

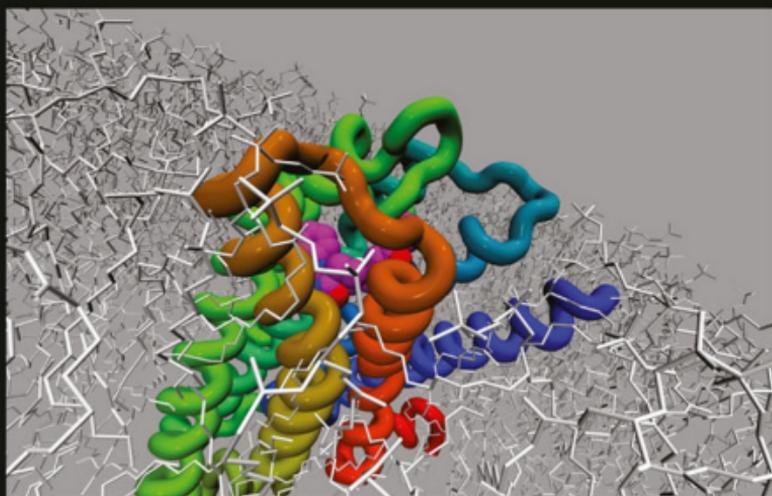
# The Dopamine Receptors

*Second Edition*

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*Edited by*

Kim A. Neve



 Humana Press

# The Dopamine Receptors

# THE RECEPTORS

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*Editor*

Kim A. Neve  
Portland VA Medical Center  
Oregon Health & Science University  
3710 SW. US Veterans Hospital Rd.  
Portland, OR 97239-2999  
USA  
nevek@ohsu.edu

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# Preface

As sites of action for drugs used to treat schizophrenia and Parkinson's disease, dopamine receptors are among the most validated drug targets for neuropsychiatric disorders. Dopamine receptors are also drug targets or potential targets for other disorders such as substance abuse, depression, Tourette's syndrome, and attention deficit hyperactivity disorder. When chapters were being written for the first edition of "The Dopamine Receptors," published in 1997, researchers were still coming to grips with the discovery of novel dopamine receptor subtypes whose existence had not been predicted by pharmacological analysis of native tissue. Although we are still far from a complete understanding of the roles of each of the dopamine receptor subtypes, the decade since the publication of the first edition has seen the creation and characterization of mice deficient in each of the subtypes and the development of increasingly subtype-selective agonists and antagonists. Many of the chapters in this second edition rely heavily on new knowledge gained from these tools, but the use of knockout mice and subtype-selective drugs continues to be such a dominant theme in dopamine receptor research that these topics are also discussed in stand-alone chapters. The field of G protein-coupled receptors has advanced significantly since the publication of the first edition, with a model of GPCR signaling based on linear, compartmentalized pathways having been replaced by a more complex, richer model in which neurotransmitter effects are mediated by a signalplex composed of numerous signaling proteins, including multiple GPCRs, other types of receptors, such as ionotropic receptors, accessory and scaffolding proteins, and effectors. Again, although many chapter topics are affected by this more complex model, key aspects of the model are specifically addressed in new chapters on dopamine receptor-interacting proteins and on dopamine receptor oligomerization.

My goal has been to produce a book that will serve as a reference work on the dopamine receptors while also highlighting the areas of research that are most active today. To achieve this goal, I encouraged contributors to write chapters that set a broad area of research in its historical context and that look forward to new research opportunities. I hope that readers will agree with me that the authors have achieved that goal.

Portland, Oregon  
March, 2009

Kim A. Neve

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# Contributors

**Anissa Abi-Dargham** Division of Translational Imaging, Departments of Psychiatry and Radiology, Lieber Center, Columbia University College of Physicians and Surgeons, NY 10032, USA, aa324@columbia.edu

**Luigi Agnati** Department of Biomedical Sciences University of Modena and Reggio Emilia, 41100-Modena, Italy

**Véronique M. André** Mental Retardation Research Center, David Geffen School of Medicine, University of California, Los Angeles, CA 90095, USA

**Emiliana Borrelli** Department Microbiology and Molecular Genetics, 3113 Gillespie Neuroscience Facility, University of California, Irvine, CA 92617, USA, borrelli@uci.edu

**Carlos Cepeda** Mental Retardation Research Center David Geffen School of Medicine, University of California, Los Angeles, CA 90095, USA

**Claudia De Mei** Department Microbiology and Molecular Genetics, 3113 Gillespie Neuroscience Facility, University of California, Irvine, CA 92617, USA

**Miriam Dörfler** Department of Chemistry and Pharmacy, Friedrich Alexander University Erlangen-Nürnberg, 91052 Erlangen, Germany

**Ursula M. D'Souza** MRC Social, Genetic and Developmental Psychiatry (SGDP) Centre, Institute of Psychiatry, King's College, London, UK, ursula.d'souza@iop.kcl.ac.uk

**Spencer S. Ericksen** Department of Physiology and Biophysics, Weill Medical College of Cornell University, New York, NY 10021, USA

**R. Benjamin Free** Molecular Neuropharmacology Section, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Bethesda, MD 30852, USA

**Zachary Freyberg** Department of Psychiatry, Columbia University College of Physicians and Surgeons, New York, NY 10032, USA

**Kjell Fuxe** Department of Neuroscience, Karolinska Institutet, 17177-Stockholm, Sweden, kjell.fuxe@ki.se

**Susan R. George** Departments of Pharmacology and Medicine, 1 King's College Circle, Centre for Addiction and Mental Health, University of Toronto, Toronto, ON M5S 1A8, Canada, s.george@utoronto.ca

**Nathalie Ginovart** Neuroimaging Unit, Department of Psychiatry, University of Geneva, Geneva, Switzerland, nathalie.ginovart@unige.ch

**Peter Gmeiner** Department of Chemistry and Pharmacy, Friedrich Alexander University Erlangen-Nürnberg, 91052 Erlangen; Laboratory of Molecular Imaging, Clinic of Nuclear Medicine, Friedrich Alexander University Erlangen-Nürnberg, 91054 Erlangen, Germany, gmeiner@pharmazie.uni-erlangen.de

**Diego Guidolin** Section of Anatomy, Department of Human Anatomy and Physiology, University of Padova, 35121-Padova, Italy

**Eugenia V. Gurevich** Department of Pharmacology, Vanderbilt University, Nashville, TN 37232, USA, eugenia.gurevich@vanderbilt.edu

**Vsevolod V. Gurevich** Department of Pharmacology, Vanderbilt University, Nashville, TN 37232, USA

**Lisa A. Hazelwood** Section of Molecular Neuropharmacology, National Institute of Neurological Disorders and Stroke, National Institutes of Health, Bethesda, MD 20852, USA

**Dawn Holmes** Department of Microbiology and Molecular Genetics, 3113 Gillespie Neuroscience Facility, University of California, Irvine, CA 92617, USA

**Chisato Iitaka** Department Microbiology and Molecular Genetics, 3113 Gillespie Neuroscience Facility, University of California, Irvine, CA 92617, USA

**Jonathan A. Javitch** Center for Molecular Recognition, Columbia University College of Physicians and Surgeons, NY 10032, USA, jaj2@columbia.edu

**Emily L. Jocoy** Mental Retardation Research Center, David Geffen School of Medicine, University of California, Los Angeles, CA, 90095, USA

**Shitij Kapur** Department of Psychological Medicine, Institute of Psychiatry, London, UK

**Noriaki Koshikawa** Department of Pharmacology, Nihon University School of Dentistry, Tokyo, 101, Japan

**Marc Laruelle** Schizophrenia and Cognitive Disorder Discovery Performance Unit, Neurosciences Center of Excellence in Drug Discovery, GlaxoSmithKline, Harlow, UK

**Frankie H.F. Lee** Centre for Addiction and Mental Health, Department of Psychiatry, University of Toronto, Toronto, ON M 5A 4R4, Canada

**Michael S. Levine** Mental Retardation Research Center, University of California, Los Angeles, CA 90024, USA, [mlevine@mednet.ucla.edu](mailto:mlevine@mednet.ucla.edu)

**Daniel Marcellino** Department of Neuroscience, Karolinska Institutet, 17177-Stockholm, Sweden

**Irina S. Moreira** Department of Physiology and Biophysics, Weill Medical College of Cornell University, New York, NY 10021, USA

**Kim A. Neve** VA Medical Center and Oregon Health & Science University Portland, OR 97239, USA

**David E. Nichols** Department of Medicinal Chemistry and Molecular Pharmacology, School of Pharmacy and Pharmaceutical Sciences, Purdue University, West Lafayette, IN 47907, USA, [rdave@pharmacy.purdue.edu](mailto:rdave@pharmacy.purdue.edu)

**Brian F. O'Dowd** Department of Pharmacology, 1 King's College Circle, Centre for Addiction and Mental Health, University of Toronto, Toronto, ON M5S 1A8, Canada

**Gerard J. O'Sullivan** Molecular and Cellular Therapeutics, Royal College of Surgeons, Dublin 2, Ireland

**Colm O'Tuathaigh** Molecular and Cellular Therapeutics, Royal College of Surgeons, Dublin 2, Ireland

**Melissa L. Perreault** Department of Pharmacology, University of Toronto, Toronto, ON M5S 1A8, Canada

**Olaf Prante** Laboratory of Molecular Imaging, Clinic of Nuclear Medicine, Friedrich Alexander University Erlangen-Nürnberg, Schwabachanlage 6, 91054 Erlangen, Germany

**Maria Ramos** Department of Microbiology and Molecular Genetics, 3113 Gillespie Neuroscience Facility, University of California, Irvine, CA 92617, USA

**Trevor W. Robbins** Department of Experimental Psychology and Behavioural and Clinical Neuroscience Institute, University of Cambridge, Cambridge CB2-3 EB, UK, [t.robbs@psychol.cam.ac.uk](mailto:t.robbs@psychol.cam.ac.uk); [twr2@cam.ac.uk](mailto:twr2@cam.ac.uk)

**Robert J. Romanelli** Helix Medical Communications, San Mateo, CA 94404, USA, [robert.romanelli@helixhh.com](mailto:robert.romanelli@helixhh.com)

**Jeremy K. Seamans** Department of Psychiatry and The Brain Research Centre, University of British Columbia, 2211 Wesbrook Mall, Vancouver BC V6T 2B5, Canada, [seamans@interchange.ubc.ca](mailto:seamans@interchange.ubc.ca)

**Philip Seeman** Department of Pharmacology, University of Toronto, 1 King's College Circle, Toronto, ON M5S 1A8 Canada, [philip.seeman@utoronto.ca](mailto:philip.seeman@utoronto.ca)

**David W. Self** Department of Psychiatry, The Seay Center for Basic and Applied Research in Psychiatric Illness, University of Texas Southwestern Medical Center, Dallas, Texas 75390-9070, USA, david.self@utsouthwestern.edu

**Weixing Shen** Department of Physiology Northwestern University, Feinberg School of Medicine, Chicago, IL 60611, USA

**Lei Shi** Department of Physiology and Biophysics and Institute for Computational Biomedicine, Weill Medical College of Cornell University, New York, NY 10021 USA

**David R. Sibley** Molecular Neuropharmacology Section, NINDS/NIH, 5625 Fishers Lane, Rockville, MD 20852-9405, USA, sibley@helix.nih.gov

**D. James Surmeier** Department of Physiology, Northwestern University, Feinberg School of Medicine, Chicago, IL 60611, USA  
j-surmeier@northwestern.edu

**Emanuele Tirotta** Department Microbiology and Molecular Genetics, 3113 Gillespie Neuroscience Facility, University of California, Irvine, CA 92617, USA

**Katsunori Tomiyama** Advanced Research Institute for the Sciences & Humanities and Department of Pharmacology, Nihon University School of Dentistry, Tokyo, Japan

**Vaneeta Verma** Department of Pharmacology, University of Toronto, Toronto, ON M5S 1A8, Canada

**John L. Waddington** Molecular and Cellular Therapeutics, Royal College of Surgeons in Ireland, Dublin 2, Ireland, jwadding@rcsi.ie

**Harel Weinstein** Department of Physiology and Biophysics and the HRH Prince Alwaleed Bin Talal Bin Abdulaziz Alsaud Institute for Computational Biomedicine, Weill Medical College of Cornell University, New York, NY 10021 USA

**John T. Williams** Vollum Institute, Oregon Health & Science University, Portland, OR 97239, USA

**Albert H.C. Wong** Centre for Addiction and Mental Health, Department of Psychiatry, University of Toronto, Toronto ON M5A 4R4, Canada, albert.wong@utoronto.ca

**Amina Woods** Intramural Research program, Department of Health and Human Services, National Institute on Drug Abuse, National Institute of Health, Baltimore, MD 21224, USA

# Chapter 1

## Historical Overview: Introduction to the Dopamine Receptors

Philip Seeman

**Abstract** A long-term search for the mechanism of action of antipsychotic drugs was motivated by a search for the cause of schizophrenia. The research between 1963 and 1975 led to the discovery of the antipsychotic receptor, now known as the dopamine D<sub>2</sub> receptor, the target for all antipsychotic medications. There are now five known dopamine receptors, all cloned. Although no appropriate animal model or brain biomarker exists for schizophrenia, it is known that the many factors and genes associated with schizophrenia invariably elevate the high-affinity state of the D<sub>2</sub> receptor or D<sub>2</sub><sup>High</sup> by 100–900% in animals, resulting in dopamine supersensitivity. These factors include brain lesions; sensitization by amphetamine, phencyclidine, cocaine, or corticosterone; birth injury; social isolation; and more than 15 gene deletions in the pathways for the neurotransmission mediated by receptors for glutamate (NMDA), dopamine, GABA, acetylcholine, and norepinephrine. The elevation of D<sub>2</sub><sup>High</sup> receptors may be the unifying mechanism for the various causes of schizophrenia.

**Keywords** Neuroleptic · Antipsychotic receptor · D<sub>2</sub><sup>High</sup> receptor · Membrane stabilization · [<sup>3</sup>H]haloperidol · Van Rossum hypothesis of schizophrenia · Dopamine supersensitivity · [<sup>3</sup>H]domperidone

### 1.1 Introduction

The background to dopamine receptors is intimately associated with the history of antipsychotic drugs. The research in this field started with the development of anti-histamines after the Second World War, with H. Laborit using these compounds to

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P. Seeman (✉)

Department of Pharmacology, University of Toronto, Toronto, Ontario, Canada, M5S 1A8  
e-mail: philip.seeman@utoronto.ca

This chapter is dedicated to the memory of Hyman Niznik and Hubert H.M. Van Tol, pioneers in dopamine receptors.

enhance analgesia [1]. In individuals receiving one of these series of medications, Laborit noticed a “euphoric quietude”; the patients were “calm and somnolent, with a relaxed and detached expression.” Compound 4560 (now named chlorpromazine) was the most potent of the Rhone Poulenc compounds in the series.

Chlorpromazine was soon tested by many French physicians for various diseases. While Sigwald and Bouttier [2] were the first to use chlorpromazine as the only medication for a psychotic individual, they did not report their observations until 1953. The 1952 report by Delay et al. [3] showed that within 3 days [4, 5] chlorpromazine reduced hallucinations and stopped internal “voices” in eight patients, a significantly dramatic finding.

With the “neuroleptic” or antipsychotic action of chlorpromazine capturing the attention of the psychiatric community, the specific target of action for chlorpromazine became a research objective for basic scientists. The working assumption then, and still is the case now, was that the discovery of such a target might open the pathway to uncovering the biochemical cause of psychosis and possibly schizophrenia.

## 1.2 Membrane Stabilization by Antipsychotics

With the introduction of chlorpromazine to psychotic patients in state and provincial hospitals in North America in the late 1950s and early 1960s, the number of patients hospitalized with schizophrenia became markedly reduced. The basic science premise gradually emerged – if the target sites for antipsychotics could be found, then perhaps these sites were overactive in psychosis or schizophrenia. In the 1960s, however, no one agreed on what schizophrenia was. Inclusion criteria varied so much that it was impossible to decide which patients to study, let alone what to study. But everyone agreed that chlorpromazine and the many other new antipsychotic drugs, most of which were phenothiazines, alleviated the symptoms of schizophrenia, however defined.

But where in the nervous system does one start to look for an antipsychotic target? Moreover, were there many types of antipsychotic targets to identify?

With the advent of the electron microscope, the 1960s was an active decade of discovery of subcellular particles and cell membranes. In those days, therefore, it seemed reasonable to start by examining the actions of antipsychotics on cell membranes. In particular, did antipsychotics readily locate to cell surfaces and cell membranes and thereby alter membrane structure and function? Did antipsychotics target mitochondria, the structure of which was being rapidly revealed by electron microscopy?

In my own research in 1963, it was important to determine whether antipsychotics permeated cell membranes and whether the drugs were membrane active. I started with an artificial lipid film floating on water, and measured the film pressure with a 1 cm square of sand-blasted aluminum hanging into the bath (Wilhelmy method; [6]). Upon the addition of an antipsychotic to the water below the film, the

aluminum plate immediately rose, showing that the film pressure had been altered by the antipsychotic. This indicated that the antipsychotic molecules had entered into the single layer of lipid molecules floating on the water surface, expanding the intermolecular spaces between the lipid molecules. Therefore, could it be that cell membrane lipids were targets for antipsychotics?

To my surprise, however, when I omitted the lipid molecules, the addition of the antipsychotic still altered the surface pressure of the water surface. In other words, I had accidentally discovered that antipsychotics were surface active [7].

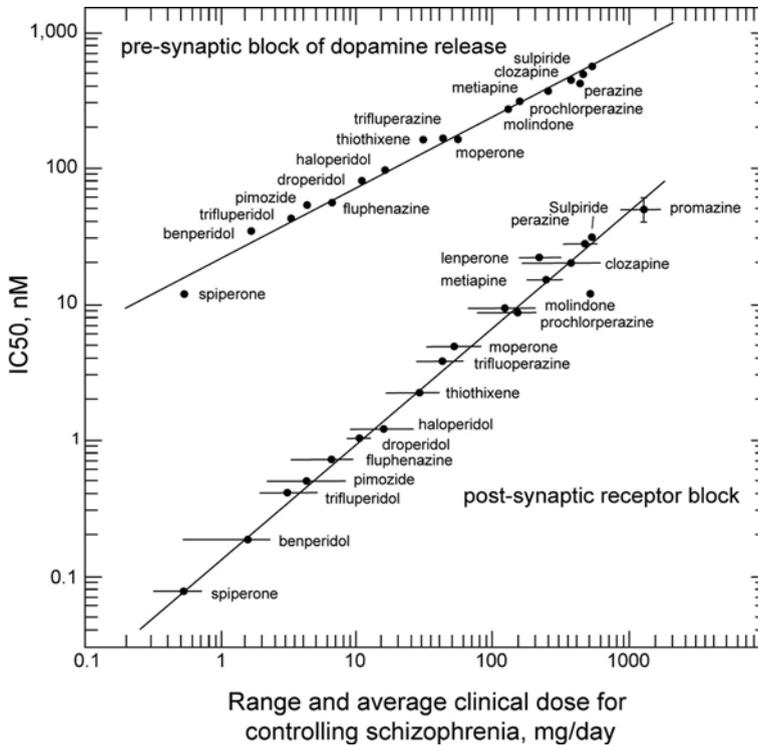
These surface-active potencies showed an excellent correlation with clinical antipsychotic potencies. However, I later realized that the antipsychotic concentrations were all in the micromolar range, a concentration subsequently found to be far in excess of that which was clinically effective in the plasma water or spinal fluid in patients taking antipsychotic medications.

Although all the antipsychotics were surface active and readily acted on artificial lipid films, it was essential to determine whether antipsychotics had similar membrane actions on human red blood cell membranes. In fact, this did occur, and it was found that low concentrations of antipsychotics readily expanded red blood cell membranes by  $\sim 0.1$ – $1\%$  and, in doing so, exerted an anti-hemolytic action by allowing the cells to become slightly larger and stabilized before hemolysis occurred [8–11].

This membrane stabilization by antipsychotics was also associated with electrical stabilization of the membrane. That is, it soon became clear that the antipsychotics were potent anesthetics, blocking nerve impulses at antipsychotic concentrations of between 20 nM and 1,000 nM (Fig. 1.1, top correlation line) [10, 12]. However, here too, these membrane-stabilizing concentrations were still in excess of those found clinically in the spinal fluid of treated patients (see following section). The driving criterion throughout this research was to find a target that was sensitive to the antipsychotic concentrations found in the spinal fluid of psychotic patients on maintenance doses of antipsychotic medications.

### 1.3 Therapeutic Concentrations of Antipsychotics

Although antipsychotics stabilize a variety of cellular and subcellular membranes [10], these antipsychotic concentrations are generally between 20 nM and 100 nM. The therapeutic molarities, however, were not known until the data on haloperidol were analyzed. In the case of haloperidol, for example, only 8% of haloperidol was free and not bound to plasma proteins [13]. Therefore, the active free concentration of haloperidol in the patient plasma water or in the spinal fluid would be between 1 nM and 2 nM [14, 15, 16]. Based on the standard pharmacological principle that the non-protonated form of tertiary amines readily permeates cell membranes [8], this concentration in the aqueous phase in the plasma is expected to be identical to the aqueous concentration of haloperidol in the spinal fluid.



**Fig. 1.1** All antipsychotic drugs inhibit the binding of [ $^3$ H]haloperidol to dopamine D<sub>2</sub> receptors (in calf striatal homogenate) in direct relation to the clinical antipsychotic potencies (*lower line*) [17,18,20]. The *upper line* indicates that antipsychotics also block the stimulated release of [ $^3$ H]dopamine (from rat striatal slices) at concentrations which correlate with their clinical potencies [12]; however, the antipsychotic concentrations required for this presynaptic action are much higher than those that inhibit [ $^3$ H]haloperidol binding to the D<sub>2</sub> receptors (*lower line*) or those which are found in the spinal fluid of patients being treated with antipsychotics [14] (re-drawn and adapted from [82] with permission)

## 1.4 Discovery of the Antipsychotic Dopamine Receptor

These latter calculations were critical for the discovery of the antipsychotic dopamine receptor [17, 18, 19]. That is, in order to detect or label a receptor with a dissociation constant of  $\sim 1$  nM for radioactive haloperidol, the specific activity of [ $^3$ H]haloperidol would have to be at least 10 Ci/mmol. However, the [ $^3$ H]haloperidol samples from Janssen Pharmaceutica (Belgium) kindly provided to the author's laboratory by Dr. J.J.P. Heykants in 1971 and by Dr. Jo Brugmans in 1972 had a specific activity of only 0.032–0.071 Ci/mmol, too low to detect specific binding for a site with an expected dissociation constant of  $\sim 1$  nM. Although New England Nuclear Corp. (Boston, MA) custom tritiated haloperidol for the author's laboratory, the specific activity was only  $\sim 0.1$  Ci/mmol.

Finally, after my extensive correspondence with Dr. Paul A.J. Janssen and Dr. J. Heykants, they asked I.R.E. Belgique (National Institut Voor Radio-Elementen, Fleurus, Belgium; Mr. M. Winand) to custom synthesize [ $^3\text{H}$ ]haloperidol for the author's laboratory. I.R.E. Belgique soon thereafter provided us with relatively high specific activity [ $^3\text{H}$ ]haloperidol (10.5 Ci/mmol) by June 1974.

This [ $^3\text{H}$ ]haloperidol readily enabled us to detect the specific binding of [ $^3\text{H}$ ]haloperidol to brain striatal tissue. Our laboratory submitted an abstract describing this to the Society for Neuroscience before the annual May 1975 deadline [17]. This report listed the following important  $\text{IC}_{50}$  values to inhibit the binding of [ $^3\text{H}$ ]haloperidol: 2 nM for haloperidol, 20 nM for chlorpromazine, 3 nM for (+)butaclamol, and 10,000 nM for (-)butaclamol. The stereoselective action of butaclamol and the good correlation between the  $\text{IC}_{50}$  values and the clinical doses indicated that we had successfully identified the antipsychotic receptor. Moreover, of all the endogenous compounds tested, dopamine was the most potent in inhibiting the binding of [ $^3\text{H}$ ]haloperidol, thus indicating that the antipsychotic receptor was a dopamine receptor.

The data of Seeman et al. [17] were confirmed by more extensive publications [18, 20, 21, 22], showing a clear correlation between the clinical potencies and the antipsychotic dissociation constants (Fig. 1.1, bottom correlation line).

At the CINP (Collegium Internationale Neuro-Psychopharmacologicum) meeting held in Paris in July 1975, during the evening courtyard reception at the City Hall of Paris, I rushed up to Dr. Paul Janssen and showed him the chart correlating the average clinical antipsychotic doses with the in vitro antipsychotic potencies. He laughed and said that averaging the clinical doses for each antipsychotic was like averaging all the religions of the world. Nevertheless, the correlation remains a cornerstone of the dopamine hypothesis of schizophrenia, still the major contender for an explanatory theory of schizophrenia causation.

## 1.5 Nomenclature of Dopamine Receptors

The receptor labeled by [ $^3\text{H}$ ]haloperidol was later named the D2 receptor [23]. It is important to note that the data for the binding of [ $^3\text{H}$ ]haloperidol identifying the antipsychotic receptor [17, 18] differed from the pattern of [ $^3\text{H}$ ]dopamine binding described by Burt et al. [24] and Snyder et al. [25]. For example, the binding of [ $^3\text{H}$ ]haloperidol was inhibited by  $\sim 10,000$  nM dopamine, while that of [ $^3\text{H}$ ]dopamine was inhibited by  $\sim 7$  nM dopamine. For several years, this latter [ $^3\text{H}$ ]dopamine binding site was termed the "D3 site" [26, 27], a term which is not to be confused with the discovery of the D<sub>3</sub> dopamine receptor [28]. As summarized in Table 1.1, there are now five different dopamine receptors that have been cloned.

At the same 1975 CINP meeting where I showed the correlation chart to Dr. Janssen, I happened to meet Dr. Sol Snyder in the lobby of the convention hotel and told him that I had custom prepared [ $^3\text{H}$ ]haloperidol and that it was now available. The pattern of [ $^3\text{H}$ ]haloperidol binding later published by Snyder et al.

[25] and by Burt et al. [24] agreed with my findings. The paper by Snyder et al. [25] kindly cited my paper of November, 1975, describing the [ $^3\text{H}$ ]haloperidol-labeled antipsychotic receptor [18]. In addition, the publication of Burt et al. [24] kindly acknowledged the receipt of the drug samples of (+)- and (-)-butaclamol from our laboratory so that they could demonstrate stereoselective binding of [ $^3\text{H}$ ]haloperidol.

**Table 1.1** Key findings related to dopamine receptors

| Year      | Key findings related to dopamine receptors                            | Authors                            | References |
|-----------|---|------------------------------------|------------|
| 1952      | Analgesia and “euphoric quietude” with RP 4560                        | Laborit (Lacomme et al.)           | [1]        |
| 1952–1953 | Chlorpromazine (RP 4560) has effective antipsychotic action           | Delay et al.; Sigwald and Bouttier | [2, 3]     |
| 1960      | Very low amount of dopamine in Parkinson’s diseased brain             | Ehringer and Hornykiewicz          | [29]       |
| 1963      | Two antipsychotics increase normetanephrine and methoxytyramine       | Carlsson and Lindqvist             | [30]       |
| 1964      | Three antipsychotics increase HVA and DOPAC; elimination delayed?     | Andén et al.                       | [31]       |
| 1965      | Dopamine can excite or inhibit neurons                                | Bloom et al.                       | [83]       |
| 1966      | Dopamine hypothesis of schizophrenia outlined                         | Van Rossum                         | [33]       |
| 1971      | Dopamine stimulates adenylate cyclase                                 | Kebabian and Greengard             | [38]       |
| 1971      | Haloperidol measured in patient’s plasma (see 1977 below)             | Zingales et al.                    | [15]       |
| 1974      | 2.5 nM haloperidol blocks tritiated dopamine receptors                | Seeman et al.                      | [19]       |
| 1974      | Haloperidol blocks excitation in Helix                                | Struyker Boudier et al.            | [84]       |
| 1975      | Tritiated haloperidol labels dopamine receptors                       | Seeman et al.                      | [17, 18]   |
| 1975      | Antipsychotic doses correlate with blockade of dopamine receptors     | Seeman et al.                      | [18, 20]   |
| 1976      | Sulpiride resolves two dopamine sites; no effect on adenylate cyclase | Roufogalis et al.                  | [42]       |
| 1976      | Two dopamine receptors proposed: inhibitory and excitatory            | Cools; Van Rossum                  | [35]       |

**Table 1.1** (continued)

| Year      | Key findings related to dopamine receptors   | Authors                        | References |
|-----------|--|--------------------------------|------------|
| 1977      | Dopamine stimulates adenylate cyclase in parathyroid                                 | Brown et al.                   | [39]       |
| 1977      | 92% of plasma haloperidol bound, indicating 2 nM free in water                       | Forsman and Öhman              | [13]       |
| 1978      | Two dopamine receptors: coupled and uncoupled to adenylate cyclase                   | Spano et al.; Garau et al.     | [36, 37]   |
| 1978      | Presynaptic action of apomorphine reduces release of dopamine                        | Starke et al.                  | [53]       |
| 1978      | Elevated D2 in postmortem schizophrenia brain  | Lee et al.                     | [59]       |
| 1979      | Names of D1 and D2 used  | Kebabian and Calne             | [23]       |
| 1979      | Dopamine inhibits adenylate cyclase in ant pituitary                                 | De Camilli et al.              | [43]       |
| 1983      | Identical antipsychotic Ki values at striatum and limbic D2 receptors                | Seeman and Ulpian              | [85]       |
| 1984      | Kd values of D2 ligands depend on final tissue concentration                         | Seeman et al.                  | [56]       |
| 1984      | D <sub>2</sub> <sup>High</sup> and D <sub>2Low</sub> affinity states of D2 receptors | Wreggett and Seeman            | [55]       |
| 1985      | D <sub>2</sub> <sup>High</sup> is functional state of D2                             | McDonald et al.; George et al. | [51, 52]   |
| 1986      | Elevated D2 measured in living schizophrenia patients                                | Wong et al.                    | [68]       |
| 1986      | Labeling of D2 receptors in living humans by positron emission tomography            | Farde et al.                   | [86]       |
| 1988      | Antipsychotics occupy 60–80% of D2 in living schizophrenia patients                  | Farde et al.                   | [70]       |
| 1988–1989 | Cloning of the rat D <sub>2Short</sub> and D <sub>2Long</sub> receptors              | Bunzow et al.; Giros et al.    | [46, 48]   |
| 1989      | Cloning of the human D <sub>2Short</sub> and D <sub>2Long</sub> receptors            | Grandy et al.                  | [47]       |
| 1989      | 90% of D2 receptors are in D <sub>2</sub> <sup>High</sup> state in brain slices      | Richfield et al.               | [54]       |
| 1989      | Endogenous dopamine lowers radio-raclopride binding; relevant to PET                 | Seeman et al.                  | [81]       |
| 1990–1991 | Dopamine D1 and D5 receptors cloned  | Sunahara; Zhou et al.          | [40,41,87] |

**Table 1.1** (continued)

| Year | Key findings related to dopamine receptors   | Authors            | References |
|------|--|--------------------|------------|
| 1990 | Dopamine D3 receptor cloned  | Sokoloff et al.    | [28]       |
| 1991 | Dopamine D4 receptor cloned  | Van Tol et al.     | [50]       |
| 1992 | Block of D2 >80% by antipsychotics associated with Parkinsonism                              | Farde et al.       | [69]       |
| 1992 | Synaptic dopamine at rest is ~2 nM, ~100–200 nM during firing                                | Kawagoe et al.     | [88]       |
| 1995 | Drug Ki depends on fat solubility of ligand  | Seeman and Van Tol | [57]       |
| 1996 | Amphetamine-induced release of dopamine is higher in schizophrenia                           | Laruelle et al.    | [80]       |
| 1998 | D <sub>2Short</sub> receptors located mostly in nigral neurones                              | Khan et al.        | [89]       |
| 1999 | Therapeutic doses of antipsychotics block 60–80% D2  | Kapur et al.       | [71]       |
| 1999 | Isoleucine at position 154 in D2 causes myoclonus dystonia                                   | Klein et al.       | [90]       |
| 1999 | Rapid release of clozapine and quetiapine from D2 receptors                                  | Seeman et al.      | [74]       |
| 2000 | New D <sub>2Longer</sub> receptor  | Seeman et al.      | [49]       |
| 2003 | Antipsychotics occupy more D2 in limbic areas than striatum                                  | Bressan et al.     | [75]       |
| 2005 | Dopamine supersensitivity correlates with elevated D <sub>2</sub> <sup>High</sup> states     | Seeman et al.      | [91]       |
| 2005 | Dopamine receptor contribution to action of PCP, LSD, and ketamine                           | Seeman et al.      | [92]       |
| 2005 | Higher D2 density in healthy identical twins of schizophrenia patients                       | Hirvonen et al.    | [66]       |
| 2006 | Markedly elevated D <sub>2</sub> <sup>High</sup> receptors in all animal models of psychosis | Seeman et al.      | [93, 94]   |

## 1.6 Antipsychotic Accelerated Turnover of Dopamine

In 1960 Ehringer and Hornykiewicz [29] discovered that the content of dopamine was extremely low in the postmortem brains of patients who died with Parkinson's disease. This discovery immediately suggested that the well-known Parkinsonism

caused by antipsychotics was probably associated in some way with interference of dopamine neurotransmission by the antipsychotics. However, there were many possible molecular modes of interference, including presynaptic and postsynaptic mechanisms.

The finding of Ehringer and Hornykiewicz naturally stimulated brain research on dopamine. Carlsson and Lindqvist [30] soon reported that chlorpromazine and haloperidol increased the production of normetanephrine and methoxytyramine, metabolites of epinephrine and dopamine, respectively. To explain the increased production of these metabolites, these authors suggested that “the most likely [mechanism] appears to be that chlorpromazine and haloperidol block monoaminergic receptors in brain; as is well known, they block the effects of accumulated 5-hydroxytryptamine . . . .”

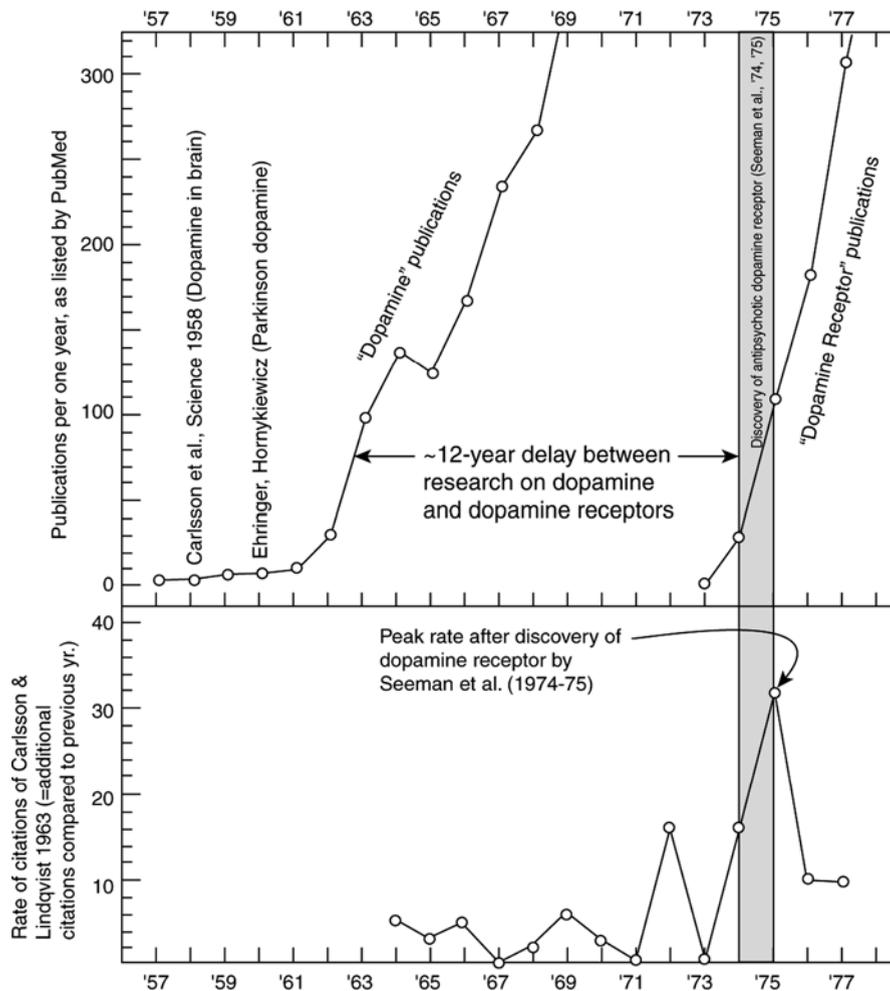
In other words, these authors proposed that antipsychotics blocked all three types of receptors for noradrenaline, dopamine, and serotonin, but they did not identify which receptor was selectively blocked or how to identify or test any of these receptors directly *in vitro*. The paper by Carlsson and Lindqvist [30] is often mistakenly cited as discovering the principle that antipsychotic drugs selectively block dopamine receptors. A year later, even the students of the Carlsson laboratory, Andén et al. [31], limited their speculation to proposing that “chlorpromazine and haloperidol delays the elimination of the (metabolites). . .,” a hypothesis no longer held. Moreover, even after 7 years, although Andén et al. [32] reported that antipsychotics increased the turnover of both dopamine and noradrenaline, they could not show that the antipsychotics were selective in blocking dopamine; for example, chlorpromazine enhanced the turnover of noradrenaline and dopamine equally. Therefore, it remained for *in vitro* radioreceptor assays to detect the dopamine receptor directly and to demonstrate antipsychotic selectivity for the dopamine receptor.

In fact, when the antipsychotic dopamine receptor was discovered [18, 20], there was a peak surge in the rate of citations of the paper by Carlsson and Lindqvist [30], a peak stimulated by the actual discovery of the dopamine receptor method, as shown in Fig. 1.2. This figure also shows that there was approximately a 12-year interval between the onset of dopamine research and the research on dopamine receptors, indicating that the two fields were stimulated by separate developments.

## 1.7 The Dopamine Hypothesis of Schizophrenia, and Dopamine Receptors in the Human Brain

As already noted, the paper by Carlsson and Lindqvist [30] is often mistakenly cited as the origin of the dopamine hypothesis of schizophrenia. However, the dopamine hypothesis of schizophrenia was first outlined in 1967 by Van Rossum [33] (see [34]) as follows:

“The hypothesis that neuroleptic drugs may act by blocking dopamine receptors in the brain has been substantiated by preliminary experiments with a few



**Fig. 1.2** *Top*: Annual number of publications on “dopamine” and on “dopamine receptors,” as listed by PubMed online. Dopamine was found in brain tissue by Montagu [95] in Weil-Malherbe’s laboratory [96, 97] and by Carlsson et al. [98]. There is a 12-year interval between the two sets of publications, suggesting that the two onsets of publications were stimulated by separate other publications. *Bottom*: Annual rate of citations (Web of Science, Thomson Scientific, Philadelphia, PA) of the article by Carlsson and Lindqvist [30], describing the increased production of noremetanephrine and methoxytyramine by chlorpromazine or haloperidol. The citation rate of this 1963 article peaked in 1975 when the dopamine receptors were discovered [17, 18, 19] (from [82] with permission)

selective and potent neuroleptic drugs. There is an urgent need for a simple isolated tissue that selectively responds to dopamine so that less specific neuroleptic drugs can also be studied and the hypothesis further tested. . . . When the hypothesis of dopamine blockade by neuroleptic agents can be further substantiated it may have

fargoing consequences for the pathophysiology of schizophrenia. Over-stimulation of dopamine receptors could then be part of the etiology.”

With the discovery of the antipsychotic dopamine receptor *in vitro*, it became possible to measure the densities and properties of these receptors directly not only in animal brain tissues but also in the postmortem human brain and, at a later time, in living humans by means of positron emission tomography. Many, but not all, of these findings directly or indirectly support the dopamine hypothesis of schizophrenia.

## 1.8 Key Advances Related to Dopamine Receptors

Many of the significant advances in dopamine receptors and the dopamine hypothesis of psychosis or schizophrenia are listed in Table 1.1. Between 1976 and 1979, it became clear that there were two main groups of dopamine receptors, D1 and D2 [23, 35, 36, 37]. The D1-like group of receptors were associated with dopamine-stimulated adenylate cyclase [38, 39], but were not selectively labeled by [<sup>3</sup>H]haloperidol. The antipsychotic potencies at these D1 receptors did not correlate with clinical antipsychotic potency [26]. The D1-like receptors now consist of the cloned D<sub>1</sub> and D<sub>5</sub> receptors [40, 41].

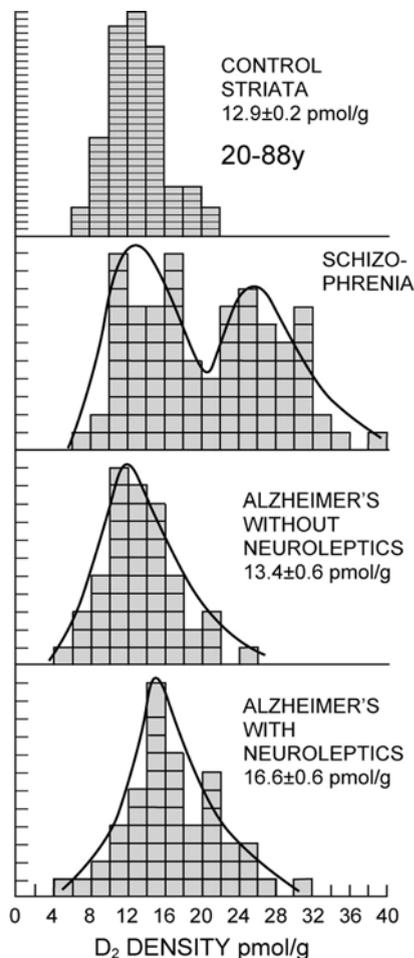
The D2-like receptors did not stimulate adenylate cyclase and are now known to inhibit adenylate cyclase [42, 36, 37, 43, 44, 45]. The D2-like group now includes the cloned D<sub>2Short</sub> [46, 47], D<sub>2Long</sub> [48], D<sub>2Longer</sub> [49], D<sub>3</sub> [28], and D<sub>4</sub> dopamine receptors [50].

Moreover, each of these receptors has a state of high affinity and a state of low affinity for dopamine, with D<sub>2</sub><sup>High</sup> being the functional state in the anterior pituitary [51, 52], in nigral dopamine terminals (presynaptic receptors [53]), and presumably in the nervous system itself. Although this latter point has not been unequivocally established, Richfield et al. [54] have found that 90% of the D<sub>2</sub> receptors in brain slices are in the D<sub>2</sub><sup>High</sup> state. The D<sub>2</sub><sup>High</sup> state can be quickly converted into the D<sub>2Low</sub> state by guanine nucleotide [55].

The differences in findings on dopamine receptors between laboratories are explained by technically different methods and ligands. For example, the dissociation constant of a ligand at the D<sub>2</sub> receptor can vary enormously, depending on the final concentration of the tissue [56]. Moreover, fat-soluble ligands, such as [<sup>125</sup>I]iodosulpride, [<sup>3</sup>H]nemonapride, and [<sup>3</sup>H]spiperone, invariably yield higher dissociation constants than less fat-soluble ligands (such as [<sup>3</sup>H]raclopride) for competing drugs [21, 57]. This technical effect also occurs with positron emission tomography ligands [58].

Although the density of D<sub>2</sub> receptors in postmortem human schizophrenia tissues is elevated [26, 59, 60–62], some of this elevation may have resulted from the antipsychotic administered during the lifetime of the patient. An example of this elevation is shown in Fig. 1.3, where it may be seen that the postmortem tissues from half of the patients who died with schizophrenia revealed elevated densities of

**Fig. 1.3** Elevation of dopamine D<sub>2</sub> receptors in postmortem caudate–putamen tissues from patients who had died with schizophrenia. Each box indicates the D<sub>2</sub> density measured by saturation analysis with [<sup>3</sup>H]spiperone (Scatchard method for B<sub>max</sub>; centrifugation method) [62]. The D<sub>2</sub> densities in the postmortem striata from schizophrenia patients exhibit a bimodal pattern, with half the values being two or three times the normal density. Most of the schizophrenia patients had been treated with antipsychotics during their lifetime. Although the Alzheimer patient tissues also revealed a small elevation of D<sub>2</sub> densities, the magnitude and pattern were different than that for schizophrenia (re-drawn and adapted from [82] with permission)



[<sup>3</sup>H]spiperone-labeled D<sub>2</sub>-like receptors in the caudate–putamen tissue. The other half of the postmortem schizophrenia tissues were normal in D<sub>2</sub> density even though most of the patients were known to have also been treated with antipsychotics during their lifetime.

It is often surprising to encounter people who are resistant to advances in science. For example, I vividly recall one British psychiatrist standing up and shouting at me from the audience: “Post-mortem dopamine receptors? Do you actually expect me to believe that these dead receptors come to life and bind your radioactive material?” I answered that the same type of question was raised a century ago when people seriously questioned whether ferments could be isolated and still have activity, but that we can now buy crystallized enzymes for a few dollars and that these ferments are fully active. And, of course, thanks to many of the contributors to the present

book on “The Dopamine Receptors,” one can now purchase frozen clones of the five different dopamine receptors.

## 1.9 Is $D_2^{\text{High}}$ the Unifying Mechanism for Schizophrenia?

Throughout the years between 1963 and the present, the overall strategy has been to identify the main target of antipsychotic medications and then to determine whether these antipsychotic targets are overactive in schizophrenia or in animal models of psychosis. Has this strategy worked? The answer is yes. First, the primary target for antipsychotics, the dopamine  $D_2$  receptor, has been identified, and, second, many avenues indicate that  $D_2^{\text{High}}$  (the high-affinity state of the  $D_2$  receptor) may be the unifying mechanism for schizophrenia.

In particular, the following facts on dopamine receptors validate the 45-year search for a basic unifying mechanism for schizophrenia:

1. All antipsychotic drugs, including the newer dopamine partial agonists such as aripiprazole [22] or OSU 6162 [63], block dopamine  $D_2$  receptors in direct relation to their clinical potency. Even the glutamate-type antipsychotic [64] has a significant dopamine partial agonist action on  $D_2$  receptors [65].
2. The brain imaging by Hirvonen et al. [66] shows that the  $D_2$  density is elevated in healthy identical co-twins of patients who have schizophrenia. This finding suggests that the elevation of  $D_2$  receptors is necessary for psychosis. At the same time, however, the findings of Hirvonen et al. also illustrate that in addition to elevated  $D_2$  receptors there is likely another factor precipitating the psychotic symptoms. This additional factor may well be that a certain proportion of  $D_2$  receptors must convert into the high-affinity state. At the same time, the elevation of  $D_2$  is becoming recognized as a valuable biomarker for prognosis and outcome in first-episode psychosis [67]. Earlier work had shown that the density of  $D_2$  receptors labeled by [ $^{11}\text{C}$ ]methylspiperone was elevated in drug-naïve schizophrenia patients [68]. However, no such elevation of  $D_2$  receptors was found in schizophrenia patients when [ $^{11}\text{C}$ ]raclopride was used (Refs in [69]).
3. It has been consistently found that psychotic symptoms are alleviated when 65% to 75% of the brain  $D_2$  receptors (as measured in the striatum) are occupied by antipsychotics [70, 69]. It is now considered unlikely that the blockade of serotonin-2 receptors assists in alleviating psychosis and affecting  $D_2$  occupancy [71, 72, 73]. The antipsychotic occupancy of  $D_2$  may or may not be higher in limbic regions [21, 74, 75, 76, 77].
4. In contrast to traditional antipsychotics such as chlorpromazine and haloperidol that can elicit Parkinsonism, clozapine and quetiapine do not produce Parkinsonism, consistent with the fact that clozapine and quetiapine dissociate rapidly from the  $D_2$  receptor [21].
5. The psychotic symptoms in schizophrenia increase or intensify when the individual is challenged with psychostimulants at doses that have little effect in

control subjects. As reviewed by Lieberman et al. [78], 74–78% of patients with schizophrenia become worse with new or intensified psychotic symptoms after being given amphetamine or methylphenidate. Psychotic symptoms can also be elicited in this way in control subjects, but only in 0–26%.

6. In a meta-analysis of 27 studies (3,707 schizophrenia patients and 5,363 control subjects), Glatt and Jönsson [79] have found that the Ser311Cys polymorphism in the D<sub>2</sub> receptor was significantly associated with schizophrenia ( $P = 0.002$ – $0.007$ ), indicating that this polymorphism in D<sub>2</sub> may contribute a significant and reliable risk for the illness.
7. Amphetamine-induced release of endogenous dopamine in humans is a possible marker of psychosis [80], using the principle worked out in animals [81].
8. Although no appropriate animal model or brain biomarker exists for schizophrenia, it is known that the many factors and genes associated with schizophrenia invariably elevate dopamine D<sub>2</sub><sup>High</sup> receptors by 100–900% in animals, resulting in dopamine supersensitivity. These factors include brain lesions; sensitization by amphetamine, phencyclidine, cocaine, or corticosterone; birth injury; social isolation; and more than 15 gene deletions in the pathways for the neurotransmission mediated by receptors for glutamate (NMDA), dopamine, GABA, acetylcholine, and norepinephrine. A list of these psychosis-precipitating factors is given in Table 1.2, along with the magnitude of the elevations that these factors elicit in the proportion of D<sub>2</sub><sup>High</sup> receptors in the striata of mice or rats. The total density of D<sub>2</sub> generally does not change.

**Table 1.2** Increase in D<sub>2</sub><sup>High</sup> receptors in dopamine supersensitive animal models for psychosis

| Percentage of increase in proportion of D <sub>2</sub> <sup>High</sup> | Treatment                    | References                            |
|--|------------------------------|---------------------------------------|
|  | Sensitization by             |                                       |
| 250%   | Amphetamine                  | [93, 94]                              |
| 180%   | Phencyclidine                | [91]                                  |
| 160%   | Cocaine                      | [99]                                  |
| 125%   | Caffeine                     | [100]                                 |
| 50%  | Quinpirole                   | [94]                                  |
| 210%   | Corticosterone               | [91]                                  |
|  | Lesions of                   |                                       |
| 270%   | Neonatal hippocampus         | [91]                                  |
| 160%   | Neonatal hippocampus         | [94]                                  |
| 130%   | Cholinergic lesion in cortex | [94]                                  |
| 100%   | Entorhinal hippocampus       | [101]                                 |
|  | Knockout of gene for         |                                       |
| 200–900%   | D4 receptor                  | [91]                                  |
| 60–340%  | GRK6                         | [91, 94]                              |
| 232%   | Alpha-Adrenoceptor-1b        | [102]                                 |
| 225%   | GABA <sub>B1</sub>           | H. Mohler and P. Seeman (unpublished) |
| 200%   | Dopamine-beta-hydroxylase    | [91, 94]                              |

**Table 1.2** (continued)

| Percentage of increase in proportion of D <sub>2</sub> <sup>High</sup> | Treatment  | References                                    |
|--|--|---|
| 160%   | Trace amine-1 receptor   | [103]   |
| 135%   | RGS9-2   | [91, 94]                                      |
| 133%   | Nurr77   | L.E. Trudeau,<br>P. Seeman<br>(unpublished)   |
| 129%   | Postsynaptic density 95  | J.-M. Beaulieu,<br>P. Seeman<br>(unpublished) |
| 120%   | Tyrosine hydroxylase (no dopamine)                             | [91]  |
| 90%  | COMT   | [91]  |
| 60–80%   | Vesicular monoamine transporter                                | [104]   |
| 48%  | RII beta (protein kinase A)                                    | [91, 94]                                      |
| 39%  | Dopamine transporter   | [104]   |
|  | Other  |   |
| 130–460%   | Cesarian birth with anoxia (rat)                               | [91, 94]                                      |
| 228%   | Rats socially isolated from birth                              | [105]   |
| 100%   | Reserpine-treated rats<br>Animals not showing supersensitivity | [91, 94]                                      |
| –7%  | Dopamine D1 receptor knockout mice                             | [91, 94]                                      |
| 19%  | Glycogen synthase kinase 3 knockout mice                       | [91, 94]                                      |
| –75%   | Adenosine A2A receptor knockout mice                           | [91, 94]                                      |
| 20%  | mGluR5 knockout mice   | [91, 94]                                      |

Abbreviations: COMT, catechol-O-methyl transferase; GABAB1, the B1 subtype of G protein-coupled receptors for GABA; GRK6, G protein-coupled receptor kinase 6; mGluR5, metabotropic glutamate receptor 5; Nurr77, orphan nuclear receptor 77; RII beta, the IIβ form of the regulatory subunit of cyclic AMP-dependent protein kinase; RGS9-2, regulator of G protein signaling 9-2

Because antipsychotic drugs directly block D<sub>2</sub> receptors, it is not surprising that antipsychotics also cause an increase in the proportion of D<sub>2</sub><sup>High</sup> receptors. In fact, it has long been known that administration of antipsychotic drugs can induce dopamine supersensitivity and antipsychotic tolerance in animals. These effects are also found in humans and presumably are the basis for supersensitivity psychosis or rebound psychosis upon drug withdrawal. Although D<sub>2</sub><sup>High</sup> receptors become elevated after long-term antipsychotics, these elevated D<sub>2</sub><sup>High</sup> states readily reverse, unlike the essentially permanently elevated D<sub>2</sub><sup>High</sup> states in the other animal models of psychosis mentioned above.

The strategy, the objective, and the questions on dopamine receptors still remain. What is the molecular pathway for antipsychotic action via the dopamine receptors? Are any of these steps specifically altered in schizophrenia? What is the intracellular biochemical mechanism of converting  $D_{2Low}$  into  $D_2^{High}$ ?

At present, the most promising direction in this field is to examine the molecular basis of dopamine supersensitivity, because up to 70% of patients are supersensitive to either methylphenidate or amphetamine at doses that do not affect control humans. Moreover, as shown in Table 1.2, a wide variety of brain alterations (lesions, drug treatment, receptor knockouts) all lead to the final common target of elevated proportions of  $D_2$  receptors in the  $D_2^{High}$  state. Therefore, the molecular control of the high-affinity state of  $D_2$  is emerging as a central problem in this field. At present, there is uncertainty as to whether this high-affinity state of  $D_2$  is controlled through  $G_o$  or one of the  $G_i$  proteins, because this varies from cell to cell.

It is currently proposed that there are multiple pathways in the various types of psychosis that all converge to elevate the  $D_2^{High}$  state in specific brain regions and that this elevation elicits psychosis. This proposition is supported by the dopamine supersensitivity that is a common feature of schizophrenia and that also occurs in many types of genetically altered, drug-altered, and lesion-altered animals. Dopamine supersensitivity, in turn, correlates with  $D_2^{High}$  states. The finding that all antipsychotics, traditional and recent ones, act on  $D_2$  receptors further supports the proposition.

Altogether, the dawn of the neurotransmitter era has proven to be an exciting chapter in neuropsychopharmacology. The art of psychiatry is becoming a science. It has been a privilege to participate in these developments. I thank my fellow students for making it possible.

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# Chapter 2

## Gene and Promoter Structures of the Dopamine Receptors

Ursula M. D'Souza

**Abstract** The dopamine receptors have been classified into two groups, the D<sub>1</sub>-like and D<sub>2</sub>-like dopamine receptors, respectively, based on molecular biology and pharmacological studies. The D<sub>1</sub>-like dopamine receptors comprise the D<sub>1</sub> and D<sub>5</sub> dopamine receptors and the D<sub>2</sub>-like dopamine receptors include the D<sub>2</sub>, D<sub>3</sub> and D<sub>4</sub> dopamine receptors. The gene structures of these two classes of receptors are dissimilar with respect to the organization of their coding and regulatory regions. First, the D<sub>2</sub>-like dopamine receptor genes have revealed the presence of coding exons separated by introns whereas the D<sub>1</sub>-like dopamine receptor genes consist of a single exon and thus are intronless. Second, examination of the 5'-regulatory regions reveals the presence of non-coding exon(s) several kilobases upstream from their coding exons in the D<sub>2</sub> and D<sub>3</sub> dopamine receptor genes, while regulatory regions of the D<sub>1</sub>-like dopamine receptor genes have only one non-coding exon that is separated by a small intron from the coding exon. However, in general, characterization of the 5'-flanking regions of the dopamine receptor genes demonstrates that they lack TATA boxes or CCAAT boxes, are GC rich and have several consensus binding sites for the transcription factor Sp1. The regulatory region of the D<sub>2</sub> dopamine receptor gene is similar to that in the D<sub>3</sub> dopamine receptor gene as they both contain an initiator-like element suggesting transcription initiation from this position and are under strong negative regulation in mammalian cell cultures. Furthermore, amongst the dopamine receptor genes, the 5'-flanking regions of the D<sub>3</sub> and D<sub>5</sub> dopamine receptors have much lower GC content than those in the D<sub>1</sub>, D<sub>2</sub> and D<sub>4</sub> dopamine receptor genes. Nevertheless, overall, the promoter regions of all the dopamine receptor genes are regulated in a cell-specific manner, including the additional promoter of the D<sub>1</sub> dopamine receptor gene located within intron 1. There are several studies that have identified transcription factors (DNA binding proteins) that regulate the dopamine receptor genes,

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U.M. D'Souza (✉)  
MRC Social, Genetic and Developmental Psychiatry (SGDP) Centre, Institute of Psychiatry,  
King's College, London, UK  
e-mail: ursula.d'souza@iop.kcl.ac.uk

with more experimental data generated for D<sub>1</sub> and D<sub>2</sub> compared to the D<sub>3</sub>, D<sub>4</sub> and D<sub>5</sub> genes. Therefore, all the evidence suggests that the genes encoding the dopamine receptor subtypes have diverse transcriptional regulation mechanisms that result in cell-specific expression patterns that are coupled with different molecular functions.

**Keywords** Dopamine receptors · Promoters · Transcriptional regulation · Gene structure

## 2.1 Dopamine Receptors

Dopamine is a catecholamine neurotransmitter that mediates several important physiological functions in both the central and peripheral nervous system. In the brain, it plays a major role in the control of motor function, reward, emotional expression, neuroendocrine release and behavioural homeostasis. Dopamine induces cellular and biochemical effects by interacting with its cell surface receptors [1, 2]. These receptors belong to the superfamily of G protein-coupled receptors having seven transmembrane domains and were first classified in the 1970s based primarily on pharmacological and biochemical studies, which included the rank order of receptor agonist and antagonist affinities [3], and the ability of dopamine to stimulate cAMP formation, by the activation of adenylyl cyclase in the central nervous system [4]. Later on in the 1980s four distinct dopamine receptor subtypes termed D<sub>1</sub>, D<sub>2</sub>, D<sub>3</sub> and D<sub>4</sub> were proposed on the basis of radioligand binding studies [5, 6]. However, this terminology was soon abandoned when the proposed D<sub>3</sub> and D<sub>4</sub> dopamine receptors were realized to be high-affinity states of the D<sub>1</sub> and D<sub>2</sub> dopamine receptors, respectively. In the 1990s, modification of this dopamine receptor classification was necessary after the development of molecular biology experimental techniques such as PCR cloning which revealed a much larger number of dopamine receptors than originally postulated (see [7] for a review). The current nomenclature for dopamine receptors is based on their structure, pharmacological specificity and effector responses. Consequently, the studies have divided the dopamine receptors into two groups called the D<sub>1</sub>-like and the D<sub>2</sub>-like dopamine receptors. The D<sub>1</sub>-like dopamine receptor group is composed of the D<sub>1</sub> and D<sub>5</sub> dopamine receptors, sometimes also referred to as D<sub>1A</sub> and D<sub>1B</sub> dopamine receptors, respectively. The D<sub>2</sub>-like dopamine receptors are the D<sub>2</sub>, D<sub>3</sub> and D<sub>4</sub> dopamine receptors which include the two D<sub>2</sub> dopamine receptor isoforms, the different isoforms of D<sub>3</sub> and the polymorphic forms of the D<sub>4</sub> dopamine receptors. Molecular cloning of the dopamine receptor genes paved the way for the characterization of their 5'-flanking and promoter regions to understand their transcriptional control. This information further enabled the identification of key polymorphisms (single nucleotide and tandem repeats) within

these regulatory regions which have been found to be associated with several neuropsychiatric and behavioural disorders. Interestingly, these genetic variants within the regulatory regions of the dopamine receptor genes have been found to have functional effects at a molecular and cellular level (reviewed in [8–11]). Thus this provides plausible molecular mechanisms underlying the aetiology of psychiatric phenotypes.

This chapter will describe the gene and promoter structures of the dopamine receptors under subheadings of the D<sub>1</sub>-like and D<sub>2</sub>-like dopamine receptor genes. The section on the D<sub>1</sub>-like dopamine receptor genes will be divided into D<sub>1</sub> and D<sub>5</sub> dopamine receptor genes. Similarly, the subdivision on the D<sub>2</sub>-like dopamine receptor genes will be separated into the D<sub>2</sub>, D<sub>3</sub> and D<sub>4</sub> dopamine receptor genes. Every section for each gene will be further divided into two parts: one focusing on the topic of gene structure and organization and the other concentrating on the regulatory and promoter regions. All this information has been summarized in Table 2.1 and should be referred for the overall description of each of the dopamine receptor subtypes. However, specific details can be obtained from original references that have been cited in each section.

The themes of transcriptional gene regulation and gene expression have been described concisely in several reports [12–17]. More recently, several other levels of gene regulation are currently being studied and include RNA interference which is important in gene silencing [18] and non-coding RNA (ncRNA) that comprise a hidden layer of internal signals that control various levels of gene expression [19, 20]. These non-coding RNAs include rRNA and tRNA involved in mRNA translation, small nuclear RNA (snRNA) implicated in splicing, small nucleolar RNA (snoRNA) involved in the modification of rRNA and microRNA (miRNA) which function as repressors at the level of post-transcriptional control. Furthermore, since DNA is packaged into a nucleoprotein complex known as chromatin, it is becoming important to understand this structure together with histone modification and cytosine methylation in gene regulation [21].

In general the first stage in characterizing the 5'-flanking and promoter region(s) of a gene involves isolation of a genomic clone that harbours the transcription initiation site and contains the upstream sequence of the gene. This is followed by the determination of the exon/intron organization to identify any untranslated region and then measurement of the transcriptional activity of the upstream regulatory sequences [12]. These strategies involve the generation of serial 5'-deletion plasmid constructs fused with a reporter gene such as luciferase or chloramphenicol acetyltransferase (CAT). These constructs are transiently transfected into mammalian cell lines to determine transcriptional activity of the mutant fragments *in vitro* or they can be used *in vivo* to generate transgenic mice. Furthermore, electrophoretic mobility assays and yeast one-hybrid studies have also focused on identifying which DNA binding proteins (transcription factors) interact within the regulatory domains of the genes coding for the dopamine receptors. The findings generated from the methods described above are described and discussed below.

**Table 2.1** Description of gene organization and transcriptional regulation of the dopamine receptor genes

|                                   | Gene organization<br>[coding and<br>5'-regulatory region]             | Features in promoter<br>region   | Upstream regulation   | Regulation by<br>transcription factors                          |
|-----------------------------------|---|--|---|---|
| <b>D2-like dopamine receptors</b> |   |  |   |   |
| D <sub>2</sub> dopamine receptor  | One non-coding exon separated from seven coding exons by large intron | Two promoter regions, initiator-like element, no CCAAT or TATA boxes, 80% GC | Two silencer regions in mammalian cell lines                              | AP1, retinoids<br>Sp1/Sp3, Zif68,<br>DRRF, nuclear<br>factor-κB |
| D <sub>3</sub> dopamine receptor  | Two non-coding exons separated from six coding exons by large intron  | One promoter region, initiator-like element, no CCAAT or TATA boxes, 52% GC  | Two silencer regions in neuroblastoma and hepatoblastoma cell lines       | DRRF  |
| D <sub>4</sub> dopamine receptor  | Four or five coding exons (depends on species) separated by introns   | One promoter region, no CCAAT or TATA boxes, CpG island, over 50% GC         | Two silencer regions in neuroblastoma and retinoblastoma cell lines       | Sp1   |
| <b>D1-like dopamine receptors</b> |   |  |   |   |
| D <sub>1</sub> dopamine receptor  | One non-coding exon separated from the coding exon by small intron    | Two promoter regions, no CCAAT or TATA boxes, 80% GC                         | Two activator regions and one silencer region in neuroblastoma cell lines | Sp1, POU, Bm4,<br>Meis2, TGF, ZIC,<br>Sp3, DRRF                 |
| D <sub>5</sub> dopamine receptor  | One non-coding exon separated from the coding exon by small intron    | One promoter region, no CCAAT or TATA boxes, not GC rich                     | One activator and one silencer region in neuroblastoma cell lines         | Not known to date   |

## 2.2 D<sub>2</sub>-Like Dopamine Receptor Genes

### 2.2.1 D<sub>2</sub> Dopamine Receptor Genes

#### 2.2.1.1 Gene Structure and Organization

The cloning of the rat D<sub>2</sub> dopamine receptor was a major breakthrough in the neuroscience field [22]. The cloning strategy that was employed utilized the coding region of the hamster  $\beta_2$ -adrenergic receptor [23]. This genomic DNA sequence was used to probe a rat genomic library for the presence of homologous fragments in Southern blot analysis. Under low-stringency hybridization conditions several clones were found, and one clone (clone RGB-2) was further characterized. This clone consisted of a 0.8 kb EcoRI–PstI fragment that revealed a high degree of similarity to the nucleotide sequence of the putative transmembrane domain of the hamster  $\beta_2$ -adrenergic receptor. The 0.8 kb EcoRI–PstI fragment of RGB-2 was then used to probe a rat brain cDNA library. A full-length cDNA of 2,455 bases was isolated that encoded a protein of 415 amino acids. A hydrophobicity plot of this amino acid sequence indicated that it belonged to the family of G protein-coupled receptors, as it consisted of seven putative transmembrane domains [24]. Subsequently, the human pituitary cDNA (hPITD<sub>2</sub>) was cloned using rat brain D<sub>2</sub> dopamine receptor cDNA as a hybridization probe [25]. The human and rat nucleotide sequences were found to be 90% identical and they indicated 96% homology at the amino acid level. When hPITD<sub>2</sub> cDNA was expressed in mouse Ltk<sup>-</sup> cells, the protein showed a pharmacological profile which was essentially identical to that obtained with the cloned rat D<sub>2</sub> dopamine receptor [22]. However, the human pituitary D<sub>2</sub> dopamine receptor encoded a protein of 444 amino acids, 29 amino acids longer than the rat D<sub>2</sub> dopamine receptor. DNA sequence analysis showed that the coding sequence had seven exons interrupted by six introns and that the additional amino acid sequence was encoded by a single exon (exon 5) of 87 base pairs, which was present in the putative third cytoplasmic loop of the receptor. These D<sub>2</sub> dopamine receptors of different sizes from the two species were referred to as the D<sub>2L</sub> (long) and D<sub>2S</sub> (short) forms and it was postulated that they were produced by alternative splicing of mRNA [25]. The human D<sub>2</sub> dopamine receptor gene was found to localize to chromosome 11q23-24 [26].

The structure and organization of the rat D<sub>2</sub> dopamine receptor gene was subsequently further delineated when demonstrated that the gene contains eight exons and spans at least 50 kb [27]. This research group identified seven coding exons (numbered as exons 2–8), including the alternatively expressed exon (exon 6), clustered in approximately 13 kb of the genome which revealed a similar structure to the human D<sub>2</sub> dopamine receptor gene. Furthermore, they also identified a non-coding exon termed as exon 1, thus generating a different exon numbering system to that previously used for the human D<sub>2</sub> dopamine receptor gene [25]. Additionally, the same research group consequently analysed the structure of the human D<sub>2</sub> dopamine receptor [28]. Like the rat D<sub>2</sub> dopamine receptor gene, the human D<sub>2</sub> dopamine receptor gene was found to contain at least eight exons and spans at least 52 kb. The

coding exons 2–8 are clustered within 14 kb and the non-coding exon 1 is separated from exon 2 by at least 38 kb. Similarly, the mouse D<sub>2</sub> dopamine receptor gene was found to span at least 30 kb with the coding exons 2–8 clustered in ~11 kb and the non-expressed exon 1 located at least 18 kb away from exon 2 revealing an analogous organization to the rat and human D<sub>2</sub> dopamine receptor genes [29]. Each intron/exon boundary was also sequenced in the mouse D<sub>2</sub> dopamine receptor gene and compared with the rat and human species [29]. The position of all boundaries was conserved in all three species except for intron 4 which contains a variant donor splice site (a GC dinucleotide instead of the canonical GT) in the mouse and rat but not in the human D<sub>2</sub> dopamine receptor gene [27].

Other studies also demonstrated that alternative splicing produces the expression of two rat D<sub>2</sub> dopamine receptor isoforms [27, 30–32]. Furthermore, similar investigations were performed on both the rat and human D<sub>2</sub> dopamine receptor isoforms [31], on the rat and bovine D<sub>2</sub> dopamine receptor isoforms [33–36] and for the mouse D<sub>2</sub> dopamine receptor isoforms [29]. In the literature the long form of the D<sub>2</sub> dopamine receptor was referred to as the D<sub>2L</sub>, D<sub>2(long)</sub>, D<sub>2A</sub>, D<sub>2(444)</sub> or D<sub>2-in</sub>, whereas the short form was termed D<sub>2S</sub>, D<sub>2(short)</sub>, D<sub>2B</sub>, D<sub>2(415)</sub> or D<sub>2-o</sub>.

### 2.2.1.2 Promoter Structure and Transcriptional Regulation

A short fragment of 500 bp from the translational start site of the rat D<sub>2</sub> dopamine receptor gene was initially sequenced [27]. No transcriptional elements such as CCAAT or TATA boxes were found but the region was 78% GC rich and consisted of several Sp1-like binding sites. Subsequently, the analysis of the promoter region of the rat D<sub>2</sub> dopamine receptor gene was comprehensively determined [37]. This analysis included cloning of exon 1, identification of its 5'-end, determination of the transcription start sites and the ability of D<sub>2</sub> promoter deletion mutants to transcribe the reporter gene chloramphenicol acetyltransferase (CAT) in various cell lines. The rat D<sub>2</sub> dopamine receptor gene spans at least 50 kb with coding exons 2–7 clustered in approximately 13 kb of genome, revealing that intron 1 is very long and over 20 kb [27]. A 21-mer oligonucleotide probe consisting of exon 1 sequences [27] was used to screen a rat genomic library [37]. A 1.3 kb region including all of exon 1, its 5'-flanking region and part of intron 1 was sequenced. S1 nuclease analysis indicated three consecutive nucleotides as the main transcription start sites and several weaker sites also noted upstream from the 3'-end of exon 1. The results also reveal no exon further upstream to the non-coding exon 1 in the D<sub>2</sub> dopamine receptor gene. The +1 was designated as the adenine that corresponds to one of the strong S1 signals and to one of the 5'-cDNA ends generated by RACE (rapid amplification of cDNA ends). The promoter region of the D<sub>2</sub> dopamine receptor gene was found to lack TATA and CCAAT boxes and is rich in GC content (reaching 80% in some portions) with several putative binding sites for the transcription factor Sp1. An initiator-like sequence was sited between nucleotides –6 and +11, suggesting transcription initiation from this position. Transient expression assays using 5'-deletion mutant constructs controlling transcription of the CAT gene were determined in murine neuroblastoma cells (NB41A3) that endogenously express the

D<sub>2</sub> dopamine receptor gene. Strongest transcriptional activity was found between nucleotides -75 and -30 and silencing activity was present between nucleotides -217 and -76. DNase I footprinting studies using nuclear extract from NB41A3 cells suggested Sp1 binding to its consensus sequence at nucleotide -48 but inhibition of Sp1 binding at nucleotide -86 by the extract. The D<sub>2</sub> promoter showed no transcription activity of the heterologous CAT gene in rat glioma C6, mouse embryonal NIH 3T3 and human hepatoblastoma Hep G2 cells, indicating that it is regulated in a tissue-specific manner.

Subsequently, another study demonstrated the transcription of the rat D<sub>2</sub> dopamine receptor gene from two promoter regions [38]. Using single-stranded ligation to single-stranded cDNA (SLIC), the gene was found to contain two transcription start sites: the major one located about 320 bp upstream from the 3'-end of the first exon and a minor site 70 bp further upstream. Transient expression assays with fusion constructs consisting of fragments of the rat D<sub>2</sub> promoter region and the luciferase reporter gene confirmed the presence of two independent TATA-lacking promoter regions. Both promoters independently induced transcription of the luciferase gene in C6 glioma cells, fibroblasts and GH3 and MMQ rat pituitary cell lines, although only the MMQ cells express the D<sub>2</sub> dopamine receptor. The transcriptional activity was enhanced in the presence of both promoters and modified by the upstream sequences. These data differ from that derived by [37] and were suggested to be due to the use of different reporter gene assays with varying sensitivities and/or the utilization of different cell lines [38].

The negative modulator of the rat D<sub>2</sub> dopamine receptor gene was further analysed [39]. In this study, a small deletion series within the negative modulator fused with the CAT reporter gene was used to transfect the D<sub>2</sub>-expressing cells, NB41A3. The results identified two *cis*-acting functional DNA sequences. The first is a 41 bp segment between nucleotides -116 and -76 (D<sub>2</sub>Neg-B) and the second is a 26 bp segment between nucleotides -160 and -135 (D<sub>2</sub>Neg-A). D<sub>2</sub>Neg-B decreased transcription from the D<sub>2</sub> promoter by 45%, whereas D<sub>2</sub>Neg-A in the presence of the downstream negative modulator reduced transcription down to the level of a promoterless vector. Furthermore, DNase I footprinting, gel mobility shift and competitive cotransfection experiments suggested that D<sub>2</sub>Neg-A functions without *trans*-acting factors, while D<sub>2</sub>Neg-B interacts with nuclear factors at its Sp1 binding sequences. Gel supershift assays with anti-Sp1 antibody and UV cross-linking experiments revealed that a novel 130 kDa factor as well as Sp1 interacts with D<sub>2</sub>Neg-B in NB41A3 cells. The novel protein that recognizes Sp1 binding sequences in the D<sub>2</sub> gene negative modulator was also found to be present in rat striatum nuclear extract.

In the case of the human D<sub>2</sub> dopamine receptor gene only a small fragment of the 5'-flanking region was isolated and sequenced which enabled screening of genetic variants [40]. A significant polymorphism in the D<sub>2</sub> promoter is the -141C Ins/Del (insertion/deletion), where one or two cytosines are found as part of a putative binding site for the transcription factor Sp1. Constructs consisting of the -141C Del allele cloned into a plasmid with the luciferase reporter gene demonstrated lower transcriptional activity in human retinoblastoma Y-79 cells (that express D<sub>2</sub>) and

human kidney 293 cells (D<sub>2</sub> non-expressing) compared to the -141C Ins allele [40]. Interestingly, it was additionally demonstrated in case-control studies that the -141C Del allele was significantly lower in schizophrenic patients than in control subjects in Japanese and Swedish populations [40, 41].

The promoter region of the D<sub>2</sub> dopamine receptor has been found to be regulated by other transcription factors including retinoids [42, 43], AP1 [44], Sp1/Sp3 [45] and Zif268 in the rat [46], by nuclear factor- $\kappa$ B in human [47] and by dopamine receptor regulating factor (DRRF) in mouse [48]. The latter report showed that DRRF is a zinc finger transcription factor that binds to GC and GT boxes in the D<sub>2</sub> dopamine receptor promoters and effectively displaces Sp1 and Sp3 from these sequences. Highest levels of DRRF mRNA were found in mouse brain in areas including olfactory bulb and tubercle, nucleus accumbens, striatum, hippocampus, amygdala and frontal cortex. Interestingly, these brain regions also express abundant levels of dopamine receptors, indicating the importance of DRRF in regulating dopaminergic neurotransmission. In the D<sub>2</sub>-expressing NB41A3 cells, DRRF potently inhibited transcription from the D<sub>2</sub> promoter, whereas it was found to activate the D<sub>2</sub> promoter in NS20Y and TE671 cells. In vivo experiments show that DRRF mRNA is significantly altered in striatum and nucleus accumbens brain regions in mice treated with acute and chronic doses of cocaine and haloperidol. Furthermore, in situ hybridization studies in mice have shown that DRRF mRNA is expressed uniquely during development with high levels observed at E12, E14 and E16 in various tissues [49]. DRRF expression during development is also found in particular brain regions such as the neopallial cortex, olfactory lobe and corpus striatum. This pattern of DRRF distribution during embryogenesis overlaps with that found in the adult brain and with the expression profile of dopamine receptors both in adult and during development. Additionally, the promoter region of murine DRRF was characterized, revealing tissue-specific activity, suggesting that it shares structural and functional similarities with the dopamine receptor genes that it regulates [50]. More recently, it has been found that DRRF auto-regulates its own promoter by competing with Sp1 and that both AP1 and AP2 modulate its expression [51]. Additionally a small segment of the rat D<sub>2</sub> promoter has been found to be regulated by corticosterone and oestrogen in NB41A3 cells in vitro [52, 53].

Moreover, DNA methylation has been demonstrated within the promoter region of the human D<sub>2</sub> dopamine receptor gene, suggesting that this transcription regulatory mechanism plays a role in controlling human D<sub>2</sub> dopamine receptor gene expression [54]. Lately, the 5'-regulatory region of the human D<sub>2</sub> dopamine receptor gene has been found to have methylated cytosines mainly in three clusters [55].

## ***2.2.2 D<sub>3</sub> Dopamine Receptor Genes***

### **2.2.2.1 Gene Structure and Organization**

The molecular cloning of the rat D<sub>3</sub> dopamine receptor gene was performed using reverse transcription polymerase chain reaction (RT-PCR) [56]. Genomic and cDNA

libraries were screened using a probe derived from the D<sub>2</sub> dopamine receptor sequence published earlier [22]. The positive clone that was obtained coded for a protein of 446 amino acid residues, and hydrophobicity analysis of the clone indicated seven putative transmembrane regions characteristic of G protein-coupled receptors. The D<sub>3</sub> dopamine receptor gene contained introns similar to the D<sub>2</sub> dopamine receptor gene, and 75% homology existed between the rat D<sub>2S</sub> and D<sub>3</sub> dopamine receptor genes within the transmembrane regions. Consistent with this high sequence homology, the pharmacological properties of the D<sub>3</sub> receptor were similar to but distinct from those of the D<sub>2</sub> dopamine receptor. The rat D<sub>3</sub> dopamine receptor gene contains six coding exons separated by five introns. In humans, this gene is located on chromosome 3, band 3q13.3 [57], with a coding region consisting of six exons over 53 kb and an open reading frame of only 400 amino acids. This difference of 46 amino acid residues between the rat and human D<sub>3</sub> dopamine receptors is located within the third cytoplasmic loop of the protein [58].

The polymerase chain reaction amplification of mRNA from rat brain revealed the existence of two shorter isoforms of the D<sub>3</sub> dopamine receptor in addition to the D<sub>3</sub> dopamine receptor itself [59]. The isoforms were suggested to result from different processes of alternative splicing. One form was produced by splicing of an exon whose absence deletes the third transmembrane domain, resulting in a protein (termed D<sub>3</sub>(TM3-del)) having no dopaminergic ligand binding activity. The second isoform resulted from splicing at a receptor site that coded for half the second extracellular loop and part of the fifth transmembrane domain (referred to as D<sub>3</sub>(O2-del)). Other research groups have also demonstrated splice variants of the D<sub>3</sub> dopamine receptor in the rat and human brain [60–62], but none of the truncated proteins encoded by these variants has dopamine receptor activity. However, the alternatively spliced short isoform of the mouse D<sub>3</sub> dopamine receptor that lacks 63 nucleotides in the third cytoplasmic loop was found to bind dopaminergic ligands [63]. This alternative splicing reflects the presence of a sixth intron found in the mouse D<sub>3</sub> receptor gene [64, 65]. The functional and physiological role of the truncated forms of the D<sub>3</sub> dopamine receptors is not known, but it has been suggested that they could be formed for controlling the amount of active D<sub>3</sub> dopamine receptors [59]. Defects in the regulation of alternative splicing of the receptor could result in formation of inactive D<sub>3</sub> dopamine receptors and may be associated with psychiatric disorders.

### 2.2.2.2 Promoter Structure and Transcriptional Regulation

The D<sub>3</sub> dopamine receptor gene has been implicated in neuropsychiatric disorders and found to be regulated following antipsychotic drug treatment [66, 67]. To begin with only a short segment of the 5'-untranslated region of the D<sub>3</sub> dopamine receptor gene was described in the mouse [65] and human [62]. However, a comprehensive investigation of the gene's transcriptional control was elucidated when the 5'-flanking region was characterized by isolating the 5'-end of its cDNA as well as 4.6 kb of genomic sequence [68]. Analysis of this region revealed the presence of two new (untranslated) exons of 196 bp and 120 bp, designated exon 1 and exon

2, that are separated by an 855-bp intron located several kilobases (at least 4 kb) upstream of the previously published coding exons. This evidence shows that the rat D<sub>3</sub> dopamine receptor gene is organized into eight exons and is comparable to the structure of the rat D<sub>2</sub> dopamine receptor gene. The rat D<sub>2</sub> dopamine receptor gene has a single non-coding exon located at least 35 kb upstream from its first of seven coding exons [27, 37, 38]. However, sequence comparison between the 5'-UTR and 5'-flanking regions of the rat D<sub>2</sub> and D<sub>3</sub> dopamine receptor genes shows substantial homology. On the other hand, the D<sub>1A</sub> dopamine receptor gene has been found to have a different organization with a non-coding exon separated from a single coding exon by a small intron [69, 70], which is 116 bp in humans (see Section 2.3). There is no sequence homology between the 5'-flanking region of the D<sub>1A</sub> and the rat D<sub>3</sub> dopamine receptor genes.

The transcription initiation site of the rat D<sub>3</sub> dopamine receptor gene determined by primer extension analysis and repeated rounds of 5'-RACE (rapid amplification of cDNA ends) was found to consist of a pyrimidine-rich consensus "initiator" sequence, similar to the rat D<sub>2</sub> dopamine receptor gene [37, 68]. The promoter region of the rat D<sub>3</sub> dopamine receptor gene did not reveal any TATA and CCAAT boxes but unlike that of D<sub>1</sub> and D<sub>2</sub> dopamine receptor genes has only 52% GC content. These results demonstrate that the rat D<sub>3</sub> dopamine gene has similarities with the rat D<sub>2</sub> dopamine receptor gene as both are transcribed from a TATA-less promoter that has an initiator element. Functional studies of rat D<sub>3</sub> promoter deletion mutants fused to the CAT reporter gene were carried out in a human medulloblastoma cell line (TE671 cells) [68]. These cells endogenously express the D<sub>3</sub> dopamine receptor [71]. Strongest transcriptional activity was determined within 36 nucleotides upstream of the transcriptional start site and a potent silencer identified between bases -37 and -86 which extends to -537 as transcriptional activity is noticeably and gradually reduced with the addition of sequences between -36 and -537 until complete inhibition. There was a small recovery of reporter gene activity with the addition of nucleotides -538 to -782, suggesting the presence of a potential activator. Additionally, another weaker silencer is located between nucleotides -783 and -1,046. These data suggest that the rat D<sub>3</sub> dopamine receptor gene is under intense negative regulation and similar to that observed with the rat D<sub>2</sub> dopamine receptor gene. Interestingly, none of the D<sub>3</sub> deletion mutant constructs showed any transcriptional activity in COS-7 (African green monkey kidney) or C6 rat glioma cells, which are not known to express the D<sub>3</sub> dopamine receptor gene endogenously. However, the shortest construct having 36 nucleotides from the transcriptional start site also showed significant transcriptional activity in OK (opossum kidney) and HepG2 (human hepatoblastoma) cells even though the evidence suggests that these cells do not express the D<sub>3</sub> dopamine receptor mRNA. However, unlike the potent silencing effect of the longer upstream regulatory regions of the D<sub>3</sub> gene in TE671 cells, these fragments showed only weak inhibition in OK cells or strong activation in HepG2 cells. Thus although the core promoter of the rat D<sub>3</sub> dopamine receptor gene is active in these three different cell types, its regulation by the upstream elements varies in D<sub>3</sub>- and non-D<sub>3</sub>-expressing cells. The presence of specific transcription factors in the different cell lines could help explain the complex differential

regulation of the rat D<sub>3</sub> dopamine receptor gene. Interestingly, the transcription factor dopamine receptor regulating factor (DRRF) was found to activate the regulatory region of the rat D<sub>3</sub> dopamine receptor gene in TE671 cells [48].

Subsequently, a 9 kb genomic fragment of the human D<sub>3</sub> dopamine receptor gene was isolated upstream from the translational start site [72]. Studies using 5'-RACE identified three additional exons, and transcriptional activity was found in two putative 500 bp 5'-regions derived from brain tissue and lymphoblast cells following transfection in human cell lines. However, interpretations of these findings were ambiguous as the transcriptional start site was not accurately determined and no series of deletion constructs tested for transcriptional activity. The main focus of this report appeared to be identification of single nucleotide polymorphisms in the 5'-region of the gene, but no association was found with schizophrenia.

### ***2.2.3 D<sub>4</sub> Dopamine Receptor Genes***

#### **2.2.3.1 Gene Structure and Organization**

The human D<sub>4</sub> dopamine receptor was cloned and characterized after screening various cell lines for other D<sub>2</sub>-like dopamine receptors [73]. The cloning strategy employed in the discovery of this receptor utilized the D<sub>2</sub> dopamine receptor sequence that encoded for the sixth and seventh putative transmembrane regions [22]. This fragment of the rat D<sub>2</sub> dopamine receptor served as a probe for screening genomic and cDNA libraries under low- and high-stringency conditions. The genomic intron–exon organization of the human D<sub>4</sub> dopamine receptor gene indicated the presence of five coding exons for a protein of 387 amino acids. Hydrophobicity analysis of the protein sequence indicated seven putative transmembrane regions, which suggested that it belonged to the family of G protein-coupled receptors. The pharmacological characteristics of the D<sub>4</sub> dopamine receptor resembled that of the D<sub>2</sub> and D<sub>3</sub> dopamine receptors. However, the “atypical neuroleptic” drug clozapine had higher affinity for D<sub>4</sub> than for D<sub>2</sub> and D<sub>3</sub> dopamine receptors.

The rat analogue of the human D<sub>4</sub> dopamine receptor gene was cloned, also revealing high affinity for clozapine [74]. This rat gene was found to have only four coding exons which encoded a protein of 368 amino acids, suggesting an additional splice site in the human D<sub>4</sub> dopamine receptor gene. However, despite the differences in gene structure the rat gene shares a high homology of 73% and 77% with the human D<sub>4</sub> gene at the amino acid and nucleic acid level, respectively. Interestingly, the amino acid homology of the gene between the two species increased to 89–96% when only the transmembrane regions were considered. The majority of the differences observed amongst the rat and human D<sub>4</sub> dopamine receptor genes occurred within the third cytoplasmic loop, which have only 50% amino acid identity. In the human gene, this region contains an unusual splice site within intron 3 (a donor/acceptor site of TC/CT is present instead of the GT/AG). Additionally, the rat D<sub>4</sub> dopamine receptor mRNA was detected in the cardiovascular system in addition to the brain, suggesting that this receptor is an important

dopamine receptor in the peripheral nervous system [74]. Similar to the rat D<sub>4</sub> gene, the murine D<sub>4</sub> dopamine receptor gene was found to have four coding exons that span over 30 kb [75]. The gene encodes a 387 amino acid protein displaying 80% and 95% homology with the human and rat D<sub>4</sub> dopamine receptors, respectively, at the amino acid level. Likewise, at the nucleotide level the mouse D<sub>4</sub> dopamine receptor gene revealed 79% and 93% homology with the human and rat D<sub>4</sub> dopamine receptor genes, respectively. The most conserved regions were seen within the transmembrane domains that are thought to form the ligand binding site.

Three polymorphic forms of the D<sub>4</sub> dopamine receptor in humans were further discovered [76]. These were the three most common variants, having 2-, 4- or 7-fold imperfect repeats of a 48 bp sequence in the putative third cytoplasmic loop of the receptor, located in exon 3 of the gene. This was the first example of polymorphic variation observed in catecholamine receptors. Although the different forms of the receptor showed slightly different pharmacological profiles with drugs spiperone and clozapine, they all coupled to G proteins [76]. Similarly, the same group later found that the polymorphic repeat sequences conferred only small differences in pharmacological binding properties [77, 78] and also in functional properties to inhibit cyclic adenosine monophosphate [79]. Therefore, it was concluded from the evidence that there was no direct relationship between length of the polymorphism and changes in these activities. The D<sub>4</sub> dopamine receptor variants were also capable of coupling to several G protein (G<sub>i</sub>  $\alpha$ ) subtypes, but no evidence of any quantitative difference in G protein coupling related to repeat length was observed [80]. However, transcriptional differences were observed when the repeat variants were cloned downstream from the luciferase gene in expression vectors and tested in a somatomammotrophic (GH4C1) cell line [81]. Constructs having 7 repeat sequences significantly suppressed expression of the reporter gene compared to those consisting of the 2 and 4 repeats, which was suggested to be via mechanisms involving RNA stability or translational efficiency. More recently, dopamine was found to be more potent at D<sub>4</sub> receptors having 2 and 7 repeats than those with 4 repeats, suggesting that the actions of dopamine and therapeutic drugs on D<sub>4</sub> dopamine receptors may vary amongst individuals depending on the variants they have [82].

At least 19 different repeat unit sequences, used in 25 different haplotypes that code for 18 different unique receptor variants, were identified in the human D<sub>4</sub> dopamine receptor gene [83]. More recently, an extra 35 different alleles have been detected in the population having single nucleotide polymorphisms [84]. The 7-repeat allele was initially reported to be associated with the personality of novelty seeking [85, 86] and then more lately with attention deficit hyperactivity disorder (ADHD) [87–90].

### 2.2.3.2 Promoter Structure and Transcriptional Regulation

The 5'-flanking region of the human D<sub>4</sub> dopamine receptor gene was isolated and sequenced, revealing a transcription initiation region located between -501 and -436 bp relative to the first nucleotide of the translational codon [91]. A CpG island

spanned the region from -900 to +500 bp (which is over 50% GC rich) but no TATA or CCAAT boxes were present in the 5'-flanking region. However, the region was found to have consensus binding sites for transcription factors including Sp1. These properties are similar in the 5'-regulatory sequences of the D<sub>1</sub>, D<sub>2</sub>, D<sub>3</sub> and D<sub>5</sub> dopamine receptor genes. Functional analysis of deletion constructs fused to the CAT reporter gene and transiently transfected into IMR32 (neuroblastoma) and Y-79 (retinoblastoma) cells demonstrated promoter activity in the region around -591 and -123 bp and the presence of a negative modulator between -770 and -679 bp. However, no transcriptional activity was observed in human epithelial (HeLa) cells, suggesting cell-specific regulation of the human D<sub>4</sub> dopamine receptor gene.

The 5'-flanking region of the human D<sub>4</sub> dopamine receptor contains several polymorphisms [92]. One of these is a -521 C/T polymorphism that showed weak association to schizophrenia. Functional studies demonstrated that this promoter polymorphism had reduced transcriptional activity compared to the C allele in human neuroblastoma cells (Y-79) [93]. However, more lately the -521 C/T polymorphism showed no significant differences in transcriptional activity in three human neuroblastoma (SK-N-F1, IMR32 and Y-79) cell lines [94]. The discrepancy in results between the two studies was suggested to be due to the use of different reporter vectors and variation in the length of the cloned fragment that harboured the polymorphism. Interestingly, the transcriptional regulation of the human D<sub>4</sub> dopamine receptor gene was also further analysed in SK-N-F1, Y-79, IMR32 and HeLa cells [94]. The highest transcriptional activity was observed between nucleotides -668 and -389 from the translational start site and a putative silencer region was located from -1,571 to -800 bp. These results together with the previous findings on the regulatory region of the D<sub>4</sub> dopamine receptor gene [91] suggest that the gene may possess two negative modulators, one of which was not functional in the cell systems utilized in the study by [94].

A tandem duplication of 120 bp located 1.2 kb upstream from the initiation codon and approximately 850 bp upstream from the transcription start site was identified in the human D<sub>4</sub> dopamine receptor gene [95]. This polymorphism has been found to be associated with ADHD [96-98]. Transient transfection in human neuroblastoma cells and other human cell lines with coupled luciferase reporter gene assays demonstrated that the duplication had lower transcriptional activity in human neuroblastoma cells (SK-N-MC, SH-SY5Y), human embryonic kidney cells (HEK293) and HeLa cells compared to the non-duplicated form [99]. These data also suggested that the D<sub>4</sub> dopamine receptor gene may have an alternative promoter in an intron region, as the tandem duplication revealed promoter activity. This is yet to be confirmed, but this speculation is in agreement with a previous report that suggested that the promoter region characterized by [91] could be in an intron region due to the discrepancy in size of mRNA from previous studies [100]. They also suggested that a large intron could separate the coding exons of the D<sub>4</sub> dopamine receptors from potential untranslated exons similar to that observed for the other D<sub>2</sub>-like receptors [100], and the interpretation of findings from the functional studies of the tandem duplication were discussed in light of these considerations [99].

A recent study has verified these functional data, also showing that the duplicated allele but this case in constructs comprising the major part of the 5'-regulatory region showed lower transcriptional activity in human cell lines Y-79, SK-N-F1 and HeLa compared to the non-duplicated form [101]. They also identified a 4-repeat allele of this polymorphism which showed dose-dependent functional effects with the lowest transcriptional activity in the cell lines tested.

Capillary electrophoretic mobility shift assays were used to compare the binding capacity of the transcription factor Sp1 to the polymorphic 120 bp sequence in the human D<sub>4</sub> dopamine receptor gene [102]. The data suggest enhanced binding capacity of the transcription factor to the duplicated form using HeLa nuclear extracts. However, these data have not been verified independently using other cell culture systems and/or other techniques such as standard electrophoretic mobility shift assays (EMSA).

## 2.3 D<sub>1</sub>-Like Dopamine Receptor Genes

### 2.3.1 *Gene Structure and Organization of D<sub>1</sub>-Like Dopamine Receptors*

The human and rat D<sub>1</sub> dopamine receptors were cloned by several groups [103–106]. This was achieved using a cloning strategy based on the nucleotide sequence of the D<sub>2</sub> dopamine receptor gene [22]. The cloned D<sub>1</sub> dopamine receptor encodes a protein of 446 amino acids and the gene consists of one coding exon and thus was found to be intronless. Hydrophobicity analysis of the amino acid sequence of the receptor indicated that it belonged to the family of G protein-coupled receptors, as it consists of the characteristic seven stretches of hydrophobic amino acid residues. The structural features of this receptor include a short third cytoplasmic loop and a long carboxyl-terminal tail, in contrast to the D<sub>2</sub> dopamine receptor with a long third cytoplasmic loop and short carboxyl-terminal tail. Furthermore, the cloned D<sub>1</sub> dopamine receptor when transfected into a cell line was able to stimulate adenylyl cyclase in response to dopamine. This clearly indicated that cellular physiological responses mediated at the D<sub>1</sub> dopamine receptor were different from those mediated at the D<sub>2</sub> dopamine receptor. A second member of the D<sub>1</sub> dopamine receptor sub-family was then cloned and referred to as the D<sub>5</sub> dopamine receptor as it had affinity for dopamine and lower expression in the brain compared to the D<sub>1</sub> dopamine receptor [107]. After the cloning of the D<sub>5</sub> dopamine receptor, the cloning of the rat D<sub>1</sub> dopamine receptor subtype was reported [108]. They referred to this receptor as the D<sub>1B</sub> dopamine receptor, and the previously cloned D<sub>1</sub> dopamine receptors were termed D<sub>1A</sub> dopamine receptor [103–106]. The cloned rat D<sub>1B</sub> dopamine receptor encoded a protein of 475 amino acids and belonged to the family of proteins that couple to G proteins. The distribution of the receptor was found to be similar to that of the D<sub>5</sub> dopamine receptor and it was suggested that the D<sub>1B</sub> dopamine receptor is the rat ortholog of the D<sub>5</sub> dopamine receptor, and therefore the terms D<sub>1B</sub> and D<sub>5</sub>

were used interchangeably to describe the same receptor [109]. The current standard nomenclature for dopamine receptors refers to these subtypes as D<sub>1</sub> and D<sub>5</sub> (<http://www.iuphar-db.org/GPCR/ChapterMenuForward?chapterID=1282>).

Interesting developments arose when three genes related to the D<sub>1</sub> dopamine receptor were identified in the human genome [110–112]. The authors demonstrated that one of the genes lacked introns and was found to function as human D<sub>5</sub> dopamine receptor. However, the other two genes were pseudogenes. The transcript of one of these pseudogenes is expressed in several brain regions and produces a protein of 154 amino acids [113]. The human D<sub>1</sub> dopamine receptor is located on chromosome 5 at q35.1 [114] and the functional human D<sub>5</sub> dopamine receptor gene is localized to chromosome 4p16.1 [115]. The first and second pseudogenes of the D<sub>5</sub> dopamine receptor genes demonstrated chromosome localization to 2p11.1-p11.2 and 1q21.1, respectively [115].

### ***2.3.2 Promoter Region of the D<sub>1</sub> Dopamine Receptor Gene***

The 5'-flanking region of the human D<sub>1</sub> dopamine receptor gene was characterized by sequencing a 2.3 kb genomic fragment from -2,571 to -236 bp relative to the adenosine of the first methionine codon [69]. S1 nuclease mapping and reverse transcription PCR revealed the presence of a small intron of 116 bp (-599 to -484) and an exon of about 440 bases in the 5'-non-coding region upstream from the coding exon in the human D<sub>1</sub> dopamine receptor gene which was previously thought to be intronless [103–105]. The rat D<sub>1</sub> dopamine receptor gene was also found to have a small intron in its 5'-untranslated region [70] and additional information on its 5'-flanking region has been described at the end of the section. The human D<sub>1</sub> dopamine receptor gene has multiple transcription initiation sites located between -1,061 and -1,040. The promoter region lacks a TATA box and a CCAAT box, is rich in G+C content (up to 80% in some regions) and has several putative binding sites for the general transcription factor Sp1 [69]. Thus the promoter region of D<sub>1</sub> dopamine receptor was similar to that in the D<sub>2</sub> gene having similar features. However, it also has consensus sequences for a putative cAMP response element and binding sites for the transcription factors AP1 and AP2. Transient expression assays suggested the presence of a positive modulator between nucleotides -1,340 and -1,102 and a negative modulator between -1,730 and -1,341 in the murine neuroblastoma cell line (NS20Y), with no or very low transcriptional activity in NB41A3, C6 and HepG2 cells which do not express the D<sub>1</sub> dopamine receptor gene, suggesting regulation in a tissue-specific manner. It was later demonstrated that the transcriptional activity of the intron within the human D<sub>1</sub> dopamine receptor gene is higher than the upstream promoter by 12-fold in SK-N-MC cells and by 5.5-fold in NS20Y cells in an orientation-dependent manner [116]. Studies in SK-N-MC cells additionally revealed that longer D<sub>1</sub> mRNAs including exon 1 are degraded 1.8 times faster than the shorter D<sub>1</sub> transcripts. Thus all this evidence indicates that the human D<sub>1</sub> dopamine receptor gene is transcribed in neural cells from a second strong promoter that is located in the intron and generates shorter transcripts

deficient in exon 1. However, only this short D<sub>1</sub> dopamine receptor transcript was present in human and rat kidneys [117]. These data demonstrate that the upstream promoter is active only in neural cells, whereas the intron promoter is active in both neuronal and renal cells. However, the activator region (nucleotides -1,154 to -1,136) that enhances transcriptional activity of the upstream promoter in SK-N-MC and NS20Y could not activate this promoter in OK cells [117]. Furthermore, gel shift assays using nuclear extracts from either OK cells or rat kidney tissue showed no protein binding to the activator region. The results suggest that differential expression of long and short D<sub>1</sub> dopamine receptor transcripts is due to tissue-specific expression of the activator protein binding to the activator region promoting transcription from the upstream promoter. It was suggested that absence of this protein would result in a non-functional D<sub>1</sub> upstream promoter in the kidney.

The activator region of the human D<sub>1</sub> dopamine receptor gene was further analysed and found to localize to two regions (-1,154 to -1,137 and -1,197 to -1,154) which increased promoter activity [118]. In addition, both the -1,197 to -1,154 region and the core promoter located downstream to -1,102 resulted in cell-specific D<sub>1</sub> dopamine receptor gene expression. Additionally, DNase I footprinting and gel shift assays revealed DNA protein interactions mainly in the region between -1,197 and -1,116. Furthermore, functional significance of nuclear factors interacting with the activator regions of the human D<sub>1</sub> dopamine receptor gene was determined in the neuroblastoma cell line SK-N-MC using competitive cotransfections with different fragments of this region. Novel transcription factors interacted with the D<sub>1</sub>-Act-1 (-1,197 to -1,152) sequence even though it does not have consensus binding sites for known transcription factors. DNA binding proteins interact with D<sub>1</sub>-Act-2 (-1,154 to -1,116) sequence as a complex that includes Sp1 or Sp1-like protein as well as a novel factor. However, even though recombinant AP2 binds to some of its consensus sequences in the D<sub>1</sub> dopamine receptor gene, it was suggested that it is unlikely that AP2 has a significant role in positively modulating the basal expression of the gene in NS20Y cells as the AP2 consensus sequences in the D<sub>1</sub> dopamine activator could not bind to nuclear extracts of these cells [118].

Supplementary transcriptional regulation studies of the human D<sub>1</sub> dopamine receptor gene by cAMP revealed location of two cAMP responsive regions in exon 1, both of which interacted with nuclear proteins in D<sub>1</sub>-expressing cells SK-N-MC [119]. The segment of D<sub>1</sub> gene between these two regions strongly interacted with nuclear proteins following forskolin/IBMX which directly increases cAMP levels. A different study demonstrated that 6.4 kb upstream region on the human D<sub>1</sub> dopamine receptor gene is sufficient to confer tissue-specific expression in specific D<sub>1</sub>-expressing brain regions of transgenic mice *in vivo* and in neuroblastoma cells *in vitro* [120].

The regulatory regions of the rat and mouse D<sub>1</sub> dopamine receptor genes have additionally been studied. The promoter region of the rat D<sub>1</sub> dopamine receptor gene was initially characterized locating the transcription start site to 864 bp upstream from the translational start site [70]. Like the human gene, the 5'-flanking region of the rat gene does not have any TATA or CCAAT boxes but is G + C rich, with binding sites for the transcription factors Sp1, Ap1 and Ap2 and with potential

cAMP and glucocorticoid response element sequences. Transfection studies using fusion constructs with the CAT reporter gene demonstrated that the rat D<sub>1</sub> promoter is active in D<sub>1</sub>-expressing neuroblastoma NS20Y cells but inactive in glioma C6 and human embryonic kidney (HEK293) cells that do not express the D<sub>1</sub> dopamine receptor. A fragment of 735 bp of the 5'-flanking region of the gene produced this cell-specific promoter activity which was responsive to cAMP, suggesting an auto-regulation mechanism by which stimulation of the gene exerts a positive feedback on its expression.

Second, the 5'-flanking region of the murine D<sub>1</sub> dopamine receptor gene was investigated to determine the utility of its promoters in brain tissue-specific expression of transgenes [121]. The presence of two functional promoters was confirmed similar to that found for the rat and human D<sub>1</sub> dopamine receptor genes [116, 117]. Transient expression analyses using CAT fusion constructs revealed that the murine D<sub>1</sub> upstream promoter fused with the activator region of the human D<sub>1</sub> gene has strong transcriptional activity in NS20Y cells that express D<sub>1</sub> but not in renal (OK), glial (C6) and hepatic (HepG2) cells. This suggests that the hybrid construct harbours neural cell-specific elements and this could be tested for the neuronal-specific expression of transgenes in vivo [121].

Most of the evidence for the interaction of DNA binding proteins with the regulatory region of the D<sub>1</sub> dopamine receptor has been generated from studies with the human gene. The transcription factors that have been found to regulate the human D<sub>1</sub> dopamine receptor gene include POU factors such as Brn-4 [122, 123] and also Meis2 (myeloid ecotropic viral integration site 1) and TGIF (5'-TG-3'-interacting factor) which belong to the family of three-amino acid extension loop (TALE) homeobox proteins [124]. Furthermore, the zinc finger protein ZIC2 and factor Sp3 were found to repress Sp1-induced activation of the human D<sub>1</sub> dopamine receptor gene, an effect that involved the activator region in the regulatory fragment of the gene [125]. The hormone oestrogen has additionally been found to upregulate transcription of the human D<sub>1</sub> dopamine receptor in neuroblastoma cell lines [126]. The zinc finger-type transcription factor DRRF has been found to repress the promoter region of the D<sub>1</sub> dopamine receptor in NS20Y cells and activate the D<sub>1</sub> dopamine receptor promoter in TE671 cells [48]. This protein binds to the GC and GT boxes in the D<sub>1</sub> dopamine receptor promoter and effectively displaces Sp1 and Sp3 from these sequences. Thus DRRF regulates dopamine receptor subtypes and has opposing effects depending on cellular context.

### ***2.3.3 Promoter Region of the D<sub>5</sub> Dopamine Receptor Gene***

There is some evidence on the transcriptional regulation of the D<sub>5</sub> dopamine receptor following characterization of the 5'-flanking and promoter regions of the human gene [127]. Comparison of genomic and cDNA sequences revealed the presence of two exons separated by a small intron. The 5'-flanking region showed no TATA and CCAAT boxes but contained several putative binding sites for the transcription factors Sp1 and Ap1, thus revealing a similar structure to the other dopamine receptor

genes. However, the D<sub>5</sub> regulatory region is not GC rich and has a major transcription initiation site determined 2,125 bp upstream from the translational start site, in contrast to [12, 127]. Constructs consisting of the luciferase gene and up to 500 bp of the 5'-transcription initiation site showed transcriptional activity in SK-N-SH cells but not COS-7, CHO (Chinese hamster ovary), NB41A3 and SK-N-MC cells. Deletion analysis indicated that the regulatory region of the D<sub>5</sub> dopamine receptor gene has a positive modulator at 119–182 bp and a negative modulator 251–500 bases upstream from the transcriptional start site in the neuroblastoma cell line SK-N-MC cells. This information resulted in an understanding of the regulatory control mechanisms of the human D<sub>5</sub> dopamine receptor genes. In addition, even though a polymorphic dinucleotide (TC) repeat in the promoter region of the human gene was identified and demonstrated to have transcriptional activity in human neuroblastoma cells (SK-N-SH), there were no significant differences in the functional effect of these genetic variants [128]. To date there are no reports on the 5'-flanking regions of the D<sub>5</sub> dopamine receptor gene from other species.

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# Chapter 3

## Structural Basis of Dopamine Receptor Activation

Irina S. Moreira, Lei Shi, Zachary Freyberg, Spencer S. Ericksen, Harel Weinstein, and Jonathan A. Javitch

**Abstract** G protein-coupled receptors (GPCRs) are seven transmembrane (TM) proteins representing the largest and most universally expressed cell surface receptors and are present in almost all species and in a wide variety of cells. Here we will focus our attention on the catecholamine-binding GPCRs and in particular on the dopamine receptors. The catecholamine-binding GPCRs form a group of rhodopsin-like GPCRs composed of adrenoceptors, which are endogenously activated by epinephrine and norepinephrine, and dopamine receptors. We review the different “molecular switches” involved in GPCR activation and we emphasize the importance of extracellular loop 2 (ECL2) in ligand binding. A better understanding of the functional role of ECL2 can be achieved after the release of the crystal structures of B2AR and rhodopsin, which are consistent with dopamine D2 receptor substituted cysteine accessibility method (SCAM) experimental data. Even though reconstituted GPCR monomers appear sufficient to activate a G protein, in the native setting their dimerization/oligomerization may modulate activation through changes at the dimerization interface or a larger-scale reorientation of the protomers. Therefore, the structural aspects of oligomerization and their importance for receptor activation and signaling are also addressed.

**Keywords** Catecholamine-binding GPCRs · Dopamine receptors · Binding site · ECL2 · GPCR oligomerization · GPCR–G Protein interaction · Activation · Structural rearrangements

### 3.1 Introduction

G protein-coupled receptors (GPCRs) are seven transmembrane (TM) proteins representing the largest and most universally expressed cell surface receptors. GPCRs

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J.A. Javitch (✉)

Center for Molecular Recognition, Columbia University College of Physicians and Surgeons,  
New York, NY 10032, USA  
e-mail: jaj2@columbia.edu

are present in almost all species and in a wide variety of cells [1–8]. They play important roles in a broad array of cellular functions and in disease and represent the targets for a large fraction of existing drugs [9–12]. GPCRs are classified into three major classes based on the size of the N termini, on sequence homology, the identity of conserved residues within the seven TM domains that participate in ligand binding, mode of action, and pharmacology [13, 14]. The largest family is Class A (more than 90%), which comprises rhodopsin as well as receptors for biogenic amines, peptides, and odorants. Class B receptors are a much smaller group and include receptors for large peptides such as secretin, cytokines, thrombin, and glucagon. Class C receptors (comprised of approximately 12 members) include the  $\gamma$ -aminobutyric acid B receptor (GABA<sub>B</sub>), eight metabotropic glutamate receptors, the Ca<sup>2+</sup> sensing receptor, as well as some pheromone and taste receptors [15]. GPCRs, upon ligand binding, induce dissociation of G proteins into their G<sub>α</sub> and G<sub>βγ</sub> components and ultimately modulate the activity of enzyme or ion channel effectors [5, 16–19].

Structurally, GPCRs are made up of seven TM segments connected by three intracellular and three extracellular loops (ICL, ECL), and Class A receptors share important functionally conserved sites identified as structural motifs that act as functional microdomains, such as the D(E)RY motif in TM3 and NPXXY in TM7 [8, 20–28]. The first GPCR structure, bovine rhodopsin, was solved in 2000 [29], and there was much anticipation that many other GPCR structures would be rapidly forthcoming. Although a number of different rhodopsin structures were solved, 7 years passed without any other GPCR structures, in support of the unique biochemical properties of rhodopsin, including its high abundance and its unusual stability, retaining function under conditions that denature other GPCRs, due to the covalently bound 11-*cis*-retinal, which maintains the receptor in an inactive conformation [30–32].

At the end of 2007, two new crystal structures of the human  $\beta$ 2 adrenergic receptor (B2AR) were solved, including the wild-type receptor bound to an antibody fragment and an engineered receptor with T4 lysozyme inserted into the third intracellular loop [31–33]. Although the B2AR crystallographic structures are quite similar to rhodopsin with a root mean square deviation of 1.6 Å, there are some interesting differences, which impact on considerations of the structure of the dopamine receptor family, for which a structure is not yet available. Very recently two new structures of the  $\beta$ 1 adrenergic receptor [34] and the adenosine A2 receptor [35] have been solved, and while there are interesting differences, the overall structures are again quite similar.

Here we will focus our attention on the catecholamine-binding GPCRs and in particular on the dopamine receptors. The catecholamine-binding GPCRs form a group of rhodopsin-like GPCRs composed of adrenoceptors, which are endogenously activated by epinephrine and norepinephrine, and dopamine receptors [36]. For the adrenoceptors, there are three main classes based on their pharmacological properties, amino acid sequences, and signaling mechanisms. These adrenoceptor classes were subsequently divided in humans into three subtypes each:  $\alpha_1$  ( $\alpha_{1A}$ ,  $\alpha_{1B}$ ,  $\alpha_{1D}$ ),  $\alpha_2$  ( $\alpha_{2A}$ ,  $\alpha_{2B}$ ,  $\alpha_{2C}$ ), and  $\beta$  ( $\beta_1$ ,  $\beta_2$ ,  $\beta_3$ ). These receptors respond to the

neurotransmitters/hormones, norepinephrine and epinephrine, which play key roles in regulation of cardiovascular function, energy metabolism, and blood pressure [15]. In contrast to adrenoceptors, dopamine receptors in human are divided into two classes: D<sub>1</sub>-like receptors (D<sub>1A</sub> or D<sub>1</sub> and D<sub>1B</sub> or D<sub>5</sub>) and D<sub>2</sub>-like receptors (D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub>). While sharing some common properties, each receptor displays unique properties including affinity for dopamine, specificity for G protein coupling and signaling, and specific neuronal distributions [37]. Furthermore, in the case of the D<sub>2</sub> receptor (D2R) subfamily, there are two isoforms: the long isoform D<sub>2L</sub> and the short isoform D<sub>2S</sub>, generated by alternative splicing of an 87-bp exon. This splicing event leads to an additional 29 amino acids in the ICL3 of the isoform D<sub>2L</sub> [38].

## 3.2 Transmembrane Segments and Activation

TM segment interactions are a key determinant in the assembly and stability of the native structure of membrane proteins [39–41]. As the sequence conservation within the membrane-spanning regions is high, it is thought that class A GPCRs share a similar architecture [16, 17, 41, 42], which has been supported to date by the four different receptors for which we have crystal structures. The catecholamine-binding GPCRs share within their TM regions 20–26% sequence identity with rhodopsin [36]. For example, the sequence identity between the TM domains of rhodopsin and B2AR is 21%, between rhodopsin and D2R is 25%, and between D2R and B2AR is 38% [36].

Some of the most important features of the TM domains are the kinks and bends generated by prolines and glycines, respectively [23, 43–46]. Serines, threonines, and cysteines can also bend the  $\alpha$ -helices that constitute the TM domains [24, 47]. In rhodopsin, TM1 possesses a proline-induced kink that bends it inward, toward the helix bundle. It was proposed that other GPCRs, which do not have this proline in TM1, including the D2R, might be packed somewhat differently with TM1 more distant from the bundle [8, 24, 48]. Consistent with such an orientation of TM1, the extracellular segment of TM1 of D2R did not seem to contribute to the binding site based on substituted cysteine accessibility method (SCAM) studies [8, 49]. The B2AR 3D structure validated this hypothesis because its TM1 is comparatively straight [32]. Moreover, although the TM segments in rhodopsin and B2AR have similar orientations, there are some differences: the angles between TM1, TM3, and TM6 and the membrane are different from their counterparts in rhodopsin, TM4 is translated away from the center of the receptor, and TM5 is translated closer to the center of the receptor [32].

It is hypothesized that GPCRs exist as an ensemble of various conformational states that are in a dynamic equilibrium, and that agonist binding and subsequent activation occur through a series of conformational intermediates [50, 51]. Ligands have the ability to stabilize or possibly induce specific conformations [52]. Mutations that disrupt stabilizing non-covalent interactions favor more active receptor conformations by increasing the movement of the TM segments relative to

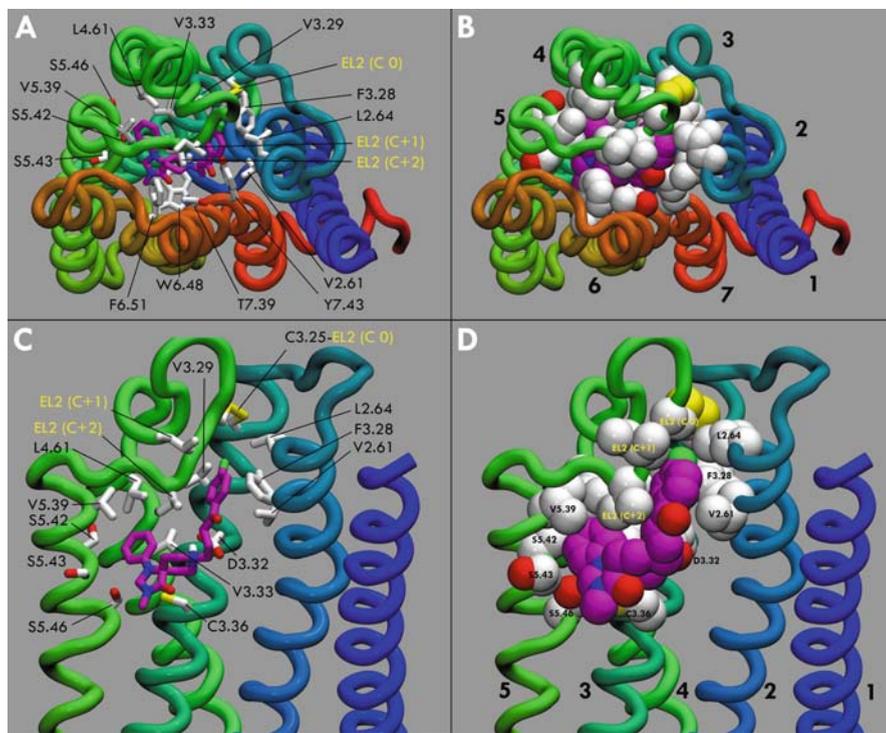
each other [52]. Although there are different ligand-binding modes in the different GPCR classes, activation processes are thought to result from similar conformational changes involving the TM domain [53–59]. In particular, rotation and outward movement of TM6 likely open a crevice allowing for interaction with the C terminus of the G protein  $\alpha$ -subunit and triggering GPCR activation [59–61].

Many GPCRs show a considerable amount of basal, agonist-independent activity, reflecting GPCR structural flexibility and the existence of conformational ensembles [52]. The study of constitutively active GPCRs has contributed to our understanding of the activation mechanism [57, 62–65]. Mutation of certain residues in GPCRs significantly increases their constitutive activation [66, 67] by breaking crucial intramolecular interactions between amino acid residues that normally constrain the receptor to its inactive state [21, 24, 62]. Many residues that produce constitutive activation when mutated are linked through packing interactions with residues that are essential for receptor activation by side chain rearrangement on adjacent TMs and/or by larger-scale TM movements [62, 68–70]. Some of the most well-known constitutively active mutants (CAMs) are those that disrupt the highly conserved (D/E)R(Y/W) amino acid sequence present in 72% of class A GPCRs. By contrast, an “ionic lock” is crucially involved in maintaining the inactive state of the receptor [21, 24, 71–73]. This is exemplified in a network of hydrogen bonding and charge interactions between Glu134<sup>3,49</sup> and Arg135<sup>3,50</sup> at the cytoplasmic end of TM3 and Glu247<sup>6,30</sup> and Thr251<sup>6,34</sup> at the cytoplasmic end of TM6 of rhodopsin (Ballesteros general number in the superscript [7]) [23, 24, 74]. In the B2AR structures, the “ionic lock” is broken, which may account for the residual basal activity of the B2AR bound to the inverse agonist carazolol [31, 33, 51]. Recent computational studies suggest that the ionic lock dynamically forms and unforms in association with conformational change in ICL2 [75].

Besides the “ionic lock,” there are other “molecular switches” involving non-covalent intramolecular interactions that must be altered to achieve an active state. The “rotamer toggle switch” involves Phe290<sup>6,52</sup>, which is accessible in the binding site crevice and serves as a “sensor,” a change in the bend of TM6 at the highly conserved residue Pro288<sup>6,50</sup>, and a change in the rotamer of Trp265<sup>6,48</sup> upon activation of rhodopsin and related family members [46]. Although carazolol does not directly interact with the “toggle switch” in the B2AR TM6, it seems to modulate the rotameric state of Trp286 indirectly by interacting with Phe289<sup>6,51</sup> and Phe290<sup>6,52</sup> [31–33, 76, 77]. These kinds of molecular switches can be studied experimentally and computationally [6, 25, 71, 72].

### 3.3 The Binding Site

SCAM studies, experimental approaches such as studies of chimeric receptors and point mutants, as well as molecular modeling allowed for the identification of amino acids that line the putative binding pocket of the D2R [48, 78–96] (Fig. 3.1). The findings for D2R are in agreement with results for other catecholamine-binding receptors [36]. The binding crevice has two polar regions common to all these



**Fig. 3.1** *N*-Methylspiperone (MSP) docked into the binding site crevice of the dopamine D<sub>2</sub> receptor (D2R). Panel (A): From an extracellular perspective, TMs 1–7 are colored from *blue* to *red*. MSP (carbon *magenta*, stick) is nestled in the binding site and capped by EL2. D2R side chains within 4 Å of MSP are shown (carbon *white*, stick) and labeled according to the Ballesteros and Weinstein indexing system. Residues in EL2, Ile183<sup>EL2(C+1)</sup>, and especially Ile184<sup>EL2(C+2)</sup> (labeled in *yellow*), provide substantial hydrophobic contacts to the ligand. Other residues within 4 Å of MSP are Val91<sup>2.61</sup>, Leu94<sup>2.64</sup>, Phe110<sup>3.28</sup>, Val111<sup>3.29</sup>, Asp114<sup>3.32</sup>, Val115<sup>3.33</sup>, Cys118<sup>3.36</sup>, Leu171<sup>4.61</sup>, Cys182<sup>EL2(C 0)</sup>, Val190<sup>5.39</sup>, Ser193<sup>5.42</sup>, Ser194<sup>5.43</sup>, Ser197<sup>5.46</sup>, Trp357<sup>6.48</sup>, Phe360<sup>6.51</sup>, Thr383<sup>7.39</sup>, and Tyr387<sup>7.43</sup> [D2R (*short*) UNIPROT sequence P14416-2]. Panel (B): To emphasize the hydrophobic packing of the EL2 and crevice residues with bound MSP, the contact side chains from A are rendered as van der Waals spheres. TMs are numbered. Panel (C): Peering into the crevice from a side view (TMs 6–7 are removed) reveals some key interactions between MSP and the D2R binding site crevice and EL2. Key interactions include a hydrogen bond-reinforced ionic interaction between Asp114<sup>3.32</sup> and the ligand’s amine moiety, deep occupancy of the MSP’s phenyl-imidazolidinone group in the primary binding cleft centered between TMs 3 and 5–6, and contacts between the fluorophenyl group with residues in EL2 and TMs 2,3, and 7 (not shown). Missing from this view are the aromatic contacts from TM6 to the ligand’s piperazine and phenyl-imidazolidinone moieties and potential hydrogen bonding between Thr383<sup>7.39</sup> and Tyr387<sup>7.43</sup> and the butyrophenonyl keto group. Panel (D): Same view as Panel C with side chains rendered as van der Waals spheres. EL2 contact residues are labeled in *yellow*. TMs are numbered

receptors: Asp<sup>3.32</sup>, which forms ionic interactions with the protonated amine of biogenic amines, and Ser<sup>5.42</sup>, Ser<sup>5.46</sup>, and Ser<sup>5.43</sup> of TM5, which interact by hydrogen bonding with the *meta*-OH and *para*-OH of the catecholamine. The  $\beta$ -hydroxyl group of (nor)epinephrine, which is not found in dopamine, interacts with Asn<sup>6.55</sup>. Phe<sup>5.47</sup>, Trp<sup>6.48</sup>, Phe<sup>6.51</sup>, and Phe<sup>6.52</sup> are also expected to interact with the aromatic ring of the ligands [36]. In an exhaustive computational study, Xhaard et al. [36] demonstrated that the docked ligand tends to be in an extended conformation because Asp<sup>3.32</sup> and TM5 residues are distant from each other, at the opposite ends of the binding pocket.

Prior to the determination of the crystal structure of rhodopsin, Simpson et al. [91] used data from SCAM studies to guide an exploration of the structural basis of the pharmacological specificity of D2R and D4R. Combined substitution of four to six of the residues that faced the binding site crevice in the D2R but were not conserved in the D4R switched the affinity of the receptors for several chemically distinct D4-selective antagonists by three orders of magnitude in both directions (D2- to D4-like and D4- to D2-like). The mutated residues were in TM2, TM3, and TM7 and were predicted to form a divergent cluster that differentiated D2R and D4R binding, which has been supported as well by subsequent studies [94, 95, 97]. Ortore et al. [98] have docked different ligands to both D2R and D4R and have proposed that another difference between the two receptors seems to be due to the extracellular loop 2 (ECL2) region (see below), which is differentially situated in the receptor models, although it should be noted that loop modeling is a complex and developing science [99, 100]. Ligand binding to many members of the GPCR family is regulated allosterically by cations. For example, Na<sup>+</sup> is important for the D2R, and Zn<sup>2+</sup> was shown to interact with D1, D2, and D4 receptors [101].

### 3.4 Extracellular Loop 2

It is widely accepted that the extracellular loops (especially ECL2) are of great importance for accommodating high molecular weight GPCR ligands (peptides and proteins). In the rhodopsin structure ECL2 forms a lid-like structure over retinal, but the precise role of ECL2 in binding other lower molecular weight, drug-like ligands is less clear [102]. In more than 800 GPCRs encoded in the human genome, the average size of ECL2 is 27 residues, with a deviation of 13 residues [103]. For nearly all rhodopsin-like GPCRs, the disulfide bond between Cys<sup>3.25</sup> (Cys-107 in D2R) and the conserved Cys in E2 (Cys\_e2, Cys-182 in D2R) connects ECL2 with the extracellular end of TM3, and this disulfide bond (SS-E2) is crucial to the structural integrity and function of many GPCRs. This disulfide bridge is found in more than 90% of GPCRs [14, 103]. The removal of SS-E2 by mutagenesis severely disrupts ligand binding to muscarinic acetylcholine receptors [104, 105] and destabilizes the high-affinity state of the B2AR [106]. Moreover, antagonist protected the B2AR from the effects of reduction by dithiothreitol [107]. Thus, SS-E2 is protected by a conformational change or steric block within the binding site.

In rhodopsin, ECL2 forms a twisted, buried  $\beta$ -hairpin structure that folds deeply into the TM domain with one strand contacting retinal and forming interactions with other extracellular loops [102]. It forms a lid-like structure that shields the retinal in a hydrophobic pocket [51]. The orientation of ECL2 is maintained by the SS-E2 described above [29, 108].

Several reports have implicated ECL2 in ligand specificity in aminergic and other small molecule ligand GPCRs. Zhao et al. [109] found that substitution of three consecutive residues in ECL2 interconverted the ligand specificity for particular antagonists between that of  $\alpha_{1B}$ AR and  $\alpha_{1A}$ AR. Substitution of a single residue in ECL2 interconverted the pharmacological specificities of canine 5-HT<sub>1D</sub> and human 5-HT<sub>1D</sub> receptor [110]. Similarly, substitution of ECL2 and TM5 changed the subtype specificity of the 5-HT<sub>1D</sub> receptor to that of the 5-HT<sub>1B</sub> receptor and vice versa [111]. Thus, although it has been argued that the presence of ECL2 within the TMD may be a feature unique to rhodopsin [112, 113], it has also been proposed that ECL2 contributes directly to forming the binding site of aminergic and certain other small molecule ligand GPCRs [114]. To address this issue, SCAM studies were carried out in the short ECL2 of D2R [115]. The reaction of five of these mutants with sulfhydryl reagents inhibited antagonist binding, and bound antagonist protected two, I184C and N186C, the second and fourth residues after the highly conserved Cys<sub>e2</sub> (C+2, C+4). The pattern of accessibility in ECL2 was consistent with a structure similar to that of bovine rhodopsin, in which E2b, the part of ECL2 C-terminal to the conserved disulfide bond, is deeper in the binding site crevice than is E2a, the N-terminal part of ECL2, and E2b was inferred to contribute directly to the binding site in the D2R and probably in other aminergic GPCRs as well (Fig. 3.1).

More recently, the effects of ECL2 mutations on agonist and antagonist binding have been studied in the V1a vasopressin receptor (Class A) ECL2 by a systematic alanine-scanning mutagenesis technique that identified four aromatic amino acids, located in the middle of the ECL2 near the conserved disulfide bond and conserved throughout this subfamily of peptide GPCRs, as important for agonist binding and receptor activation [116]. Trp206<sup>(C+1)</sup> and Phe209<sup>(C+4)</sup> were hypothesized to be important for ligand binding and Tyr218<sup>(C+13)</sup> and Phe189<sup>(C-16)</sup> appear to be important for orientation/stability of ECL2 over the binding pocket [116]. Furthermore, Klco et al. showed that disruption of ECL2 of the complement C5a receptor (C5aR) by random mutagenesis generated many receptors able to activate G proteins even in the absence of ligands [14]. The authors postulated that ECL2 acts as a negative regulator of C5aR activation possibly by making multiple contacts with the TM domain to stabilize the inactive state.

Through their studies of the serotonin 5-HT<sub>4(a)</sub> receptor Baneres et al. have suggested the existence of different arrangements of ECL2 depending whether the bound ligand was an agonist (partial or full) or an inverse agonist [117]. In contrast, antagonist binding was inferred not to induce any structural changes of ECL2. Therefore, as in the case of D2R, ECL2 appears to participate in the binding site and rearranges upon activation. Despite the constraint provided by the conserved disulfide bond between ECL2 and the top of TM3, Avlani et al. showed that the

flexibility in ECL2 of the muscarinic acetylcholine M<sub>2</sub> receptor (M<sub>2</sub> mAChR) and its capacity to achieve an open conformation is necessary for the binding of both allosteric and orthosteric ligands [4]. They postulated ECL2 as a gatekeeper with respect to entrance into the orthosteric binding site crevice.

Other studies stress ECL2's importance for ligand binding as in the M<sub>3</sub> muscarinic acetylcholine receptor (M<sub>3</sub>R) and the thyroid-stimulating hormone receptor (TSHR). ECL2 of the M<sub>3</sub>R was subjected to random mutagenesis. In contrast to the model proposed by Klco et al. [14], the results of this study suggested that specific ECL2 residues stabilize the active state of the M<sub>3</sub>R, and are required for efficient agonist-induced M<sub>3</sub>R activation [108]. The authors also proposed a mechanism in which conformational flexibility in the ECL2 loop is required for efficient receptor activation [108]. Kleinau et al. suggested an activation mechanism in which TM6 glides along ECL2 according to the diverse receptor activation states. Disruption of this critical interface by introduction of mutations in the TSHR alters its basal activity [118].

The crystal structure of B2AR provided the first non-rhodopsin ECL2 structure with which to address these hypothesized functional roles. The conformation of B2AR ECL2 and its orientation to the TMD are significantly different from that in rhodopsin, rendering the binding site crevice of B2AR directly exposed to the water phase [31–33]. Strikingly, however, the ligand-binding residue positions in E2b of rhodopsin and B2AR are remarkably consistent, if counted from CysE2, namely the C+2 and C+4 positions, even though rhodopsin has eight extra residues between CysE2 and the start of TM5 at position 5.36. This is in remarkable agreement with the SCAM studies in D2R [115], in which protection by antagonist suggests that the same two positions, Ile184 and Asn186, face the binding site crevice. In this study several residues in D2R were also found to be accessible to MTS reagent but not protected by ligand, and these were proposed to line the ligand entry pathway. This is most obvious in the C+1 position, because E2b can easily be aligned between D2R and B2AR, whereas E2a varies significantly. In the B2AR structure, C+1 is in the vestibule through which the extracellular milieu gains access to the bound carazolol [31–33]. Given the consistency between the D2R SCAM experimental data for ECL2 with both the rhodopsin and B2AR structures, it is likely that C+2 and C+4 play an important role in ligand binding in the other catecholamine receptors as well, and play an important role in ligand specificity (see Fig. 3.1).

### 3.5 GPCR Oligomerization

Class C GPCRs, including the metabotropic glutamate receptors and  $\gamma$ -aminobutyric acid type B (GABA<sub>B</sub>) receptors, have been shown to form homo- and heterodimers in the plasma membrane, with important consequences for trafficking of receptors to the cell surface and for ligand-induced activation and G protein coupling [119]. Class C GPCRs have unique characteristics with dimerization potential: an N-terminal Venus flytrap (VTF) module with structural and functional homology to bacterial periplasmic proteins [120], and cysteine-rich domains (CRDs) [121].

Although the formation of dimers for Class C GPCRs is clear, there is still some controversy regarding the existence of dimers in Class A receptors [122, 123]. Nonetheless, there is increasing agreement that Class A GPCRs can interact to form homo- or heterodimers/oligomers [40, 124–149]. Evidence for dopamine receptor homo- and heteromerization is reviewed extensively in Chapter 10; here we focus on structural aspects of oligomerization and the relationship of oligomerization to receptor activation and signaling.

For rhodopsin, dimers and higher-order oligomers have been visualized in disc membranes by atomic force microscopy [150], and an oligomeric arrangement has been inferred in its native environment [12, 151]. Oligomerization also has been inferred from ligand-binding studies [132, 152–155]. Guo et al. recently demonstrated using biophysical and biochemical approaches that the D2R forms higher-order oligomers in living cells at physiological levels of expression [147].

### ***3.5.1 GPCR Oligomerization and Signaling***

What is physiologically most relevant is understanding the role of the dimeric or oligomeric organization of GPCRs in signaling [156, 157]. Indeed, one of the great challenges in GPCR biology today is strengthening the weak mechanistic link between the physical interactions of receptors in the membrane and signaling cross talk of presumed heterodimers or hetero-oligomers. There is a great deal of evidence from many laboratories that many GPCRs interact as heterodimers (reviewed in [158, 159]). As indicated above, a number of findings support the existence of higher-order homo-oligomers as well [150, 155, 160, 161]. This raises the possibility that GPCR heteromers may interact not as heterodimers per se but rather as higher-order hetero-oligomers composed of homodimer subunits.

A large number of studies have demonstrated signaling cross talk between coexpressed GPCRs [162]. In almost all cases, however, the mechanistic link between heteromerization and signaling is tenuous. Although activation of two coexpressed receptors may be essential, signaling cross talk could nonetheless take place downstream of parallel homomeric receptor-mediated G protein activation and in such a case would not be a direct result of heteromeric signaling. Such a downstream cross talk mechanism, while often ignored, is very difficult to rule out. One example of this complexity is a recent fascinating study of a putative D1–D2R heterodimer that has been carried out both in heterologous cells [163] and in the brain [164]. These receptors appear to be coexpressed in some neurons in vivo [164]. In heterologous cells they have been inferred to physically interact based on fluorescence resonance energy transfer (FRET) [165, 166] as well as co-internalization [167, 168] and co-retention of mutants [169]. Activating both D1 and D2Rs leads to Gq-mediated signaling [163, 164], whereas D1 signaling is normally Gs/olf mediated and D2 signaling is normally Go/i mediated. These findings are intriguing and open exciting avenues of drug design targeted selectively to specific heteromers [170]. However, the plot appears thicker, as D1R-mediated Gq signaling has been observed in the brain [171, 172] where in some studies it has been shown to be insensitive to D2R

blockade [173], suggesting a role for other cellular factors in the coupling of D1R to the Gq pathway. Evidence for a priming effect for D1R-mediated Gq signaling is an example of such a potential mechanism [174, 175].

D2R has also been reported to interact with the dopamine D<sub>3</sub> receptor (D3R), and coexpression of D<sub>2</sub> and D<sub>3</sub> receptors has been reported to modulate the function of both receptors [176, 177]. More recently the D2R has been shown to modulate and to physically associate with the dopamine transporter as well [178, 179].

In addition to its reported interactions with receptors from the dopamine subfamily, there is a substantial literature on heteromerization of D2R with multiple other Class A receptors. There is evidence for direct physical interaction between D2R and the SST5 somatostatin receptor [180], D2R and adenosine A2A receptor [181, 182], and D2R and CB1 cannabinoid receptor [183]. In each of these cases, changes in signaling were observed upon receptor coexpression, with either altered D2R pharmacology by the partner protomer and/or an alteration in the properties of the partner in response to drugs acting at the D2R. In the case of the D2R–CB1 heteromer, dual-agonist mediated activation of G<sub>s</sub> was reported, although neither receptor alone is able to activate this G $\alpha$  subunit [183]. These results are intriguing and suggest the possibility of an untapped level of pharmacological diversity for new compound development, as well as a host of potential roles for *in vivo* signaling specificity for these putative heteromers. However, in none of these studies is it possible to rule out downstream signaling cross talk and thus to establish incontrovertibly that direct signaling by the D2R heteromer is responsible for the cross talk.

Such a mechanistic interrogation of heteromeric signaling in Class A GPCRs has been difficult. Our mechanistic understanding of the functional role of GPCR dimerization is more advanced in the Class C receptors, due in part to the availability of a clever adaptation of the endoplasmic reticulum (ER) retention signal from the GABA<sub>B</sub> receptor to enable controlled cell surface expression and signaling by defined metabotropic glutamate receptor (mGluR) heterodimers [184]. These studies have shown evidence for asymmetric activation of the heterodimer [185, 186]. Furthermore, one agonist can activate the dimer, but two agonists are required for full activation [187]. In addition, within the same Class C, T1R3 taste receptors are known to form functional heterodimers with either T1R1 or T1R2 in order to respond to a large panel of ligands and to trigger umami and sweet taste sensations, respectively (reviewed in [188]).

Unfortunately, related approaches with ER retention signals have been unsuccessful in Class A receptors, and it has not been possible to differentiate clearly the role of each subunit in homomeric and heteromeric signaling with coexpressed receptors. However, multiple lines of study do suggest interaction between Class A receptors in a heteromeric functional unit. Thus, for example, ligand-binding dissociation kinetics have recently been linked to the GPCR dimerization process (reviewed in [189]). In chemokine receptor heteromers, a CCR2-selective drug accelerates the dissociation of a CCR5- or CXCR4-selective drug when the receptors are coexpressed in heterologous cells and in native lymphocytes [190–192]. Moreover, although it remains to be proven conclusively, it seems reasonable to

infer that bivalent drugs engaging two different receptors, i.e., heteromer-selective compounds, might act simultaneously on two protomers in a heteromer and thereby directly activate downstream heteromer-specific signaling machinery [193–195] raising the possibility of their selective therapeutic potential [196]. Although there is evidence of G protein signaling by coexpressed nonfunctional receptor chimeras, this was proposed to occur by transmembrane domain swapping [197], which is unlikely to be universal [198]. Curiously, coexpression of two loss of function glycoprotein hormone receptors (receptors with either agonist binding or the ability to activate G proteins compromised) [199–201] led to function, but among Class A receptors such rescue seems to be limited to glycoprotein hormone receptors, which have very large extracellular N-terminal binding sites. This is similar to the transactivation seen in the Class C GABA<sub>B</sub> receptor, in which agonist binding to one protomer signals to G protein through the second protomer [184].

Another major question facing the field is the relationship between findings in heterologous cells and in *ex vivo* or *in vivo* cell systems. Most studies have focused on heterologous cells, but new approaches are being developed, including heteromer-specific antibodies (L. Devi, personal communication) as well as transgenic approaches with modified receptors.

Recent studies of purified B2AR and rhodopsin reconstituted into nanodiscs [202, 203] or in detergent solution [204] have demonstrated clearly that these receptors as monomers *can* activate G proteins. If, however, these receptors are indeed organized as dimers (or higher-order units) in native membranes, these elegant biophysical studies beg the physiologically relevant question. That is, if the receptors are capable of functioning as monomers but are closely associated as dimers or oligomers in the membrane, then what functional role does the second protomer play in drug binding and G protein activation? For example, in the GABA<sub>B</sub> receptor the GB2 subunit is necessary for high-affinity binding of agonist to GB1 [205]. Studies in the D2R indicate that conformational change at the TM4 dimer interface is part of the receptor activation mechanism [145], although we cannot as yet establish whether this is achieved by changes in one or both protomers. Similarly, in the LBT4 Baneres and colleagues have shown evidence receptor for conformational changes in protomer B upon agonist binding to protomer A [185], again consistent with a role for the dimer interface in activation.

### 3.5.2 GPCR Oligomers – Structural Considerations

Dimer interface has been the subject of various studies over the years because of its crucial value in elucidating the structural mechanism(s) for cross talk between receptors within an oligomeric arrangement [145]. Guo et al. have shown that in the D2R TM4 forms a symmetrical dimer interface and that a conformational change at this interface is part of the receptor activation mechanism [145, 206]. Based on atomic force microscopy (AFM) maps of rhodopsin, Liang et al. proposed an oligomeric model in which TM4, TM5, and ECL2 form a dimeric interface, whereas contacts between TM1, TM2, and the cytoplasmic loop connecting TM5 and TM6

facilitate the formation of oligomers [151, 160, 207, 208]. TM1 and TM4 were postulated to be the most common interfaces of oligomerization by a correlated mutation analysis-based method [143, 144, 209].

It is unclear if other dimer orientations are also permissible [119]. For example, besides TM4 and TM5 of rhodopsin [160], other TMs have been implicated in dimer interfaces [210]: TM6 of the  $\beta_2$ -adrenergic, cholecystokinin, and leukotriene B<sub>4</sub> receptors [211, 212], TM5 and TM6 of the adrenergic–muscarinic chimera [213–216], TM1 and TM4 of the D2R [145, 147, 206], TM1 and TM7 of the  $\alpha$ -adrenergic receptor [217], TM1 and TM4 of the chemokine receptor [218], TM4, TM1, and TM5/6 in the  $\beta_1$ -adrenoceptor [130], TM1, TM2, and TM4 in the complement C5a [219], and TM5 in the adenosine A2A receptor [220].

Bouvier et al. showed that a peptide derived from the TM6 of the B2AR inhibits dimerization of these receptors and proposed a helix–helix interaction involving a conserved GxxxG motif on TM6 [221]. Although TM1 and TM4 can form simultaneous symmetric interfaces in an oligomeric structure [147], TM6 cannot form a symmetrical interface in this oligomer, although it might contribute to an asymmetrical interface.

### 3.5.3 Oligomer Rearrangements upon Activation

Even though GPCR monomers appear sufficient to activate a G protein [122, 202, 203, 222], their dimerization may modulate this activation through changes at the dimerization interface or a larger-scale reorientation of the two subunits [145, 147, 162, 223, 224]. Cross-linking in the D2R homodimer suggested a conformational rearrangement at the TM4 dimer interface upon receptor activation, passing from a conformation consistent with the 1N3M pdb file to an alternative TM4 interface [145, 147]. Consequently, the D2R inactive state is consistent with the AFM model while the active state is consistent with a squid rhodopsin electron cryomicroscopy (ECM) model [145, 147]. Consistent with this proposal, cross-links of the TM4 interface activated D2R, even in the absence of agonist [145, 147]. This idea was substantiated by recent studies. Brock et al. showed that an agonist-induced rearrangement may indeed occur in the activation of the dimeric metabotropic glutamate receptors [225]. Similarly, a possible dimeric rearrangement was also observed in the mGluR1 $\alpha$  receptor. Upon ligand binding, although the distance between ICL1 and ICL2 in each protomer is unchanged, the distance between the ICL1s becomes larger, whereas that between ICL2s becomes smaller [226]. Damian et al. have also shown that in the leukotriene B<sub>4</sub> (LTB<sub>4</sub>) receptor, conformational changes take place in one of the protomers upon activation of the other [185].

These observations suggest that in addition to the activation-related conformational changes within a GPCR protomer after activation (mainly a conformational change in TM6 and an associated opening of a binding cleft for G protein between TM6 and TM3) [227], it seems that a rearrangement of the interface of the two protomers is also vital for activation [145, 147]. Mechanisms that might account for this conformational rearrangement include a rigid body clockwise rotation of

contacting TM4s upon activation, protomer displacement involving a large movement and reorganization, or partner change among protomer partners [145, 147], although Niv et al. found using computational methods that rigid body rotation of interacting TM4s is an unlikely mechanism [228].

### 3.5.4 GPCR Oligomerization and GPCR–G Protein Interactions

mGlu receptor heteromers have been inferred to activate with individual protomers in an asymmetrical relationship [186, 229]. For the BLT1 receptor, the active form of the receptor dimer also is nonsymmetric with only one subunit reaching the fully active state [230]. A single agonist per dimer appears to be sufficient for activation of heterodimeric receptors such as GABA<sub>B</sub> [205, 231] and T1R receptors [232]. Similar findings have been reported for the mGlu receptor [187], but other findings in mGlu receptors suggest that activation by agonist binding to both protomers produces greater activation [187]. G protein-specific interactions have been proposed to account for such asymmetric behavior [185, 233, 234]. Jastrzebska et al. speculated that activation of a GPCR dimer could be achieved by a single protomer and that the combination of interactions including the regions of specific trimeric G proteins and two protomers facilitates more efficient coupling [235].

In the classic view, supported by innumerable mutagenesis studies of GPCRs, a monomeric GPCR interacts through ICL2, ICL3, and/or proximal carboxyl-terminal regions with a single heterotrimeric G protein. Structural studies of the receptor–G protein interface have led to the identification of several points of contact between the G protein and the receptor on both  $\alpha$ - and  $\beta/\gamma$ -subunits [236]. When the first crystal structure of a heterotrimeric G protein was solved, it was argued that the surface area of a GPCR monomer was too small to account for the simultaneous interaction with both  $\alpha$ - and  $\beta/\gamma$ -subunits of a G protein [29, 60, 236–238]. A single G protein molecule might instead interact with a GPCR dimer [19, 29, 160, 236, 239–241]. Consistent with this, Baneres and Parelo have shown that activated leukotriene B<sub>4</sub> (LTB<sub>4</sub>) receptor BLT1 dimer and G $_{\alpha_{12}\beta_{1}\gamma_{2}}$  form an assembly containing one G protein heterotrimer and one receptor dimer (242). If the signaling unit is a GPCR dimer complexed with a heterotrimeric G protein, then both *cis*- and *trans*-activation between two protomers may occur [145].

In recent years, increasing attention has been placed on developing an improved understanding of the interaction between G proteins and the D2R. Senogles et al. have demonstrated that random point mutations in the ICL3 of D2R<sub>s</sub> modify G<sub>i</sub> protein coupling specificity. Specifically, ICL3 mutations R233G and A234T alter the predicted helical character of ICL3 and disrupt the D2R<sub>s</sub>/G protein interface [243]. Moreover, a receptor-mimetic peptide derived from the N terminus of D2R ICL3 (D<sub>2</sub>N) directly activates G<sub>i</sub>/G<sub>o</sub> proteins [244, 245]. The crystallographic structure of D<sub>2</sub>N with G $_{\alpha_{i1}}$  has further elucidated D<sub>2</sub>N/G protein interactions, suggesting that the  $\alpha 4/\beta 6$  region of G $\alpha$  (residues Q304/E308 and T321) is connected to a short basic cluster of D<sub>2</sub>N and <sup>11</sup>RRRK<sup>14</sup> (corresponding to <sup>216</sup>RRRK<sup>219</sup> in human D2R) [246].

### 3.5.5 Consequences of GPCR Oligomerization

One of the most fundamental aspects of oligomerization is its importance for GPCR pharmacology. Ligand binding to GPCRs may result in changes in the binding characteristics of additional ligands targeting the same GPCR, creating a cooperative effect on the binding of another GPCR through an allosteric mechanism [247–249]. Stabilization of a particular conformation of the dimer by a bifunctional agonist might lead to an increase of specificity and efficacy of the signaling [250]. A number of different functionalities and pharmacologic characteristics have been reported and attributed to the generation of GPCR heterodimer/oligomer complexes. Nevertheless, it is crucial to keep in mind that these effects can not only be attributed to direct protein–protein interactions but also to indirect effects produced via downstream signaling and feedback control [251].

The capacity of a GPCR to alter the binding affinity of its binding partner may ultimately be applied clinically in future drug development. More than 50% of all drugs with annual worldwide sales of more than \$50 billion regulate the function and activity of many GPCRs in attempts to treat various diseases and disorders [131, 252]. As previously mentioned, GPCR dimerization is important prior to plasma membrane delivery, and incorrect folding may interfere with dimerization and can lead to alteration in cell surface delivery and function [253–255]. In designing potential drugs that may take advantage of our growing knowledge of GPCR structure and function, taking into account oligomerization and heterodimer formation may be critical. Moreover, since receptor heterodimers can generate distinct signals from their corresponding homodimers, understanding the structural basis for higher-order receptor structure may offer a means to improve tissue selectivity and improve drug therapeutic function [251].

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# Chapter 4

## Dopamine Receptor Subtype-Selective Drugs: D<sub>1</sub>-Like Receptors

David E. Nichols

**Abstract** A survey is presented of the development of dopamine D<sub>1</sub> receptor-selective drugs, including agonists and antagonists. It is noted that there are presently no ligands that are specific for the D<sub>1</sub> vs the D<sub>5</sub> receptor isoforms. A general discussion is presented on the structure–activity features of D<sub>1</sub>/D<sub>5</sub> selective agents, with the conclusions developed that all known full D<sub>1</sub> agonists must contain a catechol moiety and, in addition, require the presence of a hydrophobic moiety (typically a phenyl ring) in the region adjacent to the beta side chain carbon of the embedded dopamine fragment. This latter structural feature is so crucial that when added to a noncatechol ergoline it gave a D<sub>1</sub>-selective partial agonist. Present evidence indicates that D<sub>1</sub> agonists may be therapeutically useful in the treatment of Parkinson's disease, as well as improving cognition and working memory in schizophrenia and age-related cognitive decline. No D<sub>1</sub> agonist has yet been commercialized, and that seems largely due to the difficulties of oral bioavailability for catechol-containing drugs.

**Keywords** D<sub>1</sub> · D<sub>5</sub> · Apomorphine · Phenylbenzazepine · Isochroman · Dihydroxynomifensine · Dihydropyridine · ABT-431 · Dinapsoline · Dinoxyline · Doxanthrine

### 4.1 Introduction

The first simple classification of dopamine receptors into D<sub>1</sub> and D<sub>2</sub> families in 1979 was based on the observation that D<sub>1</sub> receptors are positively coupled to adenylate cyclase, whereas the activation of D<sub>2</sub> receptors resulted in an inhibitory response or had no effect on adenylate cyclase [1]. Dopamine receptors are divided into two main families: the D<sub>1</sub>-like family, which includes the D<sub>1A</sub> and D<sub>1B</sub> (also referred

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D.E. Nichols (✉)

Department of Medicinal Chemistry and Molecular Pharmacology, School of Pharmacy and Pharmaceutical Sciences, Purdue University, West Lafayette, IN 47907, USA  
e-mail: drdave@purdue.edu

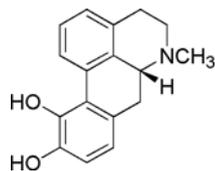
to as D<sub>1</sub> and D<sub>5</sub>), and the D<sub>2</sub>-like family, composed of the D<sub>2long</sub>, D<sub>2short</sub>, D<sub>3</sub>, and D<sub>4</sub> receptor isoforms. Of all the dopamine receptors, the D<sub>1</sub> is the most prevalent in the brain, with a proposed role in a variety of CNS functions, including motor control and memory-related processes. Antagonist radiolabeling has shown highest D<sub>1</sub> receptor density in the frontal cortex, mainly in the nucleus accumbens and olfactory tubule, but also in the substantia nigra pars compacta [2, 3]. In the peripheral nervous system it is present in the kidney and cardiovascular system [4]. All of the dopamine receptors are members of the family A G-protein-coupled receptor family (GPCR). These receptors exist as a bundle of seven alpha-helical transmembrane segments embedded in the target cell membrane.

The D<sub>1</sub> and D<sub>5</sub> receptors were first cloned in the early 1990s [5, 6]. The D<sub>1</sub> receptor consists of 446 amino acids, whereas the D<sub>5</sub> is comprised of 477 amino acids in humans and 475 in rats. These receptors are 82% homologous in the transmembrane spanning helices and 100% in the region where orthosteric ligands are thought to bind. Although we shall discuss certain molecular features of the receptor later in this chapter, a more complete discussion of the molecular biology of this seven transmembrane helix family is provided in other chapters of this book; the focus of this chapter will be on selective dopamine D<sub>1</sub> drugs and the structure–activity relationships of these molecules.

It should be noted at the outset, however, that there is presently no agonist or antagonist ligand that is specific, or even selective, for the D<sub>1</sub> vs the D<sub>5</sub> receptor isoforms; all presently available “D<sub>1</sub> ligands,” including both agonists and antagonists, have similar affinity and potency at both the D<sub>1</sub> and D<sub>5</sub> receptor isoforms. Hence, it has not been possible to employ traditional pharmacological approaches to elucidate distinct roles in brain function for these two closely related receptors. Therefore, the development of ligands specific for these two receptor isoforms still remains of extremely high importance today.

## 4.2 Apomorphine

The first drug known with D<sub>1</sub> agonist properties was apomorphine (Fig. 4.1), although this pharmacological property of the molecule was not recognized for many years. Its ready access by simple acid treatment of morphine allowed extensive studies and led eventually to its experimental therapeutic use in humans for a wide variety of ailments and conditions, including coughing, erectile dysfunction, alcohol and opiate addiction, schizophrenia and, later, Parkinson’s disease [7, 8]. Studies



**Fig. 4.1** The structure of apomorphine

of its binding in nervous tissue led to the recognition of “apomorphine receptors,” which would eventually become known as dopamine receptors [9].

*N*-alkylation of apomorphine yields ligands with improved D<sub>2</sub> affinity and reduced D<sub>1</sub> affinity, the *N*-propyl analog (NPA) being the optimum modification for maximizing D<sub>2</sub>-like selectivity [10, 11]. This observation appears to be a general property that extends to most dopaminergic molecules and has been referred to as the “propyl effect” [12, 13], and groups longer than propyl tend to be detrimental for D<sub>2</sub> receptor affinity and potency. The size of the *N*-alkyl group in dopaminergic ligands proves to be one determinant of high D<sub>1</sub> receptor affinity and agonist activity, and as a general rule, a primary or secondary amine within the structure is optimal for D<sub>1</sub> activity.

Apomorphine is characterized as a mixed D<sub>2</sub>/D<sub>1</sub> agonist and was briefly marketed in the United States (Apokyne©) as a rescue medication for the “off” motor effects observed in late-stage Parkinson patients treated with levodopa. In view of the fact that no other D<sub>2</sub>-like agonist has anti-Parkinson efficacy comparable to apomorphine, its D<sub>1</sub> agonist character [14] is likely responsible for its greater therapeutic effect [15].

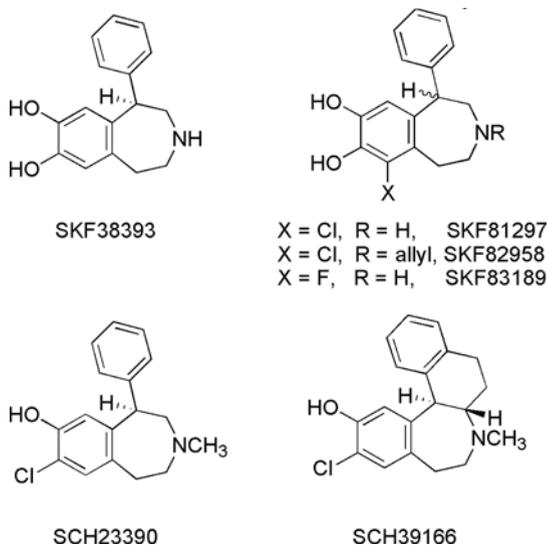
### 4.3 1-Phenyl-3-Benzazepines

The first compound discovered to possess high D<sub>1</sub> receptor selectivity was SKF38393 (Fig. 4.2), initially tested for its peripheral effects [16] but assessed soon thereafter for a central action and found to stimulate striatal adenylate cyclase [17]. The discovery of SKF38393 truly represented a breakthrough for dopamine research, as the molecule is remarkably selective for D<sub>1</sub> receptors, with affinities of 18 and 9,300 nM at the D<sub>1</sub> and D<sub>2</sub> receptors, respectively [18]. The absolute configuration of the more active enantiomer was established as R, as shown in Fig. 4.2 [19].

SKF38393 was characterized as an agonist ligand, but early studies found that it displayed little antiparkinsonian potential [20, 21]. Unfortunately, these findings were used to argue against the relevance of the D<sub>1</sub> receptor as a target for the treatment of Parkinson’s disease, an erroneous perception that still persists in many quarters today. It was ultimately realized, however, that the partial agonist character of SKF38393 [17] was likely responsible for its lack of efficacy in Parkinson’s disease. Nevertheless, great research attention was focused on this molecule and the structural characteristics that were responsible for its high affinity and selectivity at D<sub>1</sub>-like receptors.

Following the discovery of SKF38393, it was found that compounds with a halogen replacing the hydroxyl at the 7-position and an *N*-methylated nitrogen were extremely potent and selective D<sub>1</sub>/D<sub>5</sub> antagonists. The most notable example is the chloro compound SCH23390, a highly D<sub>1</sub>-selective antagonist (Fig. 4.2; D<sub>1</sub>  $K_i$  = 0.12 nM; D<sub>2</sub>  $K_i$  = 1,210 nM) [22, 23]. Most of the pharmacological characterization of D<sub>1</sub> receptors has been performed with a tritiated form of SCH23390,

**Fig. 4.2** 1-Phenylbenzazepine D<sub>1</sub>-selective ligands



which remains the ligand of choice for radioligand binding assays. This ligand has potent *in vivo* antagonist activity and virtually all of the studies of the role of the D<sub>1</sub> receptor in various behaviors also have been carried out using SCH23390. The only alternative approach to studies of the D<sub>1</sub> receptor has been the use of genetic mice that are null for the D<sub>1</sub> receptor.

Several analogs of SKF38393 also have remarkable selectivity for the D<sub>1</sub> receptor. Adding a halogen to the catechol ring led to an increase in D<sub>1</sub> affinity, yielding the selective ligands SKF81297 and SKF83189 [18, 24]. The activity of all these compounds resides in the illustrated (+)-enantiomers (Fig. 4.2). Despite their high degree of selectivity, functional assays of these agonists have generally revealed a lack of full intrinsic activity. That is, they are not able to stimulate cyclic AMP (cAMP) production to the same extent as dopamine itself in cells expressing D<sub>1</sub> receptors. A notable exception is SKF82958, which induces a robust activation of D<sub>1</sub> receptors [25].

The crystal structure of SKF38393 revealed that the pendant phenyl substituent occupies an equatorial position, twisted orthogonal to the plane of the catechol ring, and the ethylamino side chain is locked into a “*gauche*” conformation [26]. As we shall see later, both of these structural features may account for the inability of this ligand to stimulate adenylate cyclase optimally (only ca. 30–50% vs dopamine). It is unknown, of course, what conformation the molecule adopts when it binds to the receptor. Molecular modeling has indicated the existence of several low-energy conformational states, with the orientation of the pendant phenyl ring ranging between orthogonal and coplanar relationships with respect to the catechol ring plane [27]. Not surprisingly, the X-ray crystal solution of the conformation of SCH23390 also revealed a structure similar to that of SKF38393 [26].

Tethering the pendant phenyl ring of SCH23390 into a *trans*-fused tetrahydro-naphthalene led to SCH39166, a potent D<sub>1</sub> antagonist with the pendant phenyl ring constrained in a conformation that extends it in the equatorial direction and with a slight β-phenyl ring-plane twist (Fig. 4.2) [26]. Although of somewhat lower D<sub>1</sub> affinity ( $K_i = 3.3$  nM) than SCH23390, this conformation still has a high degree of complementarity to the D<sub>1</sub> binding site, suggesting that the active conformation of SCH23390 may be one where the pendant phenyl ring approaches coplanarity with the hydroxylated ring (but is not actually coplanar with it). Based on the structural similarities between SKF38393 and SCH23390, the dihydroxy analog of SCH39166 might have been expected to have high D<sub>1</sub> receptor affinity. Surprisingly, however, it had 1,000-fold lower affinity than the chlorohydroxy analog! Although this unexpected finding apparently has not raised interest, it may suggest that, despite the apparent structural similarity between SKF38393 and SCH23390, these molecules could be binding to the receptor in a fundamentally different way.

#### 4.4 4-Phenyltetrahydroisoquinolines

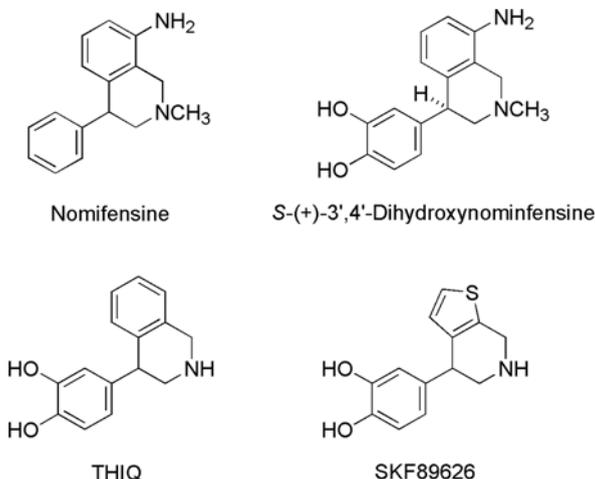
Nomifensine (Fig. 4.3) was developed in the late 1960s by Hoechst AG as a potential antidepressant with weak dopaminergic properties [28, 29]. Studies of its potential hydroxylated metabolites indicated that 3',4'-dihydroxynomifensine had significant dopaminergic agonist effects at the renal "DA1" receptor [30]. We subsequently demonstrated that its des-amino analog THIQ retained these dopamine agonist properties [12] and, further, that *N*-propylation of this compound abolished its D<sub>1</sub> activity, establishing a key difference in the SAR of D<sub>1</sub> and D<sub>2</sub> agonists, namely that *N*-alkylation is detrimental to D<sub>1</sub> affinity and functional activity. As noted earlier under the discussion on apomorphine, *N*-alkylation of dopamine agonists generally reduces activity at D<sub>1</sub> receptors, whereas it enhances activity at D<sub>2</sub>-like receptors.

Replacing the phenyl ring in THIQ with a thiophene gave a bioisosteric molecule (SKF89626) with properties virtually identical to THIQ [31, 32]. This class of compounds had efficacy comparable to dopamine in stimulating cAMP production. It will also be noted that the pendant phenyl moieties in these congeners, like the phenylbenzazepines, still possess a large degree of rotational freedom.

Dihydroxynomifensine was also resolved into its two enantiomers and the absolute configuration solved by X-ray crystallography [33]. The more active isomer had the *S* absolute configuration, shown in Fig. 4.3. It will be recognized that this stereochemistry corresponds to the active stereochemistry of the 1-phenylbenzazepines at the carbon atom where the pendant phenyl moiety is attached (the β-position of the "dopamine moiety"). Dandridge et al. [34] proposed a conceptual model of the D<sub>1</sub> receptor to accommodate this stereochemistry, as well as to be compatible with the earlier model of McDermed et al. [35].

The appearance of a "β-phenyldopamine" motif in all of these ligands led us to study β-phenyldopamine itself, and we subsequently proposed a β-phenyldopamine pharmacophore as a requirement for activation of D<sub>1</sub> receptors [36]. We compared

**Fig. 4.3** Tetrahydroisoquino  
line-type D<sub>1</sub> agonists

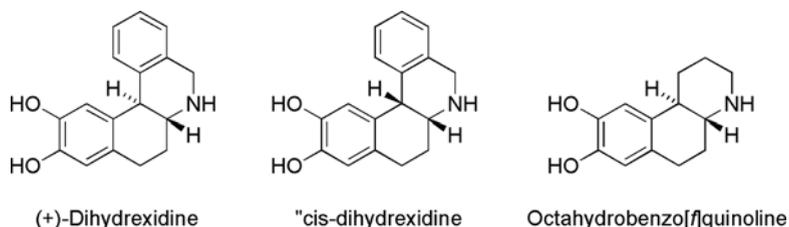


the ability of dopamine,  $\beta$ -methyldopamine, and  $\beta$ -phenyldopamine to activate the D<sub>1</sub> receptor in rat retina. Racemic  $\beta$ -methyldopamine had only one-twentieth the potency of dopamine in this assay, whereas  $\beta$ -phenyldopamine had one-half the potency of dopamine and was 10-fold more potent than  $\beta$ -methyldopamine. Clearly, the pendant  $\beta$ -phenyl ring dramatically enhanced potency, compared to the simple  $\beta$ -methyl, and suggested that this structural feature was a key determinant of D<sub>1</sub> activity in all of these molecules.

## 4.5 Benzo[*a*]phenanthridines

The demonstrated D<sub>1</sub> agonist activity of 4-(3',4'-dihydroxyphenyl)-tetrahydroisoquinoline (THIQ), coupled with the well-known dopaminergic activity of simple 2-aminotetralins, led us to tether the THIQ structure into a tetracyclic benzo[*a*]phenanthridine, dihydroxidine (DHX), the first high-potency, full-efficacy selective dopamine D<sub>1</sub> agonist [37, 38]. DHX had modest 10-fold selectivity for D<sub>1</sub> over D<sub>2</sub> receptors. The analogous benzo[*f*]isoquinoline, lacking the " $\beta$ -phenyl" moiety, lacked D<sub>1</sub> activity, demonstrating again that the interaction of the pendant phenyl moiety with some accessory binding region within the D<sub>1</sub> receptor was crucial for high activity. In this same report, the *cis*-fused compound (*cis*-DHX) also was examined and found to be inactive, demonstrating that full agonists should be relatively planar molecules (Fig. 4.4).

In a later study, the enantiomers of DHX were resolved, and the (+)-isomer, with the absolute stereochemistry shown, was the most active [39]. Thus, these studies all confirmed the requirement for a similar absolute stereochemistry at the chiral carbon that is the site of attachment of the appended " $\beta$ -phenyl" moiety in DHX, SKF38393, and 3',4'-dihydroxynomifensine.



**Fig. 4.4** The structure of dihydroxidine (DHX), its inactive *cis* isomer, and DHX with the appended phenyl ring removed, the inactive octahydrobenzo[*f*]quinoline

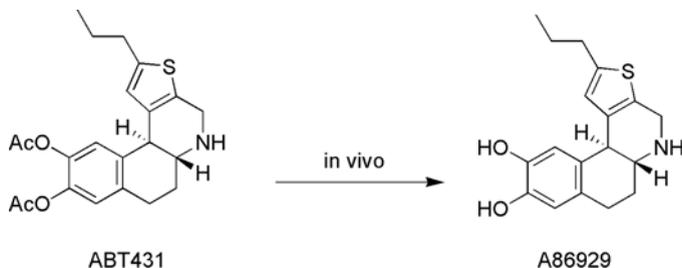
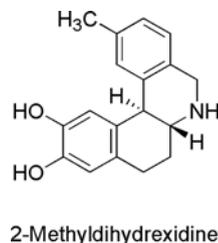
DHX produced a profound reduction of *N*-methyl-4-phenyl-1,2,5,6-tetrahydropyridine (MPTP)-induced parkinsonian symptoms in male African green monkeys [40]. In a small clinical trial, however, three of four human subjects experienced marked hypotension when the drug was rapidly administered intravenously [41]. This effect was likely the result of potent activation of renal D<sub>1</sub> receptors [42]. The fourth patient, with the highest measured blood plasma levels of DHX, displayed a significant improvement of Parkinson's disease (PD) symptoms. Not surprisingly, the D<sub>1</sub> antagonist SCH23390 blocked the behavioral effects of DHX in rodents, whereas the D<sub>2</sub> antagonist remoxipride did not [43]. In contrast to the failure of the partial D<sub>1</sub> agonist SKF38393 to show efficacy in PD, these proof-of-principle results in both humans and a nonhuman primate model of PD clearly demonstrated the need for a full D<sub>1</sub> agonist to achieve an optimal antiparkinsonian effect [44].

The presence of both catechol hydroxyl groups seems to be necessary for the high affinity of DHX; however, the *meta*-hydroxyl has been shown to be most important. Removal of the *para*-hydroxyl results in a more than a 20-fold loss in D<sub>1</sub> affinity, whereas the absence of the *meta*-hydroxyl resulted in a more than 200-fold loss of affinity [45]. Low-energy conformations of the *trans*-diastereomer (DHX) situate the conformationally restricted  $\beta$ -phenyl ring plane at an angle of approximately 56° above the plane of the catechol ring [46, 47].

Substitutions on the  $\beta$ -phenyl ring of DHX led to important structure–activity information for this series [48]. Most notably, substitution at the 2-position with a methyl group, as in 2-methyldihydroxidine (Fig. 4.5), led to a significant increase in D<sub>1</sub>:D<sub>2</sub> selectivity, resulting in a greater than 5-fold loss in D<sub>2</sub> affinity with no significant change in its D<sub>1</sub> affinity. Substitution with an ethyl group at this position also led to a highly D<sub>1</sub>-selective compound.

Although DHX passed through preclinical toxicology studies and was taken further into the drug development process, it so far has not been successfully commercialized, for at least two reasons. First and foremost, DHX is a catechol and has less than 5% oral bioavailability, which is considered to be too low to be suitable for an orally administered commercial drug. Second, DHX has a very short duration of action, something that also could be related to the rapid metabolic processes that cause the low oral availability.

**Fig. 4.5** The structure of 2-methyldihydroxidine, an analog with increased D<sub>1</sub>:D<sub>2</sub> selectivity



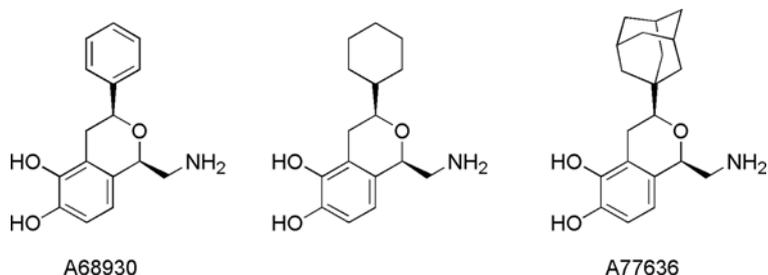
**Fig. 4.6** The structure of ABT-431, an *O,O*-diacetyl prodrug of the Abbott D<sub>1</sub> agonist A86929

A structurally related thiophene bioisostere of DHX developed by Abbott Laboratories, A-86929 (Fig. 4.6), had pharmacological properties almost identical to DHX [49–51]. Its *O,O*-diacetyl prodrug, ABT-431, was shown to have efficacy comparable to levodopa in a small trial in Parkinson patients [52, 53], but due to poor pharmacokinetic properties of this drug, further development was abandoned. ABT-431 also was reported to produce dose-related dyskinesias in patients who had already developed levodopa-related dyskinesias [53].

## 4.6 Abbott Isochromans

The compounds in this family, with examples shown in Fig. 4.7, were first synthesized by Abbott laboratories and are extremely potent and selective D<sub>1</sub> dopamine agonists with high intrinsic activity [54–57]. The postulated requirement for the *trans*- $\beta$ -phenyldopamine structure is not strictly fulfilled in this series; however, this work demonstrated that large nonaromatic hydrophobic substituents, such as the adamantyl (A77636) [58], may be substituted for the phenyl (A68930) [56, 59, 60]. Removing this bulky substituent results in a marked decrease in both D<sub>1</sub> and D<sub>2</sub> affinities. A large difference in affinities is observed in the isochromans with *cis* vs *trans* stereochemistry, with the latter being almost inactive. In the *cis* series, the potency resides mainly in the (+)-enantiomer, as shown in Fig. 4.7.

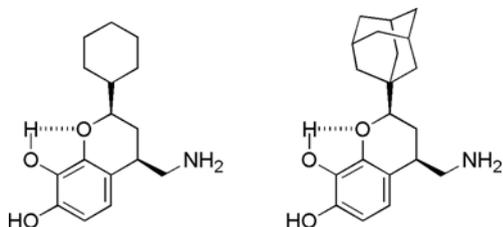
The phenyl-substituted isochroman A68930 (Fig. 4.7) has the highest D<sub>1</sub> binding affinity of the series (D<sub>1</sub>  $K_i$  = 3.1 nM, D<sub>2</sub>  $K_i$  = 776 nM), comparable to the affinity of the cyclohexyl derivative, which displayed somewhat higher selectivity



**Fig. 4.7** Abbott isochroman D<sub>1</sub> agonist ligands

(D<sub>1</sub>  $K_i = 5.4$  nM, D<sub>2</sub>  $K_i = 1,120$  nM). A prominent analog of the series was the adamantyl compound A77636 (D<sub>1</sub>  $K_i = 31.7$  nM, D<sub>2</sub>  $K_i = 1,290$  nM), making evident the tolerance of the D<sub>1</sub> accessory binding region for bulky hydrophobic groups. It can be recognized that the isochromans do contain an embedded  $\beta$ -substituted dopamine moiety, albeit the group attached to the “ $\beta$ -position” is not necessarily a phenyl group. As contrasted to the benzo[*a*]phenanthridines, however, this moiety, a phenyl or bulky hydrophobic group, also is displaced two atoms away from the  $\beta$ -side chain position, suggesting that the accessory binding site in the receptor has some flexibility or is larger than a single phenyl ring.

**Fig. 4.8** Chroman molecules with markedly reduced D<sub>1</sub> agonist activity



Although the oxygen atom in the isochromans is not essential for activity, moving the oxygen to give chromans (Fig. 4.8) led to a very dramatic loss of D<sub>1</sub> activity [61]. For example, the cyclohexyl and adamantyl congeners shown above had D<sub>1</sub> affinities of 500 and 2,500 nM, respectively, and were only 3- to 15-fold D<sub>1</sub> selective, whereas the corresponding isochromans in Fig. 4.3 had affinities of 2.4 and 3.5 nM, respectively, and were 400- to 540-fold D<sub>1</sub> selective [61]. Complete removal of the oxygen atom from the heterocyclic ring gives potent and highly selective D<sub>1</sub> agonists [62], suggesting that there is no requirement for the oxygen atom in the Abbott isochroman compounds.

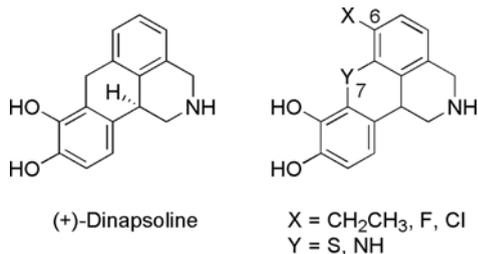
The most likely explanation for this finding would seem to be the formation of an intramolecular hydrogen bond between the chroman oxygen and the adjacent ring OH group that disrupts the hydrogen-bonding network that must form when the ligand binds to the receptor. This postulated hydrogen bond is illustrated in Fig. 4.8 as a dashed line. If this hypothesis is true, something we are now testing, it suggests

a specific hydrogen-bonding scheme for agonist ligands within the D<sub>1</sub> receptor that is probably not identical within the D<sub>2</sub> receptor.

## 4.7 Dinapsoline

A second tethering strategy that retained the  $\beta$ -phenyldopamine pharmacophore (and yielded a ligand geometry similar to DHX) led to another full D<sub>1</sub> agonist named dinapsoline (Fig. 4.9; DNS) that is as potent as DHX with respect to its D<sub>1</sub> pharmacology, although it is less D<sub>1</sub> vs D<sub>2</sub> selective [63, 64]. Interestingly, dinapsoline is a catechol, but has a much longer in vivo action than DHX [65], and was also found to have somewhat higher oral bioavailability. These observations suggest that certain molecular features can attenuate the undesirable physicochemical properties of a catechol with respect to oral bioavailability and plasma half-life. DNS was also shown to have marked and long-lasting effects in the 6-OH-DA rotating rat model, as well as efficacy in an MTPT-lesioned marmoset model of Parkinson's disease. In the MPTP-lesioned rat model of Parkinson's disease, it was shown that repeated daily dosing for 4 days with A77636 produced behavioral tolerance, whereas DNS administered once or twice daily failed to produce tolerance [65]. The authors suggested that the tolerance was likely related to the duration of D<sub>1</sub> receptor occupancy.

**Fig. 4.9** Dinapsoline and selected substituted analogs

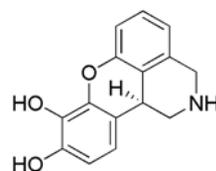


A series of substituted DNS derivatives was studied to develop preliminary structure–activity relationships [66]. Replacing the 7-methylene bridge (“Y”) with either nitrogen or sulfur (Fig. 4.9) greatly diminished D<sub>1</sub> activity and in general gave D<sub>2</sub>-selective compounds. Interestingly, the 6-ethyl-substituted compound (X = CH<sub>2</sub>CH<sub>3</sub>) had twice the D<sub>1</sub> affinity of DNS itself. The 6-fluoro-DNS analog had about one-half the affinity of DNS, but surprisingly was 10-fold selective for the D<sub>2</sub> receptor. When a chlorine was placed at the 6-position, the molecule had nearly 100-fold selectivity for the D<sub>2</sub> receptor. When considered in conjunction with the finding that 2-methyl-DHX had enhanced D<sub>1</sub> selectivity, these results suggest the presence of a region in the D<sub>1</sub> and D<sub>2</sub> receptors that may be exploited to alter D<sub>1</sub>:D<sub>2</sub> selectivity.

## 4.8 Dinoxylene

The oxygen bioisostere of dinapsoline, named dinoxylene (DNX) (Fig. 4.10), again was a full dopamine D<sub>1</sub> agonist, but in this case the ligand was not D<sub>1</sub> selective, and possessed high affinity at all five dopamine receptor isoforms [67, 68]. Nothing further has been reported on this ligand since its original discovery. It is somewhat puzzling, however, that DNX has high D<sub>1</sub> affinity and potency, whereas the chromans discussed earlier (Fig. 4.8) do not. The presence of the pendant phenyl ring must somehow compensate for changes in the hydrogen-bonding scheme when DNX binds. The two phenyl rings, through resonance overlap with the heterocyclic ring oxygen, also would be expected to reduce the electron density on the bridging oxygen, and this reduced density would decrease the strength of the intramolecular hydrogen bond. Thus, the serine residue(s) that normally hydrogen bond to the catechol “meta” OH group would not have to compete with the formation of an intramolecular hydrogen bond.

**Fig. 4.10** The structure of dinoxylene, an agonist that activates all five dopamine receptor isoforms

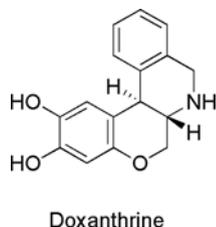


Dinoxylene

## 4.9 Doxanthrine

Most recently, an oxygen bioisostere of DHX was prepared named doxanthrine (DOX) (Fig. 4.11) [69]. The absolute configuration of the more active (+)-enantiomer of DOX had the anticipated stereochemistry, identical to DHX and DNS. In contrast to DHX, however, doxanthrine had much higher selectivity for the D<sub>1</sub> vs the D<sub>2</sub> receptor, making it perhaps one of the best of the newer D<sub>1</sub> “β-phenyldopamine”-type agonist ligands. In porcine striatal homogenates, the affinities at the D<sub>1</sub>-like and D<sub>2</sub>-like receptors for racemic DHX and DOX were 21 and 240 nM vs 22 and 3,700 nM, respectively, indicating a D<sub>1</sub>/D<sub>2</sub> selectivity of 168 for DOX vs only 11 for DHX. In cloned human D<sub>1</sub> receptors (+)-DOX had an EC<sub>50</sub> for enhancing cAMP accumulation of 29 nM, whereas the (–)-isomer was not a full agonist and had an EC<sub>50</sub> of 1,100 nM. Surprisingly, the (–)-isomer proved to be an α<sub>2C</sub>-adrenergic receptor agonist with potency at least comparable to clonidine (EC<sub>50</sub> 4.4 nM vs 17 nM for clonidine)! In the DOX series, however, and in contrast to both the DHX and DNS series, substituents on the pendant phenyl ring did not enhance D<sub>1</sub> selectivity, but in fact decreased D<sub>1</sub> activity significantly [70]. Additional studies are underway in the author’s laboratory to characterize this ligand further.

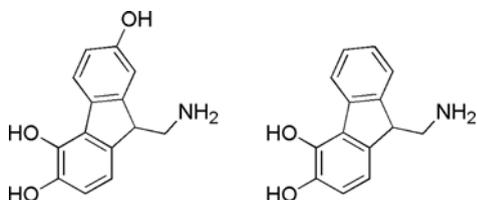
**Fig. 4.11** The structure of doxanthrine, a potent and selective dopamine D<sub>1</sub> agonist



## 4.10 Aminomethylfluorenes

In 1986, workers at Smith, Kline & French reported the synthesis of a series of phenethylamines that exploited the features of two known dopaminergic ligands, the biaryl ring system of apomorphine and the  $\beta$ -phenyldopamine skeleton of SKF38393 [71]. This fluorene series (Fig. 4.12) yielded two compounds active at D<sub>1</sub> receptors: aminomethylfluorentriol, which had modest affinity at D<sub>1</sub> receptors ( $K_i = 43$  nM), and the des-hydroxy analog aminomethylfluorenediol, which displayed 9-fold lower affinity ( $K_i = 380$  nM).

**Fig. 4.12** Aminomethyl fluorentriol (*left*) and aminomethyl fluorenediol



The D<sub>1</sub> affinities of these fluorene “ $\beta$ -phenyldopamine” analogs demonstrate that a fully coplanar  $\beta$ -phenyl ring can also lead to good receptor complementarity, at least with respect to affinity. Given the flexibility of the ethylamino side chain, however, the positioning of the ammonium moiety with respect to the coplanar  $\beta$ -substituent remains unknown [47].

## 4.11 Defining the D<sub>1</sub> Agonist Pharmacophore

Fundamentally, all full D<sub>1</sub> agonists discovered to date have a dopamine structure embedded within them, in a beta-rotameric orientation. For most of the known full D<sub>1</sub> receptor agonist molecules, the basic pharmacophoric structure can be envisioned as a  $\beta$ -substituted dopamine fragment. The pendant  $\beta$ -moiety is most typically a phenyl or aryl ring, but as evident from the Abbott isochromans, this

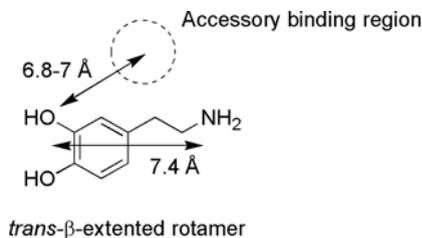
group can simply be a large hydrophobic moiety. The isochromans also illustrate that the location of the accessory binding region is not precisely fixed but has some variation with respect to the location of the appended hydrophobic moiety.

### 4.11.1 The Embedded Dopamine Fragment

The ethylamine side chain of dopamine is freely rotating and theoretically may adopt many different conformations in solution (or at the receptor). Cannon, in 1975, first designated the two possible *trans* conformational extremes of dopamine as “alpha” and “beta” [72]. Apomorphine incorporates an “alpha” rotamer, as do most D<sub>2</sub> agonist ligands, but all of the other full D<sub>1</sub> agonists contain a “beta” rotamer. Freeman et al. [35] originally developed a conceptual model that could account for the stereochemistries of 2-aminotetralines with either an alpha- or a beta-embedded side chain.

If we consider all of the foregoing discussion, we can envision the essential features of the D<sub>1</sub> agonist pharmacophore as shown in Fig. 4.13. Although the pendant phenyl ring in DHX and the phenyl ring in Abbott A68930 do not appear to reside in identical space, in fact the centroids of the pendant phenyl rings are located nearly the same distance from the key “meta” hydroxy, at a distance of 6.8–7 Å.

Fig. 4.13 The dopamine D<sub>1</sub> agonist pharmacophore



The dopamine fragment within the agonist should be in a *trans*-extended beta-rotameric form, with the distance between the meta hydroxy and the amino group being about 7.4 Å. In rigid analogs, it also has been suggested that the protonated electron pair on the nitrogen atom should be directed in a pseudoequatorial orientation [13]. Computational studies by Froimowitz were consistent with this hypothesis [73]. If all of these essential requirements are met, then the published evidence suggests that a molecule that contains these elements should have dopamine D<sub>1</sub> receptor agonist activity.

### 4.11.2 Design Limitations: The Catechol Moiety

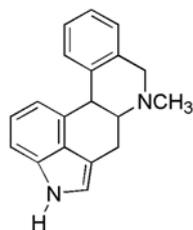
Probably the most important structural feature, and unfortunately the one that has limited the development of “druggable” selective dopamine D<sub>1</sub> agonists, is the requirement for a catechol function in the molecule. To date, no full dopamine D<sub>1</sub>

agonist has been discovered that does not possess a catechol moiety. All catechols do not have the same pharmacokinetic and metabolic properties; nevertheless, when drug companies consider the problems of developing a catechol-containing drug, they decline in favor of noncatechol alternatives. Despite modern formulation strategies and novel approaches to prodrug techniques, the historical failure to develop a catechol as a drug reinforces the notion that catechols are not good drug candidates.

Studies with monohydroxy analogs of apomorphine have shown the importance of the catechol moiety in binding at both D<sub>2</sub>- and D<sub>1</sub>-like receptors. Removal of the 10-hydroxy group, which yields 11-hydroxyapomorphine, increased D<sub>1</sub> affinity by about 10-fold [74]. By contrast, removal of the 11-hydroxy caused a marked loss of dopaminergic activity [75]. Similar observations in other series of dopaminergic compounds have established the predominant importance of the hydroxy that is “*meta*” to the ethylamine side chain fragment, whereas the “*para*”-hydroxy has a lesser contribution to binding but is necessary for full agonist activity. For example, replacing the *para*-hydroxy (10-OH) in DHX with a hydrogen results in antagonist or partial agonist properties, whereas replacement by a methoxy, halogen, or a methyl results in antagonistic properties. Removing the *meta* OH (11-OH) gave an inactive compound [45].

There is one example of a D<sub>1</sub>-selective compound that lacks a catechol: the ergoline CY208-243 developed by Sandoz (Fig. 4.14) [76]. It has been suggested that the pyrrole portion of the ergoline molecule can serve as a replacement for the catechol moiety [77], and that theory has been supported both by the synthesis of bicyclic and tricyclic partial ergolines that retain dopaminergic activity [78] and also by theoretical calculations showing similarities between the molecular electrostatic fields around simple models of apomorphine and ergolines [79].

**Fig. 4.14** The structure of the noncatechol ergoline partial D<sub>1</sub> agonist CY208-243



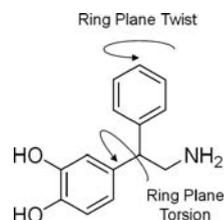
Like the benzo[*a*]phenanthridines, one can point to a  $\beta$ -phenyl moiety within CY208-243 as the basis for enhanced D<sub>1</sub> activity. Nonetheless, CY208-243, like SKF38393, failed to show efficacy in PD [80], and again that result is likely related to its partial agonist character at the D<sub>1</sub> receptor. It might be noted, however, that CY208-243 also has an *N*-methyl alkyl group, which is known in all other series of dopamine D<sub>1</sub> agonists to attenuate D<sub>1</sub> activity and enhance D<sub>2</sub> activity. Consistent with this reasoning, the reported intrinsic activity of CY208-243 for activating bovine retinal adenylate cyclase is only 57%, whereas the intrinsic activity of its *N*-des-methyl analog is reported as 82%, indicating that the latter compound is superior as a D<sub>1</sub> agonist. Unfortunately, no further results were reported

for the des-methyl analog of this compound, and it may well be that it could have therapeutic potential.

### 4.11.3 Relative Orientation of the Catechol and Pendant Phenyl Rings

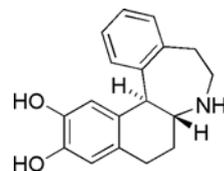
Although the presence of the  $\beta$ -substituent appears necessary for high affinity and potency in D<sub>1</sub> agonists, there are studies that demonstrate the need for a fairly specific spatial orientation of this ring, relative to the catechol ring. The two measures of this relationship can be envisioned as angles measured as ring-plane torsion and ring-plane twist, as shown in Fig. 4.15. In general, the ring-plane torsion should place the appended accessory ring in a plane at about an angle of 50–60° from the plane of the catechol ring [25]. DHX, dinapsoline, and doxanthrine are exemplary of this active conformation.

**Fig. 4.15** Angles that define the relative orientations of the aromatic rings in  $\beta$ -phenyldopamine-type D<sub>1</sub> agonists



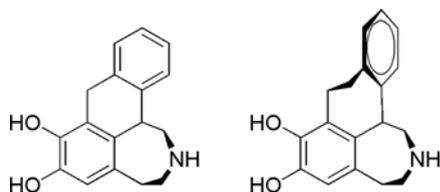
A study by Negash et al. [47] examined congeners where the C ring was expanded to seven atoms, and these molecules proved to be inactive. An example of this series is shown in Fig. 4.16. This molecule distorts not only the *trans*- $\beta$ -rotamer dopamine fragment but also the orientation of the appended  $\beta$ -phenyl moiety.

**Fig. 4.16** Inactive C-ring expanded dihydroxidine analog



Snyder et al. [27] used a methylene or an ethyl bridge to tether the pendant phenyl ring of SKF38393 to the catechol ring, molecules shown in Fig. 4.17. The methylene tether forces the  $\beta$ -phenyl moiety into a virtually coplanar orientation with respect to the catechol ring, but reduces the conformational mobility of the azepine ring. It had about 50-fold lower D<sub>1</sub> receptor affinity than SKF38393. Tethering the pendant phenyl ring with an ethyl bridge restores some conformational mobility to the azepine ring, but forces the  $\beta$ -phenyl moiety into an

**Fig. 4.17** Rigid dihydrexidine analogs with reduced D<sub>1</sub> binding affinity



orientation that is nearly orthogonal to the catechol ring. This analog had about 34-fold lower D<sub>1</sub> affinity than SKF38393, slightly better than the methyl-tethered compound.

These results are all consistent with the requirement that the  $\beta$ -phenyl moiety must reside in a *nearly* coplanar arrangement with the catechol ring and that the ethylamine side chain must be in an extended *trans*-beta-rotamer orientation. The full agonist properties of DHX, DNS, DNX, and DOX, compared to the partial agonist activity of SKF38393, also suggest that this conformation is important for full receptor activation, but is not a requirement for high D<sub>1</sub> affinity.

#### 4.11.4 Linking the Conceptual Model to the 3D Receptor Structure

Molecular modeling and mutagenesis studies of the D<sub>1</sub> receptor indicate that Asp 103 in TM3 is probably responsible for binding the protonated nitrogen of DA, whereas serines 198, 199, and 202 are involved in binding to the catechol hydroxyls [81, 82]. As noted earlier, the amino acid sequence of the D<sub>1</sub> and D<sub>5</sub> receptors in the orthosteric ligand binding domain is 100% identical.

The lack of an X-ray crystal structure for the D<sub>1</sub> receptor has compelled the use of analogies to other GPCRs as the best recourse for understanding the structural characteristics of the D<sub>1</sub> receptor binding site. The crystal structure of bovine rhodopsin, a GPCR distantly related to monoamine GPCRs, and more recently the  $\beta_2$ -adrenergic receptor [83], has enabled computationally derived hypotheses positing that the dopamine binding site is located between helices 3, 5, and 6, which traverse the cellular membrane.

In the  $\beta_2$ -adrenergic receptor, site-directed mutagenesis experiments have identified a key conserved residue, Asp 113, that has been proposed to be involved in an electrostatic interaction with the protonated amine of catecholamines [84, 85]. The cognate residue is conserved in all monoamine GPCRs and corresponds to Asp 103 in the D<sub>1</sub> receptor. Based on solid evidence using monohydroxy derivatives of DHX and serine-to-alanine mutants of these residues, as well as earlier experiments with the  $\beta_2$ -adrenergic receptor, Nichols, Mailman, and coworkers (unpublished results) have proposed that Ser 202 of the fifth transmembrane domain interacts via a hydrogen bond with the *para*-hydroxy and that Ser 198 and Ser 199 interact with the *meta*-hydroxyl of DHX. This information forms the basis for an examination of the 3D binding of agonists into the D<sub>1</sub> receptor.

Figure 4.18 is a sequence alignment for the D<sub>1</sub>, D<sub>5</sub>, and D<sub>2</sub> receptors. Residues in the D<sub>5</sub> receptor that are not identical to those in the D<sub>1</sub> receptor are shown in boldface type. The sequences of intracellular loop 3 (IL3), connecting the bottoms of helices 5 and 6, have been omitted for clarity. Sequence identity in the transmembrane regions is about 86%, but if the differences in TMs 1, 2, 4, and 8, which are too distant to affect agonist binding directly, are excluded, then the sequence identity in the transmembrane regions where the orthosteric agonist ligand binds is much higher, about 96%, and sequence similarity approaches 100%. It is apparent that the sequence similarity/identity in the orthosteric binding domain, principally in TMs 3, 5, 6, and 7, is so high that it will probably be impossible to design a molecule with D<sub>1</sub> vs D<sub>5</sub> selectivity that exploits this region of the receptor. The N-terminal portions of extracellular loop 2 (EL2), however, are sufficiently divergent that receptor-specific ligand design might be possible by differentially engaging residues in this loop. For example, there are several tryptophan residues in EL2 of the D<sub>5</sub> receptor that are absent in the D<sub>1</sub> sequence. Indeed, this portion of EL2 in the D<sub>1</sub> receptor contains no aromatic amino acids.

The 3D structure of the receptor, derived from homology models, can be reconciled with the earlier conceptual models, attesting to the insight provided by extensive experimental work over many years by numerous investigators. A number of the proposed features in the receptor can be identified, especially the catechol binding residues and the amine binding site. Figure 4.19 presents a conceptual “cartoon” model that incorporates all of the elements known to be factors in the structure–activity relationships of D<sub>1</sub> agonists.

Figure 4.20 presents a parallel illustration, but with virtual docking of doxantrine into a homology model of the D<sub>1</sub> receptor based on the crystal structure of the β<sub>2</sub>-adrenergic receptor. This figure illustrates the residues that account for the functional properties of the receptor and reflects the elements of the conceptual model that were used to drive the design of new D<sub>1</sub> ligands. In particular, serine residues 198 and 199 appear to be involved in hydrogen-bonding interactions with the more critical “meta” hydroxy group of the catechol moiety, and serine 202 appears to engage the “para”-hydroxy.

Aspartate 103<sup>(3.32)</sup> forms a salt bridge with the amino group of the ligand, a feature common to all monoamine G-protein-coupled receptors (GPCRs). In the virtual docking studies, Asp 103 approaches the protonated amine from an equatorial direction, an idea that first originated with the recognition that *N*-alkylation was detrimental to D<sub>1</sub> receptor activation, as the lower energy of an equatorial *N*-alkyl [73] would force the protonated electron pair into a pseudoaxial orientation and disfavor the equatorial approach of Asp 103.

Phenylalanine residues 288<sup>(6.51)</sup> and 289<sup>(6.52)</sup> are thought to interact with the aromatic ring of the agonist ligand, with F6.52 believed to be the most important. These residues form pi stacking complexes with the aromatic ring of the agonist ligand. The region of “steric occlusion” below the ligand is less well defined, but probably consists of a sterically crowded area with contributions from a variety of residues, including Phe203 in helix 5. Overall, viewed from the extracellular side, the orthosteric agonist binding site is a relatively narrow groove or slot in the protein, stretching somewhat linearly between helices 3 and 5.

```

D1 .....FVRIITACFLSLLIISTLLGNLTVCAAVIR.FRHLSK VTNFVVI SLAVSDLLVAVLMPWKAVAE
D5      SOWWTACLITLLIIITLLGNVLVCAAVR SRHLRAM MTNWFIVSLAVSDFVALLVMPWKAVAE
D2      ....RPHNYXATLLTLLIAIVFVGNLVCMASVR.EKALQF..TNYLIIVSLAVADLLVATLMPWVWVYLE
          1.50          2.40 2.45 2.50      2.58
=====|=====|=====|=====|=====|
          TM1
=====|=====|=====|=====|=====|
          TM2

D1 FCNIWVAFDMCSTASILNLCVIVSDRYMAIS.SPFRYERKM.TPKAAFIILISVAMTLSVLISFIPVQLSW
D5 FCDVWVAFDMCSTASILNLCVIVSDRYMAIS RPFYKRRM TQRMALVNVGLAMTLSLISFIPVQLNW
D2 HCDIFVTLDMCTASILNLCVAISDRYTAVA.MEMLYNTRYSSRRVTVMI SIVMVLSTFTSCPLLFGL.
          3.32 3.42 3.50          4.50
=====|=====|=====|=====|=====|
          TM3          TM4          TM5

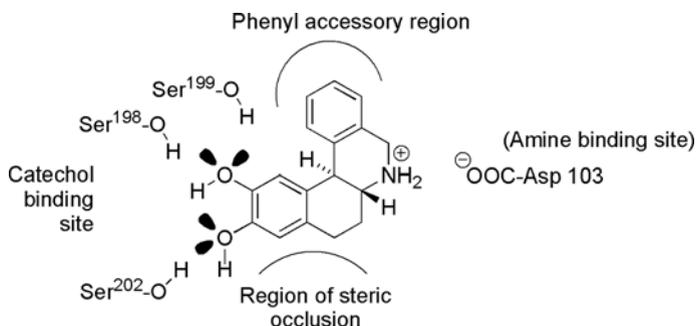
D1 HKAKFTSPDGNATSLAETIDNCDSSLSRT.....YAISSVVSFYIPVAIMIVTTRYI
D5 HRDQAAASWGLDLPNNLANWTFWEEDFWEPDVNAENCDSSLNRT YAISSLSISFYIPVAIMIVTTRYI
D2 .....NNADQNECIIANPA.....FVVYSSIVSFYVFFIVTLLVYIKIY
          5.43 5.50 5.58
=====|=====|=====|=====|=====|
          TM6          TM7

D1 MMSFKRETRVLTLSVIMGVFVCCWLPFFFLNCLILPF CGSGETQ PFCID.SNTDFVFMFGWANSLSNFIYAF
D5 RASIKKETRVLTLSVIMGVFVCCWLPFFFLNCLMVFF CGHPGPPAGPCVS ETTFDFVFMFGWANSLSNFIYAF
D2 KEKRAQMLAIVLGVFIIICWLPFFFTHILNIH CDCNIP.....PVIYSAFTMGLGYVNSAVNFIYTTTF
          6.30 6.44 6.50          7.40 7.45 7.50
=====|=====|=====|=====|=====|
          TM8          TM9

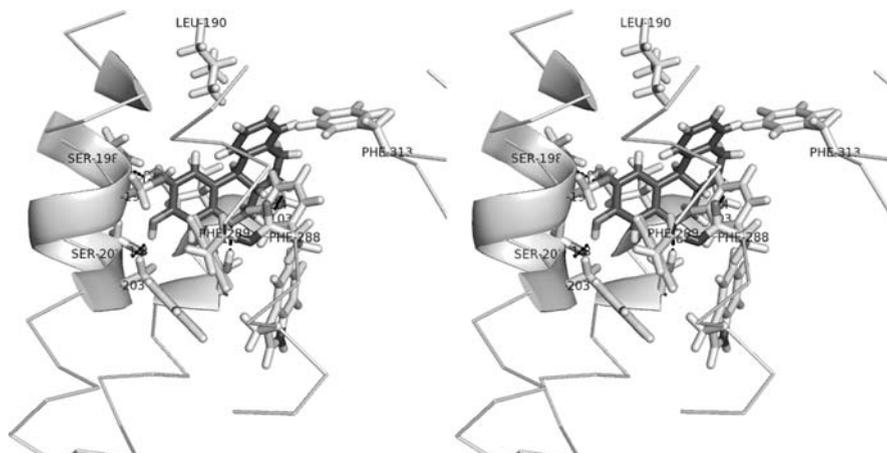
D1 NADFRKAFSTLLGCYRLCEATNNAIETVSIINNNGAAMFS.....
D5 NADFQVFAQLLGCSEHFCSTRP VETVNIENE LISYNQDIYFHKELAAAYTHMENAATVPGNREVDNDEEGGFF
          DRMFQIYQTSFDGDPVAESSWELDCGEIISLDKITPFTENGFF
D2 NIEFRKAFLLKILHC.....
          =====
          TM10

```

Fig. 4.18 Sequence alignments of the D<sub>1</sub>, D<sub>5</sub>, and D<sub>2</sub> receptors



**Fig. 4.19** Conceptual model of the D<sub>1</sub> agonist binding site



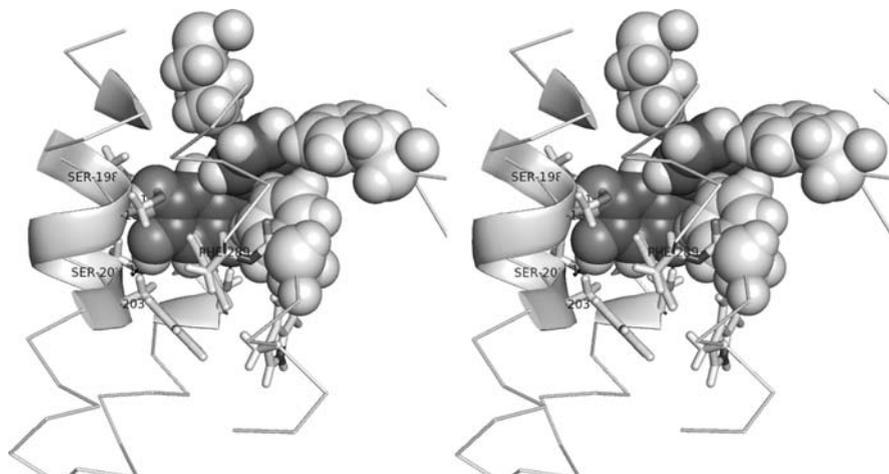
**Fig. 4.20** Sterepair view (cross eyed) of doxanthrine (*dark* central molecule) docked into a homology model of the D<sub>1</sub> receptor. The view is with TM3 in the foreground and TM5 in the right rear. The ligand is in approximately the same orientation as in the conceptual model shown in Fig. 4.19

A structural feature that has not previously been explored is the role of Ser 107<sup>(3,36)</sup>, which is one turn below the essential D103. Our finding that doxanthrine had higher selectivity for D<sub>1</sub> vs D<sub>2</sub> receptors was initially difficult to explain. After we had carried out virtual docking studies, however, it was evident that Ser 107 could probably hydrogen bond to the heterocyclic oxygen atom in doxanthrine. Yet, the D<sub>1</sub> affinity of doxanthrine was essentially identical to that of its carbon analog, dihydrexidine; it is the loss of affinity of doxanthrine at the D<sub>2</sub> receptor that gives doxanthrine its higher D<sub>1</sub> receptor selectivity. We ultimately realized that the

heterocyclic oxygen atom in the chroman ring of doxanthrine would be solvated in aqueous solution. Binding in the receptor would involve desolvation of that oxygen atom and a corresponding energy penalty as a result. For doxanthrine, this energy cost could be compensated for by the hydrogen bond with Ser 107, but no similar gain could be realized when DHX bound because it has a carbon atom adjacent to Ser 107. In the D<sub>2</sub> receptor the cognate residue is a cysteine, with much weaker hydrogen bonding potential, as well as a larger van der Waals radius. Thus, we had stumbled onto a very interesting indirect way to enhance D<sub>1</sub> selectivity that was not originally anticipated.

This difference at residue 3.36, a serine in the D<sub>1</sub> receptor, and a cysteine in the D<sub>2</sub> receptor, also could account for the loss of D<sub>1</sub> selectivity in dinapsoline, compared to DHX. Whereas dihydroxidine has an ethyl bridge in this region that will experience greater steric interference with the larger cysteine than with a serine, dinapsoline has no molecular component in this region, and thus the presence of the cysteine in the D<sub>2</sub> receptor does not create the same extent of steric impediment to binding for DNS.

As elaborated earlier at some length, one of the most important features of the D<sub>1</sub> receptor is its “β-phenyl accessory region” or accessory ring binding site. Unfortunately, the identity of this region has not yet been established. As discussed earlier, it clearly plays a very important role in conferring high D<sub>1</sub> affinity and, in catechols, full agonist activity. Virtual docking of doxanthrine into a homology model of the D<sub>1</sub> receptor does suggest some possible players, however. Phe288<sup>(6.51)</sup> is one obvious choice, except that it appears more important for antagonist binding in other GPCRs where it has been examined. A critical consideration, however, is the fact that the D<sub>2</sub> receptor has identical phenylalanine residues at these positions, so it is very difficult to conclude that Phe288 is a key part of the accessory binding region. By contrast, Phe313 in TM7 is particularly attractive as part of the accessory region because the corresponding residue in the D<sub>2</sub> receptor is a tyrosine. If this residue comprises part of the accessory binding region, it seems possible that there could be two explanations for its effect on D<sub>1</sub> vs D<sub>2</sub> selectivity. First, the para-OH of the tyrosine residue could project toward the pendant phenyl ring of ligands such as DHX or DOX. That would prevent an edge-to-face type of pi stacking interaction suggested by the virtual docking presented in Fig. 4.21. A second possible explanation is that the tyrosine in the D<sub>2</sub> receptor engages a residue in helix 2 or 3, pulling it away from an interaction with the agonist ligand. At the present time the importance of this residue remains unknown, and there are no mutagenesis studies to suggest its role in the dopamine D<sub>1</sub> receptor. It addition, it appears likely that a residue in extracellular loop 2 (EL2) may be a component of the accessory binding region, possibly serving as one of the pieces of “bread,” with the ligand accessory ring being the “meat” of a sandwich. One possibility for this role is Leu190. One study has been published where it was reported that mutation of four residues in EL2 (DSSL) containing this amino acid led to a mutant receptor with a significant 25-fold loss of affinity for SCH23390 [86]. No data were reported for binding of an agonist ligand and there is no report of a receptor with the single mutation of L190.



**Fig. 4.21** Doxanthrine docked into a homology model of the D<sub>1</sub> receptor, in the same orientation as shown in Fig. 4.20, but with the ligand and key residues shown as space-filled representations to illustrate the potential accessory binding region

## 4.12 The Future

We clearly know quite a bit about the structure–activity relationships of dopamine D<sub>1</sub> full agonists and about functional topography of the receptor. The D<sub>1</sub> receptor remains of very high importance, as it has been identified as a target for a number of potential disease states, the most important ones at the present time being Parkinson’s disease and memory and cognition enhancement, especially in schizophrenia. It seems quite likely that a “druggable” full D<sub>1</sub> agonist would be a commercially successful therapeutic agent. What chiefly prevents that from happening at the present time is the generally low oral bioavailability of catechol-containing drugs, which includes all of the present generation D<sub>1</sub> agonists. The fact that CY208-243 is not a catechol suggests that novel agonists may be discovered that are not limited by the problems associated with a catechol moiety. Nonetheless, the absence of a successful dopamine D<sub>1</sub> agonist clinical candidate also seems to have prevented major pharmaceutical companies from addressing the challenge of discovering a bioavailable full D<sub>1</sub> agonist that can be brought to market. One must have some hope that this situation will change before long, as there is every reason to believe that a D<sub>1</sub> full agonist should have a variety of very useful therapeutic indications.

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# Chapter 5

## Dopamine Receptor Subtype-Selective Drugs: D2-Like Receptors

Olaf Prante, Miriam Dörfler, and Peter Gmeiner

**Abstract** Drugs that are known to activate or block dopamine receptors are widely used for the treatment of a number of severe diseases. In most cases, dopaminergic drugs preferentially interact with the subtypes of the D2 family (D<sub>2</sub>, D<sub>3</sub>, D<sub>4</sub>). However, only minor selectivity has been observed between D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub>. Nevertheless, in recent years D<sub>3</sub> and D<sub>4</sub> subtype-selective agonists, partial agonists, and antagonist have been developed. The most interesting structural features required for high selectivity and affinity are presented as well as structure–activity relationship (SAR) studies. Moreover, the use of subtype-selective radioligands is discussed.

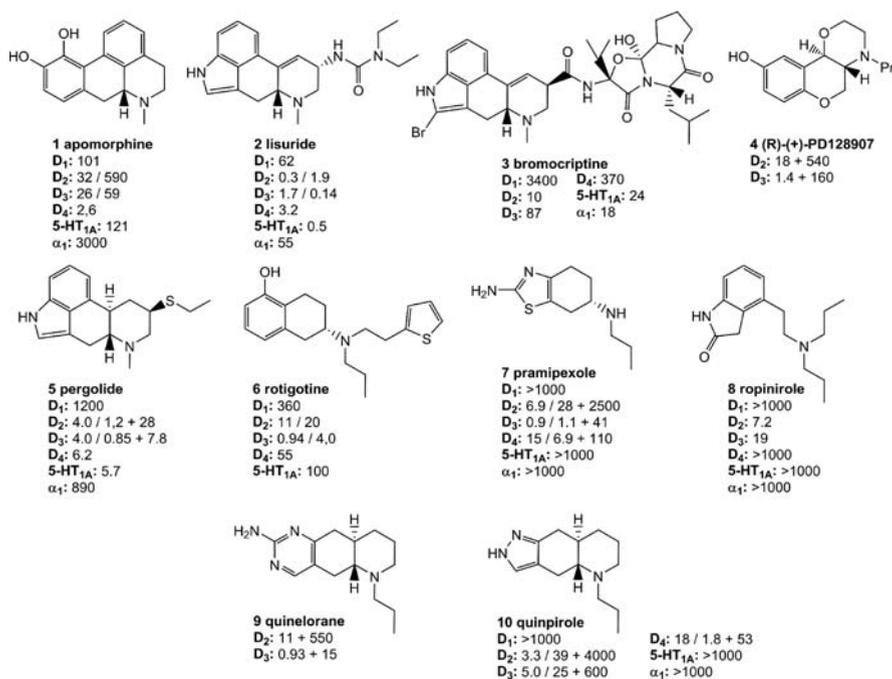
**Keywords** D2-like receptors · subtype selectivity · aminotetralins · phenylpiperazines · radioligands · D<sub>3</sub>-receptors · D<sub>4</sub>-receptors

### 5.1 Drugs on the Market and Classical Pharmacological Tools

Drugs that are known to activate or block D2-like dopamine receptors are widely used for the treatment of a number of severe diseases. Thus, dopamine receptor agonists (Fig. 5.1) such as apomorphine **1**, the ergoline derivatives lisuride **2**, bromocriptine **3**, and pergolide **5** as well as the bicyclic dopamine bioisosteres rotigotine **6**, pramipexole **7**, and ropinirole **8** are important for the treatment of Parkinson's disease and dyskinesia. Bromocriptine **3** is also employed as a prolactin inhibitor, whereas apomorphine **1** has emetic effects and has been described for the treatment of erectile dysfunction [1]. Pramipexole **7** is also approved for the treatment of restless legs syndrome [2]. Quinelorane **9**, quinpirole **10**, and PD128907 **4** are accepted as valuable pharmacological tools for the characterization of responses mediated by D2-like receptors.

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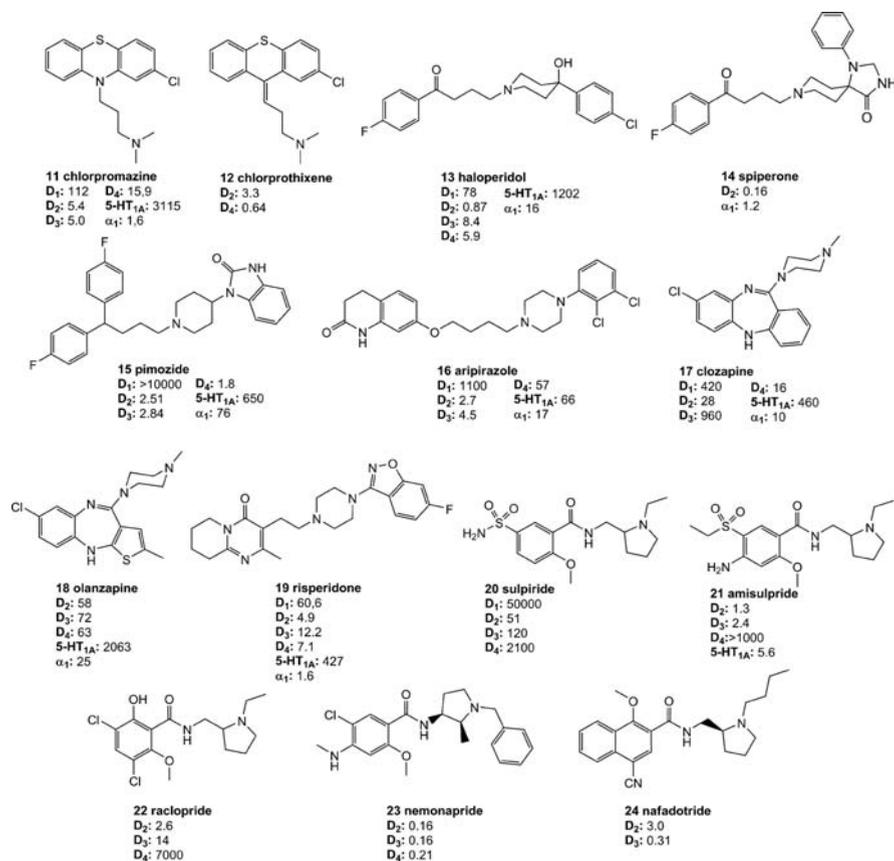
P. Gmeiner (✉)  
Department of Chemistry and Pharmacy, Friedrich-Alexander University,  
Schuhstr. 19; 91052 Erlangen, Germany  
e-mail: peter.gmeiner@medchem.uni-erlangen.de



**Fig. 5.1** Dopamine receptor agonists,  $K_i$  values in nM ( $K_{i\text{ high}}$  +  $K_{i\text{ low}}$ )

Dopamine receptor antagonists (Fig. 5.2) are used for the treatment of schizophrenia and anxiety. The pharmacological agents in clinical use are divided into classical and atypical antipsychotics [3]. The classical family of antipsychotics consists of the structural class of phenothiazines (such as chlorpromazine **11**), thioxanthenes (such as chlorprothixene **12**), butyrophenones (such as haloperidol **13**), and diphenylbutyl piperidines (such as pimozide **15**). These drugs are able to reduce the positive symptoms of schizophrenia [3]. In contrast to classical antipsychotics displaying extrapyramidal side effects [3], atypical derivatives are less likely to produce these side effects and address not only positive but also negative symptoms [3]. Major representatives for atypical antipsychotics are clozapine **17** and olanzapine **18**, binding not only dopamine  $D_4$ - and  $D_2$ -receptors but also serotonergic  $5\text{-HT}_2$ - and muscarinic receptors as well as the adrenergic  $\alpha_1$ - and the histamine  $H_1$ -receptors [3]. Risperidone **19** additionally displays a mixed binding profile [3]. Aripiprazole **16** is described as a system stabilizer for dopaminergic and serotonergic systems [4], exerting agonist effects at the presynaptic and antagonist effects at the postsynaptic dopamine  $D_2$ -receptors [5, 6]. Prominent examples of the family of methoxybenzamides are sulpiride **20**, amisulpride **21**, raclopride **22**, nemonapride **23**, nafadotride **24** which are used as antipsychotic drugs and valuable pharmacological tools. Tritiated spiperone **14** is well established as a standard radioligand for binding assays.

Figure 5.1 and Fig. 5.2 clearly indicate that the established dopamine receptor agonists and antagonists are relatively unselective and, in many cases, recognize not



**Fig. 5.2** Dopamine receptor antagonists,  $K_i$  values in nM

only the various subtypes of the dopamine receptor but also related biogenic amine receptors such as serotonergic or adrenergic receptors [1]. Nonselective dopaminergic drugs may possess therapeutic advantages in some cases, provided that effects synergistic to the dopaminergic response enhance the antipsychotic efficacy [7, 8]. To improve the pharmacological profiles of dopamine receptor-targeting drugs, selective dopamine receptor ligands have been developed in recent years. These efforts have been especially concentrated on the D<sub>3</sub>- and the D<sub>4</sub>-subtypes, since the D<sub>2</sub>-subtype is associated with side effects, such as extrapyramidal dysfunction [9].

## 5.2 D<sub>3</sub>-Selective Ligands

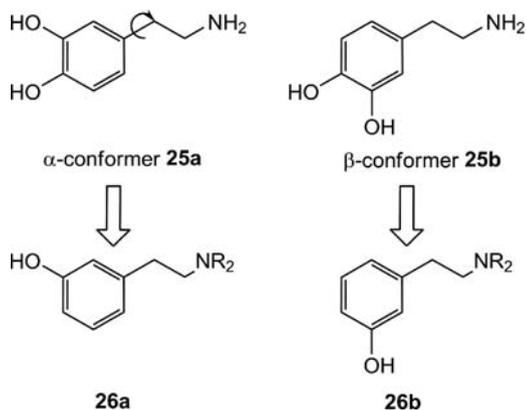
The design of D<sub>3</sub>-receptor ligands with high selectivity over the related subtypes D<sub>2</sub> and D<sub>4</sub> proved to be difficult, since the binding site crevices of these subtypes are very similar [10, 11]. Nevertheless, medicinal chemists succeeded in developing even highly selective agonists and antagonists which are summarized below.

## 5.2.1 Aminotetralins and Analogs

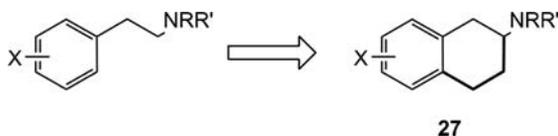
### 5.2.1.1 Aminotetralins

The neurotransmitter dopamine is able to adopt both the  $\alpha$ - and  $\beta$ -conformation according to Cannon (Fig. 5.3) [12]. Structure–activity relationship studies showed that only the *meta*-hydroxy function of the catechol system is necessary for dopaminergic activity and *N*-alkyl substituents, especially *n*-propyl groups, increase binding affinity. Formal conformational rigidization of the ethylene chain led to the structural family of aminotetralins **27** (Fig. 5.4).

**Fig. 5.3** Dopamine conformers



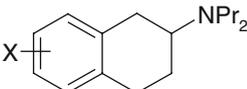
**Fig. 5.4** Design of aminotetralins



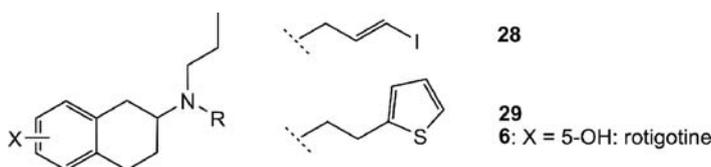
Two alternatives of bridging the dopamine structure are possible resulting in formation of the 5,6- and the 6,7-dihydroxy derivatives which represent the  $\beta$ - and  $\alpha$ -conformer of dopamine, respectively. Interestingly, the 5,6-dihydroxy derivative shows significantly higher dopaminergic potency [13, 14]. Among the monohydroxylated dipropylaminotetralins (DPATs), the 7-hydroxy substituted derivative (7-OH-DPAT; **27b**) displays the highest  $D_3$ -selectivity [15], when the (*R*)-(+)-enantiomer turned out to be significantly more active [16]. On the other hand, the (*S*)-isomer of 5-OH-DPAT **27a** reveals higher potency and a mixed  $D_2/D_3$ -affinity profile (Table 5.1) [16]. Karlsson et al. described substantial  $D_2$ -agonist activity for the (*S*)-enantiomer and weak  $D_2$ -antagonist properties for the (*R*)-enantiomer [17]. Interestingly, the unsubstituted DPAT also exhibits configuration-specific affinity profiles for receptors of the  $D_2$ -family and the 5-HT<sub>1A</sub>-receptor [18].

SAR data investigating the effect of the nitrogen substitution pattern indicated that one of the two substituents is represented in the best way by a propyl substituent, consistent with receptor modeling studies identifying a propyl cleft as an important

**Table 5.1** Binding affinities of 5-OH- and 7-OH-DPAT;  $K_i$  Values in nM

|  |              |                 |                |                                |
|---|--------------|-----------------|----------------|--------------------------------|
|   | X            | D <sub>2L</sub> | D <sub>3</sub> | D <sub>2</sub> /D <sub>3</sub> |
| (S)- <b>27a</b>   | (S)-(-)-5-OH | 6               | 0.54           | 11                             |
| (R)- <b>27b</b>   | (R)-(+)-7-OH | 56              | 0.57           | 98                             |

part of the binding pocket [15]. Structural variation of the second nitrogen substituent led to the attachment of terminal  $\pi$ -systems as realized within compounds **28** [19, 20] and **29** [21] (Fig. 5.5). 7-OH-PIPAT (**28**) is a D<sub>3</sub>-selective analog of 7-OH-DPAT, whereas 5-OH-PIPAT shows higher D<sub>3</sub>-affinity but significantly lower selectivity over D<sub>2</sub> [19, 20]. The binding profile of another prominent aminotetralin, rotigotine **6**, is very similar to that of dopamine with respect to D<sub>1</sub>, D<sub>2</sub>, and D<sub>3</sub> (Fig. 5.1) [21, 22].

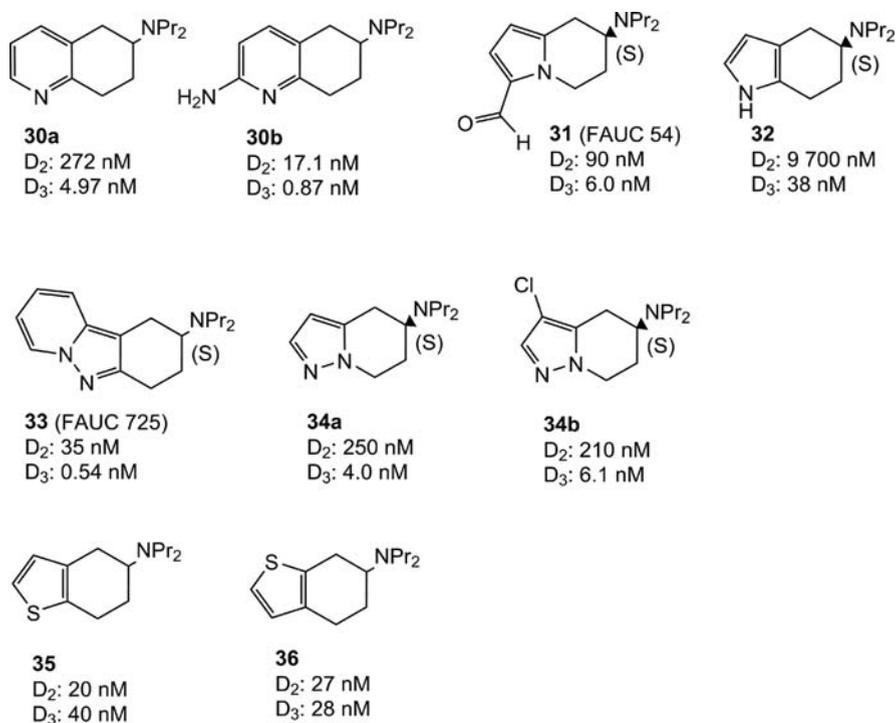
**Fig. 5.5** Side chain variations in aminotetralins

### 5.2.1.2 DPAT Bioisosteres

Since the aromatic hydroxyl function of OH-DPAT analogs is rapidly inactivated by conjugation with glucuronic acid and elimination via the kidney, the oral bioavailability of OH-DPATs is low and the duration of maximum efficacy is short [23]. To attenuate rapid metabolism an effective bioisosteric replacement has been performed [23].

#### Heterocyclic Bioisosteres

A bioisosteric replacement of the hydroxyphenyl substructure by substituted and unsubstituted 6- and 5-membered heteroarenes was investigated and resulted in compounds with different affinity and selectivity patterns (Fig. 5.1; Fig. 5.6). Thus, quinelorane **9** and quinpirole **10** (Fig. 5.1) display substantial D<sub>3</sub>-selectivity over D<sub>2</sub> [9, 24–29]. Pramipexole **7** (Fig. 5.1) behaves as a D<sub>2</sub>-, D<sub>3</sub>-, and D<sub>4</sub>-receptor agonist preferentially recognizing D<sub>3</sub> [26, 29–31]. Pramipexole **7** is also described as a selective or preferential autoreceptor agonist [32]. Interestingly, replacement of the secondary amine structure by primary amine leads to a loss of activity [33]. The pyridine analogs **30a** and **30b** are known for their significant D<sub>3</sub>-selectivity and autoreceptor agonist properties [23]. The dopaminergic agents FAUC 54 **31**



**Fig. 5.6** Binding affinities of several bioisosteric DPATs,  $K_i$  values in nM ( $K_{i\text{ high}}$  for **31**, **33**, **34a**, **34b**)

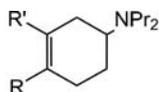
[34], FAUC 725 **33** [35], and **34a** [36] show single-digit nanomolar and subnanomolar  $D_3$ -affinities and substantial agonist effects in mitogenesis experiments. On the other hand, the ligands **32** [37] and **34b** [36] turned out to be partial agonists when compared with the full agonist quinpirole.

The tetrahydrobenzothiophene derivatives **35** and **36** are described as agonists displaying an improved bioavailability in comparison with 5-OH-DPAT **27a** [38, 39].

### Non-aromatic Bioisosteres

Until very recently, an aromatic partial structure representing the catechol function of dopamine was regarded as crucial for the pharmacophore described by the McDermid model [13]. Very recently, it has been demonstrated that such a  $\pi$ -system can also be provided by non-aromatic analogs. Chemical syntheses, pharmacological investigations, and computational studies lead to enynes, dienes, and endiynes of type **37** that display high affinity to dopamine receptors of the  $D_2$ -like family (Fig. 5.7) [40–43].

In detail, the terminal enynes FAUC 73 (**37a**) and FAUC 88 (**37b**) reveal higher affinity than the trimethylsilyl substituted analogs [42]. The ethenyl analog FAUC



|                                  |                                |                                 |
|----------------------------------|--------------------------------|---------------------------------|
| <b>37a</b> (FAUC 73)             | <b>37b</b> (FAUC 88)           | <b>37c</b> (FAUC 206)           |
| R = acetylene, R' = H            | R = R' = acetylene             | R = ethylene, R' = H            |
| D <sub>2</sub> : 250 + 12 000 nM | D <sub>2</sub> : 54 + 2 600 nM | D <sub>2</sub> : 99 + 6 400 nM  |
| D <sub>3</sub> : 5.2 + 590 nM    | D <sub>3</sub> : 3.2 + 49 nM   | D <sub>3</sub> : 5.6 + 430 nM   |
| D <sub>4</sub> : 22 + 380 nM     | D <sub>4</sub> : 6.3 + 420 nM  | D <sub>4</sub> : 260 + 3 100 nM |

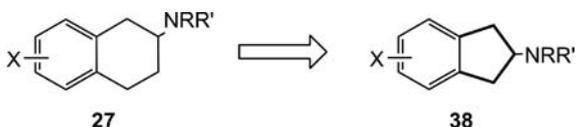
**Fig. 5.7** Binding affinities of several enynes,  $K_i$  values in nM ( $K_{i\text{ high}} + K_{i\text{ low}}$ )

206 (**37c**) shows a similar binding profile as FAUC 73 (**37a**) with an improved selectivity over the D<sub>4</sub> subtype [41]. Functional investigations were performed for FAUC 73 (**37a**) and FAUC 88 (**37b**) displaying substantial intrinsic activity [42].

## 5.2.2 Aminoindans

Formal restriction of the aminotetralin six-membered ring to a five-membered ring leads to the structural family of aminoindans **38** (Fig. 5.8). As described for the aminotetralins the substitution pattern at the aromatic substructure and the amino substituents play an essential role for the dopaminergic activity. Thus, the 4-hydroxy substituted dipropyl aminoindan **38b** displays combined D<sub>2</sub>- and 5-HT<sub>1A</sub>-affinity, reflecting the analogy both to the dopaminergic active 5-OH-DPAT and to the selective 5-HT<sub>1A</sub>-ligand 8-OH-DPAT (Table 5.2). On the other hand, the 5-hydroxy isomer **38a** displays an approximately threefold selectivity for D<sub>3</sub>-receptors [44]. Interestingly, introduction of methoxy substituents leading to the bioactive agent U 99194 (**38c**) results in an improved D<sub>3</sub>-selectivity but, on the other hand, a complete loss of intrinsic activity [44, 45].

**Fig. 5.8** Design of aminoindans

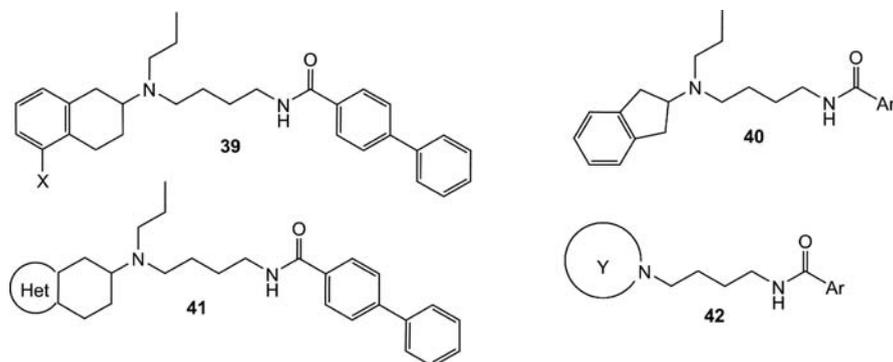


**Table 5.2** Binding affinities of several DPAIs,  $K_i$  Values in nM

|            | X          | D <sub>2</sub> | D <sub>3</sub> | D <sub>2</sub> /D <sub>3</sub> |
|------------|------------|----------------|----------------|--------------------------------|
| <b>38a</b> | 5-OH       | 53             | 14             | 3.7                            |
| <b>38b</b> | 4-OH       | 5.2            | 42             | 0.12                           |
| <b>38c</b> | 5,6-di-OMe | 992            | 31             | 32                             |

### 5.2.3 Arylcarboxamidobutyl Substituted Aminotetralins and Analogs Thereof

The exchange of an *n*-propyl side chain of the family of DPATs by an *N*-butyl-4-biphenylamido moiety results in an improvement of D<sub>3</sub>-affinity and selectivity [46]. Depending on the residue X within structure **39** (Fig. 5.9), the compounds behave as agonists or antagonists [46].



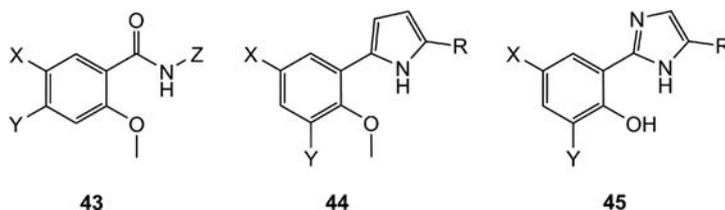
**Fig. 5.9** Binding affinities of several amides with butylene linkers, K<sub>i</sub> values in nM

As described for DPATs, heterocyclic bisoesters are also known for the amide analogs. The compounds with the general structure **41** show high D<sub>3</sub>-affinity and selectivity (Fig. 5.9) [47].

Also for this class of compounds the replacement of the aminotetralin substructure by aminoindan (**40**) proved to be a successful replacement [48]. Since compounds of type **39** can be metabolized *in vivo* by depropylation, the amino function was integrated into a ring system leading to compounds of the general structure **42** [48–51]. Besides dopamine receptor ligands with flexible linker chains, conformationally rigidized ethyl-*trans*-cyclohexyl derivatives have been described (**L6**, Fig. 5.13) [52–55].

#### 5.2.3.1 2-Methoxybenzamides and Analogs Thereof

Based on the classical representatives sulpiride **20**, amisulpride **21**, and raclopride **22** (Fig. 5.2), variations of the substituents Y and Z (Fig. 5.10) lead to an improvement of D<sub>3</sub>-selectivity. Besides this, the phenyl ring was replaced by a naphthyl system resulting in an increased D<sub>3</sub>-selectivity over D<sub>2</sub> and both  $\sigma$ -receptor subtypes [56, 57]. Bioisosteric replacement of the amide structure by certain 5-membered heteroarenes was exploited to increase D<sub>3</sub>-affinity and selectivity. Besides pyrroles **44** and imidazoles **45** as amide bioisosteres (Fig. 5.10) further 5-membered heterocycles such as oxazoles and oxadiazoles were investigated [58–61].

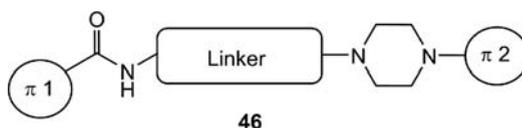


**Fig. 5.10** Benzamides and bioisosteres

### 5.2.4 Phenylpiperazines

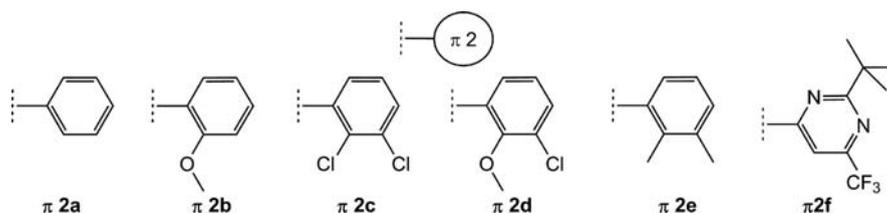
Dopamine receptor ligands of the class of phenylpiperazines contain an aryl carboxamide which is connected via a linker to a 4-aryl substituted piperazine unit (Fig. 5.11).

**Fig. 5.11** General formula of phenylpiperazines



#### 5.2.4.1 Variations at $\pi 2$

The aromatic residue  $\pi 2$  as a part of the structure **46** is usually represented by a substituted phenyl ring (Fig. 5.12). D<sub>3</sub>-selectivity is increased when the substituent is shifted from the *para*- to the *meta*- to the *ortho*-position [62]. Very frequently, 2-methoxy- and 2,3-dichlorophenylpiperazines ( $\pi 2b$  and  $\pi 2c$ ) are used when the latter usually results in higher D<sub>3</sub>-affinity compared to  $\pi 2a$  [63] or methoxy-substituted derivatives of type  $\pi 2b$  [64, 65]. Structural hybrids with 2-methoxy- and 3-chloro-substitution of type  $\pi 2d$  show binding properties ranging between  $\pi 2b$  and  $\pi 2c$  [66, 67]. Furthermore, 2,3-dimethyl substituted compounds of type  $\pi 2e$  with high D<sub>3</sub>-selectivity over D<sub>2</sub>, D<sub>4</sub>, 5-HT<sub>1A</sub> and  $\alpha_1$  [68], and heterocyclic derivatives of type  $\pi 2f$  have been described [69, 70].



**Fig. 5.12** Aromatic residues of type  $\pi 2$

### 5.2.4.2 Variations of the Linker Unit

As suitable linker units, saturated or unsaturated aliphatic and cyclic carbon-based systems are used (Fig. 5.13) when a saturated butyl linker of type **L1** results in the highest D<sub>3</sub> binding affinity [63, 64, 68, 70, 71]. Exchange of the saturated linker by a *trans*-butenyl system (**L2**) leads to antagonists [72]. Similar binding properties are described for phenylpiperazines with 3-cyclopropyl spacer of type **L4** [73]. On the other hand, D<sub>2</sub>- and D<sub>3</sub>-affinity is strongly reduced for butenyl linkers (**L3**) [72]. Replacement of the butyl chain by a cyclohexyl ring **L5** results in reduced D<sub>3</sub>-affinity [74]. However, if the cyclohexyl moiety is combined with 2-methylene units (**L6**), D<sub>3</sub>-affinity and selectivity increases [75]. A number of disubstituted phenyl systems have also been investigated [76].

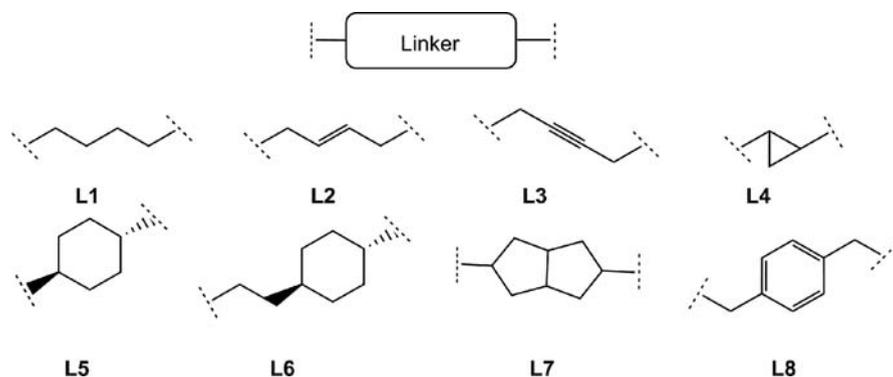
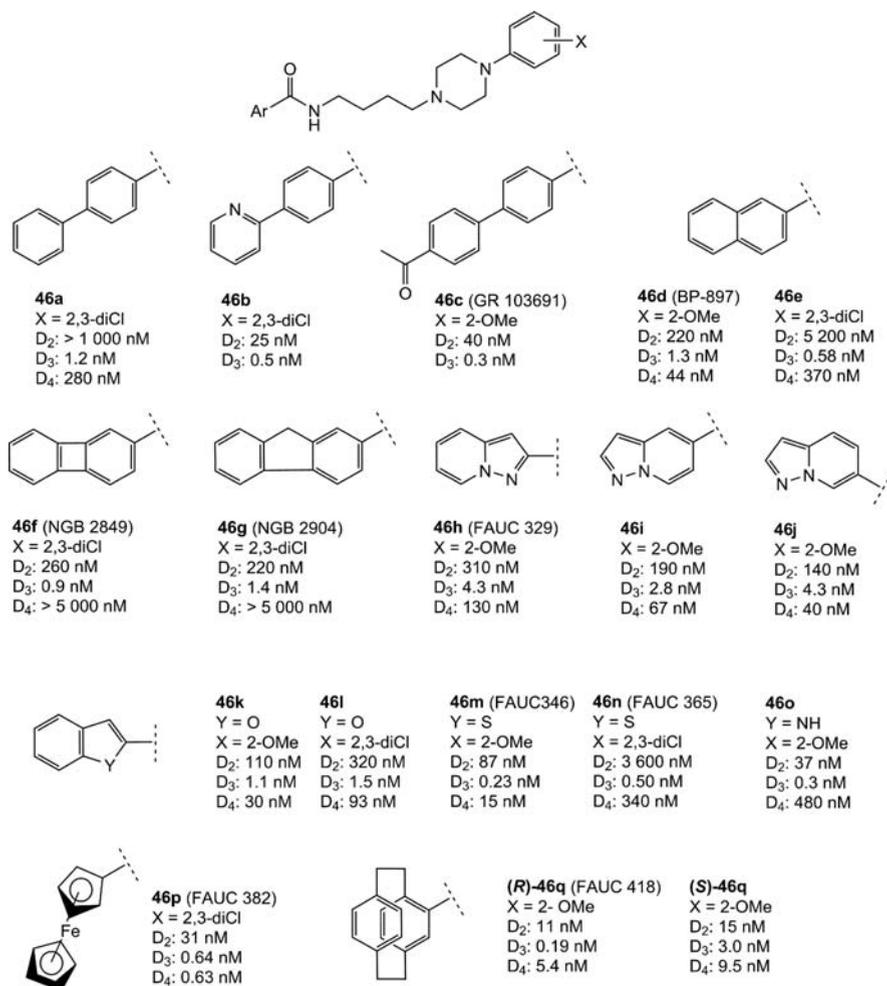


Fig. 5.13 Linker

### 5.2.4.3 Variations at $\pi 1$

For the structural unit  $\pi 1$  a great number of different carbo- and heterocyclic fused and monocyclic aromatic units was employed (Fig. 5.14). Besides substituted phenyl and biphenyl systems (**46a-c**), fused carbo- and heterocyclic rings were investigated [68, 71, 72, 77]. The most prominent representatives of this class are the D<sub>3</sub>-selective partial agonist BP-897 (**46d**), that has been successfully used for the treatment of cocaine abuse [78], and the tricyclic antagonists NGB 2849 (**46f**) and NGB 2904 (**46g**) [79]. For the 2,3-dichloro analog of BP-897 (**46e**) the D<sub>3</sub>-selectivity over D<sub>2</sub> and D<sub>4</sub> is further improved [68].

A great number of heterocyclic units have been investigated when high D<sub>3</sub>-affinity and selectivity was determined. For substituted pyrazolopyridines, affinity decreases with the substitution positions  $5 > 2 = 6 > 3 > 4 > 7$  [64, 80]. Interesting binding profiles are also displayed by the indoles (**46o**) [81], the benzofurans (**46k**, **46l**), and the benzothiophenes (**46m**, **46n**) [64]. Comparison of FAUC 365 (**46n**) and FAUC 346 (**46m**) shows significantly higher D<sub>3</sub>-selectivity for the dichloro derivative **46n** [64]. On the other hand, **46m** (FAUC 346) shows partial agonist properties, whereas **46n** (FAUC 365) is a neutral antagonist [64].



**Fig. 5.14** Binding affinities of several phenylpiperazines with butyl linker,  $K_i$  values in nM

Interestingly, bilayered systems involving metallocene or paracyclophane derivatives could be established as a novel type of dopamine receptor ligands. Depending on the type of metal that is bound between the two cyclopentadienyl systems, different binding profiles can be observed when partial agonist properties were found [66]. On the other hand, the paracyclophane derivatives show neutral antagonist properties and selective binding dependent on the planar chirality of the paracyclophane system [67].

### 5.2.5 Structural Hybrids

Combination of the aminotetralin or pramipexole moiety with the phenylpiperazine unit resulted in a hybrid structure of type **47** and **48**, respectively (Fig. 5.15). Both

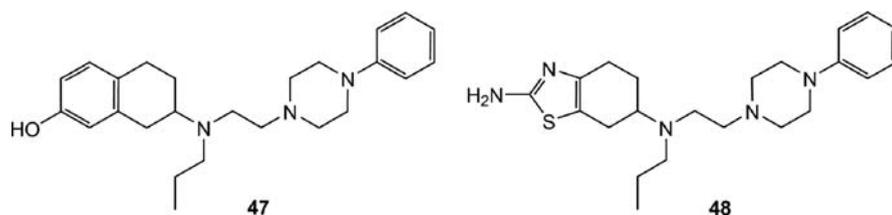


Fig. 5.15 Hybrids

compounds are partial agonists with high intrinsic activity, single-digit nanomolar  $D_3$ -affinity, and high selectivity over  $D_2$  [82, 83].

### 5.2.6 $D_3$ -Selective Radioligands

Employing autoradiography,  $D_3$ -receptors can be distinguished from  $D_2$  receptors by using both selective dopaminergic antagonists and agonists. The preferential expression of  $D_3$ -receptors in limbic areas, such as the ventromedial shell of the nucleus accumbens and the islands of Calleja, has been repeatedly demonstrated in the rat using the tritiated radioligand [ $^3\text{H}$ ]7-OH-DPAT [84–87]. Autoradiography studies with (+)-[ $^3\text{H}$ ]PD128907 (Fig. 5.1) yield a quite similar cerebral distribution in the human while additionally revealing  $D_3$ -receptors in the human neocortex [88–90]. Moreover, *in vivo* studies suggest a role of the  $D_3$ -receptor in cognition and motivated behavior [89, 90], and that  $D_3$  inhibition activates the mesocorticolimbic dopaminergic system [29]. The relevance of disturbances of  $D_3$ -receptor mediated neurotransmission in psychiatric disease is coincidentally justifying the urgent need for selective  $D_3$  imaging agents allowing the non-invasive detection of receptor disturbances (compare Chapter 13 of this book). Positron emission tomography (PET) has already gained growing importance for *in vivo* imaging of disturbances of  $D_2$ -like receptor densities using the nonselective  $D_2/D_3$  radioligands [ $^{11}\text{C}$ ]raclopride [91] and [ $^{18}\text{F}$ ]fallypride [92] (Fig. 5.16). Analogs of these most commonly used

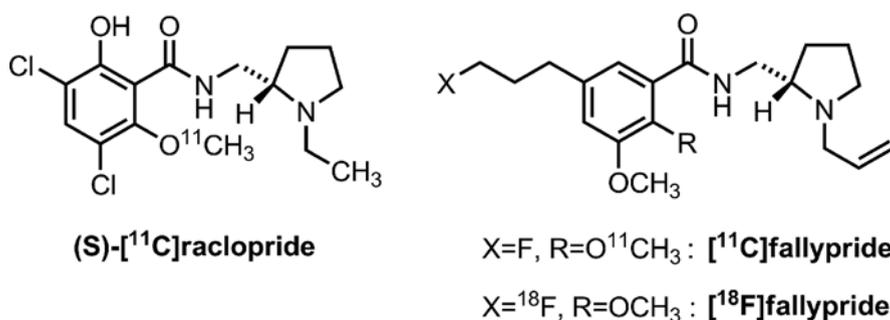


Fig. 5.16  $D_2/D_3$  radioligands for PET

PET radioligands have also been developed [93, 94]. The lack of bioavailable D<sub>3</sub>-subtype-selective PET ligands excluding cross talk with the strongly related subtypes D<sub>2</sub> and D<sub>4</sub> hampers the non-invasive investigation of the physiological role of D<sub>3</sub>. Various efforts have been made to develop selective D<sub>3</sub> PET imaging agents, including the preparation of <sup>11</sup>C-labeled imidazo[2,1-*b*]thiazolylpiperazine derivative RGH-1756 and the substituted aminotetralin [<sup>11</sup>C]GR218231 (Fig. 5.17) [95–97]. The D<sub>3</sub>-selective lead compound FAUC 365 has also been labeled with radioiodide [98], F-18 [65], or C-11 [99], yielding analogs or the <sup>11</sup>C-labeled parent compound, respectively, with high in vitro affinity and D<sub>3</sub> subtype selectivity. However, the above-mentioned D<sub>3</sub> radioligand candidates have not yet been successfully used for in vivo imaging, partly due to rapid efflux from the brain, or disappointing binding characteristics in vivo or in autoradiography experiments. Recent progress has been made by the use of comparative molecular field analysis (CoMFA) and comparative molecular similarity indices analysis (CoMSIA) guided approaches to predict D<sub>3</sub> radioligand selectivities [100, 101]; however the bioavailability of the resulting new candidates (**50a-d**, Fig. 5.17), which are derived from BP-897 and FAUC 346 (Fig. 5.14), remains to be elucidated. Thus, the future discovery of highly selective radioligands as PET tracers is critical for obtaining new insights into the role of the D<sub>3</sub>-receptor subtype in the pathophysiology of various psychiatric diseases.

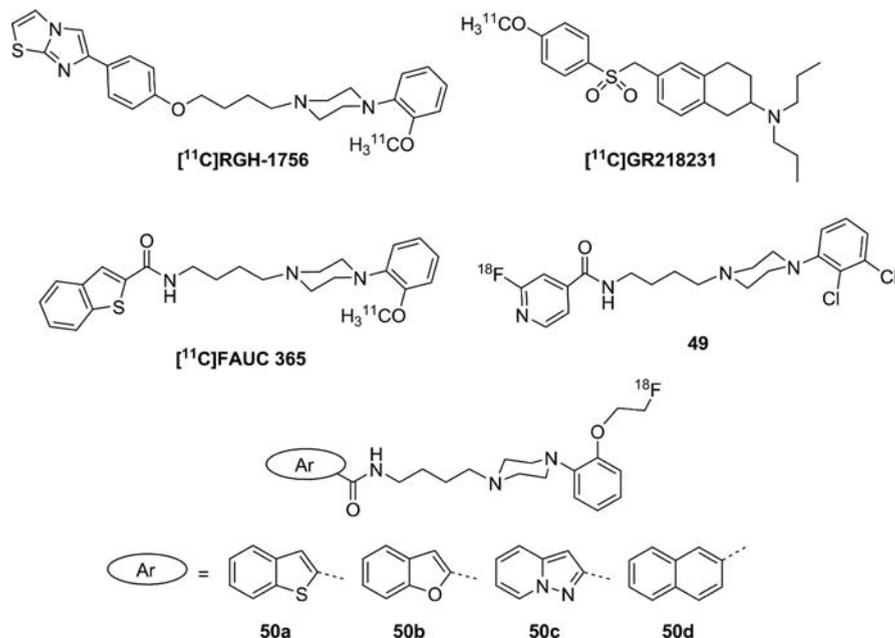


Fig. 5.17 Subtype-selective D<sub>3</sub> radioligands for PET

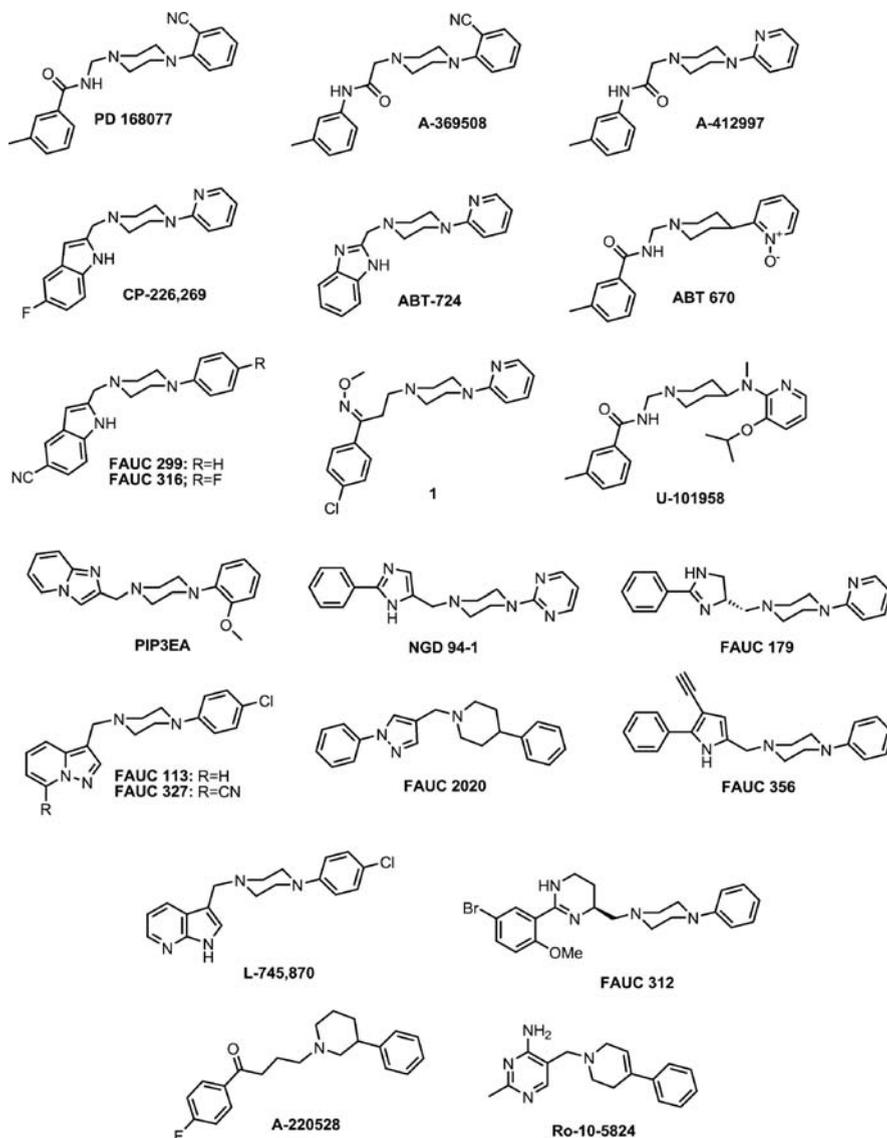
### 5.3 D<sub>4</sub>-Selective Ligands

The interest in selective D<sub>4</sub>-receptor ligands was initially driven by the finding that the atypical neuroleptic drug clozapine preferentially binds to the D<sub>4</sub>-receptor [102, 103]. Up to now, several candidates have been evaluated in vitro and in vivo, including agonists as putative agents for the treatment of sexual dysfunction and attention deficit hyperactivity disorder and antagonists as antipsychotic drugs focussing on the treatment of neuropsychiatric disorders, such as schizophrenia, as well as selective imaging agents for the D<sub>4</sub>-receptor subtype. The medicinal chemistry governing these developments has been separately summarized in recent reviews [104–106]. The crucial structural requirement for selective D<sub>4</sub> ligands consists of a basic nitrogen represented by a piperazine or piperidine core flanked by two aromatic rings with an optimal distance. A pharmacophore model for several structurally diverse D<sub>4</sub> antagonists and CoMFA studies has been successfully used to guide the design of novel selective D<sub>4</sub> ligands in recent years [107–109].

#### 5.3.1 Selective D<sub>4</sub> Agonists

One of the first selective D<sub>4</sub> agonists, PD-168077 (Fig. 5.18), was discovered by Glase et al. [110]. These authors examined a large series of *N*-methylpiperazinyl benzamides with *ortho*-substituent (2-Cl, 2-CN, and 2-OMe) at the phenylpiperazine under variation of the substitution pattern of the benzamide phenyl core. In comparison with 2-methoxy and 2-cyano derivatives, the 2-chloro compounds reveal decreased D<sub>4</sub> selectivity in binding studies using CHO K1 transfected cells. Introduction of a methyl group in the 3-position of the 2-cyano-phenylpiperazinyl compound yields PD-168077 with substantial D<sub>4</sub> affinity ( $K_i(\text{hD}_4) = 8.7 \text{ nM}$ ) and excellent subtype selectivity (>300-fold over D<sub>3</sub> and > 400-fold over D<sub>2</sub>). Stimulated mitogenesis in D<sub>4</sub>-transfected CHO pro-5 cells shows an EC<sub>50</sub> of 17 nM and 80% intrinsic activity compared with quinpirole as a reference dopamine receptor agonist. The high D<sub>4</sub>-receptor affinity of PD-168077 has also been confirmed for the human D<sub>4</sub> alleles hD<sub>4.2</sub> (6.0 nM), hD<sub>4.4</sub> (22.3 nM), and hD<sub>4.7</sub> (29.0 nM) [111]. PD-168077 has been studied in vivo in a number of pharmacological studies in rats, including behavioral studies and memory tests. The compound induces an improved memory performance [112], but dyskinesia was noticed that was insensitive to the D<sub>4</sub> antagonists L-745,870 or haloperidol [113], and thus could be ascribed to non-dopaminergic binding sites of PD-168077. The proerectile effect of PD-168077 when administered locally in the paraventricular nucleus (PVN) of the hypothalamus of male rats [114] or s.c [111] provides evidence for the role of D<sub>4</sub>-receptors mediating erectile function.

Since PD-168077 shows limited stability toward acidic medium [110], Matulenko et al. aimed at the corresponding retroamides, of which they synthesized a series of *ortho*-, *meta*-, and *para*-phenylpiperazinyl substitutes candidates [115]. Among the series of derivatives, only the 2-cyano derivative (A-369508, Fig. 5.18)



**Fig. 5.18** Selective D<sub>4</sub> ligands: partial agonists

shows equivalent efficacy ( $EC_{50} = 7.5$  nM) and increased D<sub>4</sub> potency ( $K_i(D_4) = 2.7$  nM) compared to PD-168077 as studied in a calcium flux assay using HEK 293 cells co-transfected with hD<sub>4.4</sub> and  $G\alpha_{q05}$ . Replacement of the 2-cyano group by other electron-withdrawing groups, such as fluorine or nitro, causes slightly decreased potency ( $EC_{50} = 18$  nM or 13 nM, respectively), whereas changing the

*ortho*-substituent to a *meta*- or *para*-position leads to total loss in agonist activity. Notably, some of these derivatives (3-Me, 4-Me, 3-OMe, and 4-F) retain their D<sub>4</sub> binding affinity (K<sub>i</sub>: 8–70 nM) and exhibit functional antagonism. Substitution on the aryl acetamide portion of 3-cyanopyridin-2-yl derivatives also results in compounds with good D<sub>4</sub> potency, but the intrinsic efficacy is slightly lower when compared to A-369508.

Recently, a series of structurally related analogs of PD-168077 has been developed by replacement of the amide group with a methylene-oxime moiety [116]. Introduction of a 2-pyridine ring revealed to be superior for D<sub>4</sub> agonist activity of the most potent candidate **1** shown in Fig. 5.18. This derivative shows poor D<sub>4</sub> binding selectivity over D<sub>2</sub> (K<sub>i</sub>(D<sub>4</sub>) = 38.2 nM; D<sub>2</sub>/D<sub>4</sub> = 1.7); however, it shows no efficacy at concentrations up to 10 μM in an assay using HEK-293 cells co-transfected with human D<sub>2L</sub> and chimeric Gα<sub>q05</sub> and its activity in the rat penile erection model is three times higher than that of the nonselective D<sub>2</sub>-like agonist apomorphine. Thus, this compound is a D<sub>4</sub> agonist and a moderately potent D<sub>2</sub> antagonist.

The indole CP-226,269 (Fig. 5.18), another selective D<sub>4</sub> agonist bearing a 2-pyridinylpiperazinyl moiety (K<sub>i</sub>(D<sub>4</sub>) = 6.0 nM; K<sub>i</sub>(D<sub>2</sub>) > 600 nM), has been described contemporary with PD-168077 by Zorn et al. [117]. Competition studies using recombinant human D<sub>4</sub> variants hD<sub>4.2</sub>, hD<sub>4.4</sub>, and hD<sub>4.7</sub> revealed even higher receptor affinities than PD-168077 with K<sub>i</sub> values of 2.4 nM, 3.6 nM, and 5.6 nM, respectively [111]. Despite a lack of affinity to human D<sub>2L</sub> receptors, it has been demonstrated that CP-226,269 binds to the rat D<sub>2</sub> receptor with moderate affinity (EC<sub>50</sub> = 55 nM) [118], which complicates the interpretation of its *in vivo* pharmacology in rats.

The benzimidazole derivative ABT-724 (Fig. 5.18), also bearing the 2-pyridinylpiperazinyl moiety and thus closely related to CP-226,269, has been developed by Stewart et al. [119]. Interestingly, these authors notice a distinct “*ortho*-effect” when comparing *para*-, *meta*-, and *ortho*-substituted phenylpiperazinyl derivatives with the corresponding 2-, 3-, and 4-pyridyl compounds with reference to binding affinity to hD<sub>4</sub> and efficacy measured by a calcium flux assay using HEK 293 cells co-transfected with hD<sub>4.4</sub> and Gα<sub>q05</sub>. A total loss of D<sub>4</sub> affinity and efficacy is observed for the 4-pyridyl compound, whereas the 2-pyridyl (ABT-724) and the 2-chlorophenyl derivative display satisfactory D<sub>4</sub> potency and efficacy. This study indicates that the phenylpiperazine moiety plays a key role in determining D<sub>4</sub>-receptor efficacy [119, 120]. The EC<sub>50</sub> of ABT-724 is 12.4 nM, intrinsic activity is 61%, and receptor selectivity has been confirmed by screening 70 different neuroreceptors [121]. Using the agonist D<sub>4</sub> radioligand [<sup>3</sup>H]A-369508 (Fig. 5.20) and membrane preparations expressing hD<sub>4.2</sub>, hD<sub>4.4</sub>, and hD<sub>4.7</sub>, receptor-binding experiments reveal K<sub>i</sub> values of 47–64 nM. ABT-724 has been further evaluated *in vivo*, confirming the proerectile activity of the compound when given *s.c.* at very low doses (0.03 μmol/kg) to conscious rats, an effect that is blocked by haloperidol and clozapine, but not by the peripheral dopaminergic antagonist domperidone, indicating CNS activity of ABT-724.

More recently, ABT-670 has been discovered by further structural optimization of ABT-724 introducing a (*N*-oxy-2-pyridinyl)piperidine template (Fig. 5.18),

which exhibits comparable efficacy and improved oral bioavailability in rat, dog, and monkey in comparison with ABT-724 [122].

A-412997 (Fig. 5.18) is a piperidine analog derived from the retroamide series of D<sub>4</sub> agonists [118]. In comparison with PD-168077 and CP-226,269, A-412997 ( $K_i(\text{hD}_{4.4}) = 7.9 \text{ nM}$ ;  $K_i(\text{rD}_4) = 12.1 \text{ nM}$ ) shows a better selectivity profile, with no affinity ( $> 1,000 \text{ nM}$ ) for other dopamine receptors and reveals potent full D<sub>4</sub> agonism in functional assays ( $\text{EC}_{50} = 28.4 \text{ nM}$ , intrinsic efficacy: 83% related to 10  $\mu\text{M}$  dopamine). A-412997 shows rapid blood–brain barrier penetration, induces penile erection in a conscious rat model with an effective dose of 0.1  $\mu\text{mol/kg}$ , and also induces cognitive enhancement properties in a rat model of ADHD and short-term memory [123].

An extensive series of phenylpiperazines with an indole or pyrazolo[1,5-*a*]pyridine core unit has been studied by Gmeiner et al. [124–127]. The majority of these derivatives are partial D<sub>4</sub> agonists as demonstrated by stimulated mitogenesis assays on CHO cells expressing the human D<sub>4.2</sub> receptor. Using a solid-phase supported synthesis, the influence of electropositive and electronegative substituents at C-2 of the indole core was investigated, showing that such modifications do not affect D<sub>4</sub> affinity or subtype selectivity [124, 127]. These studies reveal that a 5-cyano and the phenylpiperazinylmethyl substitution in 2-position of the indole core is most favorable for high D<sub>4</sub> affinity and substantial D<sub>4</sub> subtype selectivity. Among the series of indoles (Fig. 5.18), the phenylpiperazine FAUC 299 shows D<sub>4</sub> affinity in the subnanomolar range ( $K_i = 0.52 \text{ nM}$ ), and the corresponding *para*-fluoro derivative FAUC 316 displays high D<sub>4</sub> affinity ( $K_i = 1.0 \text{ nM}$ ) combined with substantial D<sub>4</sub> subtype selectivity of more than 8,600-fold over the other dopamine subtypes. FAUC 299 and FAUC 316 reveal partial agonism with  $\text{EC}_{50}$  values of 1.5 nM and 9.4 nM, respectively, and a relative partial agonist effect of 30–35% compared to the maximal effect of the unselective agonist quinpirole [124].

Similarly, replacing the indole moiety by conformationally restricted benzamide bioisosteres, such as a dihydroimidazole ring, led to the discovery of FAUC 179 (Fig. 5.18) [128]. The binding experiments show a biphasic curve, providing a high-affinity D<sub>4</sub> binding site ( $K_i = 0.95 \text{ nM}$ ) and a low-affinity binding site (51 nM), being comparable to the properties of quinpirole. The D<sub>4</sub> selectivity of FAUC 179 is more than 7,000-fold over the other D2-like receptors. The affinity toward serotonergic sites (5-HT<sub>1A</sub>: 45 nM; 5-HT<sub>2</sub>: 870 nM) is moderate to low, as determined by displacement studies on porcine brain homogenates using selective tritiated radioligands. FAUC 179 is finally characterized as a selective D<sub>4</sub> partial agonist ( $\text{EC}_{50} = 31 \text{ nM}$ ; efficacy: 42% relative to the reference quinpirole).

Alternative bioisosteres of the dihydroimidazole core unit of FAUC 179 have also been reported, resulting in partial agonists with retained D<sub>4</sub> affinity and efficacy including the ethenylpyrrole FAUC 356 (Fig. 5.18) [129] or the tetrahydropyrimidine FAUC 312 [130]. The latter reveals high D<sub>4</sub> affinity ( $K_i = 1.5 \text{ nM}$ ), superior subtype selectivity ( $K_i > 10 \mu\text{M}$  for the other D2-like receptors), and 83% intrinsic agonist activity ( $\text{EC}_{50} = 50 \text{ nM}$ ).

The series of pyrazolo[1,5-*a*]pyridine-based ligands demonstrate high D<sub>4</sub> affinity (1.5–2.2 nM) and selectivity [125, 126]. Starting from pyrazolo[1,5-*a*]pyridine,

which is readily available by 1,3-dipolar cycloaddition, or its 3-carboxylic ester, an extended series of 3-substituted phenylpiperazinyl derivatives, including FAUC 113 (Fig. 5.18), has been achieved by Löber et al. [126]. This study also indicates that a negative potential below and above the 5-membered ring of the heterocycle appeared to be crucial for high D<sub>4</sub> affinity, whereas an enlarged negative region below the ring appears to be responsible for substantial D<sub>4</sub> selectivity, since this molecular property obviously is not tolerated by the other dopaminergic receptors. Interestingly, non-bulky substituents in the 7-position of the pyrazolo[1,5-*a*]pyridine core are well tolerated by the D<sub>4</sub>-receptor. The 7-iodo [131], 7-methyl, 7-acetylenyl, 7-carbaldehyde, and 7-cyano (FAUC 327, Fig. 5.18) derivative shows K<sub>i</sub> values of 1.2–2.7 nM for the D<sub>4</sub>-receptor [125]. The latter has been subsequently shown to stimulate mitogenesis in CHO-D<sub>4</sub>-expressing cells inducing an intrinsic effect of 31% with an EC<sub>50</sub> of 1.5 nM. Applying a methyl group as a substituent within the piperazine template, the *R*-isomer is a partial D<sub>4</sub> agonist with an EC<sub>50</sub> of 6.2 nM, being five times more potent than the *S*-isomer [132].

As a structurally closely related analog of the pyrazolo[1,5-*a*]pyridines, the 2-methoxyphenylpiperazinyl derivative of imidazo[1,2-*a*]pyridine (PIP-3EA, Fig. 5.18) has been investigated by Enguehard-Gueiffier et al. [133]. This compound is a potent and selective D<sub>4</sub> partial agonist (K<sub>i</sub> = 2.8 nM, D<sub>4</sub>/D<sub>2</sub> > 350; D<sub>4</sub>/D<sub>3</sub> > 1,300) with EC<sub>50</sub> of 4.5 nM and an intrinsic activity of 57% (based on quinpirole) as determined in a [<sup>35</sup>S]GTPγS binding assay, whereas the 4-chlorophenylpiperazinyl analog shows weak agonist properties and the 3,4-dichloro derivative even reveals D<sub>4</sub> antagonism. PIP-3EA has been further studied in vivo. Applying systematic, intracerebroventricular (0.1–20 μg) or direct injection into the paraventricular nucleus (PVN) of the hypothalamus, PIP-3EA mediates penile erection in rats, being as potent as PD-168077 when given into the PVN, but more potent when given systematically [134]. More recently, Succu et al. provided evidence that the stimulation of dopamine receptors in the PVN, including the D<sub>4</sub> subtype, caused oxytocin release in extra-hypothalamic rat brain areas, which in turn is known to modulate the activity of mesolimbic dopaminergic neurons that are involved in rewarding effects of sexual activity [135].

As a structurally related analog of haloperidol, A220528 (Fig. 5.18) was found by conducting a high-throughput screen of an in-house library of compounds [136]. The 3-phenylpiperidine derivative (A220528, Fig. 5.1) and the respective thiazolyl analog are potent and selective D<sub>4</sub> agonists (EC<sub>50</sub> = 51 and 34 nM; IC<sub>50</sub>(D<sub>2</sub>) > 2 μM) exhibiting full agonism (91 and 94%, related to dopamine) as determined by a calcium flux assay on HEK 293 cells co-expressing hD<sub>4.4</sub> and Gα<sub>q05</sub> using a fluorometric imaging plate reader (FLIPR assay).

Another high-throughput screening approach was successful for the discovery of Ro-10-5824, a member of the biaryl type class of D<sub>4</sub> selective ligands [137]. The compound displays high D<sub>4</sub> affinity binding with a K<sub>i</sub> of 5.2 nM, a 250-fold D<sub>4</sub>-selectivity versus hD<sub>3</sub>-receptors and > 1,000-fold selectivity over the other dopamine receptor subtypes. GTPγS-binding assays in CHO-D<sub>4.4</sub> cell membranes reveal an EC<sub>50</sub> of 205 nM and a relative activation level of 36%, characterizing

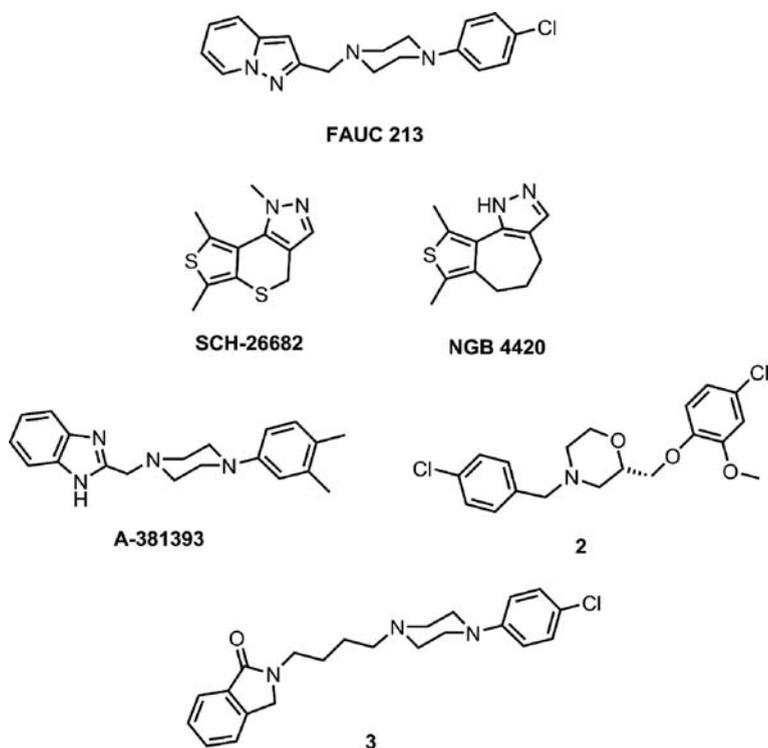
Ro-10-5824 as a selective partial D<sub>4</sub> agonist (Fig. 5.18). The compound has been tested in vivo for locomotor activity in a dose–response study and increases novel object exploration by C57BL/6 J male mice using a dose of 10 mg/kg.

Employing a modified “click chemistry” method [138] or reductive amination of the respective *N*-phenylpyrazole carbaldehyde, Löber et al. provide access to another series of biaryl analogs of NGD 94-1 including FAUC 2020 (Fig. 5.18) and its 2-fluoro- and 2-methoxyphenylpiperazinyl analogs [139]. These compounds exhibit extraordinarily high D<sub>4</sub> affinities with K<sub>i</sub> values in the subnanomolar range combined with > 50-fold D<sub>4</sub> preference over the other dopamine subtypes (K<sub>i</sub>(hD<sub>4</sub>) = 0.59 nM for FAUC 2020; K<sub>i</sub>(hD<sub>4</sub>) = 0.7 nM (2-fluorophenyl analog); K<sub>i</sub>(hD<sub>4</sub>) = 0.28 nM (2-methoxyphenyl)). In comparison with the corresponding pyrrole template, the pyrazole or a triazole scaffold increases D<sub>4</sub> affinity by a factor of 20. FAUC 2020 proves to be a partial agonist displaying intrinsic activities of 40 % and EC<sub>50</sub> of 5.6 nM using GTPγS binding and mitogenesis assays on D<sub>4</sub>-receptor-expressing CHO cells. However, discrepancies between D<sub>4</sub> selectivity in binding experiments and functional assays have been noticed.

### 5.3.2 Selective D<sub>4</sub> Antagonists

Several compounds originally reported to act as D<sub>4</sub> antagonists were revealed by subsequent investigations [140, 141] to be partial agonists, such as the selective D<sub>4</sub> ligands L-745,870 (K<sub>i</sub>(hD<sub>4</sub>)=0.43 nM, > 2,000-fold selectivity over other dopamine subtypes, > 1,000-fold selective over 5-HT<sub>2</sub> [142, 143]), U-101958 (K<sub>i</sub>(hD<sub>4</sub>) = 1.4 nM, > 460-fold selectivity over other dopamine subtypes [144]), and NGD 94-1 (K<sub>i</sub>(hD<sub>4</sub>) = 3.6 nM, K<sub>i</sub>(D<sub>2</sub>) = 2230 nM, K<sub>i</sub>(5-HT<sub>1A</sub>) = 180 nM [145]) (Fig. 5.18). Interestingly, the efficacy was only apparent in cells with high receptor density in the in vitro assays [146]. Since an increased D<sub>4</sub>-receptor density in postmortem schizophrenia brain tissue was reported by Seeman et al. [147], it is tempting to speculate that this in vivo situation could also result in partial agonist activity of these compounds in vivo, which may help explain the lack of efficacy of these compounds in clinical trials aiming at the treatment of schizophrenia [148, 149].

In the search for D<sub>4</sub>-receptor antagonists, Löber et al. studied the influence of the linkage position of the (4-(4-chlorophenyl)piperazin-1-yl)methyl moiety to the pyrazolo[1,5-a]pyridine on the functional activity of the resulting potential D<sub>4</sub> ligand [150]. Linkage in the 7-position of the heterocycle leads to loss of D<sub>4</sub> affinity, whereas in the 4-position moderate D<sub>4</sub> affinity of the resulting ligand with K<sub>i</sub> = 64 nM for D<sub>4</sub> is observed. However, the corresponding 2-substituted (FAUC 213, (Fig. 5.19)), 3-substituted (FAUC 113, Fig. 5.18), and 6-substituted compounds equally demonstrate high D<sub>4</sub> affinities with K<sub>i</sub> values of 2.3, 3.6, and 3.1 nM. Among these, the regioisomer FAUC 213 is a neutral D<sub>4</sub> antagonist as shown by ligand-induced mitogenesis experiments, with substantial D<sub>4</sub> selectivity. It was further demonstrated that the intrinsic activity of the regioisomers investigated



**Fig. 5.19** Selective  $D_4$  ligands: neutral antagonists

depends on the ability of the heterocyclic unit to interact with both elements of the  $D_4$  binding-site crevice, the aromatic microdomain in TM6, and a serine residue in TM5. FAUC 213 has been further studied in behavioral and neurochemical animal models of schizophrenia in vivo, exhibiting atypical antipsychotic properties [151]. Although FAUC 213 holds promise for further pharmacological experiments, it remains to be elucidated whether interfering receptors, such as adrenergic or serotonergic, could influence the in vivo efficacy of FAUC 213.

A series of similar azaindoles with high  $D_4$  potency ( $K_i(\text{h}D_4) = 1.4\text{--}4.7$  nM) and  $D_4$  selectivity are also characterized as  $D_4$  antagonists, and due to the methoxy substituents in some analogs, their C-11-labeled analogs are proposed as radioligands for in vivo imaging studies [152].

Varying the aromatic core unit,  $D_4$  selective pyrido[1,2-*a*]pyrazine antagonists have also been reported, including CP-293,019 ( $K_i(\text{h}D_4) = 3.4$  nM,  $K_i(\text{h}D_2) > 3$   $\mu\text{M}$ ), which inhibits apomorphine-induced hyperlocomotion in rats after oral dosing [153].

As a derivative bearing a benzenesulfonamide, U-101387 displays moderately high affinity and selectivity for the  $D_4$ -receptor in vitro ( $K_i = 10$  nM), lacking measurable affinity for other dopamine, noradrenaline, serotonin and histamine

receptors ( $K_i > 2,000$  nM) [154, 155]. U-101387 also displays favorable oral bioavailability, good brain penetration and is without effect in behavioral animal tests predictive of extrapyramidal and neuroendocrine side effects. U-101387 has been introduced in a clinical trial including 467 schizophrenia patients, where U-101387 was, however, ineffective for the treatment of patients with schizophrenia [156]. Recently, U-101387 has been used to inhibit the effects of dopamine, noradrenaline, and serotonin on G-protein-regulated inwardly rectifying potassium channels (GIRK1) in frog oocytes co-expressing D<sub>4</sub>-receptors, thus indicating that D<sub>4</sub> can be pharmacologically stimulated by any of the three major central monoamines [157].

With a unique fused thiophene structure, SCH 26682 (Fig. 5.19) has been found by a compound library screening approach and further structural optimization has been performed leading to the corresponding 2,5-dimethylthiophene NGB 4420 with a  $K_i$  of 12 nM and good D<sub>4</sub> selectivity of 170-fold over D<sub>2</sub> and > 1,000-fold over D<sub>1</sub>, D<sub>3</sub>, and D<sub>5</sub> [158]. The [<sup>35</sup>S]GTP $\gamma$ S binding assay using hD<sub>4.2</sub> receptor-expressing cells suggests that NGB 4420 functions as a neutral antagonist.

Nakane et al. identified the benzoimidazole A-381393 (Fig. 5.19) as a structurally related bioisostere of L-745,870 with potent D<sub>4</sub> binding ( $K_i = 1.5$  nM) combined with high selectivity (> 2,700-fold) over the other dopamine receptor subtypes [159]. Contrary to L-745,870, A-381393 does not show any intrinsic activity in D<sub>4.4</sub> and G $\alpha_{q05}$  co-expressing HEK cells (measured by Ca<sup>2+</sup>-flux) and significantly blocks agonist-induced GTP binding. Moreover, A-381393 also inhibits D<sub>4</sub> agonist (PD-168077)-induced penile erection in the male rat animal model, successfully demonstrating D<sub>4</sub> antagonist properties of A-381393 both in vitro and in vivo. In addition, the selective D<sub>4</sub>-receptor antagonist A-381393 reduces c-Fos expression in the PVN below control levels suggesting a tonic dopamine D<sub>4</sub>-receptor activation under basal conditions in vivo [160].

The morpholine template as an bioisostere of the piperazine core has been introduced by Audouze et al., revealing high D<sub>4</sub> affinity ( $K_i(D_4) = 2.0$ – $4.5$  nM), especially for the *S*-isomer of a 2-methoxy-4-chlorophenoxy substituted compound (**2**, Fig. 5.19), whereas the *R*-isomer is inactive [161]. A predictive 3D-QSAR model also shows that the size of the morpholine or 1,4-oxazepane ring is a prerequisite for high D<sub>4</sub> affinity.

Alternative structural features of D<sub>4</sub>-selective candidates have been reported by others, including benzylpiperazines bearing an azaindole core [162], benzamides bearing a benzylpyrrolidine scaffold [163, 164], or compounds with structurally rigid pyrimidinylpiperazines [165]. More recently, novel lactam derivatives have been prepared and evaluated for binding affinity and functional activity by Awadallah et al., including the indolinone derivative **3** (Fig. 5.19) that displays superior D<sub>4</sub> affinity ( $K_i = 0.04$  nM) and a > 43,000-fold selectivity over hD<sub>2</sub> receptor [166]. Antagonistic activity of this series of compounds was confirmed using a calcium fluorescence assay. These series of candidates could be helpful in further developments of D<sub>4</sub>-selective antagonists as potential treatments for psychiatric disorders.

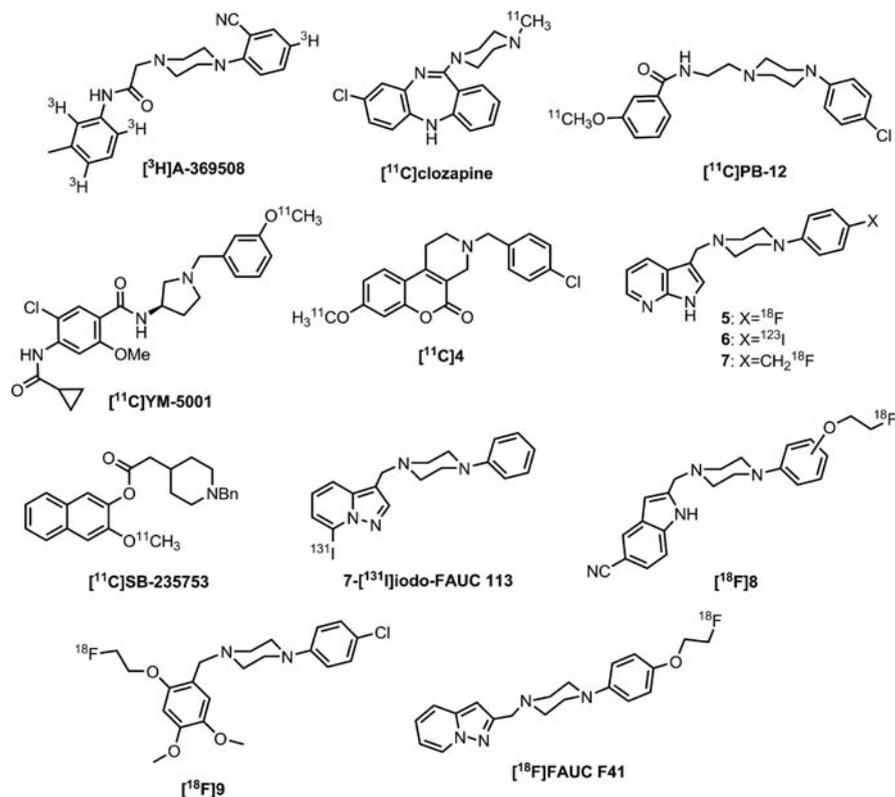
### 5.3.3 Selective $D_4$ Radioligands

Most of the  $D_4$  radioligand-binding studies were performed employing the indirect method described by Seeman et al. [147] that involves the subtraction of binding sites measured with the selective  $D_2/D_3$  radioligand [ $^3\text{H}$ ]raclopride from total  $D_2$ -like binding sites defined by the unselective radioligand [ $^3\text{H}$ ]nemonapride. This methodology has been used in various autoradiography studies [167–169] and has been extended by the use of cold raclopride ( $1\mu\text{M}$ ) in an assay system with [ $^3\text{H}$ ]nemonapride, which appears to be more adequate when estimating  $D_4$ -receptor overall population in the mouse brain [170].

Isotopically labeled radioligands derived from the above described selective  $D_4$  ligands have been used for in vitro studies on  $D_4$ -receptor expression in tissue by autoradiography [171, 172]. A detailed study by Primus et al. using  $^3\text{H}$ -labeled NGD 94-1 reveals region-specific binding that appeared to be low in density ( $< 20$  fmol/mg) in the rat brain [172]. Highest  $D_4$ -receptor density is detected in rat hippocampus, lateral septal nucleus, medial preoptic area, and entorhinal cortex, with negligible binding in the rat striatum. In several human brain regions, including hippocampus, hypothalamus, dorsal medial thalamus, entorhinal cortex, prefrontal cortex, and lateral septal nucleus, high-affinity [ $^3\text{H}$ ]NGD 94-1 binding has been determined (approx. 30 fmol/mg). Again, binding was low, if not absent, in striatal human brain regions.

Matulenko et al. synthesized the tritiated  $D_4$  agonist A-369508 (Fig. 5.20) by reaction of a suitable brominated precursor with tritium gas in the presence of a sensitive cyano group, obtaining the agonist radioligand in adequate specific activity for saturation binding experiments [173]. [ $^3\text{H}$ ]A-369508 shows high affinity to  $\text{hD}_{4.2}$  (1.7 nM),  $\text{hD}_{4.4}$  (4.0 nM), and  $\text{hD}_{4.7}$  (1.2 nM), and also binds to rat  $D_4$ -receptors ( $K_d = 4.4$  nM) [174]. The  $D_4$ -receptor-subtype selectivity of [ $^3\text{H}$ ]A-369508 is greater than 400-fold ( $D_1$ ,  $> 2,475$ -fold;  $D_{2L}$ , 434-fold;  $D_3$ , 1,022-fold;  $D_5$   $> 2,475$ -fold) and over 70 other potentially interfering neurotransmitter receptors were tested. Among these, only moderate affinity to the 5-HT $_{1A}$  receptor ( $K_i = 1219$  nM) is worth mentioning. Therefore, [ $^3\text{H}$ ]A-369508 is useful as an agonist radioligand in competition-binding experiments and in autoradiography studies.

As recently reviewed [104], there is an intriguing interest in the development of radiolabeled selective  $D_4$  ligands suitable for in vivo imaging of  $D_4$ -receptor densities by positron emission tomography (PET) to further explore the relevance of this molecular target for various neurobehavioral and psychiatric disorders, such as schizophrenia. Early PET studies using the nonselective  $D_2/D_3$  radioligand [ $^{11}\text{C}$ ]raclopride (Fig. 5.16) failed to detect dopamine receptor disturbances in drug-naïve patients [175], whereas the  $D_2/D_3/D_4$  affine radioligand [ $^{11}\text{C}$ ]spiperone markedly indicates an increase in dopamine receptors in similar patients [176]. These findings suggest elevated  $D_4$ -receptor densities in vivo, as confirmed by Seeman et al. for postmortem schizophrenia brain tissue some years later [147]. Consequently, various attempts toward the development of subtype-selective  $D_4$  radioligands labeled with the positron emitters  $^{18}\text{F}$  and  $^{11}\text{C}$  have been reported. The first study on a putative  $D_4$  radioligand was reported by Bender et al. dealing



**Fig. 5.20** Subtype-selective D<sub>4</sub> radioligands

with the synthesis of [<sup>11</sup>C]clozapine (Fig. 5.20) [177]. Using [<sup>11</sup>C]methyl iodide in DMSO, norclozapine was labeled in 70% with a specific activity in the range of 92–130 GBq/μmol. Biodistributional experiments in NMRI mice showed preferential brain uptake of [<sup>11</sup>C]clozapine in the frontal cortex, which was retained for up to 40 min.

Later on, Boy et al. applied [<sup>11</sup>C]SDZ-GLC756 for imaging of D<sub>4</sub>-receptors in the primate brain by PET, which included the need for D<sub>1</sub>, D<sub>2</sub>, D<sub>3</sub>, and D<sub>5</sub> receptor blockade by preinjection of SCH23390 and raclopride [178], indicating D<sub>4</sub>-receptor localization in the frontal cortex and neocortex by this subtractive approach.

When searching for a selective PET ligand, without the need for pharmacological blocking of interfering receptors, methoxybenzamide analogs of PD-168077, such as [<sup>11</sup>C]PB-12 (Fig. 5.20), reported as highly potent and selective D<sub>4</sub> ligands [179, 180], were labeled with [<sup>11</sup>C]methyl triflate [181, 182]; however, no specific binding was detected in the monkey and rat brain.

The same group provided evidence that a <sup>11</sup>C-labeled tetrahydrochromeno[3,4-*c*]pyridin-5-one ([<sup>11</sup>C]4, Fig. 5.20), originally reported as a selective D<sub>4</sub> antagonist

[183], preferentially binds to sigma-1 receptors in vivo as demonstrated by blocking studies with pentazocine [184]. Closely related  $^{18}\text{F}$ -labeled analogs have also been synthesized [185, 186] and one candidate showed highest uptake in frontal cortex and medulla of the rat brain [185].

$^{18}\text{F}$ - and  $^{123}\text{I}$ -labeled derivatives of pyrrolo[2,3-*b*]pyridines L-745,870 and L-750,667 (5–7, Fig. 5.20) [162, 187–190] were also evaluated in animal models and determined not to be suitable for in vivo imaging of the  $\text{D}_4$ -receptor. In addition,  $\text{D}_4$  radioligand candidates for PET have been derived from naphthyl-based  $\text{D}_4$  ligands [191], such as  $^{11}\text{C}$ -labeled SB-235753 (Fig. 5.20) [192], revealing homogeneous distribution in the rat brain suggesting non-specific tracer uptake.

In terms of the selective  $\text{D}_4$  ligands FAUC 316, FAUC 113, and FAUC 213 (Fig. 5.18, Fig. 5.19), the syntheses of radiolabeled analogs have been studied by Prante et al., including 7-iodo-FAUC 113 [131, 193],  $^{18}\text{F}$ -labeled 5-cyanoindoles ( $^{18}\text{F}$ 8) [194], benzylpiperazines ( $^{18}\text{F}$ 9) [195], and an extended series of  $^{18}\text{F}$ -labeled pyridinyl- and (2-fluoroethoxy)phenyl substituted pyrazolo[1,5-*a*]pyridines [196] (Fig. 5.20). Among these, the *para*-(2-fluoroethoxy)phenyl candidates revealed superior  $\text{D}_4$  selectivity over  $\text{D}_2$  (> 2,300-fold) combined with inverse agonism at  $\text{D}_4$  as studied in mitogenesis experiments. The  $^{18}\text{F}$ -labeled  $\text{D}_4$  inverse agonist FAUC F41 (Fig. 5.20) revealed a promising binding pattern in vitro and ex vivo, reflecting the known  $\text{D}_4$ -receptor distribution, as determined by autoradiography in comparison with [ $^3\text{H}$ ]nemonapride (1  $\mu\text{M}$  raclopride) [196].  $^{18}\text{F}$ -labeled FAUC F41 binding was blocked by FAUC 213 and eticlopride in vitro, while co-injection of rats with L-750,667 blocked binding of FAUC F41 in distinct regions of the rat brain, including the gyrus dentate region of the hippocampus, hypothalamus, the medial habenular nucleus, central medial thalamic nucleus, septum, and cortical areas, whereas low binding was detected in the striatum [196, 197]. Although FAUC F41 holds promise for further in vivo studies, a suitable selective  $\text{D}_4$  PET ligand for human use still remains to be established.

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# Chapter 6

## Dopamine Receptor Signaling: Intracellular Pathways to Behavior

Robert J. Romanelli, John T. Williams, and Kim A. Neve

**Abstract** Dopamine receptors belong to the large family of heptahelical transmembrane spanning G protein-coupled receptors (GPCRs). Five mammalian dopamine receptor subtypes have been identified and are classified into two major groups, the D1-like (D<sub>1</sub> and D<sub>5</sub>) and D2-like (D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub>) receptors. Two splice variants of the D<sub>2</sub> receptor exist, D<sub>2-Long</sub> (D<sub>2L</sub>) and D<sub>2-Short</sub> (D<sub>2S</sub>), which differ by an insertion of 29 amino acids in the third intracellular loop of D<sub>2L</sub>. In this chapter, we discuss canonical and non-canonical signaling pathways regulated by individual dopamine receptor subtypes and the contribution of these pathways to dopamine-induced behaviors. Particular focus is given to the behavioral effects of drugs of abuse, including the psychostimulants cocaine, amphetamine, and methamphetamine.

**Keywords** Dopamine · Dopamine receptor · Adenylate cyclase · G protein · Arrestin · Akt · Phospholipase C · Protein kinase A · Cyclic AMP

### 6.1 Dopamine Receptor Overview

#### 6.1.1 Introduction

Dopamine receptors belong to the large family of heptahelical transmembrane spanning G protein-coupled receptors (GPCRs). Five mammalian dopamine receptor subtypes have been identified and are classified into two major groups, the D1- (D<sub>1</sub> and D<sub>5</sub>) and D2- (D<sub>2</sub>, D<sub>3</sub>, D<sub>4</sub>) like receptors. Two splice variants of the D<sub>2</sub> receptor exist, D<sub>2-Long</sub> (D<sub>2L</sub>) and D<sub>2-Short</sub> (D<sub>2S</sub>), which differ by an insertion of 29 amino acids in the third intracellular loop of D<sub>2L</sub> [1, 2].

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R.J. Romanelli (✉)  
Helix Medical Communications, San Mateo, CA 94404, USA  
e-mail: robert.romanelli@helixhh.com

Although dopamine receptors are similar in structure, receptor subtypes differ by their affinity for dopamine and coupling to downstream effectors, including heterotrimeric guanine nucleotide-binding proteins (G proteins) [3]. These factors, in addition to the differential distribution of individual receptor subtypes, contribute to the complexity of dopaminergic signaling in the brain.

Signaling through dopamine receptors regulates neural processes such as motor activity, motivation and reward (including drug-seeking behavior), and higher cognition (including working memory) [4]. Dysfunction of dopamine signaling contributes to the pathophysiology of various neurological and psychiatric illnesses, including Parkinson's disease, Tourette's syndrome, schizophrenia, mood disorders, and drug addiction. The signaling pathways through which dopamine receptors mediate such behaviors in normal and disease states remain enigmatic. Our challenge is to understand how dopamine-regulated signaling pathways are integrated downstream of the multiple receptor subtypes to produce diverse behavioral outcomes.

In this chapter, we discuss the signaling pathways regulated by individual dopamine receptor subtypes and the contribution of these pathways to dopamine-induced behaviors. Particular focus is given to the behavioral effects of drugs of abuse, including the psychostimulants cocaine, amphetamine, and methamphetamine, which act as non-selective, indirect agonists of dopamine receptors by elevating extracellular levels of dopamine. These drugs have been well studied in rodent models of addiction, in which endogenous dopamine receptors can be modified genetically or pharmacologically. Accordingly, these studies provide a valuable tool for parsing the role of dopamine receptor signaling pathways and their behavioral correlates.

### ***6.1.2 Expression***

Dopamine receptor subtypes are expressed differentially throughout the brain. Of the D1-like receptors, D<sub>1</sub> receptors are the most abundant, with mRNA transcripts found in the neostriatum, nucleus accumbens, and olfactory tubercle. Lower levels of D<sub>1</sub> receptor mRNA are found in the cerebral cortex, hypothalamus, and thalamus [5]. D<sub>5</sub> receptor mRNA is found mainly in the hippocampus and hypothalamus [6].

Of the D2-like receptors, D<sub>2</sub> receptors are the most abundant, with mRNA transcripts found in the neostriatum, nucleus accumbens, and olfactory tubercle, as well as the midbrain, including the substantia nigra and ventral tegmental area [5]. D<sub>2</sub> mRNA transcripts also are found in the pituitary [7]. Khan and colleagues, using specific antibodies directed against the D<sub>2</sub> splice variants, report that D<sub>2S</sub> is located predominantly in cell bodies and axons of dopaminergic neurons of the primate midbrain, whereas D<sub>2L</sub> is more strongly expressed by neurons of the striatum and nucleus accumbens that are targeted by dopaminergic neurons [8]. Accordingly, in the primate brain, D<sub>2S</sub> and D<sub>2L</sub> are primarily localized to pre- and postsynaptic

membranes, respectively. The physiological role for pre- or postsynaptic dopamine receptors is discussed at length later in Section 6.7.

D<sub>3</sub> and D<sub>4</sub> receptors are less abundant and less widely distributed compared to D<sub>2</sub> receptors. D<sub>3</sub> receptor mRNA transcripts are found in the nucleus accumbens, olfactory tubercle, and hippocampus [9]. Lower levels of D<sub>3</sub> receptor mRNA are found in the hypothalamus, neostriatum, and midbrain. Finally, D<sub>4</sub> receptor mRNA is found primarily in areas of the cerebral cortex, hippocampus, cerebellum, and amygdala [10].

## 6.2 Dopamine Receptor Coupling to G Proteins

Dopamine receptor signaling is mediated chiefly through heterotrimeric G proteins, which are comprised of an  $\alpha$ ,  $\beta$ , and  $\gamma$  subunit complex [11]. The G protein  $\alpha$  subunit ( $G\alpha$ ) binds guanine nucleotides and cycles between an *inactive* GDP-bound state and an *active* GTP-bound state [12]. Upon agonist binding, receptors undergo a conformation change that activates  $G\alpha$  through the exchange of GDP for GTP, resulting in the dissociation of the constitutive dimeric G protein  $\beta$  and  $\gamma$  subunits ( $G\beta\gamma$ ).  $G\alpha$ -GTP and  $G\beta\gamma$  directly modulate downstream targets of dopamine receptors, including second messengers and ion channels [13]. Finally, G protein activity is terminated by GTP hydrolysis and the re-formation of the G protein heterotrimer [12]. It is important to keep in mind that, although we speak of “dissociation” and “re-formation” of the heterotrimer to describe what is happening functionally, the extent to which there is physical dissociation, as opposed to protein conformational changes within a stable multi-protein signalplex, is still being determined [14, 15].

A distinguishing feature of D1- and D2-like receptors is their differential coupling to heterotrimeric G proteins. In many cell types D1-like receptors couple to  $G\alpha_s$ , which activates adenylate cyclase [16, 17]; however, recent evidence suggests that  $G\alpha_{olf}$ , a G protein originally identified as a mediator of olfaction, also couples to D1-like receptors for the stimulation of adenylate cyclase. In the rodent neostriatum, where expression of  $G\alpha_{olf}$  is abundant and  $G\alpha_s$  is relatively low [18], D<sub>1</sub> receptor activation of adenylate cyclase is mediated by  $G\alpha_{olf}$  [19, 20]. In contrast, D2-like receptors couple to the pertussis toxin-sensitive  $G\alpha_i$  or  $G\alpha_o$ , which inhibit adenylate cyclase [21]. Numerous studies have reported that D<sub>2</sub> receptors are capable of coupling to and activating multiple pertussis toxin-sensitive G proteins, and it seems likely that different G protein subtypes mediate distinct signaling responses [22, 23], but evidence from a variety of experimental approaches suggests that  $G\alpha_o$  is particularly important for signaling by D<sub>2</sub> receptors [22–28] and by D<sub>3</sub> receptors [29, 30], particularly in the rodent brain [31]. Characterization of  $G\alpha_z$  null mutant mice suggests that this member of the  $G\alpha_i$  family is also important for D2-like receptor function [32].

The coupling of dopamine receptors to specific  $G\beta\gamma$  proteins is less characterized. In mice lacking  $G\gamma_7$ , a subunit enriched in the dopamine receptor-expressing medium spiny neurons of the neostriatum [33], D1-like receptor-induced adenylate

cyclase activity is reduced in this brain region [34]. Notably, these animals also display a significant and selective reduction in  $G\alpha_{olf}$  expression in the striatum. Thus, striatal D1-like receptors likely regulate adenylate cyclase through  $G\alpha_{olf}/G\beta\gamma_7$ . In HEK293 cells, reduced expression of  $G\gamma_7$  also causes a loss of expression of  $G\beta_1$ ; the loss of these two subunits is associated with decreased stimulation of adenylate cyclase by D<sub>1</sub> receptors, but not D<sub>5</sub> receptors [35].

In addition to the aforementioned G proteins, which regulate adenylate cyclase activity, increasing evidence suggests that dopamine receptors couple to G proteins that modulate alternative effectors. For example, D1- and D2-like receptor coupling to  $G\alpha_q$ , which stimulates phospholipases and the consequent hydrolysis of phosphoinositides, has been described [13]. In what follows, we discuss the coupling of dopamine receptor subtypes to G proteins in the context of specific signaling and behavioral responses.

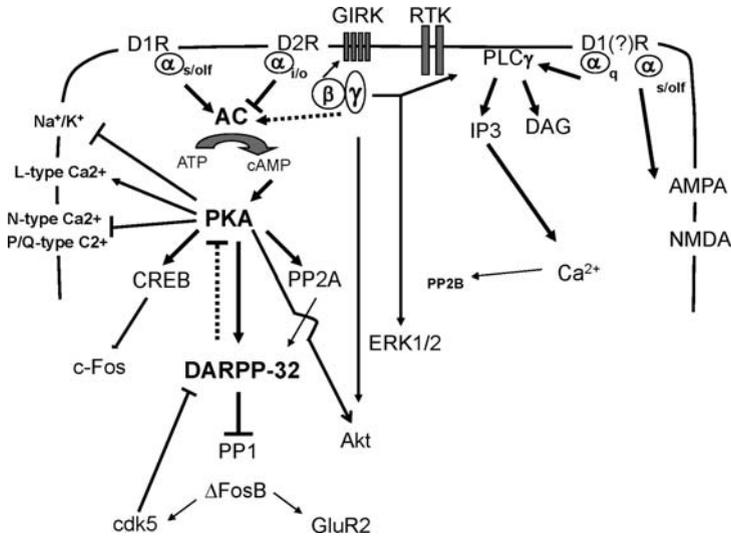
## 6.3 Regulation of Adenylate Cyclase

### 6.3.1 D1-Like Receptor Regulation of Adenylate Cyclase

D1-like receptor stimulation of  $G\alpha_s$  or  $G\alpha_{olf}$  induces the activation of adenylate cyclase, an enzyme that catalyzes the conversion of ATP to cyclic AMP, and consequently the disinhibition of the catalytic subunit of cyclic AMP-dependent protein kinase (PKA). In the striatum, D1-like receptors likely activate PKA through adenylate cyclase 5, which is highly expressed in this brain region [36], since genetic ablation of this isoform almost eliminates D1-like agonist-stimulated adenylate cyclase activity [37]. PKA in turn phosphorylates multiple downstream targets, including the cyclic AMP regulatory element-binding protein (CREB), the dopamine and cyclic AMP-regulated phosphoprotein, 32 kDa (DARPP-32), and various ion channels (Fig. 6.1).

D1-like receptor-mediated phosphorylation of CREB at Ser133 by PKA leads to the translocation of CREB to the nucleus and CREB-dependent transcription of numerous genes, including the immediate early gene *c-fos* [38]. CREB-induced gene transcription is associated with synaptic plasticity and memory formation [39] and with long-term changes in gene expression and synaptic function associated with drug addiction [40].

PKA-dependent phosphorylation of DARPP-32, a striatal-enriched phosphoprotein, at Thr34 leads to DARPP-32-dependent inhibition of protein phosphatase 1 (PP1) [41, 42]. PP1 inhibition, however, is negatively regulated through cyclin-dependent kinase 5-induced phosphorylation of DARPP-32 at Thr75, resulting in DARPP-32-mediated inhibition of PKA [43]. In contrast, PP1 inhibition is augmented by PKA-dependent activation of protein phosphatase 2A, which dephosphorylates DARPP-32 at Thr75 [44]. Therefore, DARPP-32 is regulated by phosphorylation at multiple residues through a complex positive and negative feedback system. DARPP-32 also activates the transcription factor  $\Delta$ FosB, which regulates



**Fig. 6.1** Dopamine receptor G protein-mediated signaling. D1- and D2-like receptors activate multiple signaling pathways through G proteins, including the canonical adenylate cyclase-PKA-DARPP-32 and PLC pathways, as well as the non-canonical Akt and ERK pathways. Although not depicted in the figure, many PKA-mediated responses involve both direct PKA-catalyzed phosphorylation and inhibition of dephosphorylation via DARPP-32-mediated inhibition of PP1. The D<sub>1</sub> receptor, in particular, influences the localization and function of AMPA- and NMDA-type glutamate receptors by both PKA-mediated phosphorylation and protein:protein interactions. The D<sub>1</sub>-like receptor that activates PLC might be a D<sub>1</sub> receptor, a D<sub>5</sub> receptor, or a D<sub>1</sub>/D<sub>2</sub> heteromer. AC, adenylate cyclase; CaMK, calcium-, calmodulin-dependent kinase; Cdk5, cyclic-dependent kinase 5; CREB, cyclic AMP response element-binding protein; DAG, diacylglycerol; GIRK, G protein-regulated inwardly rectifying potassium channel; IP<sub>3</sub>, inositol trisphosphate; PKA, cyclic AMP-dependent protein kinase; PLC, phospholipase C; PP1, 2A, 2B, protein phosphatase-1,- 2A, -2B; RTK, receptor tyrosine kinase

the expression of the GluR2 AMPA–glutamate receptor subunit, cyclin-dependent kinase 5, and dynorphin [45, 46].

Several lines of evidence suggest that the activity of DARPP-32 is regulated by drugs of abuse. For example, amphetamine increases DARPP-32 phosphorylation at Thr34 and Ser130 in the frontal cortex and neostriatum [47]. Acute methamphetamine administration also increases DARPP-32 phosphorylation at Thr34 in the nucleus accumbens, but chronic administration of methamphetamine decreases Thr34 phosphorylation [48]. DARPP-32 is required for cocaine-induced expression of ΔFosB [49], which persists for days to weeks following administration of various drugs of abuse and may serve as a molecular switch for long-term changes in gene expression associated with addiction [46, 50].

PKA directly phosphorylates voltage- and ligand-gated ion channels or indirectly promotes phosphorylation of these channels through DARPP-32-mediated inhibition of PP1 [13]. Multiple putative PKA phosphorylation sites have been identified in voltage-gated Na<sup>+</sup> channels [51, 52]. D1-like receptor-mediated PKA activation

decreases  $\text{Na}^+$  and  $\text{K}^+$  inward rectifying channels [53, 54] but increases L-type and decreases N and P/Q-type  $\text{Ca}^{2+}$  channel activity [55]. Direct interactions between the  $\text{D}_1$  receptor and  $\text{Ca}^{2+}$  channels may also contribute to regulation of channel distribution and function [56].

Additionally,  $\text{D}_1$ -like receptors modulate glutamatergic and GABAergic neurotransmission through protein–protein interactions [57–59] and via the phosphorylation of NMDA, AMPA, and GABA receptor subunits [60, 61], thereby altering receptor currents.  $\text{D}_1$ -like receptor-induced phosphorylation of the GluR1 AMPA receptor subunit is observed in mice after treatment with cocaine and methamphetamine, and requires DARPP-32 [62]. The regulation of ion channels by dopamine receptors is discussed at greater length in Chapters 7, 11, and 14.

### ***6.3.2 D2-Like Receptor Regulation of Adenylate Cyclase***

$\text{D}_2$ -like receptors inhibit adenylate cyclase through coupling to the pertussis toxin-sensitive G proteins  $\text{G}\alpha_i$  and  $\text{G}\alpha_o$ , thereby decreasing or preventing stimulation of cyclic AMP production [63–66]. Accordingly,  $\text{D}_2$ -like receptors act oppositely to  $\text{D}_1$ -like receptors in the regulation of substrates downstream of cyclic AMP, including PKA and DARPP-32.  $\text{D}_2$  receptor stimulation decreases DARPP-32 phosphorylation at Thr34 and increases DARPP-32 phosphorylation at Thr75, inhibiting this phosphoprotein [44, 67]. It would be expected that  $\text{D}_2$ -like receptor stimulation also decreases CREB phosphorylation. However, in sagittal brain slices (including the neocortex, neostriatum, hippocampus, thalamus, and substantia nigra) the  $\text{D}_2$ -like agonist quinpirole stimulates CREB phosphorylation, presumably through a cyclic AMP-independent mechanism [68].

The nature of functional differences between  $\text{D}_2$  receptor splice variants remains controversial; however, a few studies have reported differences in their pharmacological properties, such that  $\text{D}_{2S}$  receptors have a two to threefold higher affinity for some substituted benzamide drugs compared to  $\text{D}_{2L}$  receptors [69, 70].  $\text{D}_{2S}$  and  $\text{D}_{2L}$  receptors are also thought to couple differently to G proteins, since the alternatively spliced exon lies in a region that mediates G protein interactions. This is supported by evidence that heterologously expressed  $\text{D}_{2S}$  receptors in cell lines have a higher affinity for dopamine in the absence of GTP compared to  $\text{D}_{2L}$  receptors [69, 71, 72]. Furthermore,  $\text{D}_{2S}$  receptors more potently inhibit adenylate cyclase than  $\text{D}_{2L}$  receptors [73, 74]. Taken together,  $\text{D}_{2S}$  receptors may be more efficiently coupled to or interact with distinct subtypes of G proteins.

### ***6.3.3 Cyclic AMP-Dependent Signaling and Behavior***

Considerable evidence suggests that cyclic AMP-dependent signaling is important for modulating dopamine-induced behaviors. A null mutation of  $\text{G}\alpha_{olf}$  or adenylate cyclase 5 in mice increases spontaneous locomotor activity [19, 37], whereas when

stimulated with psychostimulants, animals deficient in either  $G\alpha_{olf}$  or DARPP-32 display an attenuated locomotor response [19, 49, 75], consistent with the phenotype of  $D_1$  receptor KO animals [76, 77]. Notably, adenylate cyclase 5 KO mice retain  $D_1$  agonist-induced locomotor behaviors, but haloperidol-induced catalepsy and the ability of sulpiride and haloperidol to suppress locomotor behavior ( $D_2$  receptor-mediated effects) are markedly impaired in these animals [37].

Although PKA-deficient mice display no change in spontaneous activity [78], psychostimulant-induced expression of *c-fos* in the dorsal medial striatum and  $D_2$  antagonist-induced catalepsy are attenuated in PKA KO mice [79, 80]. PKA KO mice display no changes in locomotor behavior after acute administration of amphetamine or cocaine but exhibit a heightened sensitization to repeated administration of amphetamine [80]. Direct infusion of cyclic AMP analogs into the nucleus accumbens, resulting in the inhibition or activation of PKA, respectively, reduces or enhances cocaine-seeking behavior [81, 82]. Thus, PKA activity is associated with psychostimulant-seeking behavior and sensitization but may not be required for acute responses to these drugs.

DARPP-32 KO mice are also unresponsive to inhibition of locomotor activity via  $D_2$  antagonists [42], and lose  $D_2$  receptor-mediated inhibition of glutamatergic neurotransmission and enhancement of intercellular coupling in nucleus accumbens spiny neurons [83]. Together, these data suggest that  $D_1$ -like receptors can regulate locomotor activity independent of cyclic AMP signaling but that normal regulation of this behavior by  $D_2$ -like receptors requires cyclic AMP.

## 6.4 Regulation of Phospholipase C

### 6.4.1 $D_1$ -Like Receptor Regulation of Phospholipase C

Stimulation of phospholipase C (PLC) induces phosphoinositide hydrolysis, leading to the production of inositol trisphosphate (IP3) and the concomitant mobilization of calcium from intracellular stores [84, 85]. Calcium release, in turn, regulates calcium-dependent proteins such as calcium/calmodulin-dependent kinase II (CaMKII) and protein phosphatase 2B (calcineurin).

A putative  $D_1$ -like receptor that stimulates PLC has been proposed. Most  $D_1$  receptor agonists stimulate accumulation of inositol phosphate in several brain regions; in addition, a  $D_1$  agonist, SKF83959, with behavioral effects similar to other  $D_1$  agonists but that antagonizes  $D_1$  receptor stimulation of adenylate cyclase, stimulates PLC rather than adenylate cyclase [86–91]. Interestingly, another ligand, SKF83822, has been identified that activates  $D_1$ -like receptor-mediated cyclic AMP accumulation but not stimulation of PLC [92]; this compound has behavioral effects that are distinct from those of most other  $D_1$ -like receptor agonists [93]. In particular, SKF83822 induces seizures that are abolished in  $D_1$  KO mice and decreased in DARPP-32 KO mice, indicating a significant contribution of this signaling pathway to the behavior [94]. As mentioned in the previous section, the existence of  $D_1$ -like

receptors that signal independently of  $G\alpha_{olf}$ /adenylate cyclase is underscored in both  $G\alpha_{olf}$  and adenylylase 5 KO mice, in which  $D_1$  agonist-induced locomotor activity is preserved [37, 95].

$D_1$ -like receptors stimulate PLC through coupling to the G protein  $G\alpha_q$  [89, 96–98]. The distribution of  $G\alpha_q$  overlaps with  $D_1$  agonist-induced PLC stimulation in brain regions in which expression of  $G\alpha_{olf}$  is low and adenylylase activation is weak, namely the amygdala and hippocampus [86, 96, 99]. However, several studies report that  $D_1$  receptor agonists stimulate PLC in neurons from other brain regions, such as the neostriatum and prefrontal cortex, and regulate neuronal excitability [100, 101].

In  $D_1$  receptor KO mice SKF83959-mediated production of inositol phosphate and the coupling of [ $^3$ H]SCH23390-binding sites to  $G\alpha_q$  have been reported to be preserved, indicating that the PLC-linked  $D_1$ -like receptor is not a product of the *drd1* gene [102]. Notably, the  $D_1$  antagonist SCH23390 attenuates  $D_1$  agonist-induced inositol phosphate production in these animals, confirming that even in the  $D_1$  receptor KO animals the response is mediated by a  $D_1$ -like receptor. This is, however, contradicted by a more recent finding that activation of  $G\alpha_q$  by dopamine receptor agonists was abolished in  $D_1$  and in  $D_2$  receptor KO mice [103]. It has also been suggested that the PLC-linked receptor is possibly of the  $D_5$  receptor subtype since genetic deletion of this receptor attenuates SKF83959-induced grooming behavior [104]. Indeed, Undie and colleagues recently reported that  $D_1$ -like receptor activation of PLC is reduced or ablated in  $D_5$  receptor KO mice [105]. On the other hand,  $D_5$  receptor abundance is low in the mouse amygdala [106], a brain region which in the rat is rich in  $D_1$ -linked PLC [86].

### 6.4.2 *D2-Like Receptor Regulation of PLC*

In contrast to  $D_1$ -like receptors, activation of  $D_2$ -like receptors stimulates PLC and calcium mobilization through mechanisms including  $G\beta\gamma$  and receptor tyrosine kinase transactivation, depending on the receptor subtype and brain region. For example, in acutely dissociated neostriatal medium spiny neurons,  $D_2$  receptor stimulation produces  $G\beta\gamma$ -mediated activation of PLC, resulting in dephosphorylation and inhibition of L-type  $Ca^{2+}$  channels [107]. In prefrontal cortical neuronal cultures,  $D_4$  but not  $D_{2L}$  receptors stimulate a rapid translocation of CaMKII to postsynaptic membranes and consequent GluR1 AMPA receptor subunit phosphorylation via the stimulation of PLC and calcium mobilization [108].  $D_2$  and  $D_3$  receptor-induced transactivation of the platelet-derived growth factor receptor (PDGFR) inhibits NDMA-evoked currents in a PLC $\gamma$ -dependent manner in prefrontal cortical neurons [109]. In cultured hippocampal neurons,  $D_4$  receptor-induced transactivation of the PDGFR inhibits NMDA-evoked currents in a  $G\alpha_{i/o}$ -, PLC $\gamma$ -dependent manner [110]. These pathways may contribute to the cyclic AMP-independent regulation of CREB observed by Yan and colleagues [68].

### **6.4.3 Regulation of PLC Through D<sub>1</sub> and D<sub>2</sub> Receptor Heteromerization**

Recent evidence suggests that pharmacologically unique D<sub>1</sub> and D<sub>2</sub> receptor heteromers stimulate PLC and induce the release of calcium from intracellular stores through G $\alpha_q$  coupling [103, 111]. In HEK293 cells co-expressing D<sub>1</sub> and D<sub>2L</sub> receptors, co-application of the D<sub>1</sub> agonist SKF81297 and the D<sub>2</sub> agonist quinpirole, or application of dopamine, stimulates calcium mobilization in a PLC- and IP<sub>3</sub>-dependent manner. The application of D<sub>1</sub> agonist alone produces only a small rise in intracellular calcium; this, however, is not observed in cells individually expressing the D<sub>1</sub> or D<sub>2L</sub> receptor, where agonist stimulation has no effect on calcium mobilization, suggesting that an interaction between the D<sub>1</sub> and D<sub>2</sub> receptor is required. A role for activation of G $\alpha_q$  in the response is indicated by its insensitivity to pertussis toxin and sensitivity to a G $\alpha_q$  inhibitor, and by the demonstration of heteromer-mediated activation of G $\alpha_q$ . Interestingly, unlike most adenylate cyclase-stimulating D<sub>1</sub> agonists, the adenylate cyclase-specific agonist SKF83822 does not increase Ca<sup>2+</sup> mobilization even in the presence of quinpirole, and the PLC-specific D<sub>1</sub> agonist SKF83959 activates the putative heteromer and Ca<sup>2+</sup> mobilization in the absence of a D<sub>2</sub> agonist [103].

Heteromerization of D<sub>1</sub> and D<sub>2L</sub> receptors is supported by studies in which both receptor subtypes have been co-immunoprecipitated from the rat neostriatum and from heterologous expression systems [111, 112]. Notably, the abundance of the putative D<sub>1</sub>/D<sub>2L</sub> receptor complex increases in the rat neurostriatum during brain development, becoming most abundant in late adulthood [103].

The aforementioned studies suggest that the formation of dopamine receptor heteromers mediates coupling to G $\alpha_q$  and consequently increases dopamine-regulated calcium signaling. The implications of this developmental “switch” for dopamine receptor signaling in the context of neural development and neurological diseases remain undefined, and significant questions remain about the extent of co-localization of D<sub>1</sub> and D<sub>2</sub> receptors in striatal neurons [113].

It is tempting to conclude that the G $\alpha_q$ -coupled D<sub>1</sub>/D<sub>2</sub> heteromer and the PLC-linked D<sub>1</sub> receptor are the same molecular entity, particularly considering the correspondence between the effects of adenylate cyclase-selective SKF83822 and PLC-selective SKF83959 in the two systems, but as alluded to above there are two significant discrepancies. First, the PLC-linked D<sub>1</sub> receptor has not been reported to require co-activation of D<sub>2</sub> receptors, whereas both receptors in the D<sub>1</sub>/D<sub>2</sub> heteromer must be activated. It has been argued that the high concentrations of D<sub>1</sub> agonists used to characterize the PLC-linked D<sub>1</sub> receptor would likely activate D<sub>2</sub> receptors, as well [114]; however, in earlier reports D<sub>2</sub> receptor antagonists did not prevent activation of G $\alpha_q$  by dopamine [96, 99], formation of IP<sub>3</sub> by SKF83959 [89], or SKF83959-induced Ca<sup>2+</sup> mobilization in hippocampal neurons [115], indicating that activation of D<sub>2</sub> receptors was not involved in these responses. Second, as mentioned above, Friedman et al. reported that dopamine- and SKF83959-induced inositol phosphate accumulation in the cortical slices and coupling of [<sup>3</sup>H]SCH23390-binding sites to G $\alpha_q$  were unaltered in D<sub>1</sub> receptor KO

mice [102] and Sahu et al. reported that D1-like receptor-induced inositol phosphate accumulation is lost in D<sub>5</sub> receptor KO mice [105], whereas Rashid et al. reported that activation of G $\alpha_q$  in neostriatal tissue by co-activation of D<sub>1</sub> and D<sub>2</sub> receptors was abolished in either D<sub>1</sub> or D<sub>2</sub> receptor KO mice [103].

#### **6.4.4 PLC and Behavior**

Compared to dopamine-induced cyclic AMP signaling, less is known about the behavioral implications of dopamine-induced PLC signaling. However, that disruption of cyclic AMP-dependent signaling results in modest effects on many D<sub>1</sub> receptor-mediated behaviors suggests that alternative pathways such as PLC might regulate those behaviors. Indeed, D<sub>1</sub> agonists that stimulate both adenylate cyclase and PLC and the atypical D<sub>1</sub> agonist SKF83959 that stimulates only PLC elicit similar behaviors when administered to rodents and primates [87, 116–118]. In addition, like other D<sub>1</sub> agonists, SKF83939 induces contralateral rotations in the unilateral 6-hydroxydopamine-lesioned rodent model of Parkinson's disease [119, 120]. In contrast, the adenylate cyclase-specific D<sub>1</sub> agonist SFK83822 induces sniffing and seizures in mice [93]. These observations suggest that many behaviors induced by D<sub>1</sub> receptor agonists require activation of PLC.

Deletion of PLC $\beta$ -1 in mice enhances locomotor hyperactivity but impairs sensorimotor gating, socialization, and cognitive skills, behaviors generally associated with schizophrenia in humans. The D<sub>2</sub> antagonists and antipsychotic drugs clozapine and haloperidol rescue some of these impairments [121, 122] suggesting a role for dopaminergic signaling in this phenotype. Furthermore, an increase and decrease of PLC $\beta$ -1 in the prefrontal cortex and superior temporal cortex, respectively, has been reported in patients with schizophrenia [123].

### **6.5 Arrestin-Dependent Signaling**

#### **6.5.1 Overview**

Originally identified as a protein involved in receptor desensitization [124] and then resensitization [125], there is increasing evidence for a role of arrestin in GPCR signaling [126, 127], particularly for signaling pathways other than the canonical heterotrimeric G protein-regulated pathways (adenylate cyclase, phospholipase C, G $\beta\gamma$ -regulated ion channels). It ought to be noted that although in some cases arrestin-mediated signaling has been shown to be independent of G proteins because it can be induced by ligands that are antagonists for receptor activation of G proteins [128, 129] or mediated by mutant receptors that are incapable of coupling to G proteins [130], in other cases it seems possible that stimulation of G proteins is *required* for receptor phosphorylation and arrestin binding prior to arrestin-dependent signaling.

Arrestin-dependent signaling may involve the spatial redistribution of dopamine receptors from the plasma membrane into endosomal vesicles, facilitating the interaction of receptors with distinct cytosolic signaling proteins not available at the cell surface, a mechanism that has been demonstrated for other receptor families such as receptor tyrosine kinases [131]. In addition, arrestin may serve as a scaffold for specific signaling proteins, such as Akt, during desensitization of G protein-mediated signaling [132].

Arrestin2 KO mice display normal spontaneous locomotor behavior but reduced apomorphine-induced climbing [133]. Arrestin3 KO mice also exhibit reduced apomorphine-induced climbing, along with reduced amphetamine-induced locomotor activity [133, 134]. (Arrestin2 and 3 are also referred to as  $\beta$ arrestin1 and 2, respectively.) These data suggest roles for arrestin2 and, in particular, arrestin3, that are independent of desensitization, because responses would be elevated in the arrestin KO mice if the primary function of arrestin were to reduce dopamine receptor responsiveness.

In the following sections we discuss the regulation of non-canonical dopamine receptor-mediated signaling pathways that have been often described as arrestin dependent, namely the MAP kinase and Akt/GSK-3 $\beta$  pathways. However, in many studies these pathways also are activated in a G protein-dependent manner. Regardless, these non-canonical pathways are important for the regulation of dopamine-induced behaviors and are discussed in the context of activation by psychostimulants and through individual dopamine receptor subtypes.

## **6.5.2 Regulation of MAP Kinases**

### **6.5.2.1 Overview of MAP Kinases**

Mitogen-activated protein (MAP) kinases regulate a variety of cellular processes including cell growth, proliferation, differentiation, and survival [135]. MAP kinases are divided into three major groups: the extracellular-regulated kinases (ERKs), the c-jun N-terminal kinases (JNKs), and the p38 kinase [135, 136]. In the brain, signaling through the ERKs, particularly ERKs 1 and 2 (ERK1/2), is involved in neuronal plasticity, memory formation, and locomotor behavior, whereas the JNK and p38 signaling pathways are involved in neuronal stress responses [137–141]. Most studies of psychostimulant regulation of MAP kinase pathways in the brain have focused on ERK1/2.

The ERK1/2 pathway is regulated by drugs of abuse through enhanced dopaminergic signaling in rodents, although there are discrepancies among studies that may reflect time- and brain region-dependent changes in ERK1/2 phosphorylation. Repeated but not acute cocaine administration induced ERK1/2 phosphorylation in the ventral tegmental area [142]. In a study by Valjent and colleagues, however, acute injection of cocaine induced phosphorylation of ERK1/2 in medium spiny neurons of the nucleus accumbens and neostriatum [143]. In other studies, both

acute and chronic administration of cocaine induced ERK1/2 phosphorylation in the prefrontal cortex, neostriatum, and amygdala [144–146].

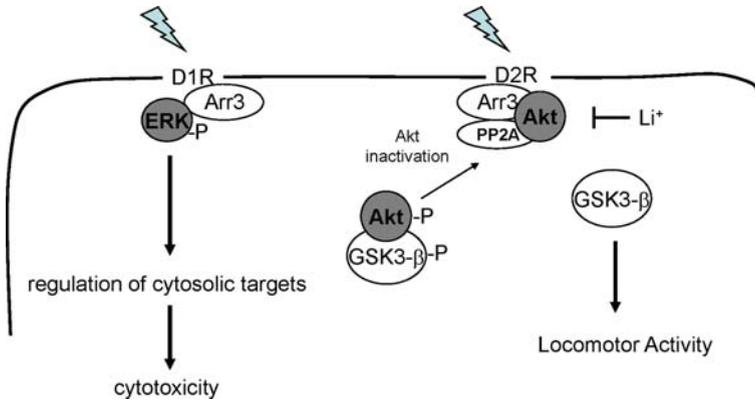
Activation of the ERK1/2 pathway, in turn, is required for the expression of many psychostimulant-induced behaviors. In mice, the blockade of the ERK1/2 pathway with MAP kinase and ERK kinase (MEK) inhibitors attenuates the rewarding properties of cocaine and amphetamine [143, 147, 148]. Furthermore, ERK1/2 inhibition prevents cocaine-induced sensitization and expression of the immediate-early gene *c-fos* [149–151]. Interestingly, the genetic deletion of ERK1 in mice results in an increased cocaine-induced sensitization and an enhanced response to the rewarding properties of morphine due to potentiated ERK2 signaling [152, 153]. These data are consistent with other studies *in vivo* and *in vitro* demonstrating that ERK1 is a less efficient kinase and consequently attenuates ERK2 signaling [154–156]. Thus, ERK1 and ERK2 may negatively and positively regulate psychostimulant-induced behaviors, respectively. The above data strongly implicate ERK1/2 activation in dopamine receptor-mediated behavioral responses to psychostimulant drugs. Evidence for the direct regulation of the MAP kinase pathways through specific dopamine receptor subtypes is discussed below.

#### 6.5.2.2 D1-Like Receptor Regulation of MAP Kinases

The regulation of MAP kinases through the D<sub>1</sub> receptor appears to be agonist-, cell-, and time-dependent. In primary striatal cultures, acute stimulation (2–20 min) with the selective D<sub>1</sub>-like receptor agonist SKF38393 induces ERK1/2 activation [157, 158]. Co-activation of D<sub>1</sub>-like receptors and metabotropic glutamate receptors also causes a PKC-dependent activation of ERK that is greater than the activation for either receptor subtype alone [158]. In contrast, acute stimulation of endogenous D<sub>1</sub> receptors with SKF38393 activates JNK and p38, but not ERK1/2 in a neuroblastoma cell line [159]. However, more prolonged (60–120 min) stimulation with dopamine or with the D<sub>1</sub> agonist SKF38393 in these cells results in activation of JNK, p38, and ERK1/2 in addition to ERK1/2-mediated oxidative stress and cytotoxicity [160]. This pathway requires an interaction between the D<sub>1</sub> receptor, phosphorylated ERK1/2, and arrestin3, which retains activated ERKs in the cytosol (Fig. 6.2).

Recent evidence suggests that ERKs activate distinct substrates in cytosol compared to the nucleus. For example, ERKs localized in the nucleus induce gene transcription leading to mitogenesis and survival, whereas ERKs localized in the cytosol are reported to induce cytotoxicity [161]. D<sub>1</sub> receptor-mediated cytotoxicity as described by Chen and colleagues [160] provides a novel mechanism by which dysfunction of dopaminergic neurotransmission, in cases such as chronic psychostimulant drug use, may cause striatal neurodegeneration [162, 163].

*In vivo*, stimulation of D<sub>1</sub>-like receptors after dopamine depletion in the neostriatum induces ERK1/2 activation [164]. Furthermore, D<sub>1</sub> receptors stimulate NDMA receptor-dependent activation of the ERK1/2, JNK, and p38 kinase pathways in the neostriatum [151, 165]. Selective antagonists to D<sub>1</sub>- but not D<sub>2</sub>-like receptors attenuate ERK1/2 phosphorylation in the neostriatum [143, 146]. Valjent and colleagues also show diminished cocaine-induced ERK1/2 phosphorylation in DARPP-32 KO



**Fig. 6.2** Dopamine receptor arrestin-mediated signaling. D1- and D2-like receptors can mediate non-canonical signaling pathways (ERK and Akt/GSK-3 $\beta$ ) through the formation of arrestin-dependent signaling complexes. Receptor-activated arrestin3 is a scaffold for both PP2A and Akt, promoting PP2A-mediated dephosphorylation and inactivation of Akt. GSK3- $\beta$  is activated by the reduced Akt-mediated inhibitory phosphorylation. Lithium disrupts the arrestin3/Akt/PP2A signaling complex and thus prevents the activation of GSK3- $\beta$ . Arr3, arrestin3 ( $\beta$ arrestin2); GSK3- $\beta$ , glycogen synthase kinase 3- $\beta$ ; PP2A, protein phosphatase-2A

mice, further suggesting a role of D1-like receptors in the activation of this pathway [150]. Similarly, direct administration of the selective D1-like receptor antagonist SCH-23390 into the prefrontal cortex of rodents attenuates ERK activation [166]. Anatomical evidence also supports a role for the D<sub>1</sub> receptor, but not the D<sub>2</sub> receptor, in psychostimulant-induced activation of ERK1/2 [167]. Thus, considerable evidence suggests that combined stimulation of ERK2 by D<sub>1</sub> and NMDA receptors mediates many psychostimulant-induced behaviors [153].

### 6.5.2.3 D2-Like Receptor Regulation of MAP Kinases

Various studies report that D2-like receptors activate MAP kinase pathways; however, the mechanism of activation appears to differ depending on D2-like receptor subtype and cell type. Such mechanisms include the pertussis toxin-sensitive  $G\alpha_{i/o}$  proteins,  $G\beta\gamma$  proteins, phosphatidylinositol-3 kinase (PI-3 K), MEK, receptor tyrosine kinase transactivation, and through arrestin binding and arrestin-mediated endocytosis.

The first evidence of D<sub>2L</sub> receptor-mediated activation of ERK1/2 was from the work of Faure et al. [168], who demonstrated a requirement for  $G\beta\gamma$ , but not activated  $G\alpha_i$ , in HEK293 cells. Subsequently, Luo et al. [169] showed that the D<sub>2L</sub> receptor expressed in C6 glioma cells activates JNK in addition to ERK1/2, and that the activation of ERK1/2 requires Ras and MEK, two upstream protein kinases in the ERK1/2 signaling cascade. In Chinese hamster ovary (CHO) cells expressing the D<sub>2S</sub> or D<sub>2L</sub> receptor, dopamine induces a rapid and transient activation of ERK1/2 in a pertussis toxin-sensitive and  $G\beta\gamma$ -dependent manner [170]. However,

D<sub>2S</sub> but not D<sub>2L</sub> receptor-stimulated ERK1/2 activation requires PKC [170]. In another study, Kim et al. [171] showed that overexpression of arrestin2 or 3 in CHO cells increases D<sub>2S</sub> but not D<sub>2L</sub> receptor-induced activation of ERK1/2. Additional evidence of a selective requirement for arrestin-dependent internalization for activation of ERK1/2 by D<sub>2S</sub> receptors is that expression of a dominant negative dynamin1 and treatment of cells with pharmacological inhibitors of receptor internalization decreases D<sub>2S</sub> but not D<sub>2L</sub> receptor-induced ERK activation. On the other hand, D<sub>2L</sub> receptor-induced ERK1/2 activation is dependent upon PDGFR transactivation [171], presumably at the cell surface, and work with an arrestin-insensitive mutant D<sub>2L</sub> receptor suggests that most D<sub>2L</sub> receptor-mediated activation of ERK1/2 in HEK293 cells is mediated by pertussis toxin-sensitive G proteins, and not by arrestin [172]. Together, these studies point to mechanistic differences in signaling through D<sub>2</sub> receptor splice variants and support the notion that D<sub>2L</sub> and D<sub>2S</sub> receptors are not functionally redundant.

Activation of D<sub>2L</sub> or D<sub>4</sub> receptors in CHO cells results in a transient, dose-dependent increase in ERK1/2 activation in a G $\alpha_{i/o}$ -, PI-3 K-, PKC-, MEK-, and PDGFR-dependent manner [173]. Studies from our laboratory corroborate the notion that D<sub>2L</sub> receptors activate ERK through transactivation of receptor tyrosine kinases. In HEK293 cells, D<sub>2L</sub> receptor-stimulated ERK1/2 phosphorylation is dependent upon the PDGFR, whereas in a neuroblastoma cell line and primary neuronal cultures D<sub>2L</sub> receptor-stimulated ERK1/2 phosphorylation is dependent upon the epidermal growth factor receptor (EGFR) [174]. Beom and colleagues, on the other hand, report that D<sub>3</sub> receptor but not D<sub>2L</sub> receptor-stimulated ERK1/2 phosphorylation requires EGFR transactivation in several non-neuronal cells [175].

Activation of D<sub>2</sub> receptors induces mitogenesis in various cell types in a PKA/cyclic AMP-independent manner [176]. D<sub>2</sub> receptor-mediated activation of ERK1/2 induces mitogenesis in C6 glioma cells [169] and an increase in the number of dopaminergic neurons in mid-brain cultures [177].

The aforementioned *in vitro* studies implicate D<sub>2</sub>-like receptors in the activation of the MAP kinase pathways, leading to mitogenesis in non-neuronal cells. Additionally, one study suggests that D<sub>2</sub> receptors activate ERK1/2 in the dopamine-denervated neostriatum, and that activation of the pathway is required for behavioral expression of D<sub>2</sub> receptor supersensitivity [178]. On the other hand, contrary evidence suggests that D<sub>2</sub>-like receptors suppress tonic activity of MAP kinases. *In vivo*, administration of D<sub>2</sub> antagonists such as haloperidol or clozapine increases ERK phosphorylation in the mouse prefrontal cortex and neostriatum [146, 179] and in D<sub>2</sub> receptor-expressing neostriatal medium spiny neurons [167]. Jiao et al. [165] demonstrated that D<sub>3</sub> receptors inhibit NMDA-induced ERK, JNK, and p38 MAP kinase pathways in the neostriatum. In primary striatal cultures, the D<sub>2</sub>-like receptor agonist quinpirole inhibits potassium-stimulated ERK1/2 phosphorylation [180], and the selective D<sub>2</sub>-like receptor antagonists haloperidol and risperidone increase the phosphorylation of ERK in primary hippocampal neurons [181].

D<sub>2</sub> receptor-mediated inhibition of ERK1/2 has also been demonstrated in neuroendocrine pituitary cells. D<sub>2S</sub> but not D<sub>2L</sub> receptors inhibited basal and thyrotropin-releasing hormone-stimulated ERK1/2 phosphorylation in pituitary cell

lines [180, 182, 183]. On the other hand, Iaccarino et al. obtained results that were similar with regard to differences between the alternatively spliced receptor isoforms, but different with regard to the effect of D<sub>2S</sub> on ERK1/2; overexpression of D<sub>2S</sub> caused activation of ERK1/2 that was associated with inhibition of lactotroph proliferation, whereas expression of D<sub>2L</sub> had little effect on phosphorylation of ERK1/2 or lactotroph proliferation [184].

### 6.5.3 Regulation of the Akt/GSK-3 $\beta$ Pathway

#### 6.5.3.1 Akt/GSK-3 $\beta$ Pathway Overview

Protein kinase B (Akt) is a well conserved serine/threonine kinase involved in the survival of most cells [185]. Classically, Akt is activated by receptor tyrosine kinases via phosphatidylinositol-3 kinase (PI-3K), although PI-3K-independent mechanisms of Akt activation have been described [186]. Akt is activated by phosphorylation at two distinct residues, Ser473 and Thr308, and in turn phosphorylates various downstream targets, leading to the inhibition of apoptosis and the regulation of gene transcription and cellular metabolism [187]. One such target of Akt is the glycogen synthase kinase (GSK)-3 $\beta$ , which is constitutively active until phosphorylated at Ser9 by Akt [186].

In recent years, the Akt/GSK-3 $\beta$  pathway has become a particularly interesting line of investigation concerning dopaminergic signaling in the brain. The Akt/GSK-3 $\beta$  pathway is regulated by drugs of abuse through enhanced dopaminergic signaling. Cocaine and amphetamine induce a rapid phosphorylation (within 10–20 min) of Akt and GSK-3 $\beta$ , respectively, in the mouse striatum [47, 157]; but other studies demonstrate that amphetamine induces dephosphorylation of Akt at later time points (30–60 min) [134, 188, 189]. Similarly, rats treated with methamphetamine display an initial increase (15 min) and subsequent decrease (120 min) in Akt phosphorylation [190]. These data suggest that enhanced dopaminergic signaling in the brain activates or inhibits the Akt/GSK-3 $\beta$  pathway depending on the duration of stimulation.

The Akt/GSK-3 $\beta$  pathway is also implicated in drug-induced behaviors and psychiatric disorders associated with dopaminergic dysfunction. Partial deletion of GSK-3 $\beta$  in mice or inhibition of GSK-3 $\beta$  with lithium – a drug commonly used to treat bipolar and other mood disorders – attenuates amphetamine-induced locomotor activity [191]. In patients with schizophrenia, total levels of Akt and phosphorylated levels of GSK-3 $\beta$  are decreased [192]. Interestingly, four studies report an association between schizophrenia and *akt1* genetic variants [192–195]. Moreover, Akt1 KO mice display impaired sensory/motor gating [192], which is also a characteristic of patients with schizophrenia [196].

The aforementioned studies strongly suggest that regulation of the Akt/GSK-3 $\beta$  pathway by dopamine receptors is a behaviorally relevant signaling response. The results of these studies are corroborated by evidence for the regulation of

the Akt/GSK-3 $\beta$  pathway through individual dopamine receptor subtypes. This evidence is discussed below.

### 6.5.3.2 D1-Like Receptor Regulation of the Akt/GSK-3 $\beta$ Pathway

In primary striatal neurons, the selective D1-like receptor agonist SKF38393 induces Akt phosphorylation at Thr308, but not Ser473, in a PI-3K-independent, MEK-dependent manner [157]. Moreover, an Akt mutant defective in kinase activity expressed in these cells blocks agonist-stimulated phosphorylation of CREB. Together, these data suggest cross-talk between the PKA, MAP kinase, and Akt signaling pathways through D1-like receptor stimulation. Interestingly, deletion of the D<sub>1</sub> receptor in mice has no effect on basal Akt or GSK-3 $\beta$  phosphorylation or on Akt phosphorylation in response to apomorphine or amphetamine in the striatum [188]. Therefore, although D1-like receptors induce Akt phosphorylation when directly stimulated with a selective agonist in striatal neurons and may be involved in psychostimulant-induced rapid activation of Akt, these receptors likely are not involved in the tonic regulation and psychostimulant-induced inhibition of the Akt/GSK-3 $\beta$  pathway.

### 6.5.3.3 D2-Like Receptor Regulation of the Akt/GSK-3 $\beta$ Pathway

In primary striatal neurons the selective D2-like receptor agonist quinpirole induces Akt phosphorylation at Thr308, but not Ser473, in a PI-3K-independent and MEK-dependent manner [157]. Additionally, a kinase-defective Akt mutant expressed in these cells blocks D<sub>2</sub> receptor-stimulated CREB phosphorylation. Thus, activation of D1- and D2-like receptors has similar effects on this pathway in neostriatal neurons. In PC12 cells heterologously expressing the D<sub>2L</sub> receptor, in a nigral cell line that endogenously expresses D<sub>2</sub> receptors, and in nigral dopaminergic neurons, the D2-like receptor agonist bromocriptine stimulates Akt (Ser473) phosphorylation through the transactivation of the epidermal growth factor receptor (EGFR) and c-src and activation of PI-3K. The D<sub>2L</sub> receptor co-immunoprecipitates with the EGFR and c-src from PC12-D<sub>2L</sub> cells, indicating that these proteins form a complex. The resulting inhibition of GSK-3 $\beta$  protects the cells against oxidative stress [197–199]. Additionally, a D<sub>4</sub>-selective agonist increases Akt kinase activity in D4-MN9D cells [200].

That Akt phosphorylation is observed at distinct residues in primary striatal neurons and cell lines suggests different mechanisms of action of endogenous and heterologous expressed dopamine receptors in the regulation of this kinase. Interestingly and in contrast to bromocriptine and ropinirole, the D2-like receptor agonist pramipexole fails to phosphorylate Akt [197–199]. Thus, certain D<sub>2</sub> receptor agonists may confer distinct conformations of the receptor, resulting in the activation of different downstream signaling pathways.

The above studies demonstrate that D2-like receptors stimulate Akt phosphorylation. Other evidence, however, implicates D2-like receptors in Akt dephosphorylation/inhibition. As noted above, this discrepancy may be in part due to

time-dependent effects of D2-like receptor stimulation on the activation state of Akt. In dopamine transporter (DAT) KO mice, which have increased dopaminergic tone due to loss of the primary mechanism for inactivation of dopaminergic neurotransmission, decreases in basal Akt (Thr308) and GSK-3 $\beta$  phosphorylation are reversed by administration of the D2-like receptor antagonist raclopride but not the D1-like receptor antagonist SCH23390 [191]. Moreover, rodents treated with D2-like receptor antagonists and commonly used antipsychotics, haloperidol, risperidone, and clozapine, display increases in Akt and GSK-3 $\beta$  phosphorylation [192, 201].

The role of D2-like receptors in regulating the Akt/GSK3 $\beta$  pathway is further confirmed by deletion studies of individual D2-like receptor subtypes [188]. D<sub>2L</sub> and D<sub>3</sub> receptor KO mice display an increase in the basal phosphorylation of Akt at Thr308; however, D<sub>2L</sub> receptor KO mice also display a decrease in the basal phosphorylation of Akt at Ser473. These data imply that D<sub>2L</sub> and D<sub>3</sub> receptors modify Akt differently. Whereas both D<sub>2L</sub> and D<sub>3</sub> receptor KO mice display an increase in basal phosphorylation of GSK-3 $\beta$ , this increase is more pronounced in D<sub>3</sub> receptor KO animals, implying that of the D2-like receptor subtypes, the D<sub>3</sub> receptor is more salient in the tonic disinhibition of GSK-3 $\beta$ . To date, Akt/GSK-3 $\beta$  phosphorylation has not been examined in D<sub>4</sub> KO mice, but mice treated with a selective antagonist to the D<sub>4</sub> receptor display no change in basal Akt or GSK-3 $\beta$  phosphorylation, suggesting that the D<sub>4</sub> receptor is not involved in the tonic regulation of this pathway in vivo [188].

Beaulieu and colleagues report that arrestin3 is necessary for the regulation of the Akt/GSK-3 $\beta$  pathway by D2-like receptors, serving as a scaffold for protein phosphatase 2A-mediated Akt dephosphorylation [134] (Fig. 6.2). Genetic deletion of arrestin3 in mice results in disinhibition of Akt, phosphorylation-induced inactivation of GSK-3 $\beta$ , and consequently an attenuated response to amphetamine-induced locomotor activity [134, 202]. The role of arrestin3 in dopamine-induced locomotor activity is underscored by the fact that arrestin3-DAT double KO mice do not display the hyperactive phenotype of DAT KO animals. Interestingly, a recent report shows that the *arrestin3* gene is associated with methamphetamine addiction in Japanese patients [203], suggesting a role for this gene in the etiology of psychostimulant-induced addiction in distinct populations.

## 6.6 D1-/D2-Like Receptor Cooperativity

### 6.6.1 Overview

D1- and D2-like receptors are thought to act cooperatively, or synergistically, to modulate dopamine-mediated behaviors, including psychiatric and motor disorders, and behavioral responses to drugs of abuse [204, 205]. Behaviorally, the requirement for activation of both receptors is reflected in the observation that administration of either D<sub>1</sub> or D<sub>2</sub> antagonists can prevent many dopamine-dependent responses [206].

Depending on the efficacy of the agonist and the endogenous dopamine tone, co-administration of D1- and D2-like agonists may be required for the full expression of some responses [207].

As reviewed by Marshall and colleagues [205], a variety of models have been proposed for D<sub>1</sub>/D<sub>2</sub> receptor synergism. The models that are most relevant for this chapter involve signal transduction pathways that require co-expression of the receptors in striatal neurons which is problematic because functionally D<sub>1</sub> and D<sub>2</sub> receptors are fairly strictly segregated in distinct populations of neostriatal neurons (e.g., [167]; see also Chapter 11). Although the two receptor subtypes are clearly antagonistic for some signaling pathways (e.g., G $\alpha_s$ - and G $\alpha_i$ -dependent regulation of adenylate cyclase), there are other pathways where stimulation of D<sub>1</sub> and D<sub>2</sub> receptors has cooperative effects. These include cyclic AMP- and G $\beta\gamma$ -dependent modulation of ion channels [208, 209], hypothesized to involve stimulation of adenylate cyclase by both G $\alpha_s$  (D<sub>1</sub>) and G $\beta\gamma$  (D<sub>2</sub>) subunits [210], inhibition of Na<sup>+</sup>,K<sup>+</sup>-ATPase [211], and activation of PLC by D<sub>1</sub>/D<sub>2</sub> receptor heteromers [103, 111]. In addition, prolonged stimulation of D<sub>2</sub> receptors can lead to enhanced D<sub>1</sub> receptor stimulation of adenylate cyclase by heterologous sensitization [212], a phenomenon discussed in more detail below.

Of particular interest is the role of individual D2-like receptor subtypes and splice variants in dopamine-induced behavior. The co-localization of D<sub>1</sub> and D<sub>3</sub> receptors in the islands of Calleja in the rat ventral forebrain raises the possibility that the D<sub>3</sub> receptor mediates synergism between D1-like and D2-like receptors [213], and although there is some evidence to support that hypothesis [213, 214], studies with dopamine receptor KO mice suggest that genetic deletion of the D<sub>3</sub> receptor has little effect on the function of D1-like receptors [77, 215]. The use of receptor subtype-selective antagonists indicates that it is the D<sub>2</sub> receptor that synergizes with the D<sub>1</sub> receptor in the neostriatum [216]. Evidence from D<sub>2</sub> and D<sub>2L</sub> receptor KO mice also suggests that D<sub>2</sub> splice variants modulate behaviors differently. For example, some behaviors induced by amphetamine, the D1/D2 agonist apomorphine, or combined administration of D1-like and D2-like agonists, are attenuated in D<sub>2L</sub> KO mice [217]. Responsiveness to the selective D1-like agonists, SKF82958 and SKF81297, was also significantly attenuated in D<sub>2L</sub> receptor KO mice but not in mice lacking both the splice variants (D<sub>2</sub> KO mice) [218], consistent with the hypothesis that D<sub>2L</sub> receptors promote D<sub>1</sub> receptor function and D<sub>2S</sub> receptors inhibit D<sub>1</sub> receptor function, but this effect on D<sub>1</sub> receptor-mediated behavior was not observed in the D<sub>2L</sub> KO mice created by Wang and colleagues [217].

### ***6.6.2 Heterologous Sensitization***

Whereas acute activation of G $\alpha_i$ /G $\alpha_o$ -coupled D<sub>2</sub> receptors inhibits adenylate cyclase, prolonged activation leads to enhanced adenylate cyclase activity (i.e., heterologous sensitization) [212]. In HEK293 and C6 glioma cells, prolonged dopamine stimulation (2 h) of G $\alpha_i$ -coupled D<sub>2</sub> and D<sub>4</sub> receptors but not D<sub>3</sub>

receptors leads to sensitization of adenylyl cyclase to subsequent activation by forskolin or  $G\alpha_s$ -coupled adrenergic receptors [219]. In vivo, repeated administration of the D2-like receptor agonist quinpirole selectively increases cyclic AMP signaling in the nucleus accumbens of rats, as measured by PKA activity and CREB phosphorylation [220]. Similarly, female hamsters that receive repeated quinpirole administration display an enhanced  $D_1$  receptor-stimulated cyclic AMP accumulation in the neostriatum [221].

The dimeric  $G\beta\gamma$ , once released from the  $G\alpha_i/G\alpha_o$ , plays a central role in heterologous sensitization.  $G\beta\gamma$  regulates the activity or subcellular localization of numerous effectors, including adenylyl cyclases type II, IV, and VII [222]. Sequestration of  $G\beta\gamma$  attenuates sensitization of adenylyl cyclase by  $G\alpha_i/G\alpha_o$ -coupled receptors [212, 223–225].

Long-term (78 h) stimulation of  $D_2$  receptors expressed in cultured cells enhances subsequent basal and forskolin-stimulated adenylyl cyclase activity, which is accompanied by a decreased expression of  $G\alpha_i$  and increased expression levels of  $G\alpha_s$  [226–229]. However, sensitization cannot be explained simply by desensitization of  $G\alpha_i$ -coupled receptors or by the downregulation of  $G\alpha_i$ , since other reports have shown that heterologous sensitization occurs in the absence of these contributing factors and very rapidly [212, 230].

As previously mentioned, enhanced cyclic AMP-dependent signaling is observed in rodents sensitized to environmental stimuli. For example, repeated psychostimulant and morphine administration enhances  $D_1$  receptor cyclic AMP-dependent signaling in nucleus accumbens and striatal neurons [231, 232]. In female Syrian hamsters, repeated sexual experience, which leads to a marked increase in extracellular dopamine levels and behavioral sensitization [233], enhances  $D_1$  receptor-stimulated cyclic AMP accumulation in the nucleus accumbens [234]. Notably, the rewarding consequences of sexual experience require D2-like dopamine receptors [235].

## 6.7 Autoreceptors

Distinct pre-synaptic dopamine receptor subtypes, termed autoreceptors, regulate the tone of dopamine neurotransmission. Autoreceptors are expressed on the cell body and dendrites of dopaminergic midbrain neurons and modulate the rate of cell firing and impulse activity [236, 237]. It is well established that autoreceptors are D2-like receptors, as both agonists (such as quinpirole) and antagonists (such as sulpiride or eticlopride) that are selective for D2-like receptors act on dopamine neurons to cause inhibition and block dopamine-induced inhibition, respectively [238, 239]. Autoreceptors are also located on dopaminergic nerve terminals where they decrease dopamine synthesis, through inhibition of the rate-limiting enzyme tyrosine hydroxylase, and dopamine release [240, 241]. D2-like autoreceptors also decrease dopaminergic activity by enhancing dopamine re-uptake via the dopamine

transporter [242–244]. Enhanced dopamine transporter activity results at least in part from increased cell surface expression of the transporter [245].

There has been considerable investigation of which D<sub>2</sub>-like receptors are capable of functioning as autoreceptors. D<sub>2</sub> and D<sub>3</sub> receptors have been commonly implicated in dopamine autoreceptor function. In a mouse mesenchymal cell line (MN9D cells), that both synthesizes and releases dopamine, heterologously expressed D<sub>2</sub> and D<sub>3</sub> receptors but not D<sub>4</sub> receptors inhibit tyrosine hydroxylase activity [246] and dopamine release [247]. Notably, D<sub>2</sub> receptors inhibit tyrosine hydroxylase activity for longer periods than D<sub>3</sub> receptors, suggesting that D<sub>2</sub> receptors have a more potent autoreceptor function. In cell expression systems, both D<sub>2</sub> and D<sub>3</sub> receptors regulate dopamine transporter function [245, 248].

Although both D<sub>2</sub> and D<sub>3</sub> receptors can function as autoreceptors in model systems, the question of which subtypes *are* autoreceptors *in vivo* has been more controversial. Initially many studies with D<sub>3</sub>-selective agonists suggested a dominant role for the D<sub>3</sub> receptor [249], but a different picture has resulted from the combined use of pharmacological and genetic tools. Genetic deletion of the D<sub>2</sub> receptor in mice abolishes all dopamine or D<sub>2</sub>-like agonist-induced inhibition of dopamine release [250–253], activation of G protein-regulated inwardly rectifying potassium (GIRK) channels [254, 255], inhibition of dopaminergic neuron firing [256], and enhancement of dopamine transporter function ([257]; but see also [252]). Pharmacological studies with D<sub>2</sub>-selective and D<sub>3</sub>-selective antagonists suggest that the autoreceptor in the guinea pig retina is also the D<sub>2</sub> receptor [258]. Mice with a genetic deletion of the D<sub>3</sub> receptor have enhanced basal dopamine levels [259, 260], but agonist-induced inhibition of dopamine synthesis and release, inhibition of GIRK channels and dopamine neuron firing, and enhancement of dopamine transporter activity are either unaltered or only modestly reduced in these mice [254, 255, 259–261]. These results indicate that the D<sub>2</sub> receptor is the predominant D<sub>2</sub> autoreceptor in the rodent brain, with the D<sub>3</sub> receptor possibly contributing to regulation of dopamine release at low concentrations of dopamine.

Surprisingly, given the similarity between D<sub>2L</sub> and D<sub>2S</sub> in heterologous expression systems, two groups have used mice in which the alternatively spliced exon 6 is deleted to identify differences in the roles that the splice variants play *in vivo* [218, 262]. These D<sub>2L</sub> receptor KO mice are deficient in behavioral and biochemical measures of postsynaptic D<sub>2</sub> receptor activation; that is, responses that are thought to be mediated by D<sub>2</sub> receptors expressed on medium spiny neurons that are postsynaptic to dopamine terminals in the basal forebrain. It is important to note that these mice express D<sub>2S</sub> receptors at approximately the levels at which wild-type mice express D<sub>2S</sub> and D<sub>2L</sub> receptors in all the neurons that normally express either variant. Even though medium spiny neurons in D<sub>2L</sub> receptor KO mice express D<sub>2S</sub> receptors, and the ability of quinpirole to stimulate binding of [<sup>35</sup>S]GTPγS is unimpaired [263], the D<sub>2S</sub> receptor does not appear to be functioning in the same way that the D<sub>2L</sub> receptor functions. Of most relevance for the topic of autoreceptors is that D<sub>2</sub> autoreceptor function is spared in D<sub>2L</sub> receptor KO mice. Thus, the ability of D<sub>2</sub>-like agonists to suppress the firing rate of midbrain neurons, to decrease the phosphorylation and activation of tyrosine hydroxylase, and, at low doses, to inhibit

locomotor activity is absent in D<sub>2</sub> receptor KO mice but spared in mice that express only the D<sub>2S</sub> receptor [218, 262–264]. Although this is often interpreted to mean that the D<sub>2S</sub> receptor is *the* D<sub>2</sub> autoreceptor, it is more accurate to interpret these data as demonstrating that the D<sub>2S</sub> receptor has the capability to function as the D<sub>2</sub> autoreceptor. Studies with D<sub>2S</sub> or D<sub>2L</sub> receptors expressed in cultured mesencephalic neurons suggest that D<sub>2L</sub> receptors can also mediate autoreceptor activity [265]. The conclusion that the D<sub>2S</sub> receptor is the autoreceptor *in vivo* is supported by one study with antibodies selective for D<sub>2S</sub> and D<sub>2L</sub> receptors reporting that, in the rhesus monkey brain, tyrosine hydroxylase-immunoreactive neurons in the substantia nigra express mainly D<sub>2S</sub> receptors. In contrast, in the striatum D<sub>2S</sub> receptor immunoreactivity is associated mainly with axons and D<sub>2L</sub> receptor immunoreactivity is in the GABAergic medium spiny neurons [8]. There is also one report that D<sub>2S</sub> receptor mRNA is more abundant than D<sub>2L</sub> receptor mRNA in the murine brainstem [266].

Several signaling pathways modulated by D<sub>2</sub> receptors might be predicted to mediate autoreceptor activity, including inhibition of adenylate cyclase activity, inhibition of Ca<sup>2+</sup> channels, and activation of K<sup>+</sup> channels. Stimulation of D<sub>2</sub> autoreceptors activates a potassium conductance as shown in brain slices [239], acutely isolated neurons [267], and cultured dopamine cells [268]. The properties of the potassium conductance indicate that the subtype is a GIRK (Kir3) channel, activated by association with the  $\beta\gamma$  subunits of the G $\alpha_{i/o}$  heterotrimeric G protein [269]. GIRK2 and GIRK3 subunits are abundantly expressed by midbrain dopamine neurons [254]; experiments using GIRK KO animals indicate that channels containing GIRK2, but not GIRK3, carry most of the D<sub>2</sub> receptor-regulated current [255]. Thus, the primary conductance underlying the D<sub>2</sub> receptor inhibition of dopamine neuron firing results from activation of the G protein dependent inwardly rectifying potassium channel [269]. Activation of potassium channels also contributes to autoreceptor regulation of dopamine release [270, 271].

Inhibition of Ca<sup>2+</sup> channels could also decrease cell firing or directly inhibit the secretory process. The high threshold P/Q calcium conductance is also regulated by activation of D<sub>2</sub>-autoreceptors [272] and regulates the intrinsic firing rate of dopaminergic neurons [273]. It is not known if the inhibition of calcium conductance resulting from the activation of D<sub>2</sub> autoreceptors is an additional mechanism that regulates the firing rate of dopamine neurons. Inhibition of calcium current does, however, decrease dendritic release of dopamine, resulting in a decrease in the inhibitory postsynaptic current that is regulated by dopamine in the cell body region [255].

Synthesis-modulating autoreceptors reduce the activity of the rate-limiting enzyme for dopamine synthesis, the tyrosine hydroxylase. Tyrosine hydroxylase contains four residues phosphorylated by PKA in its amino-terminal regulatory domain. Phosphorylation of Ser40, in particular, mediates forskolin-stimulated activation of tyrosine hydroxylase [274]. D<sub>2</sub> autoreceptor inhibition of adenylate cyclase decreases dopamine synthesis by decreasing PKA-dependent phosphorylation of Ser40 [263, 275, 276], decreasing the availability of dopamine to fill synaptic vesicles [277]. Because ERK1/2 activate tyrosine hydroxylase by phosphorylation

on Ser31 [278, 279], inhibition of ERK1/2 by D<sub>2S</sub> receptors [180] could in theory inhibit dopamine synthesis, but the existing data most solidly support the conclusion that the effect of synthesis-modulating autoreceptors is mediated predominantly by inhibition of adenylate cyclase activity.

The mechanism by which D<sub>2</sub> autoreceptor stimulation enhances dopamine transporter function and localization at the membrane is less clear. ERK1/2 constitutively increase cell surface localization of the transporter in striatal synaptosomes and in HEK 293 cells heterologously expressing the transporter [280], and also mediate recruitment of the transporter to the cell surface by D<sub>2S</sub> in HEK 293 cells [281]. Although it is tempting to attribute autoreceptor regulation of the dopamine transporter to the ERK1/2 signaling pathway, this conclusion seems premature in view of the lack of evidence for activation of ERK by D<sub>2</sub> receptors in the intact (i.e., non-denervated) neostriatum. A second mechanism by which D<sub>2</sub> autoreceptors can alter dopamine transporter localization and enhance re-uptake of dopamine is by a direct interaction between the third cytoplasmic loop of the receptor and the amino terminus of the transporter; this interaction, however, is constitutive and not influenced by D<sub>2</sub> receptor activation [282].

Not all dopamine neurons have D<sub>2</sub> autoreceptors and GIRKs [283, 284]. In fact, accumulating evidence indicates that mid-brain dopaminergic cells are a highly heterogeneous population of neurons when the expression of various ion channels and receptors is taken into consideration. The demonstration that neurons that project to the medial prefrontal cortex lack both GIRK and autoreceptors sets them apart from other dopamine neurons in the midbrain and indicates that the regulation of activity of these neurons specifically is vastly different from other dopamine neurons [269, 283].

## 6.8 Summary

Dopamine receptors regulate a variety of signal transduction pathways through which complex behaviors are expressed. In this chapter, we have focused on signaling pathways for which there is evidence of their contribution to behavior, including the PKA, PLC, ERK1/2, and Akt/GSK-3 $\beta$  pathways. Not discussed in this chapter are some signaling responses that are downstream of the adenylate cyclase-PKA-DARPP-32 pathway, such as regulation of renal Na<sup>+</sup>-H<sup>+</sup> exchange and Na<sup>+</sup>,K<sup>+</sup>-ATPase activity [13, 285], or signaling pathways, such as phospholipases other than PLC, whose contributions to dopamine-dependent behaviors have not been extensively investigated. In addition, to achieve a comprehensive understanding of the mechanisms of dopamine receptor signaling we must also consider receptor modulation of ion channels (Chapters 7 and 11), and the effects of novel receptor-interacting proteins (Chapter 9) and receptor oligomerization (Chapter 10) on function. The past decade has seen great advances on all of these fronts, producing a much richer picture of receptor function than was previously available. In

particular, the genetic deletion of individual dopamine receptors has greatly contributed to our understanding of their specific roles in regulating signaling pathways and their behavioral correlates (see also Chapter 12 on dopamine receptor KO mice and Chapter 13 on the contribution of individual receptor subtypes to behavior). Focusing the role of particular signaling pathways in behavior, our goal was to produce a chapter that would complement these other behavior-focused chapters to provide a comprehensive review of our current understanding of how the binding of dopamine to its receptors alters cellular function and behavior.

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# Chapter 7

## Dopaminergic Modulation of Glutamatergic Signaling in Striatal Medium Spiny Neurons

Weixing Shen and D. James Surmeier

**Abstract** Dopamine (DA) controls a wide variety of striatal functions, including action selection and associative learning. This is achieved by modulating cortical and thalamic glutamatergic synapses formed on principal medium spiny neurons (MSNs) and the way in which these signals are processed. Accumulating evidence suggests that D<sub>1</sub> receptor signaling enhances dendritic excitability and glutamatergic signaling in striatonigral MSNs, whereas D<sub>2</sub> receptor signaling exerts the opposite effect in striatopallidal MSNs. The functional antagonism between these two major striatal DA receptors extends to the regulation of synaptic plasticity. Using brain slices from DA receptor transgenic mice, recent studies have uncovered important differences between MSNs that shape long-term alterations in glutamatergic signaling with experience. These results are consistent with network models of striatal function, suggesting that DA acts in a push–pull fashion in action selection. Work in models of Parkinson’s disease has shown this bidirectionality is lost following DA depletion, pointing to the mechanisms underlying network dysfunction in this disease as well as in others with strong DA determinants like drug abuse.

**Keywords** Long-term potentiation · Long-term depression · Spike-timing-dependent plasticity · Basal ganglia · Voltage-dependent channels · Dendrites · Parkinson’s disease models

### 7.1 Introduction

Dopamine (DA) plays a crucial role in regulating cortical and thalamic signals carried by glutamatergic synapses on the principal neurons of the striatum – medium spiny neurons (MSNs). The regulation of this circuitry by DA is important to a wide

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D.J. Surmeier (✉)

Department of Physiology, Northwestern University, Feinberg School of Medicine,  
303 East Chicago Avenue, Chicago, IL 60611, USA  
e-mail: j-surmeier@northwestern.edu

array of striatal functions, such as associative learning and action selection [1–4]. In spite of its significance, effort to understand how this modulation is exerted has met with only a modest success. One obstacle is cellular heterogeneity within the striatum; there are at least two major populations of MSN that differ along several dimensions, including their expression of DA receptors [5, 6]. However, these subpopulations are difficult to unequivocally distinguish on the basis of their somatodendritic morphology or electrophysiological properties [7]. Moreover, both cell types are imbedded in a rich neuronal network involving both MSNs and interneurons that is modulated by DA. This has made it extremely difficult to sort out what DA is doing directly and what it is doing indirectly through effects on network properties. The recent development of mouse lines in which neurons “report” their expression of  $D_1$  or  $D_2$  receptors by co-expressing enhanced green fluorescent protein (eGFP) has greatly accelerated our pace of discovery. Electrophysiological interrogation of visually identified MSNs in tissue slices from these mice has revealed an unexpected array of functional differences between these cell types [8–13]. Another obstacle is that DA receptors are primarily found in dendrites that are inaccessible to conventional patch clamp techniques, making direct study of their actions on glutamatergic signaling and dendritic excitability difficult. Optical techniques, like two-photon laser scanning microscopy (2PLSM), are giving us access to these regions and providing new insights into their physiology and modulation by DA.

In this review, we will focus our discussion to (1) DA modulation of postsynaptic properties that influence glutamatergic synaptic events and their integration by MSNs and (2) DA modulation of the induction of plasticity at MSN glutamatergic synapses. Only the actions of the principal DA receptors in this region ( $D_1$ ,  $D_2$  receptors) will be discussed. Even with this rather narrow focus, it is impossible to faithfully summarize what has become an enormous literature in the last decade. The reader is referred to several other recent reviews [14–17]. Moreover, there are several reviews discussing the impact of glutamate on dopaminergic neurons and DA release that would not be covered [18, 19].

## 7.2 The “Classical” View of DA Modulation

The now “classical” model of how DA shapes striatal activity was advanced almost two decades ago by Albin, Young, and Penny [20]. In this model,  $D_1$  receptors excite MSNs of the “direct” striatonigral pathway whereas  $D_2$  receptors inhibit MSNs of the “indirect” striatopallidal pathway. These were envisioned as acute, readily reversible effects. The evidence for this model stemmed almost entirely from indirect measures of neuronal activity (e.g., alterations in gene expression, glucose utilization, or receptor binding). Subsequent work has proven to be largely consistent with the general principles of this model, revealing that DA activation of G protein-coupled receptors (GPCRs) “excites” or “inhibits” MSNs by modulating the gating and trafficking of voltage-dependent and ligand-gated (ionotropic)

ion channels, essentially altering cellular excitability. However, as discussed below, there are also longer lasting alterations in synaptic strength induced by DA when there is a conjunction of pre- and postsynaptic activity. These lasting changes, rather than the acute effects of DA, are thought to underlie associative learning and action selection.

### ***7.2.1 Modulation of Intrinsic Excitability and Glutamatergic Signaling by D<sub>1</sub> Receptors***

Striatonigral MSNs in the so-called direct pathway express D<sub>1</sub> receptors at high levels [5, 6]. These receptors are positively coupled to adenylyl cyclase (type V) through G<sub>olf</sub> [21]. Elevation in cytosolic cAMP levels leads to the activation of protein kinase A (PKA). PKA has a variety of intracellular targets that affect cellular excitability and glutamatergic signaling.

Several studies suggest that the D<sub>1</sub>/PKA cascade has direct effects on AMPA and NMDA receptor function and trafficking. For example, D<sub>1</sub> receptor activation of PKA enhances surface expression of both AMPA and NMDA receptors through a process that is dependent on the phosphoprotein DARPP-32 [22, 23]. The precise mechanisms underlying the trafficking are still being pursued, but the tyrosine kinase Fyn and the protein phosphatase STEP (striatal-enriched phosphatase) appear to be important regulators of surface expression of glutamate receptors [24]. Trafficking and localization might also be affected by a direct interaction between D<sub>1</sub> and NMDA receptors [25, 26].

What is less clear is whether D<sub>1</sub> receptor stimulation has rapid effects on glutamate receptor gating. Although PKA phosphorylation of the NR1 subunit is capable of enhancing NMDA receptor currents [27], the presence of this modulation in MSNs is still in debate. In neurons in which the engagement of dendritic voltage-dependent ion channels has been minimized by dialyzing the cytoplasm with Cs<sup>+</sup>, D<sub>1</sub> receptor agonists have little or no discernible effect on AMPA or NMDA receptor-mediated currents in the dorsal striatum [28]. However, in MSNs in which this has not been done, D<sub>1</sub> receptor stimulation rapidly enhances currents evoked by NMDA receptor stimulation [29]. The difference between these results suggests that the effect of D<sub>1</sub> receptors on NMDA receptor currents is indirect and mediated by voltage-dependent dendritic conductances that are taken out of play by blocking K<sup>+</sup> channels and clamping dendritic voltage. Indeed, blocking L-type Ca<sup>2+</sup> channels, which open in the same voltage range as NMDA receptors (Mg<sup>2+</sup> unblock), attenuates the D<sub>1</sub> receptor-mediated enhancement of NMDA receptor currents [30].

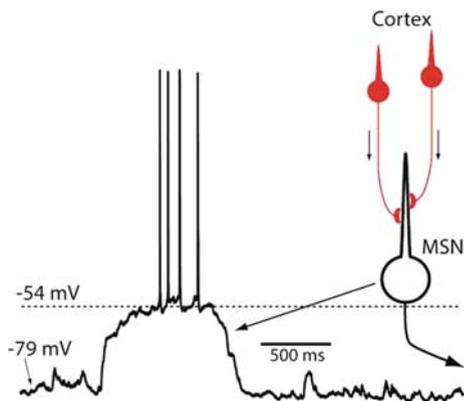
This type of interaction between voltage-dependent ion channels and ligand-gated channels appears to be common in neurons. Far from the passive entities envisioned 20 years ago, neuronal dendrites are richly invested with voltage-dependent ion channels that shape synaptic responses and plasticity. Although nearly all the studies of active dendrites to date have been in pyramidal neurons, there is evidence that similar mechanisms govern MSNs dendrites [31–33].

However, unlike pyramidal neurons, the dendrites of MSN are too small to accommodate an electrode, so indirect measures have been used to understand how DA modulates the ion channels that invest MSN dendrites. More recently, the combination of imaging (most notably 2PLSM) and patch clamp has been applied to MSN dendrites in organotypic culture and brain slices [31–33]; this approach offers a powerful alternative to conventional approaches, particularly when applied to tissue in which phenotypically homogenous neuronal populations are fluorescently tagged.

Voltage-dependent  $\text{Na}^+$  channels were the first well-characterized targets of the  $\text{D}_1$  receptor-signaling pathway in MSNs. Confirming inferences drawn from earlier work in tissue slices [34], voltage clamp work showed that  $\text{D}_1$  receptor signaling led to a reduction in  $\text{Na}^+$  channel availability without altering the voltage-dependence of fast activation or inactivation [35]. Subsequent work has shown that PKA phosphorylation of the pore-forming subunit of the  $\text{Na}^+$  channel promotes activity-dependent entry into a non-conducting, slow inactivated state that can be reversed only by membrane hyperpolarization [36]. It is likely that the  $\text{D}_1$  receptor modulation is mediated by phosphorylation of somatic Nav1.1 channels, as Nav1.6 channels are not efficiently phosphorylated by PKA [37]. The coupling of the  $\text{D}_1$  receptor cascade to dendritic (as opposed to somatic) Nav1.1/Nav1.6 channels remains uncertain and the subcellular positioning of the scaffolding interactions necessary to bring about efficient phosphorylation of  $\text{Na}^+$  channel subunits [37] has not been mapped in MSNs.

When the somatic membrane potential is held for several hundred milliseconds near the up-state ( $\sim -55$  mV; Fig. 7.1) [38],  $\text{D}_1$  receptor stimulation has a quite different effect than when it is held at nominal down-state potentials ( $\sim -80$  mV). At this up-state membrane potential, the personality of the MSN is transformed, as the constellation of ion channels governing activity is re-configured. Perhaps the most dramatic change is the closure or inactivation of Kir2, Kv1, and Kv4  $\text{K}^+$  channels that oppose the depolarizing influences of glutamate receptors. In this state,  $\text{D}_1$  receptor stimulation elevates (rather than lowers) the response to intrasomatic current injection [39]. The augmented response is attributable in part

**Fig. 7.1** Up- and down-states in MSNs. In the absence of convergent glutamatergic input, the membrane potential of MSNs resides close to the potassium equilibrium potential ( $\sim -80$  mV). This is called the down-state. In response to strong glutamatergic input, MSNs depolarize to a second preferred membrane potential around  $-55$  mV, near spike threshold. This is called the up-state. Redrawn, with permission, from [92]



to enhanced opening of L-type  $\text{Ca}^{2+}$  channels following PKA phosphorylation [40, 41]. L-type channels with a pore-forming Cav1.3 subunit are likely to be major targets of this modulation; these channels have a voltage threshold near  $-60$  mV and are anchored near glutamatergic synapses in spines through a scaffolding interaction with Shank [42]. Enhanced opening of these channels and NMDA receptors [29, 43–45] accounts for the ability of  $\text{D}_1$  receptor stimulation to promote synaptically driven plateau potentials of MSNs (resembling up-states in vivo) in corticostriatal slices [46], as in cortical pyramidal neurons [47].  $\text{D}_1$  receptor stimulation also reduces opening of Cav2  $\text{Ca}^{2+}$  channels that couple to somatic SK  $\text{K}^+$  channels [48], potentially further augmenting dendritic electrogenesis but Cav2 channels appear not to be important in MSN dendrites [31].

Taken together, these results suggest that  $\text{D}_1$  receptor signaling through PKA elevates the responsiveness of striatonigral neurons to sustained synaptic release of glutamate that generates up-states but reduces the response to transient or uncoordinated glutamate release that fails to significantly depolarize the dendritic membrane for more than a few tens of milliseconds from the down-state.

### ***7.2.2 Modulation of Intrinsic Excitability and Glutamatergic Signaling by $\text{D}_2$ Receptors***

$\text{D}_2$  receptors are expressed at high levels in neurons of the striatopallidal or “indirect” pathway.  $\text{D}_2$  receptors couple to  $\text{G}_{i/o}$  proteins, leading to inhibition of adenylyl cyclase through  $\text{G}\alpha_i$  subunits [49]. In parallel, released  $\text{G}\beta\gamma$  subunits are capable of reducing Cav2  $\text{Ca}^{2+}$  channel opening and of stimulating phospholipase C  $\beta$  isoforms, generating diacylglycerol (DAG) and protein kinase C (PKC) activation as well as inositol trisphosphate (IP3) liberation and the mobilization of intracellular  $\text{Ca}^{2+}$  stores [50, 51].  $\text{D}_2$  receptors also are capable of transactivating tyrosine kinases [52].

As with  $\text{D}_1$  receptor signaling, there are a number of studies showing that  $\text{D}_2$  receptor signaling alters glutamate receptor function in dorsal striatal MSNs. Activation of  $\text{D}_2$  receptors has been reported to decrease AMPA receptor currents of MSNs recorded in tissue slices [29]. Subsequent work using acutely isolated neurons and voltage clamp techniques supports a direct action on dendritic AMPA receptors [53].  $\text{D}_2$  receptor signaling leads to dephosphorylation of S845 of GluR1 subunit, which should promote trafficking of AMPA receptors out of the synaptic membrane [54].  $\text{D}_2$  receptor stimulation also diminishes presynaptic release of glutamate [55]; however, it is not clear whether this is mediated by presynaptically or postsynaptically positioned  $\text{D}_2$  receptors [56].

Studies of voltage-dependent channels are largely consistent with the proposition that  $\text{D}_2$  receptors act to reduce the excitability of striatopallidal neurons and their response to glutamatergic synaptic input.  $\text{D}_2$  receptor-mediated mobilization of intracellular  $\text{Ca}^{2+}$  leads to negative modulation of Cav1.3  $\text{Ca}^{2+}$  channels through a calcineurin-dependent mechanism [42, 50].  $\text{D}_2$  receptor activation also reduces opening of voltage-dependent  $\text{Na}^+$  channels, presumably by a PKC-mediated

enhancement of slow inactivation [35]. This coordinated modulation of ion channels provides a mechanistic foundation for the ability of D<sub>2</sub> receptor agonists to reduce the responsiveness of MSNs in slices at up-state membrane potentials [50].

### 7.3 Long-Term Depression of Glutamatergic Synaptic Transmission

Although it modulates short-term network activity, DA's role in associative learning and habit formation is commonly thought to be in the regulation of corticostriatal synaptic plasticity. The best-studied form of synaptic plasticity in the striatum is long-term depression (LTD). When postsynaptic depolarization is paired with high-frequency stimulation (HFS) of glutamatergic fibers, a long-lasting reduction in synaptic strength of glutamatergic synapses is seen in most MSNs. Unlike LTD induced by low-frequency stimulation in the ventral striatum [57], LTD induction in the dorsal striatum is not NMDA dependent. This form of LTD (HFS-LTD) is initiated postsynaptically, but expressed through a presynaptic reduction in glutamate release. There is a general agreement that striatal LTD requires activation of Cav1.3 L-type Ca<sup>2+</sup> channels, G<sub>q</sub>-linked mGluR1/5 receptors, and the generation of endocannabinoids (ECs). ECs exert their effect presynaptically by acting at CB1 receptors [58–60]. There is less agreement that activation of D<sub>2</sub> receptors is necessary for LTD induction. Activation of D<sub>2</sub> receptors is a very potent stimulus for EC production [61] and the ability of D<sub>2</sub> receptors to activate PLC [50] certainly is consistent with a direct involvement in EC production. However, attempts to test for the necessity of D<sub>2</sub> receptor expression using bacterial artificial chromosome (BAC) mice have met with mixed results [11, 13]. Kreitzer and Malenka (2007) [11] reported that LTD was inducible only in striatopallidal MSNs using a minimal local stimulation. However, our group and Lovinger's found that HFS-LTD was inducible in both striatonigral and striatopallidal MSNs when using macroelectrode stimulation of the cortex [13], consistent with the high probability of induction seen in previous work [62]. We have reproduced the Kreitzer and Malenka finding using minimal local stimulation, suggesting that the method of induction is important. This result underscores the difficulties inherent in stimulation paradigms that do not activate just glutamatergic fibers, but also a heterogeneous population of dopaminergic, cholinergic, and interneuronal fibers that might influence the induction of plasticity. An example of how we have attempted to sort this out is given below.

One strategy for gaining better control over which fibers are activated in studies of plasticity is to develop *in vitro* preparations that preserve connectivity between nuclei. Consider the glutamatergic synapses formed on MSNs. Most reviews have focused almost entirely on the cortical innervation of MSNs, leaving the thalamic input to a virtual footnote. Studies using nominal white matter or cortical stimulation of coronal brain slices typically assume that the glutamatergic fibers being stimulated are of cortical origin, but very few of these fibers are left uncut in this preparation [63]. The thalamic innervation of MSNs is similar in magnitude to

that of the cerebral cortex, perhaps constituting as much as 40% of the total glutamatergic input to MSNs, terminating on both shafts and spines [7]. Anatomical studies suggest that the intralaminar nuclei target primarily striatonigral neurons in primate striatum; however, this might not be the case in rodents [64], where “motor” nuclei (ventroanterior (VA) and ventrolateral (VL) nuclei) project primarily to striatopallidal neurons [65, 66]. This apparent dichotomy between motor and “associative” inputs is consistent with recent studies suggesting that input to striatopallidal neurons comes largely from pyramidal neurons contributing to descending motor control circuits, whereas the input to striatonigral neurons comes from neurons whose axons are largely intra-telencephalic [67]. Recently, several studies have shown that parahorizontal slices can preserve both cortical and thalamic connectivity, allowing each to be selectively stimulated [68, 69]. However, these preparations have not been used to date to study the rules governing the induction of plasticity at these two types of synapse.

#### **7.4 Long-Term Potentiation of Glutamatergic Synaptic Transmission**

Much less is known about the mechanisms controlling induction and expression of long-term potentiation (LTP) than LTD. Studies in tissue slices have argued that LTP induced by HFS of corticostriatal glutamatergic inputs (HFS–LTP) depends upon co-activation of D<sub>1</sub> and NMDA receptors [70, 71]. Given the apparent requirement to dramatically lower extracellular Mg<sup>2+</sup> concentration in the slice to induce LTP, there had been some question about the physiological relevance of LTP in MSNs, but this issue has been resolved by the demonstration that it is readily inducible in vivo [72]. The discrepancy presumably stemmed from the difficulty in depolarizing MSN dendrites enough to overcome Mg<sup>2+</sup> block of NMDA receptors with focal stimulation in a brain slice. How HFS–LTP is expressed has not been carefully examined. As with HFS–LTD, the dependence of a nominally widespread form of synaptic plasticity upon a receptor with restricted distribution is puzzling.

#### **7.5 A Reconciliation of Models of Striatal Synaptic Plasticity**

As is apparent from the presentation thus far, there are several obstacles that have slowed progress toward a sound understanding of the dopaminergic modulation of synaptic plasticity in the striatum. Cellular heterogeneity has been the biggest of these in our view. The development of D<sub>1</sub> and D<sub>2</sub> receptor BAC transgenic mice has made this problem tractable. Another issue is the induction protocol. Until very recently, plasticity studies have not attempted to engage the postsynaptic membrane and dendrites in a physiological way during the induction of synaptic plasticity (e.g., Cs<sup>+</sup> loading cells and voltage clamping).

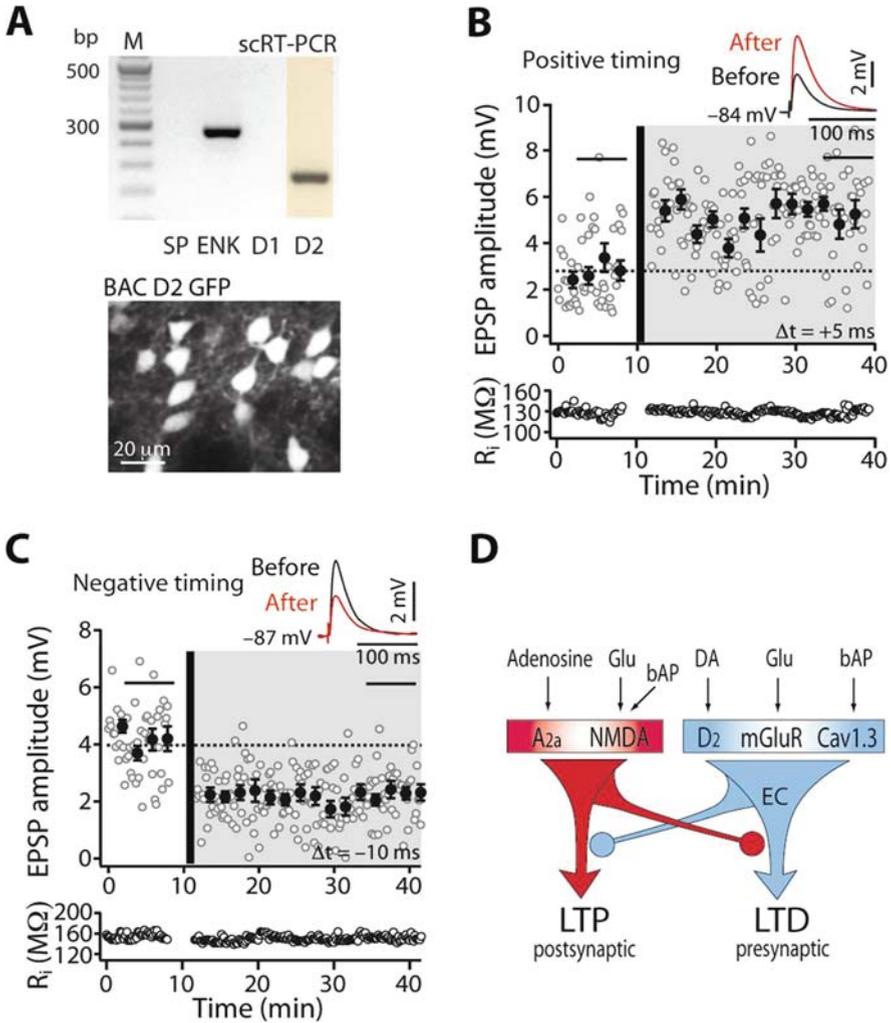
Why is this important? Most learning theories postulate that changes in synaptic strength reflect the precise temporal relationship between presynaptic and postsynaptic activity. Hebb's classic postulate asserts that excitatory, glutamatergic synaptic activity that consistently leads to postsynaptic spiking induces a strengthening or potentiation of the active synapses. An unstated corollary is that synaptic activity that follows postsynaptic activity (and hence cannot be causally linked to spiking) should be weakened or depressed. Dendrites are an integral part of this learning equation, forming the conduit between the axon initial segment where spikes are initiated and synaptic sites where plasticity is induced. DA receptors richly invest dendrites of MSNs [73], putting them in a position to modulate this linkage. The extended Hebbian postulate has been tested in several types of neuron by examining how the temporal relationship between presynaptic and postsynaptic spiking influences lasting changes in synaptic strength [74–76]. Spike-timing-dependent plasticity (STDP) of this sort depends upon back-propagating action potentials (bAPs) that serve to depolarize synaptic regions before, during, or after glutamate release. At most synapses, Hebb's postulate appears to be correct. That is, when presynaptic activity precedes postsynaptic spiking, LTP is induced, whereas reversing the order induces LTD [77–80].

Using perforated patch recordings (to preserve intracellular signaling mechanisms) and minimal local electrical stimulation of glutamatergic afferent fibers in tissue slices from BAC transgenic mice, we have used STDP protocols to examine the rules governing the induction of plasticity at striatonigral and striatopallidal MSN synapses [81]. These studies have revealed a set of rules that are largely consistent with those inferred from studies using conventional induction protocols (see above), but pushed us beyond our current conceptual model by showing that DA controls the induction of Hebbian synaptic plasticity in a receptor- and cell-type-specific manner.

Specifically, D<sub>1</sub> receptor signaling in striatonigral MSNs was necessary for the induction of Hebbian long-term potentiation whereas D<sub>2</sub> receptor signaling in striatopallidal MSNs was necessary for the induction of Hebbian long-term depression. More importantly, our studies demonstrate that DA, in concert with adenosine and glutamate, makes STDP at MSN glutamatergic synapses bidirectional and Hebbian [81].

In striatopallidal MSNs (Fig. 7.2a), repeated pairing of a synaptic stimulation with a postsynaptic spike later (positive timing) resulted in LTP of the synaptic response (Fig. 7.2b). In contrast, preceding synaptic stimulation with a short burst of postsynaptic spikes (negative timing) induced LTD (Fig. 7.2c). The timing-dependent LTP relies upon activation of NMDA and A2a receptors, as blocking them disrupts the potentiation of synaptic response in striatopallidal MSNs (Fig. 7.2d). As with conventional LTD, timing-dependent LTD is disrupted by antagonizing mGluR5, CB1, or D<sub>2</sub> receptors (Fig. 7.2d).

The bidirectionality of STDP appeared to be controlled by a balanced interaction between “opponent” GPCR signaling cascades controlling the induction of LTP and LTD [79, 82, 83]. D<sub>2</sub> and A2a receptor signaling cascades have long been known



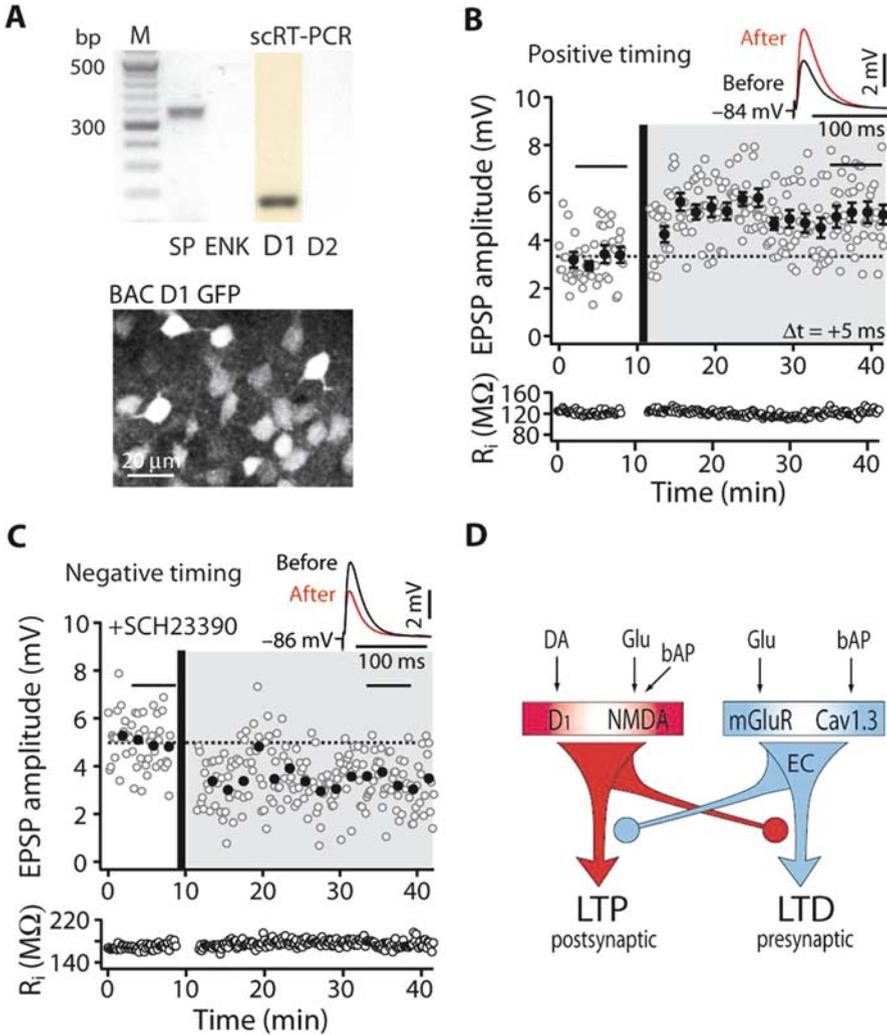
**Fig. 7.2** Striatopallidal MSNs displayed bidirectional STDP dependent upon D<sub>2</sub> and A<sub>2a</sub> receptors. **(A)** *Upper*, single cell RT-PCR (scRT-PCR) amplicons from an individual BAC D<sub>2</sub> eGFP-labeled neuron confirmed co-expression of enkephalin and D<sub>2</sub> receptor mRNA. M, marker; SP, substance P; ENK, enkephalin. *Bottom*, two-photon laser scanning microscopic image of eGFP-labeled MSNs in a slice from a BAC D<sub>2</sub> mouse. **(B)** LTP induced in eGFP-labeled striatopallidal MSN by a positive timing pairing. Plots show EPSP amplitude and input resistance as a function of time in a single cell. The *dashed line* shows the average EPSP amplitude before induction. The induction was performed at the vertical bar. *Filled symbol* shows the averages of 12 trials ( $\pm$  SEM). The averaged EPSP traces before and after induction are showed at the *top*. **(C)** LTD induced by a negative timing pairing. Plots and EPSP traces as in **B**. **(D)** Schematic illustration shows that activation of A<sub>2a</sub> and NMDA receptors leads to LTP and activation of D<sub>2</sub> and mGluR5 receptors and Cav1.3 channels leads to LTD. Moreover, A<sub>2a</sub> and D<sub>2</sub> receptor activation oppose each other in inducing plasticity. Glu, glutamate; EC, endocannabinoid. From Shen et al. 2008 [81]

to oppose one another at several levels [84, 85]. In the STDP paradigm, elevating D<sub>2</sub> receptor stimulation by bath application of quinpirole resulted in a robust LTD even when postsynaptic activity followed presynaptic activity, a protocol that would normally induce LTP. In contrast, elevating A2a receptor signaling by bath application of CGS21680 restored LTP, even when presynaptic activity followed postsynaptic activity (Fig. 7.2d).

In striatonigral MSNs (Fig. 7.3a), pairing presynaptic activity with a trailing postsynaptic spike induced robust LTP (Fig. 7.3b). As in striatopallidal MSNs, STDP LTP was dependent upon NMDA receptors (Fig. 7.3d). However, when presynaptic activity followed postsynaptic spiking, EPSP amplitude did not change. In light of the opponent signaling hypothesis, we reasoned that this failure could be due to the activation of the GPCR responsible for LTP induction. To test this hypothesis, D<sub>1</sub> receptors were blocked by SCH23390. In the absence of D<sub>1</sub> receptor activity, pairing postsynaptic spiking with a presynaptic volley led to a robust LTD (Fig. 7.3c). Moreover, the CB1 receptor antagonist AM251 blocked the LTD, establishing a mechanistic parallel to LTD in striatopallidal MSNs. To determine whether attenuating D<sub>1</sub> receptor signaling altered the timing dependence of plasticity, the effects of the positive timing protocol (presynaptic activity followed by postsynaptic activity) were re-examined. In control conditions, this protocol induced a robust LTP (Fig. 7.3b). Blocking D<sub>1</sub> receptors not only prevented LTP induction, it led to the induction of LTD (Fig. 7.3d).

The recognition that DA is not essential for all forms of synaptic plasticity in MSNs resolves the apparent paradox posed by the segregation of DA receptors in the two MSN populations. The finding that STDP plasticity at MSN glutamatergic synapses is Hebbian is consistent with a recent study [80], but conflicts with another [86]. The discrepancy could be attributable to the engagement of GABAergic interneurons in the striatum, confounding modifications in the strength of glutamatergic synapses [87]. Indirect, modulatory influences of other striatal interneurons also have been implicated in the induction of plasticity at glutamatergic synapses when large regions of the striatum are stimulated [13, 62]. Our reliance upon focal stimulation near synaptic sites minimized the involvement of these interneurons and helped to resolve how DA receptors expressed by postsynaptic MSNs shaped the induction process.

These studies suggest that while DA makes STDP in striatal MSNs bidirectional and Hebbian, it is not necessary for the induction of synaptic plasticity. This stands in contrast to previous work asserting that DA is essential for plasticity and that striatal DA depletion in Parkinson's disease models eliminates both LTD and LTP [11, 62]. To test this hypothesis, BAC mice were rendered parkinsonian by unilateral 6-OHDA lesions, sacrificed a week later and slices prepared from their brains. What we found was consistent with the work in unlesioned brains. That is, in striatopallidal MSNs pairing pre- and postsynaptic activity induced LTP, regardless of the order of presentation; in contrast, in striatonigral MSNs, pairing pre- and postsynaptic activity induced LTD, again regardless of order. Thus, synaptic plasticity is not lost in PD models, but it ceases to be bidirectional and dependent upon the timing of pre- and postsynaptic activity [81].



**Fig. 7.3** Striatonigral MSNs displayed bidirectional STDP dependent upon D<sub>1</sub> receptors. (A) *Upper*, scRT-PCR amplicons from an individual eGFP-labeled neuron from a BAC D<sub>1</sub> mouse confirmed co-expression of substance P and D<sub>1</sub> receptor mRNA. M, marker; SP, substance P; ENK, enkephalin. *Bottom*, two-photon image of eGFP-labeled MSNs in a slice from a BAC D<sub>1</sub> mouse. (B) LTP induction in labeled striatonigral neuron by a positive timing pairing protocol (+5 ms) coupled with postsynaptic depolarization to -70 mV. EPSP amplitude and input resistance of the recorded cell were plotted as a function of time. The *dashed line* shows the average of EPSP amplitude before induction. The induction was performed at the vertical bar. *Filled symbol* shows the averages of 12 trials ( $\pm$  SEM). The averaged EPSP traces before and after induction are shown at the *top*. (C) In the presence of SCH23390, a negative timing pairing revealed a robust LTD. Plots and EPSP traces are from a single cell as in B. (D) Schematic drawing shows that activation of D<sub>1</sub> and NMDA receptors evokes LTP and activation of mGluR5 receptor and Cav1.3 channels evokes LTD. Moreover, D<sub>1</sub> and mGluR5 receptor activation oppose each other in inducing plasticity. Glu, glutamate; EC, endocannabinoid. From Shen et al. 2008 [81]

In addition to reconciling a discordant literature on the role of DA in the modulation of glutamatergic synaptic plasticity, these studies establish a parallel between the short-term and long-term effects of DA on MSNs. As reviewed above, the short-term effects of DA are receptor specific, tending to diminish the excitability of striatopallidal MSNs through D<sub>2</sub> receptors and to increase the excitability of striatonigral MSNs through D<sub>1</sub> receptors. Now it is clear that the effects of DA on synaptic plasticity are also receptor and cell-type specific. That is, by promoting LTD, D<sub>2</sub> receptors diminish the excitatory synaptic input to striatopallidal MSNs, decreasing their activity; conversely, by promoting LTP, D<sub>1</sub> receptors increase the excitatory synaptic input to striatonigral MSNs, enhancing their activity.

## 7.6 What Might This Mean for Behavior?

What does this mean in the broader functional context of the basal ganglia? One of the most popular theories of the striatum is that it is involved in action selection [3, 88, 89]. When faced with a choice of what to do, the striatum helps us choose the action that will maximize our chances of reward or pleasure and minimize the chances of punishment or aversion. This is where DA comes in. Learning the reward (or punishment) probabilities of particular actions is thought to depend upon DA release in the striatum, where it changes the synaptic weights of cortical inputs associated with particular actions. The two parallel pathways in the striatum have been envisioned to act as a push–pull system with the striatonigral pathway serving to select an action and the striatopallidal pathway serving to inhibit a competing action. Computational models of the striatum suggest that this parallel organization enhances the ability of the system to resolve small differences in reward probability [90].

The recognition that DA affects these two pathways differently, particularly insofar as synaptic plasticity is concerned, is beautifully consistent with this model. In principle, reward-associated elevations in striatal DA promote the strengthening of corticostriatal synapses – that are linked to sensory stimuli that preceded the act and to the internal representation of the act that led to the reward – just on striatonigral MSNs while weakening them on striatopallidal MSNs. When an act leads to a negative consequence, striatal DA levels are thought to fall [91]. Again, in principle, this should promote the strengthening of corticostriatal synapses on striatopallidal MSNs (leading to suppression of the action) and weakening of synapses on striatonigral MSNs (leading to a reduced probability of selection of the action).

Because the induction of synaptic plasticity is controlled by opponent processes, disease states that alter the levels of DA receptor stimulation should distort how experience shapes these connections of these two pathways. So, for example, in Parkinson's disease models the absence of DA should be interpreted by the striatum as equivalent to a situation in which all acts lead to punishment and, hence, all acts should be suppressed. Phenomenologically at least, this is what happens. In contrast, drugs of abuse that dramatically elevate striatal DA should lead to a diminished ability to inhibit action selection. This could help explain some aspects of drug-seeking behavior.

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# Chapter 8

## Regulation of Dopamine Receptor Trafficking and Responsiveness

Melissa L. Perreault, Vaneeta Verma, Brian F. O'Dowd, and Susan R. George

**Abstract** The magnitude of cellular responses resulting from dopamine receptor activation is highly dependent on the balance between exocytic and endocytic trafficking pathways, which together, influence the level of receptor expression at the cell surface. Over the past decade, it has been revealed that the mechanisms involved in dopamine receptor transport are extremely complex, involving numerous protein–protein interactions that assist in targeting the receptors to distinct intracellular compartments. In addition, the importance of oligomerization in dopamine receptor trafficking is becoming increasingly evident, providing new perspectives on the mechanisms of receptor transport. This chapter will review the recent advances that have contributed to the understanding of the molecular mechanisms involved in dopamine receptor trafficking, their role in cellular responsiveness and discuss briefly the significance of receptor trafficking in health and disease.

**Keywords** Receptor sensitivity · Receptor trafficking · Desensitization · Internalization · Post-translational modifications · Receptor oligomerization

### 8.1 Introduction

Activation of dopamine receptors induces a cascade of intracellular signaling events, involving numerous effector systems, which mediate the pharmacological and physiological effects of both the receptors' endogenous ligand and exogenous

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S.R. George (✉)

Departments of Pharmacology and Medicine, Centre for Addiction and Mental Health, University of Toronto, Medical Sciences Building, 1 King's College Circle, Toronto, ON M5S 1A8, Canada  
e-mail: s.george@utoronto.ca

Vaneeta Verma and Melissa L. Perreault are co-first authors and have contributed equally in the writing of this chapter

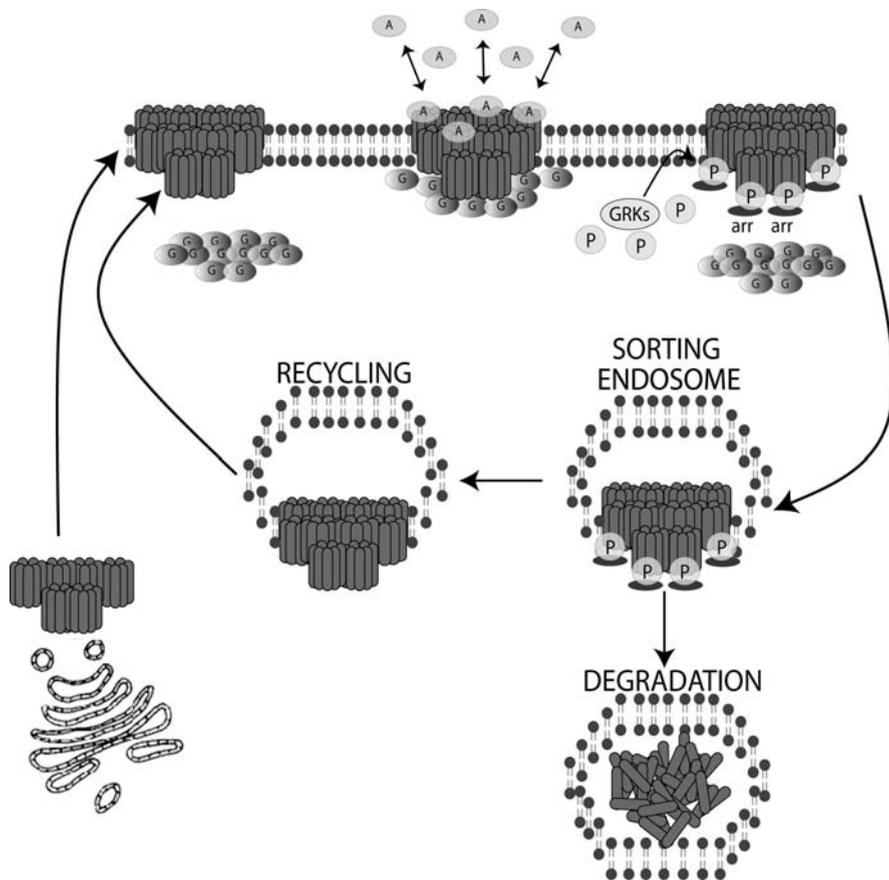
therapeutic agents. Dopamine receptor-mediated signaling is a tightly regulated process that is highly dependent on the accessibility of receptors to agonist binding at the cell surface. This availability of functional surface receptors is governed by a strict balance of the various intracellular receptor trafficking pathways that, in association with receptor sensitivity, work in concert to regulate the amplitude of agonist-mediated cellular responsiveness.

In recent years, the focus to uncover the mechanistic processes involved in each step of the trafficking pathway has yielded significant progress. In addition to a number of accessory proteins, molecular chaperones, and receptor motifs that have been identified in the past decade as contributing to dopamine receptor transport (reviewed [1, 2]), the significant role of receptor complexes in signal transduction and trafficking has also been revealed, challenging classical perceptions of receptor stoichiometry and opening up exciting new avenues of research. While traditional thinking has depicted dopamine receptors, and other G-protein-coupled receptors (GPCRs), as monomeric species, an increasing amount of evidence indicates that these receptors are assembled as higher order homo- and heteromers, complexes whose composition contributes to the regulation of receptor trafficking.

### ***8.1.1 GPCRs Traffic as Oligomers***

Evidence suggests that the oligomerization of GPCRs occurs early in the biosynthetic process, likely within the endoplasmic reticulum (ER) [3–5], and in some instances, oligomer formation appears to be obligatory to achieve successful export from the ER to the plasma membrane [6–10]. Once the receptor oligomers are correctly assembled, they are then transported through the Golgi, where they receive additional posttranslational modifications, such as glycosylation, for example, to achieve mature status, and are then trafficked to the plasma membrane as functionally active complexes (Fig. 8.1). Upon acute exposure to agonist, these receptors may undergo an agonist-induced decrease in receptor responsiveness over time or desensitization. Agonist-induced desensitization begins with phosphorylation of the receptor by specific kinases, predominantly G-protein receptor kinases (GRKs). In addition, receptor phosphorylation promotes its uncoupling from the G protein and interaction with arrestin proteins, which recruit the receptor complexes for internalization into endosomal compartments (reviewed [11, 12]). Receptors are then recycled back to the plasma membrane, retained in intracellular compartments, or targeted for degradation, processes that are central to the continued maintenance or the resultant termination of the receptor-mediated signal (Fig. 8.1).

This chapter will review in detail the currently known mechanisms that are involved in the regulation of dopamine receptor exocytic and endocytic trafficking and their role in cellular responsiveness. As an abundance of studies have focused on the D<sub>1</sub> and D<sub>2</sub> receptors, this review will focus predominantly on these two receptor



**Fig. 8.1** Schematic of a GPCR trafficking as an oligomer. A GPCR oligomer traffics from the Golgi-ER network to the plasma membrane. Exposure to agonist leads to GPCR phosphorylation by G-protein-coupled receptor kinases, which promote its uncoupling from the G protein and its interaction with arrestin proteins, which recruit the receptor complex for internalization into endosomal compartments. The receptor complex is then recycled back to the plasma membrane or targeted for degradation. A, agonist; G, G protein; GRK, G-protein-coupled receptor kinase; P, phosphate; Arr, arrestin

subtypes, both as homomers and as part of the recently identified D<sub>1</sub>-D<sub>2</sub> heteromer (reviewed [13]).

## 8.2 Biosynthesis, Export, and Cell-Surface Stabilization

Dopamine receptors are seven transmembrane receptors that regulate neuronal activity by responding to their endogenous ligand dopamine. The magnitude of the agonist-induced neuronal response is mitigated by the availability of functional

receptors at the cell surface which is contributed to, in part, by the processes of receptor biosynthesis and export trafficking.

### ***8.2.1 Biosynthesis and Cell-Surface Trafficking of Dopamine Receptors***

Similar to all GPCRs, the synthesis and folding of dopamine receptors takes place in the ER. At the completion of this process, the receptors are subjected to a stringent ER quality control system that functions to ensure only correctly configured receptors can exit the ER and continue their migration through the endoplasmic compartments toward the Golgi complex. Vital contributors to the ER quality control process are the molecular chaperones, a group of ER resident proteins that have the dual function of assisting in the overall speed and efficiency of glycoprotein folding, and inhibiting the export of misfolded proteins from the ER.

#### **8.2.1.1 Calnexin**

Calnexin is a chaperone protein with lectin-like activity that recognizes and binds monoglucosylated N-linked oligosaccharides that have been attached to GPCRs during the translational process. This interaction not only functions to prevent the formation of aggregates and promote receptor folding but also serves to anchor the glycoproteins within the ER until their native conformation is attained or until they are targeted for degradation. An involvement of calnexin in the biosynthesis of D<sub>1</sub> and D<sub>2</sub> receptors has recently been reported [14]. The association of calnexin with the receptors is mediated, at least in part, by glycosylation as the inhibition of glycosylation, through mutation or with the inhibitor tunicamycin, diminished calnexin interactions with the receptors. However, the finding that their association was not completely abolished in the absence of glycosylation is indicative of a direct interaction also with the receptor protein [14]. It has been postulated that these glycan-dependent and glycan-independent actions of calnexin on dopamine receptors may mediate, respectively, the chaperone versus ER retention functions of the protein. This hypothesis was supported by the finding that while the inhibition of glycosylation restricted the cell-surface expression of the D<sub>1</sub> receptor, the increase in calnexin binding that was observed to a trafficking-impaired D<sub>1</sub> receptor was insensitive to glycosylation inhibitors [14].

Although calnexin has been demonstrated to be involved in the biosynthesis of GPCRs [15, 16], a role for this chaperone in oligomerization has not been identified. Indeed, it has been shown that calnexin may not even associate with D<sub>1</sub> and D<sub>2</sub> receptor oligomeric complexes, but only bind to monomeric species [14]. However, while these findings may appear to exclude a role for calnexin in oligomer assembly, it has been suggested that the ability of calnexin to retain individual receptor monomers may function to facilitate the formation of oligomeric complexes [14].

While the mechanisms underlying this hypothesis require further investigation, one possibility is that calnexin may simply restrain each subunit in a spatial orientation that makes the monomer more readily accessible for receptor–receptor interactions. Evidence for self-oligomerization of calnexin [17] suggests a mechanism by which this chaperone may facilitate these interactions by assisting monomers into close proximity so as to promote oligomer assembly.

### 8.2.1.2 The Triple Phenylalanine Export Motif and DRiP78

Export from the ER has been shown to be a critical rate-limiting step in the trafficking of GPCRs to the cell surface [18]. For many GPCRs the selection for ER export appears to be dependent on the proximal portion of their carboxyl terminus [19–23] and through the use of site-directed mutagenesis, several motifs within the carboxyl terminus have been identified that may serve as ER export signals [19, 24–26]. One such motif has been reported for the D<sub>1</sub> receptor [24]. It was established that the highly conserved triple phenylalanine motif, FxxxFxxxF, was integral for the cell-surface expression of the D<sub>1</sub> receptor as substitution mutations within the motif resulted in ER retention and loss of ligand binding. Moreover, fusion of the motif to an intracellularly trapped receptor protein restored its ER export properties and conferred normal protein transport to the cell surface. Evidence suggests that the motif may promote vesicular transport from the ER or downstream from the ER, by interacting with the vesicular coat protein complex COPI [27], a complex that has been implicated in transport pathways throughout the ER-Golgi network (reviewed [28]) including exit from the ER [29]. Precipitation assays revealed that the D<sub>1</sub> receptor could associate specifically with the  $\gamma$ -subunit of COPI. Although such an interaction between carboxyl terminal motifs and coat protein complexes has not yet been reported for other GPCRs, it has been exhibited for a number of non-GPCR proteins [30–32].

The export capabilities of the FxxxFxxxF motif can be regulated by the molecular chaperone dopamine receptor interacting protein 78 (DRiP78), a membrane-associated ER resident protein [24]. Transport of the D<sub>1</sub> receptor appeared to be highly sensitive to the intracellular levels of DRiP78 as overexpression of the protein led to ER retention. It has been suggested that DRiP78 may function to mask the ER export signal thereby preventing the interaction of the motif with another complex associated with vesicular transport, such as the coat protein complexes, for example. However, given that DRiP78 sequestration similarly resulted in reduced D<sub>1</sub> receptor cell-surface expression, these results suggested that discrete levels of the protein may be required for sufficient export trafficking of the D<sub>1</sub> receptor from the ER [24]. It is possible that, in addition to its role in ER retention through motif binding, DRiP78 may function to assist in protein folding and/or oligomer assembly. Such a role has been recently demonstrated for DRiP78 in the assembly of G-protein  $\beta\gamma$  heterodimers [33]. If such was the case for D<sub>1</sub> receptors, insufficient levels of DRiP78 could result in misfolded or unformed oligomer complexes leading to ER retention and reduced cell-surface expression.

### 8.2.1.3 Role of Glycosylation in Receptor Cell-Surface Targeting

Studies have shown that glycosylation is requisite for the optimal expression of certain dopamine receptor subtypes at the plasma membrane. It has been previously reported that the loss of N-linked glycosylation by the inhibitor tunicamycin, or the mutation of a single N-linked glycosylation site (Asp<sup>4</sup>), did not attenuate the cell-surface expression of the D<sub>1</sub> receptor [34]. Yet it has been more recently reported that tunicamycin, under similar treatment conditions, inhibited the cell-surface expression of the D<sub>1</sub> receptor by approximately 27% [14]. Furthermore, this study demonstrated that a D<sub>1</sub> receptor mutant missing both N-linked glycosylation sites (Asp<sup>4</sup> and Asp<sup>174</sup>) exhibited diminished D<sub>1</sub> receptor cell-surface expression that was comparable to that observed with tunicamycin [14]. The findings from the receptor mutants indicate that mutation of both glycosylation sites, and hence a complete loss of glycosylation, may be required to attenuate D<sub>1</sub> receptor trafficking. However, given that the sole mutation of the Asp<sup>174</sup> residue was not performed, an important role for this individual site in the cell-surface transport of the D<sub>1</sub> receptor cannot be excluded.

Unlike the D<sub>1</sub> receptor, the inhibitor tunicamycin has been shown to completely abolish the cell-surface localization of the D<sub>5</sub> receptor in cells [34]. Mutation of the three individual N-linked glycosylation sites revealed that it was the Asp<sup>7</sup> residue that was critical for the cell-surface transport of this receptor as its mutation resulted in an almost complete abolishment of plasma membrane D<sub>5</sub> receptor expression [34].

The elimination of N-linked glycosylation by mutation or tunicamycin resulted in a reduction of both total cellular or plasma membrane expression of D<sub>2</sub> receptors [14, 35]. Additionally, post-ER glycosylation has also been implicated in the discrete trafficking of the D<sub>2</sub> receptor isoforms, D<sub>2short</sub> (D<sub>2S</sub>) and D<sub>2Long</sub> (D<sub>2L</sub>). Using pulse-chase procedures it was demonstrated that, under certain conditions, D<sub>2S</sub> was rapidly processed from a newly synthesized protein to a partially, and then fully glycosylated mature state. In contrast, a significant amount (approximately 20%) of the D<sub>2L</sub> isoform was only partially glycosylated and remained intracellularly sequestered [36]. In concordance with these findings, it has recently been demonstrated that, in the absence of agonist, D<sub>2S</sub> was predominantly localized to the plasma membrane, whereas the D<sub>2L</sub> isoform was found both at the cell surface and intracellularly [37]. Similarly, it has been demonstrated that D<sub>2L</sub> was retained further upstream and more strongly than D<sub>2S</sub> in early compartments of the secretory pathway [35]. The D<sub>2S</sub> and D<sub>2L</sub> isoforms differ from one another by a 29 amino acid insertion found in the third intracellular loop of D<sub>2L</sub>. Therefore, it is plausible that the differential trafficking rates and targeting of these receptor isoforms are associated with this sequence of amino acids. Specifically, it is possible that this sequence, in full or in part, may function as a retainment motif, whereby interactions of the motif with an as yet unidentified accessory protein may serve to retain the D<sub>2L</sub> isoform intracellularly. Given that D<sub>2S</sub> and D<sub>2L</sub>, respectively, function pre- and postsynaptically [38], and work together to mediate dopamine transmission, understanding the mechanisms underlying the differential trafficking of these

two isoforms may have significant implications in understanding the physiological regulation of dopamine transmission in the brain.

## ***8.2.2 Stabilization of Dopamine Receptors at the Cell Surface***

It has been demonstrated that GPCRs are not static within the plasma membrane but can move in the plane of the membrane by the passive process of lateral diffusion [39–41]. One of the key factors that govern the dynamics of lateral diffusion of GPCRs is their association with other cellular proteins. The formation of these protein complexes can serve to restrict the movements of the GPCRs, effectively stabilizing the receptors in specific microdomains within the membrane, such as the synapse for example. Numerous protein–protein associations of this type have been reported between dopamine receptors and a variety of cellular proteins, examples of which are discussed below.

### **8.2.2.1 The NMDA-D<sub>1</sub> Receptor Trap**

Movement by lateral diffusion has been reported for several GPCRs, including vasopressin V<sub>2</sub> [39], serotonin 1<sub>A</sub> [40], and dopamine D<sub>1</sub> receptors [41]. In cultured neurons, approximately 65% of D<sub>1</sub> receptors are mobile with the remaining receptors anchored within the membrane [41]. This ratio of mobile to anchored receptors is not fixed, but fluctuating, and has recently been shown to be influenced by other receptors within the plasma membrane. One such receptor is the NMDA receptor whose activation has been reported to recruit D<sub>1</sub> receptors to the cell surface from intracellular compartments [42] and, furthermore, restrict the lateral movements of D<sub>1</sub> receptors within the membrane [41]. The modulation of D<sub>1</sub> receptor flow dynamics by NMDA activation at the cell surface stems in part from the ability of the two receptors to physically interact. Particular regions of the D<sub>1</sub> receptor carboxyl tail have been shown to bind to the NR-1 and NR-2 subunits of the NMDA receptor [43]. It is the interface with the NR-1 subunit, however, that has been identified as the critical region for both NMDA-mediated cell-surface trafficking and trapping of D<sub>1</sub> receptors [41]. With regard to the functional mechanisms underlying D<sub>1</sub> receptor trapping, the influx of calcium that results from NMDA receptor activation does not appear to be involved. Rather it appears to be the result of an allosteric transformation, induced through occupation of the NMDA binding site, which facilitates the interaction between the D<sub>1</sub> receptor and the NR-1 subunit [41]. It has been established that NMDA receptors are stabilized at the membrane via anchorage to the postsynaptic density. Thus, the formation of NMDA–D<sub>1</sub> receptor complexes functions in localizing and stabilizing the D<sub>1</sub> receptor at the synapse. Presumably, increased synaptic localization would make these receptors more susceptible to activation, culminating in enhanced signal transduction and neuronal responsiveness.

### 8.2.2.2 Role of Scaffolding Proteins in Dopamine Receptor Cell-Surface Stability

Perhaps one of the most well-known functions of scaffolding proteins is to maintain the structural integrity of the cell membrane. However, it is becoming more evident that scaffolding proteins may also serve additional important functions, one of which involves the stabilization of GPCRs at the plasma membrane. With regard to dopamine receptors, several scaffolding proteins have been identified that serve in this capacity. Two examples are protein 4.1 N and filamin A (actin-binding protein 280), both of which have been shown to influence the expression of D<sub>2</sub> and D<sub>3</sub> receptors through interactions at their third intracellular loops [44–47].

The association of a truncated mutant of protein 4.1 N with D<sub>2</sub> and D<sub>3</sub> receptors significantly reduced the expression of either receptor in cells, results that implicate a positive role for protein 4.1 N in the cell-surface stabilization of these receptors [44]. Similarly, the actin-binding protein filamin A positively contributed to D<sub>2</sub> receptor plasma membrane expression [46, 47], and moreover, has been shown to play a role in enhanced D<sub>2</sub> receptor-mediated signaling [45]. It is possible that the functional mechanism underlying this increase in signaling stems from filamin A-assisted formation of D<sub>2</sub> receptor clusters at specific locales on the cell surface. Such clusters may function to increase the efficiency of receptor–effector coupling by aggregating components of the signaling pathway. Filamin A also has been reported to contribute to efficient signaling and sequestration of the D<sub>3</sub> receptor [48], although to date, a role for this protein in D<sub>3</sub> receptor cluster formation has not been reported.

In addition to increasing receptor stability, scaffolding proteins can also destabilize receptors at the plasma membrane. The cytoskeletal subunit neurofilament-M (NF-M), for example, has been shown to negatively affect the cell-surface expression of the D<sub>1</sub> receptor [49]. Specifically, coexpression of NF-M with the D<sub>1</sub> receptor in cells resulted in a significant reduction in D<sub>1</sub> receptor cell-surface number and ligand-mediated cyclic AMP (cAMP) accumulation. Interestingly, receptors that remained at the cell surface exhibited a resistance to agonist-induced desensitization. Although the mechanism underlying this insensitivity was not identified, it was postulated that formation of the NF-M/D<sub>1</sub> complex might preclude associations of the D<sub>1</sub> receptor with kinases and/or arrestin, two events that are fundamental in the initiation of receptor trafficking into the cell.

## 8.3 Desensitization

### 8.3.1 D<sub>1</sub>-Like Receptors

Desensitization of D<sub>1</sub>-like receptors (D<sub>1</sub>, D<sub>5</sub>) has been extensively studied over the past several years and indicates that dopamine-induced attenuation of signaling by these receptors occurs within minutes of exposure [50–56]. As with the majority of

GPCRs, the predominant form of D<sub>1</sub> receptor desensitization has been identified as being mediated through GRKs. Truncated mutant constructs of the rat D<sub>1</sub> receptor have shown that multiple residues located downstream of Gly<sup>379</sup> in the distal carboxyl terminus regulated dopamine-mediated phosphorylation and desensitization of the D<sub>1</sub> receptor, which was suggested to reflect the removal of potential GRK2 and/or GRK3 phosphorylation sites [50]. Carboxyl terminal sequences located upstream of Gly<sup>379</sup> (between Cys<sup>351</sup> and Gly<sup>379</sup>) were shown to be important for phosphorylation but not for desensitization [50]. Site-directed mutagenesis studies of the human D<sub>1</sub> receptor, on the other hand, have provided evidence to suggest that GRK2 acts as a critical regulator of rapid agonist-induced receptor desensitization through phosphorylation of a single motif containing the residues Thr<sup>360</sup> and Glu<sup>359</sup> in the proximal segment of the carboxyl terminus [51]. Both of these studies have used differential methodology which may play a role in the discrepant results observed. Site-directed mutagenesis studies may be a more reliable method for identifying the importance of specific residues since there is little change in the intact structure of the receptor. Carboxyl terminal truncations, however, can alter the structure of the receptor which permits access to previously sterically hindered receptor domains, such as the third intracellular loop.

The third cytoplasmic loop has also been implicated in desensitization of the D<sub>1</sub> receptor. It was previously demonstrated that the mutation of specific residues in the third intracellular loop did not affect desensitization of the D<sub>1</sub> receptor [51]. However, a subsequent report has demonstrated that these same residues were involved in D<sub>1</sub> receptor phosphorylation and desensitization [57]. A possible reason for this discrepancy may be the use of differential cell lines, where one study used CHO cells and the other HEK 293 cells. It has been shown that the rate of agonist-induced desensitization of the D<sub>1</sub> receptor in CHO cells occurs more slowly than in other cell types [58]. Thus, it has been postulated that D<sub>1</sub> receptor phosphorylation may be GRK isoform dependent and these isoforms may be lacking in the CHO cell line [57].

Given the evidence demonstrating the importance of the carboxyl terminus and third intracellular loop, it has been proposed that D<sub>1</sub> receptor phosphorylation takes place in both the carboxyl terminus and the third intracellular loop in a sequential manner, where primary phosphorylation of the carboxyl terminus is permissive for secondary third intracellular loop phosphorylation, which then allows for the desensitization response [57].

In contrast to GRK2 phosphorylation, which requires receptor activation, GRK4 has been shown to regulate the constitutive phosphorylation and desensitization of the D<sub>1</sub> receptor [59] suggesting that specific GRK isoforms may serve discrete functions in the regulation of dopamine receptor activity.

Other kinases, such as protein kinase A (PKA), may also play a role in homologous or agonist-specific forms of GPCR desensitization (reviewed [11]). Although it has been demonstrated that the mutation of a potential D<sub>1</sub> receptor PKA phosphorylation site reduced the rate of agonist-induced desensitization [60], and moreover, that D<sub>1</sub> receptor desensitization was blunted in cells deficient in PKA [58], it has also been shown that the inhibition of PKA, either by substitution mutations

[51, 52] or pharmacologically [52], appeared to have no effect on D<sub>1</sub> receptor-mediated increases in cAMP.

The D<sub>5</sub> receptor exhibits very high sequence homology with the D<sub>1</sub> receptor; however, there are major differences in the intracellular loops and carboxyl termini. Unlike the D<sub>1</sub> receptor, the D<sub>5</sub> receptor exhibits higher levels of constitutive activity [61–63], a characteristic that has been shown to be regulated by the third cytoplasmic loop [64], as well as sequence-specific motifs within the carboxyl terminus [61, 62]. Similarly, the D<sub>5</sub> receptor also exhibits higher affinity for agonists, such as dopamine, than the D<sub>1</sub> receptor (reviewed [65]). A series of truncation/deletion mutants of the D<sub>5</sub> receptor identified the region encoded by amino acids 438–448 and particularly Gln<sup>439</sup> as necessary and sufficient for full expression of higher agonist affinities and constitutive activity relative to the D<sub>1</sub> receptor. The last 40 amino acids of the D<sub>5</sub> receptor, on the other hand, were shown unnecessary for the observed distinguishing pharmacological and functional characteristics [61]. Given that the carboxyl terminus has been implicated in a variety of GPCR regulatory events (reviewed [66]) elucidation of further motifs or residues within the carboxyl terminus of the D<sub>5</sub> receptor is needed to help delineate the specific mechanisms underlying D<sub>5</sub> receptor trafficking.

### 8.3.2 D<sub>2</sub>-Like Receptors

Early studies examining the functional desensitization of D<sub>2</sub>-like receptors (D<sub>2</sub>, D<sub>3</sub>, D<sub>4</sub>) have generated variable results but, in general, indicate that they desensitize much more slowly than D<sub>1</sub>-like receptors and require prolonged agonist treatment [53, 67]. Similar to the D<sub>1</sub> receptor, the mechanisms underlying D<sub>2</sub>-like receptor desensitization appear to involve GRKs, although their role in D<sub>3</sub> receptor desensitization as yet remains uncertain. Only by overexpression of GRK2, GRK5 [68], or GRK3 [69] was there increased phosphorylation of the human D<sub>2</sub> receptor and receptor internalization, indicating the sensitivity of the D<sub>2</sub> receptor as a substrate for GRK phosphorylation is lower than the D<sub>1</sub> receptor. These kinases, however, did not appear to influence phosphorylation and desensitization of the D<sub>3</sub> receptor [48, 69]. Indeed, only when D<sub>3</sub> chimeras were generated containing the second and third cytoplasmic loops of the D<sub>2</sub> receptor, was GRK-mediated phosphorylation evident, possibly revealing the importance of these receptor domains in GRK functioning [69]. It has also been reported, however, that GRK2 and GRK3 levels may regulate the stability of the D<sub>3</sub> receptor interaction with filamin A [70], a scaffolding protein that has been shown to be involved in the stability of D<sub>3</sub> receptor expression at the plasma membrane [48]. In addition, gene deletion of GRK6 was shown to lead to enhanced coupling of D<sub>2</sub>-like receptors to their respective G proteins *in vivo*, an effect that was associated with increased susceptibility to the locomotor-activating effects of psychostimulants [71], and suggests that GRK6 plays a role in regulating the responsiveness of the D<sub>2</sub> and/or D<sub>3</sub> receptors.

The second messenger kinase, protein kinase C (PKC), has also been suggested to regulate the D<sub>2</sub> and D<sub>3</sub> receptors in a heterologous manner since PKC activation was shown to attenuate the ability of both these receptors to inhibit cAMP accumulation [48, 72]. PKC phosphorylation of the D<sub>2</sub> receptor was demonstrated to take place on two internal domains within the third intracellular loop, but only one residue, Ser<sup>355</sup>, was shown to be involved in the PKC-induced desensitization response [72]. Site-directed mutagenesis of all the possible phosphorylation sites within the intracellular loops of the D<sub>3</sub> receptor identified Ser<sup>229</sup> and Ser<sup>257</sup> as the critical amino acids responsible for PKC-induced phosphorylation, desensitization, and internalization [48]. Additionally, PKC activation was shown to induce specific effects on each D<sub>2</sub> receptor isoform (D<sub>2L</sub> and D<sub>2S</sub>) with regard to receptor-stimulated calcium mobilization [73]. It has been reported that although PKC is able to effectively desensitize D<sub>2S</sub>-induced increases in intracellular calcium, the D<sub>2L</sub> isoform is insensitive to PKC-induced desensitization of calcium signaling due to the presence of a pseudosubstrate domain. A pseudosubstrate domain is a site that resembles a substrate domain except that the serine phosphorylation site is replaced by alanine or other residues and therefore may permit association with the kinase without resulting in functional phosphorylation [73]. This difference in substrate sensitivity of D<sub>2S</sub> and D<sub>2L</sub> appeared to be the result of intramolecular competition between different substrate domains on the D<sub>2L</sub> receptor for PKC recognition and a pseudosubstrate domain, which is not found in the D<sub>2S</sub> receptor. Given the importance of the D<sub>2</sub> receptor in numerous physiological processes, the presence of pseudosubstrate domains may potentially have significant implications for the regulation of the receptor by PKC.

### 8.3.3 The D<sub>1</sub>-D<sub>2</sub> Heteromer

Although D<sub>1</sub> and D<sub>2</sub> receptors are biochemically and functionally distinct, some physiological functions require the coactivation of both receptors [74, 75]. At a mechanistic level this has been difficult to reconcile since coactivation of the D<sub>1</sub> and D<sub>2</sub> receptors can result in both opposing and synergistic physiological responses. The recent discovery, however, of a common functional output generated by the concurrent activation of D<sub>1</sub> and D<sub>2</sub> receptors within the same cells resulting in activation of a novel Gq/11-linked phospholipase C-dependent calcium signal [76] has provided a possible biochemical mechanism by which the D<sub>1</sub> and D<sub>2</sub> receptors work in concert to mediate these molecular and behavioral functions. Additionally, in cultured cells coexpressing both receptors, the existence of D<sub>1</sub>-D<sub>2</sub> heteromers was established by fluorescence resonance energy transfer [77], cotrafficking studies [77], and visualization of D<sub>1</sub>-D<sub>2</sub> heteromers in live cells [78]. Accordingly, a heteromeric D<sub>1</sub>-D<sub>2</sub> signaling complex that could rapidly activate the Gq/11 protein and result in intracellular calcium release was demonstrated to exist in the adult rodent striatum [76, 77, 79].

Although little is known regarding the regulation of D<sub>1</sub>-D<sub>2</sub> heteromer responsiveness, it has been shown that desensitization of the agonist-induced calcium signal occurs within minutes of agonist exposure and is initiated by agonist occupancy of either receptor subtype, even though the signal is generated only by occupancy of both receptors [80]. Additionally, the attenuation of receptor internalization did not result in a concomitant decrease in the extent of signal desensitization, suggesting desensitization of the signal occurred prior to recruitment of the complex into vesicles by endocytic machinery. Although GRK5 or GRK6 or any of the second messenger kinases did not play a role in the desensitization, GRK2 and GRK3 appeared to have a role in the extent of desensitization. Inhibition of GRK-mediated phosphorylation, however, did not inhibit this desensitization [80], suggesting that, in addition to phosphorylating receptors, GRKs may also mediate signal desensitization by phosphorylation-independent mechanisms. It has been suggested that GRK2 and GRK3 may sequester Gq/11 proteins, which interact with the RGS domain on these GRKs [81]. Thus, this may provide a mechanism by which GRK2 and GRK3 contribute to desensitization of the calcium signal mediated by the D<sub>1</sub>-D<sub>2</sub> receptor heteromer [80]. It is of note, however, that heteromeric D<sub>1</sub> and D<sub>2</sub> receptors exhibit conformations that permitted cross-phosphorylation of the D<sub>2</sub> receptor by D<sub>1</sub> receptor activation [77], a finding that implicates a discrete mechanism by which the D<sub>1</sub> receptor within the D<sub>1</sub>-D<sub>2</sub> complex may regulate heteromer functioning.

## 8.4 Internalization

### 8.4.1 D<sub>1</sub>-Like Receptors

The acute administration of dopamine agonists has been demonstrated to induce robust internalization of the D<sub>1</sub> receptor in both cultured cells and neurons [82, 83], as well as in vivo [84]. While in the absence of agonist the D<sub>1</sub> receptor remained predominantly on the cell surface, the addition of dopamine induced rapid internalization of approximately 70% of the receptors, with a half-life of less than 5 min [56, 85]. Although endocytosis of the D<sub>1</sub> receptor has been consistently documented in both heterologous expression systems and neuronal cultures, the underlying mechanisms have shown to be more variable. While earlier studies have identified a role for PKA-mediated internalization in cells endogenously expressing the D<sub>1</sub> receptor [86], mutagenesis of the PKA sites of the human D<sub>1</sub> receptor [51], the rat D<sub>1</sub> receptor [60], and the non-human primate D<sub>1</sub> receptor [52] did not affect agonist-induced internalization.

Consistent with the role of GRKs in D<sub>1</sub> receptor desensitization, this group of kinases appears to play an essential role in D<sub>1</sub> receptor internalization, although the residues identified as being important for desensitization are not the same as for internalization. Receptor mutagenesis has revealed that specific residues in the distal portion of the carboxyl terminus (Thr<sup>446</sup>, Thr<sup>439</sup>, and Ser<sup>431</sup>) are involved in GRK2-mediated internalization of the human D<sub>1</sub> receptor [51]. However, rat D<sub>1</sub> receptor

mutants with carboxyl terminal truncations implied that sequences located between Cys<sup>351</sup> and Gly<sup>379</sup> are pivotal to receptor internalization [50]. Although there appear to be discrepancies regarding the relative importances of specific residues in D<sub>1</sub> receptor internalization, the carboxyl terminus seems to be essential in this stage of the endocytic trafficking pathway. It has also been postulated, however, that GRK-mediated D<sub>1</sub> receptor phosphorylation on the third intracellular loop may be of relevance in promoting receptor interactions with arrestins [57], adaptor proteins that have been shown to be essential for the internalization of a number of GPCRs including the D<sub>1</sub> receptor (reviewed [87]). Specifically, it has been suggested that the phosphorylation of residues within the carboxyl terminus and third intracellular loop dissociates the two domains, allowing for arrestin to bind to the activated third loop [57]. Activation of the D<sub>1</sub> receptor leads to translocation of both arrestin2 and arrestin3 to the cell membrane, with arrestin3 being the more predominant translocated subtype. Following arrestin membrane localization, the D<sub>1</sub> receptor is internalized and arrestin subsequently dissociates from the receptor at or near the membrane [57, 88, 89]. Similarly, colocalization between endogenous D<sub>1</sub> receptors and arrestins in rat neostriatal neuronal cultures demonstrated that the D<sub>1</sub> receptor preferentially interacts with arrestin3 [90].

In addition to arrestins, studies assessing the internalization pathway of D<sub>1</sub> receptor membrane trafficking have demonstrated the involvement of numerous other proteins, including the scaffolding proteins PSD-95, clathrin, and caveolin-1, and the GTPase dynamin [85, 91, 92]. In cultured cells, the coexpression of PSD-95 with the D<sub>1</sub> receptor resulted in a robust internalization of the receptor in the absence of agonist. Additionally, the abolishment of PSD-95 in mice accentuated D<sub>1</sub> receptor-mediated behavioral responses, suggesting that PSD-95 may also serve an inhibitory role in the regulation of D<sub>1</sub> receptor signaling *in vivo* [92]. Evidence suggests that facilitation of D<sub>1</sub> receptor internalization by PSD-95 is mediated through interactions with the carboxyl terminus of the D<sub>1</sub> receptor and furthermore is dependent on the presence of dynamin [92]. As dynamin has been previously shown to be involved in dopamine-induced clathrin-mediated endocytosis of the D<sub>1</sub> receptor [56, 85], these findings implicate the clathrin-mediated endocytic pathway in the internalization of the D<sub>1</sub> receptor.

In addition to clathrin-mediated internalization, it has been shown in cultured cells that the D<sub>1</sub> receptor can be localized to low-density caveolin-enriched membrane domains and can associate with caveolin-1 in rat brain through a specific binding motif found in transmembrane domain 7 [91]. Agonist stimulation of the D<sub>1</sub> receptor caused its translocation into caveolin-1-enriched membrane fractions, which was determined to be the result of D<sub>1</sub> receptor endocytosis through caveolae. However, unlike the relatively rapid clathrin-dependent mechanism of internalization in which approximately 70% of activated receptors were internalized within 5 min [85], caveolin-dependent D<sub>1</sub> receptor endocytosis appeared to be kinetically slower, reaching approximately 55% internalization within 45 min of agonist stimulation [91]. These findings suggest that both clathrin- and caveolin-mediated processes may play functionally distinct roles in regulating D<sub>1</sub> receptor responsiveness *in vivo*. It would be of clinical relevance to determine whether

the relative contribution of each of these pathways differs in specific regions of the brain.

### 8.4.2 *D<sub>2</sub>-Like Receptors*

The endocytosis of the D<sub>2</sub> receptor is a highly complex process that has been shown to be both isoform and cell specific, as well as to exhibit both dynamin-dependent and independent mechanisms [1, 57, 69, 85, 93].

Internalization of the D<sub>2</sub> receptor requires increased levels of GRKs in heterologous cells and appears to be a relatively slow process taking approximately 2 h to plateau [68, 93, 94]. Whereas little or no internalization was observed in the absence of exogenous GRKs or in the presence of the dominant negative GRK2 (DN-GRK2), coexpression of GRK2, GRK5 [68], or GRK3 [69] caused significant D<sub>2</sub> receptor internalization.

Similar to the D<sub>1</sub> receptor, internalization of the D<sub>2</sub> receptor involves GRK-dependent receptor phosphorylation, followed by the translocation of arrestin2 and arrestin3 to the cell membrane [69, 95] which function to promote receptor internalization [57]. The endogenous dopamine D<sub>2</sub> receptor in neurons, however, has been shown to preferentially interact with arrestin2 [95]. The D<sub>2</sub> receptor isoforms also showed differential regulatory mechanisms for internalization. For example, although both isoforms displayed a similar level of phosphorylation and arrestin translocation, the actual internalization of the two isoforms was differentially regulated by GRKs and arrestins, where the internalization of the D<sub>2S</sub> receptor was preferentially enhanced by GRK2 or GRK3, but the D<sub>2L</sub> receptor was preferentially enhanced by arrestin3 [96]. As discussed previously, given that the two receptor isoforms differ by a 29 amino acid insertion in the third intracellular loop of the D<sub>2L</sub> receptor, it is plausible that this region may play a role in isoform-specific trafficking.

In contrast to the D<sub>1</sub> receptor, D<sub>2</sub> receptor internalization appears to be mediated by specific dynamin isoforms, suggesting specificity between dynamin isoforms and dopamine receptor subtypes. It has been reported that the internalization of the D<sub>2S</sub> receptor is dynamin dependent, implicating the clathrin-coated endocytic pathway in the internalization of this receptor [57, 69, 93]. There are conflicting reports, however, as to the importance of dynamin-mediated mechanisms in the internalization of the D<sub>2L</sub> receptor. While it has been suggested that the D<sub>2L</sub> receptor internalizes in a dynamin-independent manner [57, 85], these studies assessed only the role of the dynamin1 isoform, whereas the dynamin2 isoform has been more recently implicated. In cultured cells and primary striatal neurons dynamin2 was shown to localize to sites of D<sub>2</sub> receptor internalization and associate with the D<sub>2</sub> receptor in the rat brain [1]. Furthermore, when high-resolution immunoelectron microscopy was used to study internalization patterns of the D<sub>2</sub> receptor in the primate prefrontal cortex, the D<sub>2</sub> receptor was demonstrated to undergo clathrin-mediated endocytosis via clathrin-coated pits and clathrin-coated vesicles [97].

In contrast to the D<sub>2</sub> receptor, the D<sub>3</sub> receptor demonstrated little internalization in response to dopamine stimulation and only in the presence of overexpressed

GRKs [48, 69, 96]. In addition, there appeared to be no noticeable translocation of arrestin in cells expressing the D<sub>3</sub> receptor [96].

PKC activation also led to 50% of the D<sub>2</sub> receptor being internalized when PKC $\beta$  was overexpressed [72]. Mutagenesis studies suggest that both of the PKC phosphorylation domains identified within the third intracellular loop were involved in regulating its internalization from the cell surface [72]. It has also been demonstrated that PKC activation induced significant internalization of the D<sub>3</sub> receptor that appeared to be dependent on both dynamin and filamin A [48], a result that supported previous evidence of a clathrin-mediated mechanism in D<sub>3</sub> receptor endocytosis [69].

Mechanisms underlying the regulation of the D<sub>4</sub> receptor are poorly understood. An interesting feature of the D<sub>4</sub> receptor, however, is the highly polymorphic region within the third cytoplasmic loop. The human D<sub>4</sub> receptor has a variable number of tandem repeats within the third intracellular loop as well as multiple putative Src homology 3 (SH3)-binding motifs that may regulate the trafficking properties of this receptor. Deletion of all the putative SH3-binding domains, but not the tandem repeat, in the third intracellular loop of the D<sub>4</sub> receptor resulted in constitutive internalization [98]. Similarly, deletion of one of the two SH3-binding sites abolished arrestin3 translocation [96], suggesting that the SH3 domains may be important in the regulation of D<sub>4</sub> receptor responsiveness.

### **8.4.3 The D<sub>1</sub>-D<sub>2</sub> Heteromer**

Given the relatively recent discovery of the D<sub>1</sub>-D<sub>2</sub> receptor heteromer, there is much yet unknown regarding the trafficking properties of this complex. It has been determined that selective agonist occupancy by either a D<sub>1</sub> agonist or a D<sub>2</sub> agonist leads to D<sub>1</sub>-D<sub>2</sub> heteromer cointernalization [77]. This is an interesting finding that indicates activation of only one receptor within the D<sub>1</sub>-D<sub>2</sub> complex is sufficient for internalization, whereas coactivation of the D<sub>1</sub> and D<sub>2</sub> receptors is required for the PLC-mediated calcium signal. It was also shown that heteromerization resulted in altered steady-state cellular distribution of the D<sub>1</sub> and D<sub>2</sub> receptors within cells that were distinct from that of the D<sub>1</sub> and D<sub>2</sub> receptor homomers [77]. Together, these findings emphasize the unique trafficking responses of the heteromer compared to its constituent D<sub>1</sub> and D<sub>2</sub> receptors, a characteristic that may elucidate differences in physiological function.

## **8.5 Resensitization**

### **8.5.1 D<sub>1</sub>-Like Receptors**

Investigations into the trafficking fate of the D<sub>1</sub> receptor after agonist-induced internalization have generally reported that the D<sub>1</sub> receptor recycles back to the plasma membrane [50, 51, 83-85, 99, 100], as opposed to being targeted to lysosomes for receptor degradation. With the use of immunohistochemistry or fluorescence

microscopy, the D<sub>1</sub> receptor expressed in cultured cells or neurons was demonstrated to recycle back to the plasma membrane after removal of agonist within approximately 20–30 min [83, 85, 99]. In accordance with these studies, dopamine-stimulated D<sub>1</sub> receptor phosphorylation has been shown to be rapidly reversed within 30 min, although resensitization of the D<sub>1</sub> receptor-mediated cAMP response occurred much more slowly, taking a minimum of 5 h to reach control levels. It was suggested that internalization was not mandatory for D<sub>1</sub> receptor dephosphorylation since pretreatment of the cells with hypertonic sucrose or concanavalin A did not alter D<sub>1</sub> receptor dephosphorylation after agonist removal [54]. The efficient recycling of the D<sub>1</sub> receptor, however, was recently reported to require a specific sequence within the proximal portion of the carboxyl terminus of the receptor [99]. This sequence spans amino acid residues 360–382 of the human D<sub>1</sub> receptor and is distinct from those previously identified as being required for efficient recycling of other GPCRs [101–105]. The importance of this sequence as a sorting signal was further established by demonstrating that the motif could induce the recycling of the  $\delta$ -opioid receptor, a receptor that traffics preferentially to lysosomes after agonist-induced internalization [99].

Attempts have been made to elucidate the accessory proteins that may contribute to the regulation of D<sub>1</sub> receptor postendocytic sorting. GPCR-associated sorting protein (GASP) has been shown to interact with the D<sub>1</sub> receptor, and to a greater degree, the D<sub>2</sub> receptor [100, 106]. However, while GASP was demonstrated to promote receptor degradation in the D<sub>2</sub> receptor, a role in D<sub>1</sub> receptor sorting was not observed [100]. A recent study involving a number of mutant GPCRs, including the D<sub>1</sub> receptor, demonstrated that the presence of a GASP interaction in and of itself is not sufficient to induce receptor degradation but rather it is the robustness of the GASP–receptor interaction that regulates the targeting to lysosomes [106]. It was shown that although deletion of the recycling motif in the D<sub>1</sub> receptor prevented recycling, it also was not targeted for degradation, suggesting that preventing recycling does not necessarily promote D<sub>1</sub> receptor degradation unless affinity for sorting proteins such as GASP that mediate degradation is altered as well [106].

Although the endocytic sorting mechanisms of the D<sub>5</sub> receptor are poorly understood, it has been shown that the carboxyl terminus of the receptor binds to sorting nexin 1 (SNX1) [107], a trafficking protein that has been implicated in the lysosomal targeting of the thrombin receptor PAR1 [108]. Although the role of SNX1 in D<sub>5</sub> receptor trafficking has yet to be defined, these results suggest that the postendocytic sorting of the D<sub>5</sub> receptor may involve sorting to lysosomes that is mediated by SNX1.

### **8.5.2 D<sub>2</sub>-Like Receptors**

While it has been previously demonstrated that the D<sub>2</sub> receptor can recycle within approximately 30 min of dopamine exposure in cultured cells [85], more recent evidence suggests that the D<sub>2</sub> receptor is predominantly degraded after dopamine

exposure in cells and neurons [100]. As discussed previously, unlike the D<sub>1</sub> receptor, the sorting fate of the D<sub>2</sub> receptor appears to be mediated by GASP in non-neuronal cells. Moreover, it was shown that dopaminergic neurons endogenously expressing GASP did not exhibit a functional recovery of neuronal responses following D<sub>2</sub> receptor agonist administration, whereas disrupting the GASP–D<sub>2</sub> receptor interaction facilitated the recovery of functional D<sub>2</sub> receptor responses [100]. In addition to GASP, the PKC-interacting protein, ZIP, has been shown to associate with the D<sub>2</sub> receptor in both cultured cells and endogenous brain tissue. Overexpression of ZIP reduced D<sub>2</sub> receptor cell-surface expression via enhanced trafficking of the receptors to lysosomes, suggesting that the ZIP protein functions as a negative modulator of D<sub>2</sub> receptor expression [109]. Such differences in D<sub>2</sub> receptor sorting as compared to the D<sub>1</sub> receptor may have significant implications with regard to dopaminergic signaling since *in vivo* both the D<sub>1</sub> and D<sub>2</sub> receptors respond to dopamine and thus may lead to an altered signaling profile depending on the extent of previous dopamine exposure.

## 8.6 Dysregulation of Receptor Trafficking in Health and Disease

In many instances the acute activation of dopamine receptors leads to a reduction in receptor number as they internalize into the cell. For some receptors, such as the D<sub>1</sub> receptor, this effect is generally transitory with a subsequent recovery of receptors back to the cell surface. However, evidence indicates that the D<sub>2</sub> receptor may be preferentially targeted to degradation pathways (see Section 8.5.1), suggesting that persistent alterations in extracellular dopamine could potentially have long-term consequences on dopamine receptor trafficking and responsiveness. Indeed, chronic alterations in dopamine tone have been associated with brain region-specific alterations in dopamine receptor expression for a number of neurological disorders, including schizophrenia (reviewed [110]), Parkinson's disease (reviewed [111]), and drug abuse [112] and have been readily observed in animal models of enhanced dopamine transmission [113–115].

The pharmacological modification of dopamine transmission has long been employed as a therapeutic tool in the treatment of many dopamine-related disorders. It has been repeatedly shown, however, that the long-term use of dopamine receptor drugs can lead to the development of negative secondary symptoms that may be linked with changes in dopamine receptor trafficking. Long-term levodopa administration, for example, can be associated with the development of dyskinesias, a behavioral manifestation that has recently been postulated to be the result of impaired D<sub>1</sub> receptor desensitization processes [116]. Similarly, the chronic administration of various antipsychotics also has been reported to result in the manifestation of extrapyramidal motor symptoms (EPS) (reviewed [117, 118]) that may be associated with altered dopamine receptor densities in the brain [119–122].

As a result of the current undesirable consequences underlying some of the pharmaceutical agents used in the treatment of dopamine disorders, new avenues of

research continue to be explored in an attempt to identify novel drug therapies that have pharmacological benefits in the absence of behavioral side effects. Our improved understanding of dopamine receptor trafficking has greatly contributed to this goal. One such area of research involves the development of agonists that exhibit functional selectivity, that is, agonists that exhibit discrete receptor affinities, receptor trafficking profiles, and/or differ in their ability to induce specific downstream signaling events. Several agonists have been identified for the D<sub>1</sub> receptor, for instance, that differentially induce internalization and/or the targeting of internalized receptors to discrete trafficking pathways [123, 124]. Furthermore, while antipsychotics generally function as D<sub>2</sub> receptor antagonists (reviewed [125]), the antipsychotic aripiprazole has been shown to act as an agonist at presynaptic D<sub>2</sub> receptors [126] and additionally exhibit cell line-specific partial agonism, or functional antagonism, at postsynaptic D<sub>2</sub> receptors [126–128]. In a cell line where the drug displayed partial agonist activity, aripiprazole exhibited functional selectivity for both D<sub>2</sub> receptor-mediated trafficking and signaling. In contrast to dopamine, aripiprazole did not induce D<sub>2</sub> receptor internalization and, unlike typical agonists, this drug exhibited low potency for the mitogen-activated protein kinase effector pathway compared to other D<sub>2</sub> receptor-mediated signaling pathways [129]. As aripiprazole has been demonstrated to have an excellent side-effect profile (reviewed [130]), the differential mediation of D<sub>2</sub> receptor trafficking and signaling by the drug may be of relevance to its ability to provide therapeutic benefits without inducing the manifestation of EPS.

Another group of functionally selective agonists are those that affect the receptor export pathways by acting as pharmacological chaperones. These membrane permeable molecules would bind to partially folded or misfolded dopamine receptor monomers or oligomers, correct their folding, and rescue them from ER retention. It has been reported, for instance, that membrane permeable agonists could rescue an intracellularly sequestered D<sub>1</sub> receptor homomer by inducing a conformational change that permitted its cell-surface trafficking from the ER [7]. Similarly, the antipsychotic pipamperone has been shown to both increase the trafficking of D<sub>4</sub> receptors to the plasma membrane and also effectively rescue a D<sub>4</sub> receptor mutant from intracellular sequestration [131]. Thus, the exogenous manipulation of ER retention mechanisms through the use of pharmacological chaperones may provide another useful means to regulate dopamine receptor trafficking.

## 8.7 Concluding Remarks

Although the detailed mechanisms of trafficking of the five individual dopamine receptors and their isoforms have yet to be fully elucidated, what is currently known clearly highlights the complexity of dopamine receptor trafficking and its role in cellular responsiveness. From the biosynthesis of dopamine receptor complexes to desensitization and internalization, it is now apparent that dopamine receptor trafficking is regulated by an incredibly wide array of protein–protein interactions

that can be highly specific not only to each receptor subtype but also within each subcellular compartment. The importance of oligomerization in dopamine receptor trafficking has also become increasingly evident, and together with the exciting discovery of a novel D<sub>1</sub>–D<sub>2</sub> receptor heteromer, these findings have provided new insights into the mechanisms of receptor transport. Undoubtedly, it is an exciting time for dopamine receptor research as intracellular accessory proteins, and oligomeric receptor models are incorporated into strategies for drug discovery. It is hopeful that the next decade will clarify further specific aspects of dopamine receptor trafficking, their contribution to cellular responsiveness, and their role in health and disease.

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# Chapter 9

## Dopamine Receptor-Interacting Proteins

Lisa A. Hazelwood, R. Benjamin Free, and David R. Sibley

**Abstract** Historically, dopamine receptors (DARs) and other G protein-coupled receptors (GPCRs) were believed to be independent signaling units in the plasma membrane, interacting only transiently with G proteins to initiate a downstream signaling cascade. However, in recent years it has become clear that DARs do not function in isolation, but in fact exist as members of macromolecular protein complexes. The DAR protein complex, or the signalplex, consists of a variety of protein interactors that may be transient or stable in nature and that are collectively referred to as dopamine receptor-interacting proteins (DRIPs). Ultimately, the goal of the signalplex is to organize the cellular machinery or signaling components that are critical to the DAR at any given time in an orderly fashion. This higher level of organization around the DAR enables the receptor to process all information, from extracellular ligands or intracellular signaling molecules, and propagate the necessary cellular response in a timely and efficient manner.

**Keywords** Interacting proteins · Signalplex · Yeast two-hybrid · Immunoprecipitation · Proteomics

### 9.1 Introduction to the Signalplex

Historically, dopamine receptors (DARs) and other G protein-coupled receptors (GPCRs) were believed to be independent signaling units in the plasma membrane, interacting only transiently with G proteins to initiate a downstream signaling cascade. However, in recent years it has become clear that DARs do not function in isolation, but in fact exist as members of macromolecular protein complexes [1, 2]. The DAR protein complex, or the signalplex, consists of a variety of protein interactors that may be transient or stable in nature and that are collectively

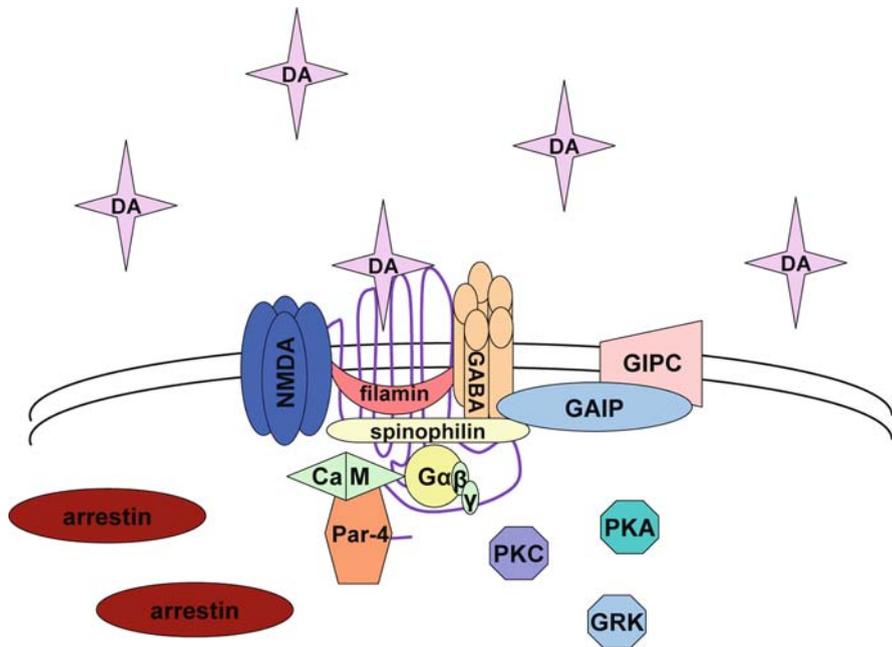
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D.R. Sibley (✉)

Molecular Neuropharmacology Section, NINDS/NIH, 5625 Fishers Lane, Rockville,  
MD 20852-9405, USA

e-mail: sibley@helix.nih.gov

referred to as dopamine receptor-interacting proteins (DRIPs). Once assembled into the signalplex, DARs and DRIPs can operate as a distinct unit to receive and process information critical to the cell from sources including ligands and cytosolic molecules (Fig. 9.1). To process this wide array of informational input, the constituents of the signalplex must change throughout the lifecycle of the receptor. The purpose of the signalplex then is to enable the DAR to adapt and function optimally and rapidly within a changing cellular milieu, based on factors as diverse as receptor maturity, cytosolic pH, calcium concentration, and ligand binding. In the absence of the signalplex, cellular signaling would be dependent on diffusion of a multitude of protein effectors, thus greatly reducing the speed and efficiency of the cellular response. Indeed, the signalplex provides a heightened level of organization within the cell for spatial and temporal control of signaling, and likely facilitates the diverse functions mediated by dopamine in different organs and even different cell types. Although we are only beginning to unravel the components of the DAR signalplex, it has become clear that the DRIPs involved may determine a multitude of receptor properties, including preference for signal transduction pathways and organization into cellular compartments or microdomains.



**Fig. 9.1** The dopamine receptor has been demonstrated to interact with a multitude of proteins, including trafficking, scaffolding, and adaptor proteins, kinases, ion channels, and various signaling molecules, a few of which are illustrated in this “signalplex.” The complement of interacting proteins likely changes throughout the life span of the cell, and can be impacted by dopamine stimulation and other extracellular events

### ***9.1.1 Constituents of the Signalplex – DRIPs and DRAPs***

The discrete components of the DAR signalplex likely change throughout the life span of the receptor, and depend upon the state of receptor maturation, ligand binding to the receptor, and various components of the cellular milieu. For a newly synthesized receptor, trafficking and targeting proteins such as calnexin [3] can begin their association with DARs at the translational machinery and remain with the receptor until insertion in the plasma membrane. This mechanism ensures correct spatial and temporal placement of the DAR in a direct manner. Receptor retention at the plasma membrane, as well as compartmentalization into microdomains, may be governed by scaffolding and accessory proteins such as spinophilin [4]. These scaffolding/accessory proteins may also act as tethers, linking the DAR to other proteins by indirect association (tethered proteins are termed DRAPs or dopamine receptor-associated proteins). Ligand binding to the DAR can initiate interaction with a variety of signaling proteins, including G proteins and kinases. Intracellular calcium levels can also activate subsets of signaling proteins, such as calcineurin [5], that interact with DARs. In both cases, the signaling proteins may directly interact with the receptor, facilitated by proximity within a microdomain, or they may be transiently tethered to the receptor by a scaffolding protein. Finally, after the DAR has been desensitized via interactions with protein kinases, it interacts with proteins such as arrestin that lead to internalization of the receptor. Once internalized, the DARs are sorted for recycling or degradation based on their interaction with specific trafficking proteins such as GASP [6] or GIPC [7].

As mentioned above, the association between DARs and members of the signalplex may be direct (DRIPs) or indirect (DRAPs). Most indirect interactors are likely downstream effectors, such as ion channels or adenylyl cyclase. While it is not necessary for DARs and DRAPs to be in direct contact with one another, signal propagation is far more efficient because the signalplex maintains the effector in close proximity to the receptor–G protein complex. In contrast, DRIPs must interact directly with the DAR, as is the case with kinases or G proteins. Scaffolding proteins are also DRIPs that may interact stably with the DAR in order to promote associations between DARs and a variety of other proteins, including DRAPs. In all cases, the signalplex provides the most efficient use of space and time for optimal cellular efficacy.

### ***9.1.2 Points of Interaction for DRIPs***

DRIPs may associate with various portions of the DAR to form the signalplex. The most common area for these protein–protein interactions to occur is on the intracellular face of the DAR, specifically within the third intracellular loop or the carboxyl terminus. In addition to facing the cytosol and, therefore, the vast majority of putative protein interactors, the third intracellular loop and carboxyl terminus are also the largest soluble spans of the DARs and are considered to be quite flexible. These

large regions of accessible protein provide ample room for binding of DRIPs and, indeed, many identified DRIPs have been proven to associate with the DAR in these two regions. In addition to the size and accessibility of these two receptor domains, they are also both targets of multiple protein kinases; many putative interactors utilize such phosphorylated residues to anchor protein associations. Finally, crystallography has recently uncovered a short eighth transmembrane domain within the carboxyl terminus of many GPCRs that appears to be important for ligand activation of the receptor and, subsequently, G protein coupling [8]. This region thus takes on significance as an activator “switch,” and the possibility that proteins interacting with the DAR in this region may respond directly to ligand stimulation is quite intriguing. Aside from the intracellular face of the DAR, it is also possible for other membrane-spanning proteins to associate with the DAR through their transmembrane domains. In fact, this has recently been demonstrated as the likely mechanism for D<sub>2</sub> receptor oligomerization [9]. Importantly, the transmembrane domains involved in protein interactions are predicted to undergo conformational shifts upon ligand binding, allowing the receptor to communicate this activation directly to the interacting partner without intermediary signaling molecules. For interactions between DARs and other large, membrane-spanning proteins, the transmembrane surfaces provide ample surface and opportunities for interactions and direct communication without second messengers.

### ***9.1.3 The Signalplex as the Most Efficient Unit for Transmission***

Ultimately, the goal of the signalplex is to organize the cellular machinery or signaling components that are critical to the DAR at any given time in an orderly fashion. This higher level of organization around the DAR enables the receptor to process all information, from extracellular ligands or intracellular signaling molecules, and propagate the necessary cellular response in a timely and efficient manner. By altering the components of the signalplex throughout the life span of the DAR and in different physiological environments, the DAR is able to respond best to the needs of the specific organ and cell at that moment.

## **9.2 Discovery Mechanisms**

The protein constituents of the DAR signalplex can be quite dynamic with respect to space and time. Elucidating the complete array of interacting proteins involved in the regulation and signaling mediated by DARs has become an important goal of this field. This identification presents a formidable task; first and foremost is the dynamic nature of the signalplex. As mentioned above, the signalplex is very likely constantly changing depending on the needs of the cellular environments, the state of the receptor, or in response to signaling. Therefore, the very nature of the signalplex itself greatly complicates discovery of proteins that interact with DARs.

Second, cellular and tissue-specific environments may very well dictate the components of a given DAR signalplex. Different tissues and cell types are likely to contain a mixture of different specific proteins. Proteins that are integral parts of the signalplex in one tissue may not even be present in another tissue. Luckily, a number of different techniques have been developed to address some of these concerns. While all of the current techniques have their pitfalls, they all also have powerful value in determining interacting proteins. Taken together these represent diverse ways of looking at a similar problem – discovery of the DAR signalplex.

### ***9.2.1 Membrane-Based Two-Hybrid and Split-Ubiquitin Systems***

The yeast two-hybrid, bacterial two-hybrid, and split-ubiquitin systems address the issue of cellular/tissue-specific interactions being a problem for identifying signalplex components by taking cellular environment completely out of the assay, and screening entire libraries of potential protein interactors. These systems use either yeast or bacteria as a model organism to determine potential protein interactions on a genomic scale. The general basic premise of the classical yeast two-hybrid revolves around transcriptional activation of screenable reporter genes. The classical yeast two-hybrid system has limited usefulness for membrane proteins such as DARs since the transcription factors are in the nucleus and membrane proteins are generally trafficked away from the nucleus. However, fragments of the receptor can be used as bait in this system and have been useful in identifying some interactors to non-membranous regions of the DAR. Therefore, classical two-hybrid is mostly useful for identifying soluble protein–protein interactions. However, modifications of these techniques such as the split-ubiquitin system [10] or membrane yeast two-hybrid [11] have allowed for use of this kind of technology for intact membrane proteins. In this system instead of using parts of transcription factors, ubiquitin can be split and separate parts attached to bait and prey proteins. The bait protein also contains a transcription factor for a reporter gene. If the bait and prey proteins interact (i.e., bind), then the ubiquitin pieces come together and are then cleaved by the yeast's ubiquitin-specific proteases and the transcription factor is liberated, where it travels to the nucleus and activates the reporter gene. If the two proteins do not interact, there is no transcription of the reporter gene since the transcription factor is locked at the membrane surface. This allows for selection of proteins that interact with the intact DAR.

The bacterial two-hybrid system is based on the transcriptional activation in *E. coli*, where an arbitrary pair of interacting proteins can mediate transcription of a synthetic promoter – one protein is tethered near the promoter via fusion to a DNA-binding domain, while the other protein is fused to a subunit of the *E. coli* RNA polymerase. The resulting transcription can be measured as an increase in expression of a selectable reporter gene. The most significant benefit to this system is the ability to rapidly assess very large libraries greater than  $10^8$  in size – however, the technique is limited by the inability of host bacteria to post-translationally modify

or properly express eukaryotic proteins, however, it has proved possible to identify protein–protein interactions using this technique [12].

This assay has proven a powerful technique in identifying direct protein interactions and is able to examine interactions with entire proteomes at one time. However there are also multiple pitfalls of the system. The system is notorious for false positives, requiring that all found interactions be confirmed by additional methods. The system is also only able to identify proteins that directly interact with the receptor. It is possible, and maybe even likely, that many members for the signalplex form a complex that would not allow them to directly bind to the receptor, but bind to other members of the signalplex. Furthermore, this system cannot take into account modifications of a protein that may be needed for binding to the bait. Therefore it is difficult to envision that this technique alone would be able to find all the signalplex members. Regardless, several DAR-interacting proteins have been identified this way, and the technique can also be used to identify regions of protein interaction by utilizing truncated protein pieces.

### **9.2.2 Biochemical Approaches: GST-Fusion Protein Pull Downs**

Another technique that has been developed and proven to be effective in elucidating protein–protein interactions are pull-down assays. Glutathione (GSH) is a protein that contains a free thiol group, normally involved in protection of cells against oxidative stress. Glutathione-S-transferase (GST) is a protein that participates in detoxification of many reactive substances by forming adducts through the thiol group. GST binds GSH with very high affinity. This natural chemistry is exploited in the GST pull-down assay where a recombinant protein of interest is made containing GST. This protein can then be coupled to GSH agarose for affinity chromatography to pull down interacting proteins, thus making an ideal way to separate and purify proteins that interact with your GST bait protein [13]. Because of the difficulty in identifying the interacting proteins through subsequent immunoblots, this assay has been used in a largely confirmatory way to show that two known proteins interact, the problem being that one has to know or at least suspect what the proteins are so that you can choose an appropriate antibody. However, if this is coupled with mass spectroscopy (MS) for identification of the interacting proteins (see more in Section 9.2.4) it becomes a more powerful technique for identifying novel interactions.

There are several primary advantages to this technique over the more traditional two-hybrid systems described above. These include: the isolation correlates to the strength of the interaction, the isolation is independent of a down-stream detection (such as transcriptional activation), the technique can internally be controlled for specificity by utilizing an unrelated negative control protein, one can isolate more than one interacting partner at a time, and entire genomes can be queried with the sequencing results found via MS.

While this highlights the power of this approach, there are indeed also significant pitfalls that make this approach miss some interacting proteins and make it entirely

unsuitable for others. The approach depends entirely on a recombinant/non-native protein. There is no guarantee that the protein will express properly in bacteria or fold properly to allow for native interacting partners to bind either in the host bacteria or after coupling to the agarose. Furthermore, weak or low-abundant interactions are likely to be missed or not interact with a strong enough affinity to be pulled down after washing in the chromatography steps. Interference can also arise from detergents or pre-formed protein complexes in the samples that are being used as prey. Finally, this is clearly a non-native artificial environment and many interactions likely rely on the cellular environment of the proteins. Therefore, not all proteins found will be direct members of the signalplex, but may be alternative binding partners of one of the signalplex members, that may form in solution before the bait protein is even tested.

### ***9.2.3 Protein Microarrays***

Protein microarrays have emerged as a complementary procedure for studying protein interactions *in vitro*. Microarray-based assays require purified proteins, which are usually obtained as tagged fusion proteins. By arraying sets of recombinant proteins in the microarray format one can screen dozens or even thousands of potential interactors. Prefabricated arrays can be purchased and used for detection. When you screen proteins like this you can either use an antibody against your bait protein of interest, or use a fusion protein bait with an available antibody to the fusion tag. The principle comes down to a miniaturized ligand-binding reaction, with your bait protein serving as the ligand [14].

While this approach in principle is very powerful it is limited by several factors, including the need for dedicated very expensive microarrayers and arraying robots. Current technology allows for arraying of only mostly soluble proteins, and purification both positive and negative controls for the assay is still being optimized. Regardless, the use of protein microarrays promises to be a powerful technique to screen many possible interaction partners in the future.

### ***9.2.4 Mass Spectroscopy-Coupled Co-immunoprecipitation Proteomics***

In MS-based proteomics, the protein itself is used as an affinity reagent to isolate its binding partners. The primary advantages over the above-mentioned methods are that the protein is used in its fully processed form, the interactions are in the protein's native environment, and multi-component complexes can be isolated in a single step. With the sequencing of the human genome and the emergence of advanced peptide-based mass spectroscopy (MS), recent studies have documented that these approaches may be more useful for identifying proteins involved in the biological regulation of neuronal responses.

Recently, MS proteomic-based methods have proven useful for identifying interacting proteins with neurotransmitter receptors, including NMDA [15], P2X<sub>7</sub> [16], and 5-HT<sub>2C</sub> [17] receptors. Additionally, both D<sub>1</sub> and D<sub>2</sub> receptor-interacting proteins [3] have been successfully identified using this approach. There are three essential components for successfully identifying neuronal proteins using MS-based proteomics: immunoprecipitation of the protein bait, purification of the complex, and the identification of the interacting partners.

The ability to immunoprecipitate a protein bait of interest from the desired system must be established before further isolation of the complex can occur. Ideally, an antibody is available allowing immunoprecipitation of the native protein from tissues. If this is the case, then the bait can be an endogenous protein in native neuronal tissue. However, suitable antibodies are often not readily available. In these instances, the bait protein can be affinity tagged and expressed in an appropriate cell system, followed by immunoprecipitation with commercially available antibodies directed against the affinity tag.

Successful immunoprecipitation of the bait is followed by a series of washes of varying stringency and then separation of proteins by denaturing polyacrylamide gel electrophoresis. The coupling of MS technologies with successful co-immunoprecipitation allows rapid and specific identification of discrete members of the protein complex and provides an attractive alternative for the discovery of novel interacting partners that cannot be detected using two-hybrid or fusion pull-down analyses.

While MS-based proteomics can be a sensitive and effective tool for identification of interacting proteins, this procedure relies on a relatively strong affinity between bait and targets. Furthermore, many biological interactions are transient in nature and depend on cellular environment. Proper controls, manipulations, and optimization techniques can help limit some of these pitfalls [18]. When used to its full capability, co-immunoprecipitation coupled with MS analysis provides a useful assay for discovering previously unknown protein partners, thus expanding our existing knowledge of dynamic protein regulation and control.

### 9.3 Experimental Manipulations

Following the initial identification of a putative DRIP, much care must be taken to confirm the interaction and to determine the significance of the DRIP association with DARs. After verifying the occurrence and determining the functional significance of the interaction, the physiological location of the interaction should be assessed. It is possible that for many different DRIPs association with the DAR occurs in specific organs, and may even vary across cell types within the tissues. Determining the physiological location of the interaction will greatly assist in ascertaining the role of the DRIP in cellular or receptor regulation. Finally, the ultimate goal of DRIP discovery is to enhance the understanding of the workings and regulation of the DAR as a unit and its role in governing various cellular processes.

Thus, once we understand the function and location of the DAR–DRIP interaction, we can begin to ascribe a unique role in governing normal physiological processes to each DRIP. Moreover, we can determine the relevance of each DRIP–DAR interaction to known disease states and etiologies, perhaps even altering current forms of pharmacotherapy or creating novel drugs to better treat DAR-associated disorders.

### ***9.3.1 Verification and Significance of the Interaction***

After initial DRIP identification, preliminary experiments must be conducted to ensure that the interaction is valid, and not a false positive result. Many of the assays described in Section 9.2 can be employed in this secondary screening stage. In the DRIP literature, the most common methods for DRIP verification are co-immunoprecipitation or GST-fusion pull-down assays. In addition, FRET and BRET analyses can be used to verify DAR interactors and are also essential tools for determining direct interaction between DARs and DRIPs (discussed further in Section 9.3.2).

After verifying the interaction, the experimenter should next examine the significance of the DAR–DRIP association. This is commonly performed in cultured cell expression systems, and ideally utilizes cells that do not endogenously express either DAR or DRIP. If such cells are available, then multiple parameters of DAR and DRIP can be investigated individually and after co-expression, including protein localization and function. If such an expression system is unavailable, overexpression of one or both proteins is also a feasible mechanism to examine the relevance of the DAR–DRIP interaction. These are popular approaches, and were successfully utilized in the characterization of multiple DRIPs, including calnexin and S100B [3, 19].

In the event that all available cell systems contain both proteins, multiple investigation methodologies are still available. The DAR can be pharmacologically manipulated in conjunction with measurements of DRIP function and/or trafficking response. Another promising method for systems that express both proteins is the inhibition of endogenous DAR or DRIP using siRNA technology. This approach enables investigation of various cellular parameters and protein function both with and without the interacting partner. Many of the proteins highlighted in the following sections utilized these investigational tactics – studies of prostate apoptosis response 4 and the  $\text{Na}^+, \text{K}^+$ -ATPase employed siRNA technology [20, 21], and dopamine transporter experimentation employed pharmacological manipulations of both the transporter and DARs [22].

Finally, using a peptide inhibitor approach, it is possible to biochemically disrupt the interaction of DAR and DRIP without altering the expression levels of either protein. This is a valuable tool for cellular environments where full expression of both proteins is necessary for normal biological function, as it enables functional investigation of the consequence of targeted DAR–DRIP disruption. This approach was successfully employed in the study of DAR interactions with the dopamine transporter and G protein inwardly rectifying potassium channels [22, 23].

### ***9.3.2 Location of the Interaction – Tissues and Protein Domains***

Occasionally, elucidation of important organs for DAR–DRIP interactions is straightforward – when the DRIP is only present in a particular tissue, for example. However, because of the wide physiological distribution of DARs, and because many DRIPs have multiple homologues expressed across a variety of tissues, identifying significant organs for a given DAR–DRIP association can be challenging. If it is known that DAR and DRIP are both expressed in a given organ, then immunohistochemistry can be used to look at protein distribution at the cellular level. Once a cellular source for DAR–DRIP co-localization is identified, it is possible to generate primary cultures of these cells for functional analyses. Functional experimentation in primary cell cultures is likely to incorporate many of the methods detailed in the previous section, including pharmacological manipulation and biochemical inhibition of the proteins. Such experiments were performed by investigators studying DAR interactions with S100B and the G protein-coupled receptor-associated sorting protein [6, 19].

In addition to determining organ localization for the DAR–DRIP association, the DAR and DRIP protein domains that mediate the interaction are also of relevance. Many DRIPs were discovered using yeast or bacterial two-hybrid systems. In these instances, the DAR “bait” is the receptor-interacting domain and only the DRIP interaction point remains to be determined. For some DRIPs, especially scaffolding and anchoring proteins, the protein sequence contains a series of well-defined domains including protein-interaction domains. For such proteins, interaction mapping is straightforward and mutagenesis experiments can be employed. The task of mapping interaction domains is far more challenging if the DRIP, like DARs, is a transmembrane protein. In these circumstances all regions of both DAR and DRIP, including the hydrophobic transmembrane regions, are potential interacting sites. Mutagenesis and truncation mapping studies were performed when determining the DAR–DRIP interaction sites for many soluble DRIPs, including GAIP-interacting protein C terminus [7], as well as for soluble regions of the transmembrane-spanning dopamine transporter [22, 24].

Determining the domains that are critical for the protein–protein interaction does not necessarily indicate that the proteins directly interact – it is possible that the mapped regions on each protein are required for binding to an intermediary, scaffolding protein, as is the case with DRAPs. Indeed, most methods for examining DAR–DRIP interaction only support that the two proteins are in a complex and in close proximity to one another, but not that they can directly interact. The closest approximations of direct DAR–DRIP interactions are ascertained from co-localization studies and FRET or BRET analysis [25].

Co-localization studies require either transfection of fluorescent-tagged proteins or fluorescent-conjugated antibody staining of endogenous proteins to determine whether the DAR and DRIP are found in overlapping regions of the cell. This method for determining direct protein–protein interaction is most convincing if there is evidence for alternative distribution patterns of at least one of the proteins – for example, if the DRIP is commonly stored in vesicles, but when interacting with the

DAR it is localized to the plasma membrane. Such a finding was presented with the interaction of the transient receptor potential channel 1 with DARs [26].

FRET or BRET analysis provides the most detailed information on the proximity of DAR to DRIP. For these assays, the interacting proteins must be within 10 Å of one another in order to achieve proper luminescence transmission between the two tagged proteins. However, even in such close range, it is still possible that a scaffolding or adaptor protein may govern the association of DAR and DRIP. Nonetheless, FRET and BRET are currently the best estimation of protein proximity and, when possible, have been employed to assess whether DAR–DRIP interactions are direct. Notably, FRET and BRET analysis have been used to study DAR interactions with other GPCRs, a topic that will be covered in Chapter 10. BRET was also used to study interactions between the D<sub>2</sub> DAR and arrestin3 [27].

### ***9.3.3 Model Systems and Disease Relevance***

After complete biochemical characterization of the DAR–DRIP interaction, it is often desirable to generate a model system for further study. This is most notably the case when the DAR–DRIP complex has important cell regulatory functions that imply a role for the interaction in human disease. Transgenic and knockout mouse models have been utilized in the characterization of several DRIPs, including prostate apoptosis response 4 and arrestin3 [21, 28]. Experimentation with animal models has revealed formerly unappreciated aspects of dopaminergic signaling and regulation, and revealed new potential pathways for future therapeutic intervention in a variety of disease states including depression and addiction [6, 21, 22].

## **9.4 Protein Members of the Dopamine Receptor Signalplex**

As the members of the DAR signalplex have been identified, it has become clear that DRIPs are not necessarily shared across the D1 and D2 families of DARs. In fact, even within the D1 and D2 families, protein interactors may associate with one DAR subtype and not another. This phenomenon may help to explain the wide array of physiological functions that are performed by DARs with the same G protein-coupling profile. It is likely, then, that unique signalplexes exist not only across cell types and throughout the lifecycle of the receptor, but also depend upon the complement of receptors present within the cell. Continued identification of proteins within the DAR signalplex will undoubtedly shed light on the unique signaling and regulative processes for each DAR.

### ***9.4.1 Targeting and Trafficking Proteins***

Proteins in this category can be subdivided into two groups – DRIPs that assist with trafficking and correct targeting of a newly synthesized DAR to the cell surface, and

those that are involved in the desensitization/internalization/recycling pathway of the DAR. DRIPs that target newly synthesized DARs to the cell surface are likely to first associate with the receptor in the ER; these DRIPs may also play a role in the proper folding and membrane insertion of the DAR. After receptor stimulation, a subset of DRIPs is necessary for binding to the receptor for removal from the plasma membrane. After endocytosis of the DAR, the fate of the receptor must be determined – resensitization and recycling to the cell surface versus lysosomal degradation of the receptor. These post-endocytic determinations of DAR fate are made by the complement of DRIPs that associate with the receptor.

#### 9.4.1.1 Calnexin

The protein calnexin functions as both an endoplasmic reticulum (ER) retention protein and chaperone, thus enabling the proper folding and assembly of glycoproteins prior to their export to the Golgi [29–31]. Both D<sub>1</sub> and D<sub>2</sub> DARs have been found to interact with calnexin via co-immunoprecipitation-based mass spectroscopy studies [3]. The interaction with calnexin in the ER is critical for the optimum expression of both DARs, and interestingly appears to be tightly regulated; there is an optimal degree or duration of calnexin interaction that results in the maximum amount of receptor being expressed at the cell surface. The interaction of calnexin with the DARs appears to be complex and dependent upon at least two different mechanisms. This has been demonstrated by using receptor mutants and pharmacological approaches. Most calnexin interactions are associated with glycoproteins based on their N-linked oligosaccharide side chains; however, some newer data suggest that calnexin may also target and bind non-glycosylated membrane proteins [3]. These data support the idea that the DARs actually associate with calnexin via both mechanisms: interaction of protein components as well as their carbohydrate side chains. Demonstration that calnexin interacts with the DARs via two distinct mechanisms raises the possibility that these different interactions may serve distinct biological functions. Although calnexin functions as a chaperone protein to assist in protein folding and assembly, it also serves as an ER retention protein that prevents misfolded proteins from exiting the ER and going on to the Golgi. Furthermore, it is possible that it is involved in heteromeric and homomeric assembly of dimers in the ER, and some data suggest that it may play a role in the proper assembly of these complexes. It has been suggested based on data with trafficking-deficient DAR mutant receptors, as well as glycosylation-deficient DAR mutant receptors, that glycan-dependant receptor–calnexin interactions may mediate the chaperone functions of calnexin, whereas the glycan-independent protein–protein interactions may be more relevant to ER retention and quality control [3]. Regardless of mechanisms it is clear that optimal receptor–calnexin interactions critically regulate D<sub>1</sub> and D<sub>2</sub> receptor trafficking and expression at the cell surface, a mechanism that is likely to be of importance for many GPCRs. This highlights the essential nature of trafficking DRIPs in DAR physiology.

#### 9.4.1.2 Dopamine Receptor-Interacting Protein-78

One of the first targeting and trafficking proteins identified to be a member of the D<sub>1</sub> DAR signalplex was DRIP78, so named because of its dopamine receptor interaction and its molecular mass of 78 kDa. It was identified in a yeast two-hybrid screen using the carboxyl terminus of the D<sub>1</sub> DAR as bait [32]. The specificity of this interaction location was subsequently verified with GST pull-down assays. Studies have shown that DRIP78 is an important member of the signalplex and is not likely to be totally specific to the D<sub>1</sub> DAR. DRIP78 closely co-localizes intracellularly with several ER membrane proteins and is clearly distinct from the Golgi. When DRIP78 is co-expressed with the D<sub>1</sub> DAR in heterologous cell lines, there is a marked change in D<sub>1</sub> DAR localization from the cell surface to intracellular stores containing DRIP78. Interestingly, when a mutant form of DRIP78 that does not bind to the D<sub>1</sub> DAR was overexpressed with the receptor, the D<sub>1</sub> DARs remained on the cell surface. These findings indicate the ability of DRIP78 to have a negative regulatory function when overexpressed with the D<sub>1</sub> DAR. Experiments that disrupt the DRIP78–D<sub>1</sub> DAR interaction also showed effects on transport to the cellular surface—hence, disruptions in the endogenous levels of this interaction appear to compromise the normal transport of the receptor to the cellular surface [32]. DRIP78 most likely acts as an ER retention protein by binding to, and thereby masking, a portion of the D<sub>1</sub> DAR carboxyl-terminal tail that is essential for export from the ER. If the completely formed receptors are not transported from the ER in a timely fashion then they are rapidly degraded, and it appears that the DRIP78 interaction is an essential part of this quality control mechanism. D<sub>1</sub> DAR transport to the cell surface is highly sensitive to the levels of DRIP78, and either interference or augmentation of those levels slows the ER export of the receptors. This suggests a dual function in both ER retention and quality control, as well as assistance in transport, reminiscent of the D<sub>1</sub> DAR interaction with calnexin described above.

#### 9.4.1.3 ALG-2-Interacting Protein 1

Recently ALG-2-interacting protein 1 (AIP1) was identified as a D<sub>1</sub>-interacting protein through a yeast two-hybrid screen using the carboxyl-terminal domain of the receptor. AIP1 is a known modulator of caspase-dependent and caspase-independent neuronal cell death. The protein is also known to be part of the endosomal transport system. AIP1 was also found to interact with the D<sub>3</sub> DAR in a similar yeast two-hybrid experiment. This interaction was verified for both receptors via GST pull-down assays and co-immunoprecipitation from mouse brain lysates [33]. Interestingly, AIP1 may represent an important functional link between D<sub>1</sub> and D<sub>3</sub> DAR-mediated signaling. It has been suggested that the D<sub>1</sub> and D<sub>3</sub> DARs and AIP1 proteins may all form a single complex. These findings have led to studies investigating the interaction of AIP1 in affecting the trafficking, stability, and recycling of these two DARs. Overexpression of all three proteins in heterologous cell lines leads to the accumulation of the proteins in the cytoplasm, indicating a possible effect on trafficking. Furthermore, it has been suggested that AIP1 could also be involved in

recycling of the receptors because AIP1 is known to interact with ESCRT (endosomal sorting complex required for transport) proteins [34]. This protein is known for sorting proteins for degradation or recycling to the plasma membrane. While the exact influence of AIP1 is not yet fully characterized, it is a DRIP that may play a prominent role in DAR biology.

#### **9.4.1.4 Neurofilament-M**

Neurofilament-M (NF-M), a neuronal cytoskeletal protein, was identified in a yeast two-hybrid screen to be a DRIP with the D<sub>1</sub> DAR. It was not found to interact with the third cytoplasmic loops (the region of interaction with the D<sub>1</sub> DAR) of the D<sub>2</sub>, D<sub>3</sub>, or D<sub>4</sub> receptors, but it did show weak interaction with the D<sub>5</sub> DAR. Co-expression of NF-M with the D<sub>1</sub> receptor resulted in a decrease in both expression and function of the receptor in heterologous cell lines. The other subtypes were not affected by NF-M expression in the same system. NF-M also appears to play a role in D<sub>1</sub> DAR trafficking and desensitization. When NF-M is expressed with the D<sub>1</sub> DAR in cells there is a decrease in cell surface expression and apparent accumulation of the receptor in the cytosol. Interestingly, the D<sub>1</sub> DARs expressed at the cell surface in the presence of NF-M were resistant to agonist-induced desensitization. These findings indicate that this interaction may play a critical role in both receptor expression and desensitization [35]. The D<sub>1</sub> DAR–NF-M interaction has also been investigated *in vivo* where approximately 50% of medium-sized striatal neurons express both proteins. Co-localization was also observed in pyramidal cells and interneurons within the frontal cortex. In addition, when NF-M-deficient mice were examined via immunohistochemistry, it was determined that they showed a decrease in D<sub>1</sub> receptor expression as compared to control mice. These data support a role for NF-M in the brain modifying D<sub>1</sub> DAR expression and regulation [35]. NF-M is encoded by the NEF3 gene. Point mutations in the NEF3 gene have been identified in patients with Parkinson's disease, however, no association of these variants and the disease has been shown [36]. Of note, when a clinical antipsychotic response study was conducted in schizophrenic patients, it was found that patients carrying specific genetic variants of NEF3 may be more likely to respond early to treatment than those not carrying the variants [37]. These findings demonstrate some potential clinical aspects of the importance of this DRIP.

#### **9.4.1.5 Dynamin-2**

It is well established that many GPCRs are desensitized and internalized via the arrestin–clathrin pathway. One of the key players in this pathway is the protein dynamin. In addition to its role in the clathrin endocytic pathway, dynamin can also assist with internalization of GPCRs via caveolae and in late-endosomal trafficking [38, 39]. Because of its important role in GPCR trafficking, dynamin was investigated as a potential interactor with the D<sub>2</sub> DAR. The D<sub>2</sub> DAR and dynamin-2 were found to co-localize in both synaptic and non-synaptic regions of rat striatum and could be co-immunoprecipitated from transfected cells [40]. Interestingly,

only the dominant negative dynamin-2 construct prevented D<sub>2</sub> DAR internalization; the dominant negative dynamin-1 construct did not alter D<sub>2</sub> internalization. This is in contrast to findings with the D<sub>1</sub> DAR, where both dynamin-1 and dynamin-2 were found to associate with and contribute to receptor internalization [40]. These findings highlight the critical role of dynamin-2 in D<sub>2</sub> DAR internalization. The difference in dynamin requirements for the D<sub>2</sub> versus the D<sub>1</sub> DAR may be mediated by the cellular location of protein expression, or may be caused by differences in protein interaction domains between the receptors. It is also interesting to note that dynamin isoforms can dimerize, and this dimerization process may be critical to DAR–dynamin pairing. It is possible that interaction of DARs with dynamin is not only necessary for receptor internalization and trafficking, but also serves to scaffold the receptor to other members of the DAR signalplex.

#### 9.4.1.6 GAIP-Interacting Protein, C Terminus

GAIP-interacting protein C terminus (GIPC) was first identified as an interacting protein with RGS19 (regulator of G protein signaling 19) or GAIP [41]; GAIP specifically acts as a GTPase for G $\alpha_{i/o}$  G proteins and has been shown to interact with D<sub>2</sub> DARs (Section 9.4.3.9). GIPC also interacts with other membrane-spanning receptors [42, 43] and transporters [44] and has been hypothesized to play a role in receptor expression, trafficking, and G protein signaling. Using the carboxyl terminus of the D<sub>3</sub> DAR as bait in yeast two-hybrid assays, GIPC was identified as a DRIP [7]. Interestingly, GIPC was found to interact with the D<sub>2</sub> and D<sub>3</sub> receptors, but not with the D<sub>4</sub> DAR, both in vitro and in rat striatum. In a transfected cell system, the D<sub>2</sub> and D<sub>3</sub> DARs caused translocation of GIPC to the plasma membrane and GIPC was co-internalized with the DARs following agonist treatment; the D<sub>4</sub> DAR neither recruited nor co-internalized with GIPC. In addition to its role in D<sub>2</sub> and D<sub>3</sub> DAR internalization, GIPC was also found to diminish the D<sub>3</sub> receptor response; this is likely caused by GIPC recruiting GAIP to the signaling form of the receptor. Finally, GIPC increased the number of D<sub>2</sub> and D<sub>3</sub>, but not D<sub>4</sub>, binding sites in transfected cells. This is likely the result of an increase in receptor recycling, as opposed to DAR degradation, following co-internalization with GIPC. The variance observed in GIPC-D2 family interactions implies that differences in D2 DAR internalization kinetics may be produced by a different complement of trafficking DRIPs associated with each receptor. Taken together, these data suggest that GIPC plays a role in trafficking of the D<sub>2</sub> and D<sub>3</sub> DARs via internalization and recycling of the receptors to the plasma membrane. These results also implicate GIPC as a scaffolding protein because of its known ability to recruit GAIP (discussed below in signaling proteins, Section 9.4.3) and other membrane-bound receptors.

#### 9.4.1.7 N-Ethylmaleimide-Sensitive Factor

N-Ethylmaleimide-sensitive factor (NSF) is an ATPase shown to be involved in membrane vesicle trafficking [45]. This protein has also been found to interact with the  $\beta_2$  adrenergic receptor where it is likely involved in both internalization and

recycling of the receptor [46]. NSF has also been identified via GST pull-down assays to be a DAR DRIP. It binds tightly to both the D<sub>1</sub> and D<sub>5</sub> receptor's carboxyl termini, but was reported to bind weakly to D<sub>2</sub>-like receptors [47]. Regardless, it is likely that NSF also affects trafficking and recycling of these DARs. Despite the reportedly weak interaction in GST pull-down assays between NSF and the D<sub>2</sub> DARs, co-immunoprecipitation from solubilized rat hippocampal tissue documents that D<sub>2</sub> DARs and NSF do, in fact, form a complex [48]. Interestingly, when the interaction sites were mapped using GST-pull-down assays, the NSF interaction site identified on the D<sub>2</sub> DAR is the same site that mediates the receptor's interaction with the AMPA receptor (see Section 9.4.4.5). It has been further proposed that, in fact, NSF mediates the interaction of the D<sub>2</sub> DAR and the AMPA receptor. This complex appears to play an important role in controlling glutamate-mediated excitotoxicity. Activation of the D<sub>2</sub> receptor results in a decrease in toxicity and this effect appears to be mediated by the shuttling of NSF between the D<sub>2</sub> DAR and the AMPA receptor [48]. This highlights how a DRIP can potentially mediate other interactions and demonstrates how two receptors can communicate through common interacting proteins.

#### **9.4.1.8 Sorting Nexin-1**

Sorting nexin-1 (SNX1) was originally found to interact with the epidermal growth factor receptor and was subsequently shown to be responsible for the efficient targeting of the thrombin receptor, PAR1, from sorting endosomes to lysosomes [49]. SNX1 has also been found to bind strongly to the carboxyl terminus of the D<sub>5</sub> DAR and weakly to the D<sub>1</sub> and D<sub>3</sub> DAR [47]. The overall importance of the DAR interactions with sorting nexin proteins continues to be investigated.

#### **9.4.1.9 G Protein-Coupled Receptor-Associated Sorting Protein**

The DRIP, G protein-coupled receptor-associated sorting protein (GASP), was first discovered as an interactor with the  $\delta$ -opioid receptor [50]. Because the D<sub>2</sub> receptor, like the  $\delta$ -opioid receptor, can be down-regulated in response to agonist treatment, the ability of GASP to interact with the D<sub>2</sub> DAR was also investigated [6]. Interestingly, the D<sub>1</sub> DAR has not been consistently shown to down-regulate in response to agonist. As such, GASP was found to interact with the carboxyl terminus of the D<sub>2</sub> but not the D<sub>1</sub> DAR [6, 51]. This D<sub>2</sub>-GASP interaction occurred in both transfected cell lines and endogenously in the rat brain. Both a dominant negative form of GASP and an antibody against GASP prevented degradation of D<sub>2</sub> DARs, but had no impact on desensitization or internalization of the receptor. This supports the hypothesis that GASP is solely involved in sorting the D<sub>2</sub> DARs to a degradative pathway, but not in desensitizing or internalizing the receptor. In fact, examination of neurons from the rat ventral tegmental area revealed that treatment with the GASP antibody prevented receptor degradation, and allowed desensitization and internalization, followed by resensitization and recovery of D<sub>2</sub> DAR response to agonist [6]. This successful manipulation of the GASP-D<sub>2</sub> DAR

interaction provides insight into potential therapeutic utility for selective blockade of GASP–D<sub>2</sub> interactions in addiction and other disorders where recovery of the D<sub>2</sub> DAR response to agonist is critical.

### ***9.4.2 Anchoring, Scaffolding, and Adaptor Proteins***

DRIPs in this category may associate with the cytoskeletal architecture. Often, this cytoskeletal association occurs via binding to actin, and functions to assist with anchoring of the DAR to the plasma membrane and DAR retention at the cell surface. Such DRIPs may also act to retain the DAR within discrete membrane microdomains. DRIPs in this category may also contain multiple protein-binding domains. DRIPs with multiple interaction sites can associate with the DAR and recruit other DRIPs and DRAPS to the signalplex, thus acting as an adaptor or scaffold protein between the DAR and its interactors. Finally, it is possible for proteins in this category to serve both purposes – they may tether the DAR to the cell surface and simultaneously scaffold the DAR to other DRIPs and signaling machinery.

#### **9.4.2.1 Filamin-A**

Filamin-A was initially termed actin-binding protein 280 and was discovered as a DRIP with the D<sub>2</sub> DAR [52]. The interaction between filamin-A and the D<sub>2</sub> DAR was found to occur on the third intracellular loop of the D<sub>2</sub> DAR by yeast two-hybrid analysis. It was subsequently determined that filamin-A can interact with both the D<sub>2</sub> and the D<sub>3</sub> DARs, but not with the D<sub>1</sub> or D<sub>4</sub> DARs [52–54]. Transfection of D<sub>2</sub> DARs into cells without endogenous filamin-A revealed both an intracellular and a diffuse membrane-bound distribution of the DAR [52, 54]. Upon transfection of filamin-A into these cells, DAR expression became localized to discrete regions of the plasma membrane, and the intracellular stores of DAR were eliminated [52, 54]. These data indicate that filamin-A is important for anchoring the DAR to the plasma membrane, and that it may play a critical role in tethering the DAR to specific membrane microdomains. It is interesting that while many GPCRs require membrane-anchoring by an actin-binding protein, a single actin-binding protein is not capable of interacting with all DARs, even within the D<sub>2</sub> family of receptors. It may be that the ability to interact with specific anchoring proteins is based on similar distributions and co-localization. Of note, D<sub>2</sub> DAR and filamin-A were found to co-localize in neuronal soma and astrocytes from cultured rat striatum [54]. In brain regions where all members of the D<sub>2</sub> DAR family are expressed, there may be a single actin-associated protein which is able to interact with all receptors.

#### **9.4.2.2 Protein 4.1 N**

Protein 4.1 N was identified as a DRIP for D<sub>2</sub> and D<sub>3</sub> DARs using the yeast two-hybrid assay with the third intracellular loop of D<sub>2</sub> or D<sub>3</sub> DARs as bait [55]. The

interaction between DARs and protein 4.1 N was subsequently confirmed by co-immunoprecipitation of the two proteins from transfected cells. Protein 4.1 N is known to interact with actin via an actin-binding domain that is separate from the region of the protein necessary for DAR interaction. As such, it was determined that protein 4.1 N and the D<sub>2</sub> and D<sub>3</sub> DARs co-localize at the plasma membrane of transfected cells. Importantly, a dominant negative version of 4.1 N caused a largely intracellular distribution of both D<sub>2</sub> and D<sub>3</sub> DARs, indicating that DAR interaction with 4.1 N is critical for receptor stability at the plasma membrane. It is notable that both protein 4.1 N and filament-A bind to the same region of the third intracellular loop of D<sub>2</sub> and D<sub>3</sub> DARs [52–55]. As such, the ability of 4.1 N and filament-A to compete for DAR binding was assessed. It was determined that the presence of 4.1 N did not interfere with the binding of filament-A to the DARs [55], indicating that the binding sites are, in fact, different. It is not presently known if the different DAR isoforms preferentially bind to either filament-A or 4.1 N for membrane-retention, or if there are alterations in DAR interactions with these DRIPs across various cell types.

#### **9.4.2.3 Spinophilin**

Using the third intracellular loop of the D<sub>2</sub> DAR as bait, spinophilin was identified as a DRIP in a yeast two-hybrid screen [4]. The interaction between D<sub>2</sub> and spinophilin was confirmed by co-immunoprecipitation and co-localization studies in transfected cells. Spinophilin is an actin-binding protein with multiple interaction domains for protein binding. It has been shown to interact with a variety of other proteins, including protein phosphatase 1 (PP1). In fact, experiments revealed that spinophilin can simultaneously bind both D<sub>2</sub> DAR and PP1, indicating that PP1 may also be a part of the D<sub>2</sub> DAR signalplex. Spinophilin serves as a membrane anchor for the D<sub>2</sub> DAR, and most likely performs the important function of scaffolding a variety of other protein partners to the D<sub>2</sub> signalplex in a time- and cell-dependent manner.

#### **9.4.2.4 Radixin**

Radixin belongs to the ERM (ezrin, radixin, moerin) family of proteins and is capable of simultaneously binding actin and interacting proteins [56]. Radixin was discovered as a D<sub>3</sub> DAR DRIP by yeast two-hybrid assay and was found to interact with the D<sub>3</sub> DAR carboxyl terminus [57]. The cellular role of radixin with the D<sub>3</sub> DAR is not presently known, but it likely acts as both a membrane anchoring protein and a scaffold to other members of the D<sub>3</sub> DAR signalplex.

#### **9.4.2.5 Multi-PDZ-Domain-Containing Protein 1**

Multi-PDZ-domain-containing protein 1, or MUPP1, is a scaffolding protein consisting of 13 protein-binding PDZ-domains. It has been shown to interact with a variety of other proteins, including the serotonin 5-HT<sub>2C</sub> receptor [58, 59]. Recently,

it was identified by yeast two-hybrid assay as an interactor with the carboxyl terminus of the D<sub>3</sub> DAR [57]. The precise function or localization of this interaction has not yet been determined, but MUPP1 most likely serves as a scaffold between the D<sub>3</sub> DAR and other proteins in the DAR signalplex.

#### 9.4.2.6 Heart-Type Fatty Acid Binding Protein

Heart-type fatty acid binding protein (H-FABP) is expressed in a variety of tissues, including heart, kidney, and brain [60]; it is known to bind and traffic fatty acids and other hydrophobic ligands [61]. H-FABP was identified as a DRIP using the third intracellular loop of the D<sub>2L</sub> receptor as bait in yeast two-hybrid screens [62]. Interestingly, H-FABP did not co-localize with or interact with the D<sub>2S</sub> receptor in co-immunoprecipitation assays. Of note, Takeuchi and Fukunaga demonstrated that the D<sub>2L</sub> isoform was predominantly intracellularly distributed, while the D<sub>2S</sub> isoform was localized to the plasma membrane in a transfected cell system. Although this study indicates that H-FABP is important for differential D<sub>2</sub> DAR isoform distribution, it is also plausible that, given H-FABPs known role in fatty acid binding, it is significant in D<sub>2</sub>-mediated arachidonic acid signaling. While the role of H-FABP in the D<sub>2</sub> DAR signalplex has not been defined, DRIPs that interact with the variable region of the D<sub>2</sub> DARs third intracellular loop may determine subtle differences in localization or functionality between these two receptors.

#### 9.4.2.7 Caveolin-1

Caveolae are subtypes of lipid rafts that exist as distinct invaginations in the plasma membrane. This dynamic structure is thought to play a role in cell-surface signaling, possibly by forming a signaling platform for the integration of various signaling molecules. The caveolin proteins are found only in caveolae, and form a scaffolding complex that binds to a large number of receptors, signaling molecules, and adaptor proteins [63]. It was initially found that the D<sub>1</sub> DAR contains a caveolin-1 binding motif in the seventh transmembrane domain, thereby implying a role in D<sub>1</sub> DAR function and piquing interest in the study of this protein as a potential DRIP [64]. Subsequent studies determined that caveolin-1 and the D<sub>1</sub> DAR are localized in the same caveolae-related lipid raft domains. Co-immunoprecipitation assays from both heterologous cell lines and rat brain, as well as BRET studies in transfected cell lines, verified the direct nature of the interaction. It was subsequently determined that agonist-induced internalization through caveolae was dependent upon the direct interaction of the D<sub>1</sub> DAR and caveolin-1. When the caveolin-1 binding domains were mutated in the D<sub>1</sub> DAR, the receptor failed to internalize. Furthermore, this interaction with caveolin-1 also appears to be important for signal transduction as a mutated D<sub>1</sub> DAR lacking the caveolin-1 binding domain also showed diminished ability to stimulate cAMP production [64]. Taken together, these findings indicate that the caveolin-1–D<sub>1</sub> DAR interaction may have important implications for regulation and signaling by dopamine in the brain.

#### 9.4.2.8 Arrestin

Arrestin proteins directly interact with DARs to mediate signal termination and internalization of the receptors, as well as to propagate alternate signaling pathways. Using GST-fusion protein pull-down assays, it was determined that arrestin2 and arrestin3, isolated from striatal homogenates, could bind to the third cytoplasmic loop of the D<sub>2</sub> DAR [65]. Similar experiments also showed that purified arrestin2 and arrestin3 could bind to the second and third cytoplasmic loops as well as the carboxyl terminus of the D<sub>2</sub> DAR [65]. Furthermore, the D<sub>2</sub> DAR was shown to co-immunoprecipitate with both arrestin2 and arrestin3 solubilized from neostriatal membranes [65]. Direct interactions between the D<sub>1</sub> DAR and arrestins have also been characterized. Both arrestin2 and arrestin3 interact (demonstrated using both GST-fusion protein and co-immunoprecipitation assays) with the carboxyl terminus of the D<sub>1</sub> receptor in striatal membranes, with arrestin3 binding more strongly [66].

Recently, arrestin has also been demonstrated to act as a scaffold between the D<sub>2</sub> family of DARs and regulation of the Akt signaling pathway [28]. Akt is a serine/threonine kinase that negatively regulates glycogen synthase kinase 3 (GSK3) and has been shown to be regulated by dopamine [67, 68]. Arrestin has been found to scaffold other GPCRs to G protein-independent signaling pathways that are slower than traditional G protein-mediated signaling pathways [69, 70]. Arrestin3 knockout mice were thus employed to investigate the role of arrestin-scaffolded signaling in dopaminergic pathways [28]. Experiments in mice lacking arrestin3 revealed that amphetamine-induced phosphorylation of Akt was greatly diminished in knockout mice as compared to wild-type littermates [28]. However, knockout versus wild-type mice exhibited no alterations in the phosphorylation of DARPP-32, a downstream target of the cAMP pathway. Using GST-pull-down assays, it was determined that Akt, arrestin3, GSK3, and protein phosphatase 2A can all interact [28]. The formation of this complex was also found to occur *in vivo* and was regulated by dopamine levels. Taken together, these data implicate arrestin3 as the scaffold necessary for linking the D<sub>2</sub> DAR with the Akt/GSK3 signaling pathway.

#### 9.4.3 Signaling Proteins

This category of DRIPs contains the most classical DAR interactors – members of the downstream signaling cascade. Such DRIPs include all manner of signal initiators and propagators, from the traditional G proteins (discussed in Chapter 6) to the more recently discovered signaling proteins – calcium-sensing molecules and arrestin. In addition, this class of proteins also includes signal terminators, such as RGS proteins and kinases (see Chapter 8). To achieve maximal efficiency in signaling, it is important for the DARs to be near the machinery within their respective signaling cascades. As such, it has been demonstrated that several of the proteins in this category are scaffolded in close proximity to the receptor, and then recruited to the DAR when necessary by the DRIPs discussed in Section 9.4.2.

#### 9.4.3.1 Calcium-Dependent Activator Protein for Secretion 1

Calcium-dependent activator protein for secretion 1, or CAPS1, is a calcium-triggered protein that assists in fusion and release of large dense-core vesicles (LDCV) to the plasma membrane [71]. LDCVs can package neurotransmitters, including dopamine, and are present along with CAPS1 and 2 in several cell lines. CAPS1 was discovered as a DRIP using the second intracellular loop of the D<sub>2</sub> dopamine receptor in yeast two-hybrid screens and was verified using co-immunoprecipitation assays [72]. Further investigation revealed that a serine within this second intracellular loop was necessary for CAPS1 binding, indicating a possible phosphorylation event that mediates D<sub>2</sub>-CAPS1 interaction. Interestingly, no other DARs were found to interact with CAPS1, but D<sub>2</sub> DARs could also bind the closely related protein, CAPS2. CAPS1, CAPS2, and the D<sub>2</sub> DAR are all endogenously expressed, and co-localize, in rat pheochromocytoma PC12 cells. Transfecting PC12 cells with a truncated version of the D<sub>2</sub> receptor disrupted the D<sub>2</sub>-CAPS interaction, thus allowing investigation of the importance of this DRIP in a D<sub>2</sub>-specific manner. Significantly, disrupting the D<sub>2</sub>-CAPS association caused a specific decrease in K<sup>+</sup>-evoked dopamine release from PC12 cells, without altering release of any other neurotransmitters [72]. This implies that CAPS binding to the D<sub>2</sub> DAR or other GPCRs confers specific information regarding synaptic neurotransmitter requirements and may promote or delay LDCV fusion and exocytosis in a neurotransmitter-dependent fashion.

#### 9.4.3.2 Neuronal Calcium Sensor-1

The neuronal calcium sensor (NCS) proteins are a family of EF-hand calcium-binding proteins that are highly evolutionarily conserved and bind calcium with high affinity [73]; within this grouping, NCS-1 belongs to the recoverin subfamily [73]. NCS-1 has been shown to regulate channel activity and, interestingly, recoverin can modulate GRK phosphorylation of rhodopsin [74]. Using the carboxyl terminus of the D<sub>2</sub> DAR as bait in a yeast two-hybrid assay, NCS-1 was identified as a DRIP [75]. Further investigation revealed that the D<sub>3</sub> and D<sub>5</sub> DARs could also interact with NCS-1, but not the closely related D<sub>1</sub> or D<sub>4</sub> DARs [75]. Although the significance of these selective interactions is not yet understood, it could be related to physiological distribution of the DARs and NCS-1. Investigations of the striatum revealed co-localization of NCS-1 and D<sub>2</sub> DAR. In a transfected cell system, NCS-1 overexpression was found to decrease the level of D<sub>2</sub> phosphorylation and internalization, even in the presence of GRK overexpression. This decrease in D<sub>2</sub> DAR phosphorylation and internalization was accompanied by a parallel increase in D<sub>2</sub> signaling. These data imply that NCS-1 can modulate the GRK phosphorylation-dependent desensitization of D<sub>2</sub> DARs. Indeed, all three proteins – D<sub>2</sub> DAR, GRK2, and NCS-1 – could be co-immunoprecipitated from transfected cells [75]. Moreover, the formation of this protein complex was regulated by forskolin-induced increases in cAMP and by increased Ca<sup>2+</sup> concentration, highlighting the potential significance of this complex in neuronal signaling and receptor regulation.

### 9.4.3.3 S100B

S100B is a member of the diverse S100 family of proteins that bind calcium via two EF-hand domains [76]. S100 proteins have been implicated in an array of cellular processes, including regulation of protein phosphorylation and  $\text{Ca}^{2+}$  homeostasis; S100B has been shown to interact with and modulate the function of more than 20 other cellular proteins [76]. Recently, S100B was identified as a DRIP using the third intracellular loop of the  $\text{D}_2$  DAR in a bacterial two-hybrid screen [19]. S100B was capable of interacting with the  $\text{D}_2$ , but not with the  $\text{D}_3$  DAR, implicating a unique region of the  $\text{D}_2$  third intracellular loop as the putative binding domain for S100B. The  $\text{D}_2$  DAR and S100B could be co-immunoprecipitated from transfected cells or from striatum, and the two proteins were found to co-localize in neostriatal neurons. When S100B was overexpressed in transfected cells,  $\text{D}_2$  DAR-stimulated ERK activation and  $\text{D}_2$  DAR-mediated cAMP inhibition were both enhanced. These results imply that S100B can act as a  $\text{D}_2$  DAR DRIP to augment the dopamine-stimulated  $\text{D}_2$  DAR signaling response. Whether S100B produces this effect alone or as a dimer, scaffolding the DAR to another protein, is not yet known.

### 9.4.3.4 Calcineurin

Immunoprecipitation experiments have shown that protein phosphatase 2B, also known as calcineurin, is a DRIP of the dopamine  $\text{D}_1$  DAR [5]. It has become apparent (see Chapter 8) that phosphorylation and dephosphorylation play an essential role in the regulation of many aspects of DAR signaling, especially desensitization and resensitization as well as trafficking. Calcineurin has been linked to the dephosphorylation of a large number of proteins in the  $\text{D}_1$  DAR signaling pathway, although its role in dephosphorylation of the  $\text{D}_1$  DAR remains unclear [77]. These data indicate that, in addition to mediating signaling for the  $\text{D}_1$  DAR, calcineurin is also physically linked to the receptor – thus making it a DRIP.

### 9.4.3.5 Calmodulin

Calmodulin [17] is a small protein that, upon calcium binding, undergoes large conformational changes that enable protein binding [78]. A CaM-binding motif in the third intracellular loop of the  $\text{D}_2$  DAR led to the discovery that CaM is a DRIP [79]. CaM was able to bind either solubilized  $\text{D}_2$  DAR [79] or to co-immunoprecipitate from transfected cells with the  $\text{D}_2$  DAR [80], and agonist treatment increased the co-localization of  $\text{D}_2$  and CaM in transfected cells or primary neuronal cultures [80]. Moreover, it was determined that the  $\text{D}_2$  DAR could interact with CaM and the  $\text{G}\alpha_{i1}$  G protein simultaneously, indicating that there is no competition for binding between these two proteins [79]. Furthermore, addition of  $\text{Ca}^{2+}$ /CaM, but not  $\text{Ca}^{2+}$  alone, to  $\text{Ca}^{2+}$ /CaM-depleted cells caused a decrease in G protein turnover [79]. These data indicate that CaM binding to the  $\text{D}_2$  DAR can act to inhibit the receptor signal. Subsequent studies have shown that mutating the  $\text{D}_2$  DAR residues required for CaM binding decreases  $\text{D}_2$ -CaM interactions without altering  $\text{D}_2$ -G

protein binding [80]. However, this CaM-binding mutation does cause a decrease in D<sub>2</sub>-mediated cAMP and ERK signaling [80]. The conflicting results between these two groups may be explained by the role of other calcium-sensing DRIPs in receptor signaling and should be further investigated to determine the precise function of CaM–D<sub>2</sub> interactions.

#### 9.4.3.6 Prostate Apoptosis Response 4

Prostate apoptosis response 4 (Par-4) was identified as a DRIP by yeast two-hybrid analysis using the D<sub>2</sub> DAR third intracellular loop as bait [21]. The D<sub>3</sub> DAR and all other GPCRs tested did not interact with Par-4. Par-4 is expressed in neurons and other tissues, though its role in these regions is unclear, and it contains a leucine zipper domain that is critical for interacting with the D<sub>2</sub> DAR [21]. The D<sub>2</sub>–Par-4 interaction was verified by co-immunoprecipitation and co-localization in striatum. Silencing Par-4 expression by siRNA caused a decrease in D<sub>2</sub>-mediated signaling in transfected cells. To examine the effect of disrupting this protein interaction in living animals, the D<sub>2</sub>-binding leucine zipper domain of Par-4 was mutated and transgenic mice expressing this mutated Par-4 gene were generated. Cultured cells from these mice displayed elevated levels of cAMP after dopamine treatment, suggesting a loss of D<sub>2</sub> DAR signaling. These mice were also more prone to depressive behaviors as assessed by both Porsolt's forced swim test and the tail suspension test, with no alteration in anxiety-like behaviors [21]. These data present a possible role for Par-4 in the brain, and for the importance of Par-4–D<sub>2</sub> DAR interactions in neurological disorders. Of note, it was also determined that Par-4 and calmodulin compete for binding in the same region of the D<sub>2</sub> DAR third intracellular loop [21]. This implies that disrupting the Par-4–D<sub>2</sub> DAR interaction may have an appreciable impact on the association of D<sub>2</sub> DARs with other DRIPs, including calmodulin, and that the consequences of Par-4 inhibition may be due to other proteins interacting with D<sub>2</sub> DAR.

#### 9.4.3.7 Post-synaptic Density 95

Ultrastructural studies have demonstrated that many D<sub>1</sub> DARs are located in the post-synaptic density of neurons. Post-synaptic density 95 (PSD-95) is a scaffolding protein that is highly enriched in post-synaptic densities and is a member of the guanylate kinase family. This complex protein contains several important domains that have been shown to be involved in its interaction with a number of different partners, most notably the NMDA receptor. Via these interactions, PSD-95 organizes proteins into functional signaling complexes in the PSD [81]. It has subsequently been appreciated that PSD-95 may also play an important role in dopaminergic signaling. PSD-95 directly interacts with the D<sub>1</sub> DAR through the amino terminus of PSD-95 and the carboxyl terminus of the D<sub>1</sub> DAR [82]. It was first determined that the two proteins interacted via co-immunoprecipitation assays which utilized both recombinant cell lines and mice (both wild-type and PSD-95 knockout mice). This interaction was then confirmed by localization studies using confocal microscopy

and the interaction sites were subsequently determined using GST pull-down assays and specific domain probes [83]. PSD-95 is able to regulate surface expression, and therefore subsequent signaling, by inducing agonist-independent internalization of D<sub>1</sub> DARs that are otherwise located on the plasma membrane. This provides an interesting mechanism by which localization and signaling is regulated by a DRIP in a cellular compartment – in this case the PSD. It has further been determined that mice lacking PSD-95 show enhanced effects of D<sub>1</sub> agonist treatment, indicating a functional significance to this protein–protein interaction that is possibly related to drugs of abuse [83].

#### **9.4.3.8 Protein Kinases**

In addition to serving as second messenger molecules, cAMP-dependent protein kinase (PKA) and protein kinase C (PKC) have both been shown to phosphorylate the DARs [77, 84, 85]. The DARs are also regulated by GPCR kinase (GRK) phosphorylation, particularly by GRKs 2, 3, 4, and 6 [86–89]. Phosphorylation of DARs is thought to uncouple the receptors from G proteins and to facilitate the recruitment of trafficking/scaffolding proteins, such as arrestins, that are necessary for receptor internalization. In addition to their role in DAR trafficking and signal termination, kinases can also regulate the binding sites for DRIPs and DAR insertion at the plasma membrane. The details of DAR phosphorylation and, therefore, interaction with protein kinases, has been detailed elsewhere in this volume and extensively reviewed in the literature [90, 91].

#### **9.4.3.9 Protein Kinase C- $\zeta$ -Interacting Protein 1**

Protein kinase C- $\zeta$ -interacting protein 1 (ZIP1) was identified as a DRIP in yeast two-hybrid screens using the third intracellular loop of the D<sub>2</sub> DAR as the bait protein [92]. Subsequent yeast two-hybrid assays revealed that ZIP1 does not interact with any other D<sub>2</sub> or D<sub>1</sub>-family DARs. The D<sub>2</sub> DAR–ZIP1 interaction was verified by co-immunoprecipitation from both transfected cells and mouse brain. Of note, ZIP1 transfection caused a decrease in D<sub>2</sub> DAR expression and signaling in mammalian cells. This was apparently caused by an increase in lysosomal trafficking of D<sub>2</sub> DARs following ZIP1 overexpression. Interestingly, there was no alteration in PKC $\zeta$  phosphorylation of D<sub>2</sub> DAR following ZIP1 overexpression, and the D<sub>2</sub> DAR was found to interact with the PKC $\zeta$ -interaction domain of ZIP1 [92]. These data imply that, while there is a D<sub>2</sub> DAR–ZIP1 interaction, a D<sub>2</sub> DAR–ZIP1–PKC $\zeta$  complex is not likely to form.

#### **9.4.3.10 Regulator of G Protein Signaling 19**

GAIP, or regulator of G protein signaling 19 (RGS19), specifically acts as a GTPase for G $\alpha_{i/o}$  G proteins, and has been shown to interact with GIPC [41]. Because GIPC was previously identified as a DRIP for both D<sub>2</sub> and D<sub>3</sub> receptors ([7];

Section 9.4.1.6), the possibility that GAIP was also a member of the DAR signalplex was investigated [93]. GAIP, GIPC, and the D<sub>2</sub> DAR were all found to co-immunoprecipitate from transfected cells. Furthermore, GAIP was found to co-localize with activated D<sub>2</sub> DARs in a GIPC-dependent manner. Importantly, recruitment of GAIP to activated D<sub>2</sub> DARs was shown to attenuate the D<sub>2</sub> DAR signal. When the GAIP GTPase domain was mutated, GAIP could still translocate to active D<sub>2</sub> DARs, but could not diminish the D<sub>2</sub> DAR signal. However, disrupting the interaction between GAIP and GIPC prevented translocation of GAIP to D<sub>2</sub> DARs. These data indicate that GAIP is recruited to the D<sub>2</sub> signalplex by GIPC which is both a trafficking and a scaffolding protein for the D<sub>2</sub> DAR. Once recruited to the signalplex, GAIP attenuates the D<sub>2</sub> signaling response via its GTPase activity.

### ***9.4.4 Ion Channels and Pumps***

It has long been accepted that the DARs can modulate the function of a variety of voltage- and ligand-gated ion channels. In recent years, several of these ion channels have been shown to associate directly with the DAR, allowing for rapid adjustments in cellular ionic balance by the DAR-activated signalplex. In addition to the interaction between DARs and ion channels, ATP-driven ionic pumps have also been shown to associate with the DARs. The ionic pumps are responsible for maintaining resting membrane potentials and normal ionic balance within cells. DARs are important regulators of neuronal excitability, and the association of DARs with ion channels and pumps is likely critical for appropriate ionic response to stimulus and recovery from events such as DAR-stimulated membrane depolarization. Their interaction with DARs allows ion channels and pumps to receive efficient signal cross talk from DARs, and also raises the interesting possibility of a more direct method of modulating ion channel function via DAR conformational changes.

#### **9.4.4.1 Chloride Intracellular Channel 6**

CLIC6, a member of the chloride intracellular channel family, was found to interact with the carboxyl terminus of the D<sub>3</sub> receptor through a yeast two-hybrid screen [57]. Little is known about the function of CLIC6, but the CLIC family has been implicated in the subcellular transport of chloride ions. In addition to interacting with the D<sub>3</sub> receptor, CLIC6 was also able to bind the carboxyl terminus of D<sub>2</sub> and D<sub>4</sub> DARs in yeast two-hybrid screens, and to co-localize with the D<sub>3</sub> DAR in transfected cells. Moreover, CLIC6 was also found to interact with the scaffolding proteins MUPP1 and radixin, raising the possibility of these three DRIPs scaffolding together within the DAR signalplex. Unfortunately, co-expression of the D<sub>3</sub> DAR with CLIC6 revealed no effect on chloride transport or D<sub>3</sub> function, therefore the role of CLIC6 in the DAR signalplex remains unclear. It is possible that the significance of CLIC6 is cell-type specific, and analysis of other cell lines or primary tissues will reveal a function for this DRIP.

#### 9.4.4.2 Transient Receptor Potential Channel 1

Transient receptor potential channel 1 (TRPC1) was found to interact with the D<sub>2</sub> dopamine receptor by yeast two-hybrid analysis [26]. TRPC proteins have been shown to mediate Na<sup>+</sup> and Ca<sup>2+</sup> entry, phospholipase C signaling, and lipid raft integrity [94]. TRPC proteins can also homo- or heterodimerize, with TRPC1 commonly forming heterodimers with TRPC4 and 5 [95]. As such, the ability of D<sub>2</sub> DARs to interact with TRPC4 and 5 was also evaluated, and it was determined that these two TRPC proteins are also DRIPs. The D<sub>2</sub>–TRPC1 protein complex could be co-immunoprecipitated from rat brain and the two proteins were also found to co-localize in post-synaptic compartments of cortical neurons. Examination of human embryonic kidney cells that endogenously express TRPC1 revealed that D<sub>2</sub> DAR transfection caused an increase in plasma membrane expression of the TRPC1 protein, with no change in the total expression level of TRPC1. While the precise role of TRPC1 in the D<sub>2</sub> signalplex is unclear, it appears that D<sub>2</sub> expression is important for membrane expression of the TRP channel.

#### 9.4.4.3 G Protein-Activated Inwardly Rectifying Potassium Channels

Dopamine receptors are known to regulate the activity of G protein-activated inwardly rectifying potassium channels (GIRKs or Kir3 [96]), likely via Gβγ activity. Based on the presence of G proteins and other effector molecules in various GPCR signalplexes, the presence of GIRKs in the DAR signalplex was investigated [23]. In these experiments, GIRK was found to co-immunoprecipitate with both D<sub>2</sub> and D<sub>4</sub> DARs from transfected cells and rat striatum. Agonist treatment and pertussis toxin treatment both had no effect on the DAR–GIRK interaction, indicating that the association was stable and not dependent upon the signaling cascade. Interestingly, the assembly of the DAR–GIRK complex was dependent upon the presence of Gβγ, but once assembled, the complex did not require Gβγ for maintained stability. It is likely that close association with GIRKs and other effectors enables rapid communication following agonist stimulation of the DARs.

#### 9.4.4.4 Na<sup>+</sup>,K<sup>+</sup>-ATPase

The Na<sup>+</sup>,K<sup>+</sup>-ATPase (NKA, sodium pump) is a ubiquitous protein important for regulation of cellular ion balance. In the brain, NKA is critical in restoring neuronal polarity after membrane depolarization events. Dopamine signaling cascades have previously been shown to regulate the vesicular insertion or endocytosis of NKA at the plasma membrane [97, 98]. Recently, however, using mass spectroscopy coupled with co-immunoprecipitation from DAR-transfected cells, endogenous NKA was found to interact with both the D<sub>1</sub> and D<sub>2</sub> DARs [20]; the NKA–D<sub>2</sub> DAR interaction was also verified by co-immunoprecipitation of native proteins from striatum. Enhancing the association of NKA with DARs caused a decrease in both D<sub>1</sub> and D<sub>2</sub> DAR function. This could be reversed by pharmacological blockade of NKA, or by diminishing the NKA–DAR interaction via siRNA inhibition of NKA. The DARs

were also found to modulate NKA activity, even in the absence of ligand. This novel association of NKA with DARs in the signalplex allows for conformational changes in the proteins for exchange of cellular information, providing a more direct and rapid means of communication than traditional signaling pathways and allowing for reciprocal modulation of function between the two proteins in response to cellular stimuli.

#### 9.4.4.5 AMPA Receptors

AMPA receptors are ligand-gated ion channels that are regulated via downstream second messenger signaling pathways stimulated through GPCRs [99, 100]. However, recent studies have revealed additional mechanisms of cross talk between AMPA receptors and GPCRs – specifically an interaction of the AMPA receptor with the D<sub>2</sub> DAR. This interaction presents a unique story of how DAR signalplex members can regulate one another via multiple mechanisms resulting in a complex regulatory paradigm between signaling systems. While data from *in vitro* binding assays suggest that the D<sub>2</sub> DAR and the AMPA receptor may not directly interact, they certainly form a protein complex that is mediated by the GluR2 subunit and the third intracellular loop of the D<sub>2</sub> DAR [48]. Co-immunoprecipitation and GST-fusion pull-down assays both indicate that the D<sub>2</sub> DAR and the AMPA receptor form a complex. Interestingly, NSF (see Section 9.4.1.7) interacts with both the D<sub>2</sub> DAR and the GluR2 subunits implicating it as the possible accessory protein in this D<sub>2</sub> DAR–AMPA interaction. There is considerable evidence that D<sub>2</sub> DAR receptors can modulate AMPA receptor-mediated neurotoxicity [101]. The mechanism for this physiological effect may partially involve the protein–protein coupling of these two systems as outlined above. It has been proposed that agonist stimulation of D<sub>2</sub> DARs promotes the formation of protein–protein interactions between the D<sub>2</sub> DAR and NSF, while at the same time uncoupling NSF from the carboxyl-terminal tail of the GluR2 subunit of the AMPA receptor, thereby resulting in a decrease in AMPA receptor membrane expression and subsequent inhibition of AMPA-mediated neurotoxicity. These findings demonstrate the importance of the D<sub>2</sub> DAR-NSF-AMPA interaction and show how a member of the D<sub>2</sub> DAR signalplex can regulate other receptors through a common interacting protein [48].

#### 9.4.4.6 NMDA Receptors

The NMDA receptor complex has become a primary target for CNS drug development. Dopamine and glutamate are known to extensively interact in several brain areas and to regulate a number of physiological functions including attention, working memory, and positive reinforcement. Evidence continues to mount connecting these two signaling pathways in several pathologies including Parkinson's disease and schizophrenia. While different mechanisms are probably important in the

interaction of these pathways, including second messenger-mediated phosphorylation of the NMDA receptor by D<sub>1</sub> DAR activation and coordinated regulation of receptor trafficking, the D<sub>1</sub> DAR–NMDA receptor interaction makes the NMDA receptor an important member of the DAR signalplex. The direct interaction of the D<sub>1</sub> DAR and NMDA receptor has been reported in the striatum and hippocampus and has been shown to influence both signaling and trafficking of both receptors [24, 102, 103]. These direct interactions were primarily shown using co-immunoprecipitation experiments from various areas of the brain, including striatal PSDs. This interaction has been further characterized by using heterologous cell lines and fusion pull-down assays which demonstrated that both the NR1 and the NR2a subunits of the NMDA receptor interact directly with the D<sub>1</sub> DAR through the carboxyl-terminal domains. Two separate domains in the D<sub>1</sub> DAR's carboxyl terminus mediate the direct interaction with the two different NMDA receptor subunits. The direct nature of this interaction (in an attempt to rule out the possibility of linker proteins) was investigated using BRET assays. These assays confirmed the direct interactions between the D<sub>1</sub> DAR and the two NMDA receptor subunits while also determining that the D<sub>1</sub> DAR does not interact with the NR2b subunit of the NMDA receptor. Furthermore, stimulation of these receptors by dopamine, glutamate/glycine, or both, failed to change the interaction in any way, indicating the constitutive nature of this DRIP formation [102]. Functionally, the interaction of D<sub>1</sub> DAR with the NR1 subunit has been shown to cause an increase in trafficking to the membrane, inhibition of dopamine-mediated DAR internalization, and the suppression of NMDA-mediated cell death. The D<sub>1</sub> DAR interaction with the NR2A subunit has been demonstrated to cause a decrease in NMDA currents [24, 102, 103].

#### **9.4.4.7 GABA Receptors**

GABA receptors mediate fast inhibitory interneuronal synaptic transmission, and it is now realized that DARs can influence this system by dramatically regulating signal strength through a G protein-independent mechanism. This mechanism involves direct coupling of the DAR to the GABA receptor – making it another member of the DAR signalplex. This interaction was originally found by using GST fusion proteins of the D<sub>5</sub> DAR in rat hippocampal membranes to pull down the GABA receptor. This was subsequently verified via co-immunoprecipitation assays using specific antibodies [104]. This direct interaction suggests cross talk between these two systems. When GABA and D<sub>5</sub> DAR receptors were expressed in the same cells, D<sub>5</sub> DAR-mediated cAMP accumulation was decreased by GABA receptor stimulation. Furthermore, whole-cell current measurements of GABA function were decreased when dopamine was applied to the cells, indicating that dopamine stimulation can inhibit GABA function [104]. These data provide yet another finding of two distinct receptor classes that, in addition to being intimately linked via signaling pathways through second messengers, are also directly interacting in a manner to influence each other's physiology.

### **9.4.5 Neurotransmitter Transporters and Other GPCRs**

Neurotransmitter transporters are located pre-synaptically and are responsible for clearing excess neurotransmitter from the synaptic cleft. Recent investigations have revealed an association between DARs and these transporters. It has also recently been shown that DARs are capable of direct interaction with other GPCRs, including other DARs, to form receptor oligomers; the topic of DAR oligomerization is covered extensively in Chapter 10.

#### **9.4.5.1 Dopamine Transporter**

The dopamine transporter (DAT) is located pre-synaptically and facilitates the re-uptake of synaptic dopamine for degradation or vesicular re-packaging. It is well documented that the DAT can be regulated by phosphorylation, including phosphorylation events downstream of DAR activation [105]. Recently, using co-immunoprecipitation assays, it was shown that the D<sub>2</sub> DAR can directly interact with the DAT [22]. Co-expression of the D<sub>2S</sub> DAR with DAT enhanced re-uptake of dopamine. The increase in DAT-mediated dopamine clearance could be blocked by expressing a peptide that binds to the D<sub>2S</sub> DAR and prevents its interaction with the DAT; transfection of this peptide in the absence of D<sub>2S</sub> DAR had no impact on DAT function. Interestingly, the observed increase in DAT function was independent of agonist binding to the D<sub>2</sub> DAR, indicating that D<sub>2</sub> DAR signaling alone was not required for the enhanced DAR function. DAT localization was also impacted by D<sub>2</sub> DAR expression – the presence of D<sub>2</sub> DAR caused DAT to translocate from a diffuse intracellular distribution to the cell surface. This DAT translocation could be reversed by expression of the D<sub>2S</sub>-DAT blocking peptide. Physiologically, the interaction of D<sub>2S</sub> DAR and DAT would be predicted to enhance clearance of dopamine from the synapse, and disrupting this interaction would result in hyperlocomotion. To examine this possibility, the D<sub>2S</sub>-DAT blocking peptide was administered to mice. As predicted, the peptide caused a decrease in synaptosomal dopamine uptake and an increase in activity and rearing behaviors. This direct interaction between D<sub>2S</sub> DAR and DAT provides a mechanism for rapid regulation between the two proteins, and disruption of this interaction clearly impedes normal synaptic function.

## **9.5 Conclusions**

The growing literature identifying and characterizing DAR-interacting proteins has revealed a great deal of information about the dynamic nature of the DAR signalplex. The components of the DAR–DRIP complex can vary with time and across cells and can influence many aspects of DAR and DRIP regulation, including signaling, pharmacology, and desensitization and resensitization/recycling pathways. Not only does this information about DAR–DRIP interactions/reveal previously unappreciated aspects of both receptor and cellular regulation, it also provides a unique

perspective on DAR diversity and a new set of tools to the experimenter for receptor manipulation. In addition, the specificity of DRIP interactions to distinct DAR isoforms and cell types reveals a new set of therapeutic targets and a new arena for drug design.

The selective interaction between DRIPs and closely related DARs can provide investigators with new information about functional differences both across and within DAR families. Regardless of tissue distribution, it is clear that even within D1 and D2 receptor families not all DARs can interact with each DRIP, thus highlighting a previously unappreciated outcome of sequence variation. Given the ability of DARs to bind specific DRIPs and the limited distribution of many interactors, it is likely that physiological receptor location alone does not determine each DAR's unique functional properties. Instead, the array of DRIPs within a cell that can interact uniquely with a DAR isoform shapes the functional role of each receptor.

As illustrated by the DRIPs discussed in this chapter, specific reinforcement or disruption of DAR–DRIP interactions has already provided useful information to investigators regarding the mechanism underlying various aspects of receptor regulation and signaling. It may now be possible to exploit the individual properties of these DAR–DRIP interactions in the treatment of dopaminergic disorders. Indeed, manipulating DAR interactions with GASP, DAT, and Par-4 has already demonstrated potential therapeutic utility for such manipulations [6, 21, 22]. Many neurological and psychiatric disorders are characterized by abnormalities in dopaminergic transmission and/or responsiveness to dopaminergic drug therapy, including schizophrenia, Parkinson's disease, and depression. However, most of the currently available drug treatments produce adverse side effects that limit their therapeutic utility. It is possible that the underlying dopaminergic abnormality involves alterations in a specific DAR–DRIP interaction; indeed, there is evidence for alterations in the levels of the D<sub>2</sub> DRIP, NCS-1, in schizophrenic patients [106]. Manipulating this and other DAR–DRIP interactions may provide a new course of treatment with more limited side effects – by focusing on a specific, dysfunctional DAR–DRIP interaction, unaffected brain regions under normal dopaminergic control can be avoided, and undesirable consequences of therapy thus eliminated.

While identifying DRIPs and characterizing the various permutations of the DAR signalplex is a challenging endeavor, much progress has already been made. Certainly, the advent of proteomic-based protein identification will expedite the identification process even further and generate many new DRIP targets for characterization. Elucidating the role of DRIPs in an organ-, region-, and cell-specific manner will undoubtedly further our understanding of variation in dopaminergic signaling and provide novel molecular tools, as well as targets for drug design and therapeutic intervention.

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# Chapter 10

## Dopamine Receptor Oligomerization

Kjell Fuxe, Daniel Marcellino, Diego Guidolin, Amina Woods,  
and Luigi Agnati

**Abstract** Each dopamine (DA) receptor subtype physically interacts with its own kind (homomers) or other receptors (heteromers) in the plasma membrane of neurons in the basal ganglia to form dimeric or high-order receptor oligomers, termed dimeric or high-order receptor mosaics (RMs). Two types of heteromeric DA RMs are primarily discussed, namely type 1 receptor mosaic (RM1) formed by different DA receptor (DA-R) subtypes that display classical cooperativity and type 2 receptor mosaic (RM2) formed by DA-R subtypes physically interacting with other receptors that display non-classical cooperativity. The D<sub>2</sub> receptor can form a RM1 with either D<sub>1</sub> or D<sub>3</sub> receptor subtypes as well as different types of RM2 with A<sub>2A</sub>, mGluR5, CB<sub>1</sub>, neuropeptide receptors (SSR5, NTS1, CCK-2), and *N*-methyl-D-aspartate (NMDA) receptors. Trimeric A<sub>2A</sub>-D<sub>2</sub>-mGluR5 and A<sub>2A</sub>-D<sub>2</sub>-CB<sub>1</sub> RM2 may exist in striatal neuronal networks and are also discussed. D<sub>1</sub> receptors can form RM1 with D<sub>3</sub> receptors and different types of RM2 with A<sub>1</sub>,  $\mu$ -opioid, and NMDA receptors. D<sub>3</sub> receptors can form a RM2 with A<sub>2A</sub> receptors and D<sub>5</sub> receptors can form a RM2 with  $\gamma$ -aminobutyric acid (GABA)-A receptors. Through existing as part of a horizontal molecular network, RMs fine-tune multiple effector systems already at the level of the membrane, involving Ca<sup>2+</sup>, Na<sup>+</sup>, and K<sup>+</sup> and including G protein-regulated inwardly rectifying potassium channels (GIRK), adenylyl cyclase (AC), phospholipase C (PLC), and dopamine transporter activity. The synaptic strength is particularly modulated by DA receptors within DA receptor RM2 that involve ligand-gated ion channels such as GABA-A and NMDA receptors. The existence of a RM2 formed by D<sub>2</sub> receptors and receptor tyrosine kinase (RTK) receptors is also likely to exist and bears high relevance for the integration of trophic and informational signals within striatal networks. A novel neuropsychopharmacology may develop on the basis of DA receptor-containing RMs in the brain from the unique pharmacological properties afforded by their receptor–receptor interactions.

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K. Fuxe (✉)

Department of Neuroscience, Karolinska Institute, 17177-Stockholm, Sweden  
e-mail: kjell.fuxe@ki.se

**Keywords** Dopamine receptor subtypes · Receptor–receptor interactions · Dopamine homomers · Dopamine heteromers · Receptor mosaic · Cooperativity · G protein-coupled receptors · Ion channel receptors · Receptor tyrosine kinase

## 10.1 Introduction

This chapter describes the functional existence of dopamine receptor (DA-R) homomers and heteromers in the brain, especially within the basal ganglia, while highlighting their clinical relevance (for general reviews, see [1–8]). Special focus will be placed on how DA receptor subtypes directly interact with other G protein-coupled receptors (GPCRs) and with two types of ligand-gated ion channels, specifically the *N*-methyl-D-aspartate (NMDA) and GABA-A receptors (see [2, 9, 10]). However, it should also be emphasized that D<sub>2</sub> and D<sub>4</sub> receptors immunoprecipitate with G protein-regulated inward rectifying potassium (GIRK) channels, form stable complexes with these channels that are opened via the G protein  $\beta\gamma$  dimers from activated DA-R, and lead to marked reductions in neuronal excitability [11]. Furthermore, evidence also exists for a direct association of GABA-B receptors with GIRK (Kir3) channels and the regulator of G protein signaling RGS4 [12], forming a signaling complex also involving G proteins. DA-R oligomers likely participate in such signaling complexes.

DA receptor homomeric and heteromeric complexes participate in horizontal and vertical molecular networks including effectors such as GIRK channels and various types of DA-R-interacting proteins. At the prejunctional level, D<sub>2</sub> receptors have been demonstrated to form stable complexes with the dopamine transporter (DAT) [13], enabling the DA re-uptake process to be properly fine-tuned to the ongoing activity of the D<sub>2</sub> autoreceptor-formed heteromers including for example, the neurotensin receptor 1 (NTS1)/D<sub>2</sub> autoreceptor heteromer (see [14]) and the non- $\alpha$ 7 nicotinic/D<sub>2</sub> receptor heteromer in the dorsal striatum [15–17]. The existence of unique DA-R-oligomeric receptor complexes at both the pre- and postjunctional level, due to the differential location of the D<sub>2L</sub> and D<sub>2S</sub> isoforms, may also give rise to a different neuropsychopharmacology at the pre- and postjunctional D<sub>2</sub> receptors. These differences may lead to novel DA agonists or antagonists for the treatment of neurological and mental disease (see [18]) with reduced side effects by fine-tuning DA transmission toward increases or reductions in specific DA-R heteromeric complexes [19, 20].

## 10.2 Receptor–Receptor Interactions

In previous papers [21–27], it has been demonstrated that direct interactions among GPCRs at the level of the plasma membrane can occur based on analysis of neuropeptide/monoamine receptor interactions. Initial observations at the level of

agonist recognition in membrane preparations from the CNS suggested the existence of receptor heteromers. In the past years, accumulating data have demonstrated that GPCRs can homodimerize and heterodimerize as well as form oligomers of unknown stoichiometry [1, 3, 4, 6–8, 20, 28–31]. However, the present techniques used to measure receptor–receptor interactions cannot distinguish between domain-swapped dimers and contact dimers [32, 33].

It is our opinion that both types of interactions (domain swapping and domain contact) may occur that allow the formation of high-order heterooligomers (high-order receptor mosaics) depending on the receptor type and the chemophysical characteristics of the environments in which the receptors are embedded that affect GPCR conformation. It is likely that several points of contact exist between two receptors in view of the available data on protein–protein interactions [34]. Most interaction interfaces are made up of relatively large protein surfaces (larger than  $600 \text{ \AA}^2$ ) with complementary conformations and electrostatic salt bridging for enhanced stability. Furthermore, a small set of hot-spot residues at the interfaces contribute significantly to the free energy binding of the protein–protein interaction and are mainly clustered at the center of these interfaces.

It should also be pointed out that electrostatic and hydrogen bond-based interactions are weaker in a water medium than within the lipid environment plane of the membrane. Hence, the interactions in the plane of the membrane involving the transmembrane domains (TMD) may form the backbone of the receptor–receptor interactions. It is likely that additional interactions between receptors in the extra- and intracellular environments are more plastic and can be easily modified [35].

It is of basic importance to discuss not only the process through which receptors physically interact but also the factors affecting such interactions, thereby modulating the transfer of the information within the receptor mosaic (RM, dimeric, or high-order receptor oligomers). In fact, hydrogen bonds (whose strength depends on the charge of acceptor and donor atoms), electrostatic interactions (whose strength depends on distance and markedly on the dielectric constant of the medium), and van der Waals forces (whose strength clearly depends on the distance and falls rapidly beyond  $4 \text{ \AA}$  of separation) have an energy that differs little from the average thermal energy of molecules. Since the assembly of protein modules is owed to the sequential formation of these types of atom–atom interactions, if two protein modules approach one another in a non-optimal way or if two protein modules that are not intended to interact initiate the interaction process, the thermal threshold can stop the process by disrupting the few weak bonds formed.

In addition, it should also be considered that receptors can assume different large-scale conformations according to several environmental conditions, including ionic strength, pH, and temperature, all of which influence receptor–receptor interactions. The existence of stable conformations, which differ on the larger scale, can be explained in terms of the free energy landscape of the receptor. The free energy landscape describes the free energy of all possible receptor protein structures for a given primary sequence in a space of  $3N$  dimensions, where  $N$  is the number of atoms. Each individual conformation is represented by a valley with a given depth in this free energy hypersurface [36], and proteins can shift from one minimum to the

nearest one if the relevant parameters are changed. This motion would correspond to intervalley motion, compared with intravalley fluctuations [37].

The various stabilized conformations in such a free energy landscape are viewed as wells into which receptors may enter or leave according to energetic and entropic considerations. Since receptor–receptor interactions depend on receptor conformations, we propose that different receptor–receptor interactions develop according to the wells in which the interacting receptors are located and hence according to their free energy. It should again be pointed out that the extramembrane parts of a GPCR are highly flexible structures immersed in a polar medium (water). Therefore, they can be remodeled in their environment and be particularly suited for “fishing,” e.g., for ligands and epitopes of other receptors and proteins in the extracellular and intracellular media, respectively. This will also lead to the transfer of information in the receptor mosaic via allosteric interactions causing development of negative or positive cooperativity in, e.g., the transmitter binding pockets of the RM.

### 10.3 The Concept of Receptor Mosaics

In the year 1982 we suggested that clusters of receptors could exist in the plasma membrane. These clusters of receptors, termed RMs [8, 38, 39], are built up of several receptors and interact via receptor–receptor interactions (i.e., via allosteric interactions). The denomination RM provides a better relationship to the biochemical fingerprint of the receptor cluster, i.e., the receptor–receptor interactions and its topology, than the term receptor oligomer (Fig. 10.1). In each RM, each receptor represents a single tessera within the mosaic; however, the receptor mosaic functions as an integrated unit with emergent properties unique to the intracellular biochemical machinery associated with each RM. We also introduced the RM hypothesis of the engram in 1982 that claims the existence of clusters of receptor proteins (G protein- and ion channel-coupled receptors) at the level of the plasma membrane that operates as computational units. These are hypothesized to play an important role in “information handling” by the cell and can contribute to the modulation of the synaptic weight of cells in neuronal networks thereby altering learning and memory processes [8, 38, 39].

A cluster of receptors operates as a high-order RM (high-order oligomer) only if each of the participating receptors modulates the biochemical/functional features of at least one other receptor within the cluster. The transitions of each receptor among its possible conformational states within the RM are constrained by the conformations of the other participating receptors through direct receptor–receptor interactions. Thereby, each receptor will respond to its ligand in a way that depends on its interactions with the other receptors in the RM. The term dimeric RM may be used instead of dimeric oligomers to consistently use the term RM [20].

A situation analogous to that of hemoglobin [40] may exist for RM consisting of the same receptor or isoreceptors, i.e., of receptors that share the same transmitter. We have defined these as RM1 (type 1 RM) representing RMs that are formed by

**type 1 Receptor Mosaics (RM1)****Dimeric RMs**

homodimers



one functional outcome possible

heterodimers of isoreceptors



two functional outcomes possible

Differential degree of receptor activation determining A over B or B over A dominance

A &gt; B

B &gt; A

**type 2 Receptor Mosaics (RM2)****High-order heteromeric RMs**

heteromers



six functional outcomes possible

Differential degree of receptor activation based on rank order of agonist concentration

A &gt; B &gt; C

B &gt; A &gt; C

C &gt; A &gt; B

A &gt; C &gt; B

B &gt; C &gt; A

C &gt; B &gt; A

**Fig. 10.1** Theoretical functional outcomes from homo- and heterodimeric (isoreceptors) type 1 receptor mosaics (RM1) and from high-order heteromeric type 2 receptor mosaics (RM2). The rank order of agonist concentration for each of the participating receptors determines the different functional outcomes. Thus, the rank order of receptor activation, dependent on agonist concentration, establishes the integration of receptor signaling that ultimately leads to the different emerging properties within RMs. In RM1 all the receptors consist of receptor subtypes having similar binding sites and share the same ligand. Thus, the *black* and *grey* receptors are subtypes of receptors sharing the same ligand such as DA. In RM2 the *black*, *grey*, and *light grey* receptors of the trimer have different ligands such as adenosine, dopamine, and glutamate activating for example A2A, D2, and mGluR5 receptors

one type of receptor (homomers) or by isoreceptors (heteromers formed by different subtypes of receptors for the same neurotransmitter). RM2 are those RMs formed by different types of receptors, i.e., receptors that bind different ligands [8, 41] (see Fig. 10.1). Dimers and tetramers for DA-R exist as discussed below. In fact, a tetrameric form of the DA-D<sub>3</sub> receptor has been reported to be the predominant form in the brain [42] but can also interact with the D<sub>3</sub> receptor splice variant D<sub>3nf</sub> [43]. Furthermore, the early demonstration of negative cooperative interactions among the β-adrenergic receptors in frog erythrocyte membranes gave additional support to the existence of RM1 and gave functional implications [44]. Also, the findings of Armstrong and Strange demonstrated negative cooperativity in DA D<sub>2</sub>-R ([45]; and

see [46]). Thus, RM1 formed by the same type (or subtype) of receptors shows classical cooperativity. Furthermore, the demonstrated receptor–receptor interactions in RM2 at the level of agonist recognition that involve receptors with different ligands gave evidence for the existence of non-classical cooperativity for these RMs (see [20, 41]). According to Koshland and Hamadani [40] classical cooperativity demands initial conditions with essentially identical binding sites.

## **10.4 On the Existence of Different Types of DA Receptor Mosaics**

### ***10.4.1 DA Type 1 Receptor Mosaics***

Beginning in the early 1990s, evidence for the existence of sodium dodecyl sulfate (SDS)-resistant homodimers of D<sub>1</sub> and D<sub>2</sub> receptors was obtained in cell lines, and subsequently in brain tissue [47, 48]. High-order oligomers (high-order RM) of D<sub>2</sub> receptors may also exist [49]. Dimers may in fact be building blocks for high-order RMs [50, 51], and linear and ring models of RMs have been introduced based on atomic-force microscopy (see [8, 41]). Multiple sites of interactions participate in the D<sub>2</sub> homodimer formation [52] where the TM domain 4, but not the disulfide bonds, plays a major role in the interface [53]. It seems possible that contact dimers are formed from monomers in the endoplasmatic reticulum, allowing their expression in the cell surface membrane (see [1, 49]) and the development of negative cooperativity [45]. Evidence for the existence of D<sub>3</sub> dimers and D<sub>3</sub> tetramers in the brain has also been obtained (see above; [42]).

#### **10.4.1.1 The D<sub>2</sub>/D<sub>3</sub> Heteromer**

Coimmunoprecipitation experiments in D<sub>2</sub> and D<sub>3</sub> cotransfected HEK-293 cells have given evidence for D<sub>2</sub>/D<sub>3</sub> heteromeric complexes [54]. Furthermore, split D<sub>2</sub>/D<sub>3</sub> heteromeric complexes may be formed through domain swapping mechanisms ([32]; see also [55]) which may contribute to their altered pharmacology allowing the D<sub>2</sub>-like agonists including ropinirole and pramipexole to be more potent at the D<sub>2</sub>/D<sub>3</sub> heteromer binding pockets [56]. The D<sub>2</sub>/D<sub>3</sub> RM may also allow the D<sub>3</sub> receptor to become more strongly coupled to adenylyl cyclase (AC) with an increased inhibition of its activity [54]. It is also possible that D<sub>2</sub>/D<sub>3</sub> RMs may exist in discrete nerve cell systems of the brain, since D<sub>2</sub> and D<sub>3</sub> receptors may be colocalized only in certain peptide nerve cells of the nucleus accumbens [57].

#### **10.4.1.2 The D<sub>1</sub>/D<sub>2</sub> Heteromer**

Phospholipase C (PLC)-coupled D<sub>1</sub>/D<sub>2</sub> receptor RM1s have been discovered in D<sub>1</sub>/D<sub>2</sub> cotransfected cells [58, 59] and D<sub>1</sub> and D<sub>2</sub> receptors coimmunoprecipitate in rat striatal membranes [60]. Also, the two receptors may be colocalized in discrete

ventral striatal nerve cell populations [61]. It is of substantial interest that the two receptors, when coactivated in the same cell, produce a novel PLC-mediated calcium signal not seen when the receptors are activated alone. The pharmacological analysis of this RM1 indicated a specific coupling to the  $G_{q/11}$  pathway that produces a unique pharmacology of the  $D_1/D_2$  RM1. The  $D_1$ -like agonist SKF 83959 exhibits a relative specificity for the  $G_{q/11}$ -coupled  $D_1$ -like receptor participating in  $D_1/D_2$  heteromers with an additional ability to act as a partial agonist at the  $D_2$  receptor. The unique pharmacology of this RM1 exhibits high PLC activation and low AC activation (see [62]). It seems possible that in the coactivated  $D_1/D_2$  RM1, due to the receptor–receptor interaction, the conformational state of the two receptors is such that it will only allow  $G_q$  to couple to the  $D_1/D_2$  heteromer. This is mainly detected in older animals and causes the activation of calcium/calmodulin-dependent protein kinase II $\alpha$  in the ventral striatum, thereby contributing to plasticity changes in the local circuits of the striatum. This RM may be of special relevance for schizophrenia in view of the observations of a reduced link of  $D_1$  and  $D_2$  receptors in this disease [63].

#### 10.4.1.3 The $D_1/D_3$ Heteromer

It has been shown that  $D_3$  receptors are overexpressed in the  $D_1$ -enriched direct GABA pathway upon DA denervation and intermittent L-DOPA therapy. This  $D_3$  receptor expression may therefore contribute to the  $D_1$  sensitization and development of L-DOPA-induced dyskinesias [64, 65]. Thus, a facilitating receptor–receptor interaction between  $D_1$  and  $D_3$  receptors should be considered as well as a role for  $D_3$  antagonists as an anti-dyskinetic therapy. It is therefore of substantial interest that it has been possible to demonstrate  $D_1/D_3$  heteromers in living cells and to demonstrate striatal intramembrane  $D_3/D_1$  receptor interactions [66, 67]. Heteromer formation was demonstrated by FRET and BRET techniques in cotransfected mammalian cells. Biochemical binding experiments performed in striatal membrane preparations exhibited facilitatory  $D_3/D_1$  receptor interactions with  $D_3$  agonist-induced increases in the affinity of the  $D_1$  agonist-binding sites. In line with these results,  $D_3$  receptor activation enhanced the motor stimulation effects of  $D_1$  agonists in reserpinized mice. Thus, the  $D_1/D_3$  heteromer may operate by enhancement of  $D_1$  receptor recognition and signaling with relevance for  $D_1$ -mediated motor functions and when exaggerated by prolonged L-DOPA treatment may contribute to development of dyskinesias in Parkinson's disease [66].

In view of the above, it seems likely that the major functional forms of  $D_1$ ,  $D_2$ , and  $D_3$  receptors in brain are dimers and high-order oligomers such as tetramers. Thus, in the brain the DA-R subtypes can in part exist as RM1s built up of homo- and heterooligomers formed by  $D_1$ ,  $D_2$ , and  $D_3$  receptors (dimeric and high-order RM1). As discussed earlier in this section, these RMs can show classical cooperativity, since all the receptor binding sites are similar (see [8, 20, 41]). The same may also be true for  $D_4$  and  $D_5$  receptors. However, in all these DA type 1 receptor mosaics the stoichiometry and topography are unknown.

## 10.4.2 DA Type 2 Receptor Mosaics

### 10.4.2.1 The Somatostatin SSTR5/D<sub>2</sub> Receptor Heteromer

This RM2 was not constitutively formed, but formed after treatment with agonist in cotransfected CHO-K1 cells, demonstrated by photobleaching fluorescence resonance energy transfer (FRET) microscopy [68]. In this heteromer, D<sub>2</sub> agonist could enhance the binding affinity of somatostatin agonist at the SSTR5 and its G protein coupling while simultaneous agonist treatments increased the inhibitory cAMP signaling. These facilitatory intramembrane receptor–receptor interactions within this RM2 may help explain the positive somatostatin–DA interactions found in the brain after treatment with D<sub>2</sub> agonists or somatostatin. However, the population of nerve cells in the brain where SSTR5 and D<sub>2</sub> are colocalized needs to be further established and defined. It is of substantial interest that a study using the mutant  $\Delta$ 318-SSTR5 receptor (a partially active C-tail deletion mutant of human SSTR5) in CHO-K1 cells indicated that a cross-activation of the D<sub>2</sub> receptor can occur in the absence of DA by a direct receptor–receptor interaction in the interface of the SSTR5/D<sub>2</sub> RM2 after somatostatin activation of the SSTR5. Similar to the DA receptor subtypes, the somatostatin receptor subtypes can assemble as functional homo- and heterodimers [69].

### 10.4.2.2 Putative Neuropeptide Receptor/D<sub>2</sub> Heteromers

*Putative CCK2/D<sub>2</sub>heteromers:* It was demonstrated very early in the 1980s that both cholecystokinin-8 (CCK-8) and CCK-4 (selective ligands for CCK2 receptors) could increase the affinity of the D<sub>2</sub> antagonist-binding sites while reducing the affinity of the D<sub>2</sub> agonist-binding sites in striatal membrane preparations [24, 25, 70]. Such an antagonistic receptor–receptor interaction may contribute to the neuroleptic-like actions of CCK-8 and indicated the existence of CCK2/D<sub>2</sub> heteromers. A substantially stronger modulation of D<sub>2</sub> receptor affinity at its agonist-binding sites by CCK-8 was found in rat striatal sections most likely due to the intact cell structure including the plasma membrane [71]. The actions of CCK-8 on D<sub>2</sub> receptors were counteracted by a CCK2 receptor antagonist demonstrating its specificity [72]. These results underlined the previous evidence for the existence of CCK2/D<sub>2</sub> receptor interactions in the striatum and strongly supported the view of the existence of striatal CCK2/D<sub>2</sub> heteromers.

Further evidence for this view was obtained in receptor binding studies performed in a mouse fibroblast cell line (L-hD<sub>2L</sub>/CCK2), expressing both human D<sub>2</sub> receptors (long form, D<sub>2L</sub>) and human CCK2 receptors [73]. Thus, CCK-8 caused a significant decrease in the affinity of the D<sub>2</sub> agonist [<sup>3</sup>H]NPA binding sites in the L-hD<sub>2L</sub>/CCK2 cell membranes, blocked by a CCK2 receptor antagonist. However, in contrast to rat neostriatal membranes where CCK-8 increases the affinity of D<sub>2</sub> antagonist binding [25], CCK-8 decreased the affinity of the D<sub>2</sub> antagonist [<sup>3</sup>H]raclopride binding sites in the L-hD<sub>2L</sub>/CCK2 cell membranes. This may

be related to the absence of the D<sub>1</sub> receptor in the D<sub>2</sub>/CCK2 cell membranes. As a matter of fact, CCK-8 was found to increase the affinity of DA for the D<sub>2</sub> receptors labeled by the D<sub>2</sub> antagonist [<sup>3</sup>H]raclopride in the rat neostriatal membranes when the D<sub>1</sub> receptors were also activated, but to decrease it when the D<sub>1</sub> receptors were blocked, indicating a control by D<sub>1</sub> receptors of the CCK receptor regulation of D<sub>2</sub> receptors. In view of the existence of D<sub>1</sub>/D<sub>2</sub> heteromers ([58] and see above), it seems possible that a high-order RM may exist in the striatal membranes containing D<sub>1</sub>, D<sub>2</sub>, and CCK2 receptors. Within this novel postulated RM2, D<sub>1</sub> receptors will strongly modulate the CCK2/D<sub>2</sub> receptor interaction. Thus in vivo, the activity of D<sub>1</sub> receptors will determine whether CCK-8 via CCK2 receptors will act as an endogenous inhibitor or enhancer of D<sub>2</sub> receptor function.

*Putative NTS1/D<sub>2</sub> heteromers:* Experimental evidence indicates that neurotensin (NT) and in particular, but not exclusively, the NT receptor subtype 1 (NTS1) play a key role in the regulation of the functional activity of the basal ganglia and that NTS1 receptors are widely expressed on dopaminergic neurons in the substantia nigra. In the dorsal striatum, their expression appears to be limited to the dopaminergic terminals of the nigral neurons and glutamatergic terminals from cortical inputs (see [14, 74, 75]).

A large number of studies have well documented the existence of a functional neurotensin/dopamine interaction in the central nervous system. The regulation of dopaminergic transmission, especially the nigro-striatal and mesocorticolimbic DA pathways, by NT [76] is mainly due to an antagonistic action of the activated neurotensin receptor (NTR) on D<sub>2</sub> receptor recognition and signaling by decreasing the affinity of D<sub>2</sub> receptor agonist binding [14, 74, 75, 77–84]. The NT-induced changes in D<sub>2</sub> receptor agonist affinity have been demonstrated to be strong in striatal sections [78, 85] but exist also in striatal membrane preparations [86]. The effects are blocked by a NTS1 receptor antagonist (SR 48692). These results demonstrate a direct allosteric NTS1/D<sub>2</sub> receptor–receptor interaction that results in a reduction in the agonist affinity of the D<sub>2</sub> receptor and indicates the existence of a striatal NTS1/D<sub>2</sub> heteromer.

The microdialysis findings in the dorsal striato-pallidal GABA pathway have provided a functional in vivo correlate to the antagonistic NTS1/D<sub>2</sub> receptor–receptor interaction observed in ligand binding experiments. These microdialysis findings demonstrated the antagonistic effects of threshold concentrations of NT on striatal D<sub>2</sub> autoreceptor signaling and D<sub>2</sub> postjunctional receptors [14, 75, 79–81, 86, 87]. The NT-induced reduction of D<sub>2</sub>-mediated signaling at both the striatal pre- and postjunctional levels leads to increased activity in the striato-pallidal GABA neurons, and DA transmission is switched toward a D<sub>1</sub>-mediated transmission that leads to increased activity of the striatonigral GABA pathway. The former action will contribute to the motor inhibition and catalepsy exhibited after NT treatment and underlies the use of NT receptor antagonists as a novel treatment strategy for Parkinson's disease (see [14, 75]). The demonstration of the antagonistic NTS1/D<sub>2</sub> autoreceptor interaction in the DA terminals of the caudate-putamen gave the first indication of the existence of a D<sub>2</sub> autoreceptor heteromer in this case with NTS1 receptors.

#### 10.4.2.3 The D<sub>2</sub>-non- $\alpha$ 7 nAChR Heteromer

Molecular interactions have been demonstrated between the  $\beta$ 2 subunits of non- $\alpha$ 7 nAChRs and the D<sub>2</sub> autoreceptor as determined in coimmunoprecipitation experiments on membrane preparations from cotransfected mammalian cells and striatum, suggesting the existence of a RM built up of non- $\alpha$ 7 nAChR channels and D<sub>2</sub> autoreceptors [15, 17]. Thus, prejunctional dorsal striatal DA transmission is also modulated by these receptor heteromers, and previous studies had demonstrated that single nicotine injections could modulate the affinity of striatal D<sub>2</sub> receptors for antagonists [16]. The D<sub>2</sub>/non- $\alpha$ 7 nAChR heteromer makes it possible for the D<sub>2</sub> autoreceptor to decrease the stimulatory effects of non- $\alpha$ 7 nAChR activation on DA release. The induction of DA release takes place via direct actions on the protein networks involved in vesicular fusion through increased calcium influx via the nicotinic channels and/or opening of N- and P/Q-type voltage-dependent calcium channels (see [15]).

#### 10.4.2.4 The A<sub>2A</sub>/D<sub>2</sub> Heteromer

A<sub>2A</sub>/D<sub>2</sub> receptor heteromers forming type 2 RM (RM2) [88–91] may exist in the dorsal and ventral striato-pallidal GABA pathway in which activation of A<sub>2A</sub> receptors reduces D<sub>2</sub> receptor recognition, coupling, and signaling [2, 7, 9, 26]. In the striato-pallidal GABA neurons, three types of RM may exist in equilibrium on the neuronal surface membrane, the type 1 RM formed by either A<sub>2A</sub> or D<sub>2</sub> homomers and the type 2 RM formed by A<sub>2A</sub>/D<sub>2</sub> heteromers. It seems possible that high-order A<sub>2A</sub>/D<sub>2</sub> RM2 of unknown stoichiometry and topology may also exist, containing, e.g., D<sub>2</sub> homodimers and A<sub>2A</sub> homodimers. In such a case, antagonistic A<sub>2A</sub>/D<sub>2</sub> receptor interactions can still take place by assuming that the A<sub>2A</sub> receptors can enhance the negative cooperativity in such participating D<sub>2</sub> receptor homodimers. Such events may also take place in the A<sub>2A</sub>/D<sub>3</sub> and A<sub>1</sub>/D<sub>1</sub> heteromers (see below). A major component of the interface in the A<sub>2A</sub>/D<sub>2</sub> heteromer is the electrostatic interaction between the positively charged arginine-rich epitope in the N-terminal domain of the third intracellular loop (IC3) of the D<sub>2</sub> receptor and the negatively charged epitopes in the C-terminal tail of the A<sub>2A</sub> receptor, especially the epitope (aa 370–378) containing a phosphorylated serine [89, 92]. Thus phosphorylation events may modulate the strength of the receptor–receptor interactions within these RMs. These results were also supported by studies using D<sub>1</sub>/D<sub>2</sub> chimeras [93].

A<sub>2A</sub> receptor activation results in an A<sub>2A</sub>-induced inhibition of inhibitory D<sub>2</sub> receptor signaling. This produces a net increase in the activity of the striato-pallidal GABA neurons that leads to the reduced activity of the glutamate-mediated motor drive to the cortical motor regions with reduction of both motor and reward functions. In Parkinson's disease where D<sub>2</sub> receptor signaling is markedly reduced, A<sub>2A</sub> receptor antagonists may therefore be used as a therapeutic agent to enhance D<sub>2</sub> receptor signaling in A<sub>2A</sub>/D<sub>2</sub> receptor heteromers of the dorsal striato-pallidal GABA pathway [19, 94, 95]. In schizophrenia and drug addiction, with a likely pathological increase in D<sub>2</sub> receptor signaling in the A<sub>2A</sub>/D<sub>2</sub> receptor heteromers

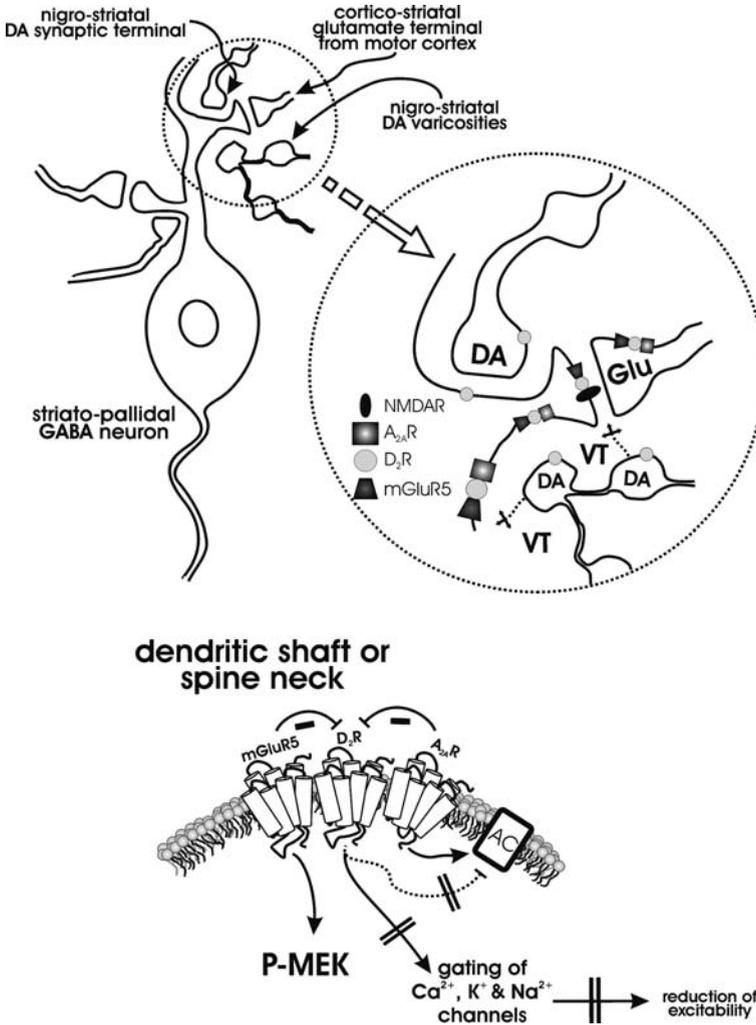
in the ventral striato-pallidal GABA pathway,  $A_{2A}$  receptor agonists may instead be useful as therapeutic agents [9, 20, 96–98]. In this way, reducing  $D_2$  receptor signaling in the  $A_{2A}/D_2$  receptor heteromer in the ventral striato-pallidal GABA pathway may inter alia counteract the deficit found in the glutamate drive to the prefrontal cortex in schizophrenia. The understanding of the structure and pharmacology of the  $A_{2A}/D_2$  receptor heteromer may offer novel treatments of inter alia Parkinson's disease, schizophrenia, and drug addiction [2, 7, 8, 19, 20, 22, 26, 65, 95, 96, 99–103]

#### 10.4.2.5 The Putative mGluR5/ $A_{2A}/D_2$ Heteromer (High-Order RM2)

There exists evidence for the colocalization of mGluR5,  $A_{2A}$ , and  $D_2$  receptors mainly located on dendritic spines of the striato-pallidal GABA neurons in perisynaptic zones around glutamate and DA boutons (see [15]). As discussed above,  $A_{2A}/D_2$  heteromers have been demonstrated in striatal tissue. Furthermore, coimmunoprecipitation studies show  $A_{2A}/mGluR5$  heteromeric receptor complexes in membrane preparations from cotransfected HEK-293 cells and in striatal membrane preparations [104]. It therefore seems possible that these three receptors can form a trimeric RM (Fig. 10.2) with the three receptors in direct contact with each other in the dendritic spines of the striato-pallidal GABA neurons and on corticostriatal glutamate terminals. Furthermore, indications of intramembrane receptor–receptor interactions between mGluR5/ $D_2$  receptors have previously been obtained. Glutamate Group I mGlu receptor agonists and mGluR5 agonists have been found to decrease the affinity of the  $D_2$  receptor for its agonists [105–107]. Furthermore, combined activation of  $A_{2A}$  and mGluR5 exerts enhanced effects on the antagonistic modulation of the  $D_2$  agonist-binding site. In various behavioral and other biochemical models, significant antagonistic  $A_{2A}/D_2$  and mGluR5/ $D_2$  have been observed, as well as synergistic  $A_{2A}/mGluR5$  receptor interactions [2, 7, 8, 15].

However, it remains to be identified to which extent this membrane cross talk may involve indirect interactions via scaffolding, adapter proteins, and cytoskeletal proteins such as protein 4.1 N [108], Filamin A [109, 110], and spinophilin [111]. It also seems possible that the  $A_{2A}$  and  $D_2$  receptors, besides mGluR5 [112], could be linked to the NMDA receptor scaffold. There may be a docking to some extent of the mGluR5,  $D_2$ , and  $A_{2A}$  receptors to the NMDA receptor-associated PSD-95 complex, although they are predominantly located extrasynaptically. To support this notion, PSD-95 has in fact been identified as a regulator of DA-mediated synaptic and behavioral plasticity [113]. Furthermore, ischemic damage can be reduced by perturbing NMDA receptor/PSD-95 protein interactions [114], demonstrating its impact on excitotoxicity.

In this way, a horizontal molecular network [7] may be identified in dendritic microdomains at the membrane surface where heteromers of GPCRs, scaffolding proteins, adapter proteins (e.g., homers), and glutamate-gated ion channels (such as NMDA receptors) participate. This may allow the development of the necessary



**Fig. 10.2** Schematic representation of postulated A<sub>2A</sub>/D<sub>2</sub>/mGluR5 RMs mainly located in the striato-pallidal GABA neurons but also in corticostriatal glutamate terminals. They mainly exist extrasynaptically on the neck of the spines and on the dendritic shafts but also on the glutamate terminals. Junctional (shown) and extrajunctional (not shown) NMDA receptors may be regulated by D<sub>2</sub> receptors. Increased action potentials reaching the corticostriatal glutamate terminals will lead to increased glutamate spillover and increased formation of extracellular adenosine due to increased release of ATP from the glutamate terminals. This will lead to increased concurrent activation of mGluR5 and A<sub>2A</sub> receptors in the extrasynaptic A<sub>2A</sub>/D<sub>2</sub>/mGluR5 RM, which will synergize to inhibit D<sub>2</sub> signaling in these RMs resulting in increases in glutamate release and reduced ability of postjunctional D<sub>2</sub> receptors to inhibit firing in the striato-pallidal GABA neurons via gating of Ca<sup>2+</sup>, K<sup>+</sup>, and Na<sup>+</sup> channels. (volume transmission; VT)

molecular circuits in the membrane and cytoplasm for the glutamate, adenosine, and DA cross talk where the receptor–receptor interactions importantly participate via direct (dimeric and high-order type 2 RMs) or indirect (adapter proteins) interactions. It now becomes possible to begin to understand the integrative molecular basis of the regulation of the excitability, firing rates, metabolism, and trophism in the striato-pallidal GABA neurons and the glutamate release process.

#### 10.4.2.6 The A<sub>2A</sub>/D<sub>3</sub> Heteromer

A recent study by Torvinen et al. [115] demonstrates a specific and high FRET efficiency in cells transiently cotransfected with A<sub>2A</sub>-YFP and D<sub>3</sub>-GFP<sup>2</sup> receptors, suggesting that A<sub>2A</sub> and D<sub>3</sub> receptors form an A<sub>2A</sub>/D<sub>3</sub> heteromer. Evidence was also obtained in membranes prepared from stably transfected CHO cell lines that A<sub>2A</sub> activation reduces D<sub>3</sub> receptor agonist binding and D<sub>3</sub> receptor signaling. This provided the evidence for an antagonistic A<sub>2A</sub>/D<sub>3</sub> receptor interaction in A<sub>2A</sub>/D<sub>3</sub> heteromers similar to those observed in the A<sub>2A</sub>/D<sub>2</sub> receptor heteromer. A<sub>2A</sub>/D<sub>3</sub> receptor heteromers may therefore exist in the D<sub>3</sub>-rich nucleus accumbens if coexpressed in the same neuron. In view of the existence of D<sub>3</sub> receptor dimers and tetramers in brain [42] and the existence of D<sub>2</sub>/D<sub>3</sub> receptor heterodimers [54], the existence of high-order RM2 should be considered in this region where A<sub>2A</sub>, D<sub>3</sub>, and D<sub>2</sub> receptors may participate (see [8, 19, 20]). The D<sub>3</sub> receptor is considered a target for anti-schizophrenic drugs [116], and therefore A<sub>2A</sub>/D<sub>3</sub> RMs offer possibilities for novel treatment strategies of this disease.

#### 10.4.2.7 The CB<sub>1</sub>/D<sub>2</sub> Heteromer and the Putative A<sub>2A</sub>/D<sub>2</sub>/CB High-Order RM2

In the year 2003 it was proposed that the anti-parkinsonian actions of cannabinoid CB<sub>1</sub> receptor antagonists involve the counteraction of antagonistic CB<sub>1</sub>/dopamine D<sub>2</sub> receptor interactions within CB<sub>1</sub>/D<sub>2</sub> heteromeric complexes [2]. Subsequent work in 2005 indicated the existence of CB<sub>1</sub>/D<sub>2</sub> heteromers in HEK-293 cell lines based on coimmunoprecipitation experiments and demonstrated that the putative CB<sub>1</sub>/D<sub>2</sub> heteromers were enhanced through their concurrent agonist stimulation [117]. The existence of CB<sub>1</sub>/D<sub>2</sub> heteromers was further established in living HEK-293 cells using FRET-based analysis and was found to be independent of receptor occupancy [118]. The CB<sub>1</sub> receptor agonist CP 55,940 reduced the affinity of D<sub>2</sub> receptor agonist binding sites in both the dorsal and the ventral striatum including the nucleus accumbens shell giving indications for the existence of antagonistic CB<sub>1</sub>–D<sub>2</sub> receptor interactions taking place in striatal CB<sub>1</sub>/D<sub>2</sub> heteromeric complexes. The evidence suggests a co-location of CB<sub>1</sub> and D<sub>2</sub> striatal receptors predominantly in the soma and dendrites of the ventral striato-pallidal GABA neurons and also in corticostriatal glutamate terminals where A<sub>2A</sub> receptors are also present (see [119, 120]).

Antagonistic CB<sub>1</sub>/D<sub>2</sub> interactions were also detected at the behavioral level through an analysis of quinpirole-induced locomotor hyperactivity in rats. The CB<sub>1</sub> receptor agonist CP 55,940 at a dose that did not alter basal locomotion was able to block quinpirole-induced increases in locomotor activity. In addition, not only the CB<sub>1</sub> receptor antagonist rimonabant but also the specific A<sub>2A</sub> receptor antagonist MSX-3 blocked the inhibitory effect of CB<sub>1</sub> receptor agonist on D<sub>2</sub>-like receptor agonist-induced hyperlocomotion. These results indicated the specific involvement of A<sub>2A</sub> receptors in the behavioral inhibition exerted by the CB<sub>1</sub> receptor agonist on D<sub>2</sub> receptor agonist-induced hyperlocomotion [118].

In agreement with the above, A<sub>2A</sub> receptor antagonists counteract the striatal CB<sub>1</sub> receptor-mediated motor depression, and striatal A<sub>2A</sub> and CB<sub>1</sub> receptors form functional heteromeric complexes [121]. It is of substantial interest that CB<sub>1</sub> agonists like CP 55,940 and Δ<sup>9</sup>-tetrahydrocannabinol can promote PKA-dependent phosphorylation of DARPP-32 in A<sub>2A</sub>-expressing medium spiny neurons probably representing the striato-pallidal GABA neurons [122, 123], and this phosphorylation is dependent on the presence and likely tonic activation of both A<sub>2A</sub> and D<sub>2</sub> receptors [122]. CB<sub>1</sub>-induced DARPP-32 phosphorylation may be a consequence of the antagonistic CB<sub>1</sub>/D<sub>2</sub> interaction demonstrated by Marcellino et al. [118]. A possible major mechanism for this event may be the ability of the antagonistic CB<sub>1</sub>/D<sub>2</sub> receptor interaction to release the A<sub>2A</sub>-activated AC from D<sub>2</sub>-mediated inhibition [9, 20] in putative CB<sub>1</sub>/D<sub>2</sub>/A<sub>2A</sub> RMs. In fact, in the brain there exists a high molecular weight form of CB<sub>1</sub> devoid of G proteins, which may represent such a trimeric RM [124].

#### 10.4.2.8 The A<sub>1</sub>/D<sub>1</sub> Heteromer

Evidence suggests the existence of A<sub>1</sub>/D<sub>1</sub> heteromers with antagonistic A<sub>1</sub>/D<sub>1</sub> receptor interactions [8, 26, 125–128] in the basal ganglia and prefrontal cortex, and especially in the direct striatonigral–striatoentopeduncular GABA pathways. The neurochemical and behavioral findings demonstrating antagonistic A<sub>1</sub>/D<sub>1</sub> receptor interactions can be explained by the existence of such A<sub>1</sub>/D<sub>1</sub> heteromers and/or by antagonistic interactions at the level of second messengers [26, 126, 129, 130]. The topology and stoichiometry of the A<sub>1</sub>/D<sub>1</sub> RMs are unknown. However, even if the number of D<sub>1</sub> receptors may dominate in these RMs with the formation of D<sub>1</sub> receptor dimers and tetramers, a single A<sub>1</sub> receptor in this RM may still have powerful inhibitory influence. The A<sub>1</sub> receptor could still enhance the negative cooperativity in the activated D<sub>1</sub> receptor dimers and tetramers within the RM via direct interactions with one of the D<sub>1</sub> receptor subunits. These results suggest a role of A<sub>1</sub> receptor agonists and antagonists in the treatment of diseases with dysfunction of D<sub>1</sub> receptor signaling via their actions on the A<sub>1</sub>/D<sub>1</sub> heteromers. Such diseases may include attention deficit hyperactivity disorder, drug addiction, and dyskinesias where A<sub>1</sub> receptor agonists may have a therapeutic value and Parkinson's disease where A<sub>1</sub> receptor antagonists may show anti-parkinsonian effects [19, 22, 26, 131].

#### 10.4.2.9 The $\mu$ -Opioid Receptor/D<sub>1</sub> Heteromer

The  $\mu$ -opioid receptor is colocalized with the D<sub>1</sub> receptor in nerve cells of the dorsal striatum [132] to which a novel approach, using a method that harnessed the mechanism for transport of proteins to the nucleus, was used to demonstrate the heteromerization between these two receptors in living cells (see Chapter 8). The nuclear translocation pathway was adapted for the visualization of the  $\mu$ -opioid receptor/D<sub>1</sub> heteromer, which caused an increased surface expression of the  $\mu$ -opioid receptor [132]. The interface in this heteromer involved the carboxyl tail of the D<sub>1</sub> receptor, since its substitution with the carboxyl tail of the dopamine D<sub>5</sub> receptor failed to increase surface expression of the  $\mu$ -opioid receptor. It is presently unknown how the  $\mu$ -opioid receptor/D<sub>1</sub> heteromer is linked to the A<sub>1</sub>/D<sub>1</sub> heteromer within the striatonigral–striatoentopeduncular GABA pathways.

#### 10.4.2.10 The D<sub>1</sub>/NMDA Receptor Mosaic

Dr. Fang Liu and collaborators [133, 134] have obtained evidence for a dual regulation of NMDA receptor function by direct receptor–receptor interactions with the DA D<sub>1</sub> receptor. Two regions of the C-terminal tail of the D<sub>1</sub> receptor interact with the NMDA receptor. One region has been found to directly interact with the NMDA receptor subunit NR1-1A. Upon D<sub>1</sub> receptor activation this direct interaction is disrupted making it possible for the C-terminal tail of NR1 to recruit calmodulin and PI-3 kinase, leading to PI-3 kinase activation causing a reduction of NMDA excitotoxicity. The other region of the D<sub>1</sub> receptor region directly interacts with the NR2A. This direct interaction seems to be involved in reducing NMDA receptor surface expression and leads to a reduction in NMDA receptor signaling witnessed by an inhibition of NMDA receptor-gated currents. In contrast, D<sub>1</sub>-mediated phosphorylation mechanisms appear to enhance NMDA surface expression and signaling (see [92]). Further evidence for the direct D<sub>1</sub>/NMDA receptor interaction has recently been obtained in cotransfected COS-7 cells using the bioluminescence resonance energy transfer (BRET) technique [135]. A reciprocal D<sub>1</sub>/NMDA receptor–receptor interaction also exists in this RM by which NMDA receptor activation can recruit D<sub>1</sub> receptors to the plasma membrane, thereby leading to an increase in D<sub>1</sub> signaling and cAMP accumulation. It is of substantial interest to note that the NR1-1 C1 cassette contains an arginine-rich epitope, whereas the interacting D<sub>1</sub> C-terminal portion contains an acidic epitope with an adjacent glutamic acid and a serine residue that is susceptible to phosphorylation by casein kinase 1 (CK1) [92]. In fact, mass spectrometry demonstrated that these two peptide epitopes could interact via an electrostatic interaction. A similar electrostatic interaction is involved in producing the A<sub>2A</sub>/D<sub>2</sub> heteromerization [89] and may be a general mechanism for direct physical receptor–receptor interactions [92].

In the striatum, the direct D<sub>1</sub>/NMDA receptor interaction probably takes place in the direct D<sub>1</sub> receptor-enriched GABA pathway. The D<sub>1</sub> receptors are predominantly located extrasynaptically, and this direct receptor interaction probably occurs

with extrajunctional located NMDA receptors in the perisynaptic zones surrounding the glutamate boutons on the head of the dendritic spines. This is of special interest since the extrasynaptic NMDA receptor signaling easily leads to excitotoxic consequences involving the cyclic-AMP response element binding protein (CREB) dephosphorylation,  $\text{Ca}^{2+}$  loading, and depolarization of mitochondria producing the activation of cell death pathways. These can be counteracted by  $\text{D}_1$  activation.

Instead, the synaptic NMDA receptor signaling may be mainly regulated via intracellular molecular networks involving PKA-dependent phosphorylation (see [136]; for review, see [11]). DARPP-32 plays a role in this cAMP-mediated process that leads to increased synaptic NMDA receptor signaling [137].

Still another site of  $\text{D}_1$ /NMDA interaction in the direct GABA pathway could be the endoplasmic reticulum (ER) [92], where PKA- and PKC-induced phosphorylation of sites close to the arginine-rich epitope of the NR1-1 subunit counteracts ER retention favoring its membrane surface recruitment [138]. This may be one of the mechanisms underlying  $\text{D}_1$ -induced increases of synaptic NMDA receptor expression at the plasma membrane [139]. It should be mentioned that the  $\text{D}_1$ /NR1-1 subunit complex only translocates to the surface membrane when bound to the NR2 subunit [135]. Furthermore, the  $\text{D}_1$ /NMDA receptor heteromerization may be strengthened by NMDA receptor-induced  $\text{D}_1$  phosphorylation by activation of CK1 [92].

#### 10.4.2.11 The $\text{D}_2$ /NMDA Receptor Mosaic

This receptor mosaic is formed by a direct interaction between the C-terminal portion of the NR2B subunit and the N-terminal portion (within the first 32 residues adjacent to the calmodulin-binding domain) of the third intracellular loop (IC3) of the  $\text{D}_2$  receptor as demonstrated by blot overlay assays [140]. Through coimmunoprecipitation, this receptor mosaic is found to be located within microdomains of postsynaptic densities of striatal glutamate synapses. It was found to be constitutively present but enhanced through an increased  $\text{D}_2$  activation produced by cocaine administration. The functional consequences are an interference with the binding of  $\text{Ca}^{2+}$ /calmodulin-dependent protein kinase II to NR2B that leads to the diminished phosphorylation of NR2B and a reduction of NMDA receptor signaling (an inhibition of NMDA-mediated currents). Thus,  $\text{D}_2$  receptors by participating in different receptor mosaics in the striato-pallidal GABA neurons and in the glutamate terminals that innervate them can exert powerful inhibitory actions on these neurons. Multiple actions of  $\text{D}_2$  receptors in separate RMs in discrete local circuits lead to inhibition of glutamate release ( $\text{A}_{2\text{A}}/\text{D}_2/\text{mGluR5}$  RM in glutamate afferents), reduction of synaptic NMDA signaling ( $\text{D}_2$ /NMDA RMs in glutamate synapses), and inhibition of L-type voltage-dependent calcium channels (perisynaptic  $\text{A}_{2\text{A}}/\text{D}_2/\text{mGluR5}$  RMs). Such a panorama of actions allows  $\text{D}_2$  receptors to effectively silence striato-pallidal GABA neurons and remove motor inhibition. Electrostatic epitope–epitope interactions play a critical role in the formation of such RMs as shown in the pioneering work of Dr. Amina

Woods and collaborators where the arginine–phosphate interaction represents a general mechanism for protein–protein interactions [141]. This work also emphasizes that phosphorylation–dephosphorylation processes play an important role in these receptor–receptor interactions, since phosphate stabilizes these intermolecular interactions [141].

#### 10.4.2.12 The D<sub>5</sub>/GABA-A Receptor Mosaic

The D<sub>5</sub>/GABA-A receptor heteromerization was discovered by Dr. Fang Liu et al. [142] and was the first demonstration of a GPCR/ligand-gated ion channel receptor mosaic. Along with this discovery came the first evidence that GPCRs can modulate synaptic strength via direct receptor–receptor interactions in the membrane (see [7, 8, 10, 143]). There exists an interaction between the C-terminal tail of the D<sub>5</sub> receptor and the  $\gamma 2$  (short) subunit of the GABA-A receptor. The results indicated that agonist coactivation of D<sub>5</sub> and GABA-A receptors was required for the formation of the RM. This appears to allow a direct bidirectional cross talk within the RM resulting in a reduction of the synaptic strength of GABA-A signaling and reduced D<sub>5</sub> signaling via reduced D<sub>5</sub>/G<sub>s</sub> protein coupling. This receptor mosaic may also allow a cotrafficking of the D<sub>5</sub> receptors. It seems that these receptor mosaics may exist not only in hippocampal neurons but also in striatal medium-sized neurons and striatal interneurons in view of the existence of both D<sub>5</sub> and GABA-A receptors in these neuronal systems [144]. However, so far the decrease of GABA-A receptor signaling in striatum via D<sub>1</sub>-like receptors has mainly been found to be a result of changes in phosphorylation involving the PKA/DARPP-32 cascade [145]. Regarding the possible existence of D<sub>2</sub>/GABA-A receptor mosaics, it may be commented that there exists evidence for striatal GABA-A/D<sub>2</sub> receptor–receptor interactions in membrane preparations, as studied at the level of D<sub>2</sub> recognition (see [146]). In the prefrontal cortex there exists evidence that D<sub>2</sub> activation can reduce GABA-A receptor signaling that may include transactivation of the platelet-derived growth factor receptors [147]. However, it is unknown if this receptor interaction involves a direct D<sub>2</sub>/GABA-A receptor–receptor interaction.

#### 10.4.2.13 Putative D<sub>2</sub>-Receptor Tyrosine Kinase Receptor Mosaics

It has recently been discovered that the DA D<sub>2</sub> receptor stimulation of mitogen-activated protein kinases is mediated by a cell type-dependent transactivation of receptor tyrosine kinases (RTK) [148]. There may also exist RTK ligand-independent mechanisms for RTK transactivation with participation of both GPCRs and the RTK in a multi-receptor signaling complex [149, 150]. In fact, D<sub>2</sub> receptor agonist increases the coimmunoprecipitation of D<sub>2</sub> and epidermal growth factor (EGF) receptors in neuroblastoma cells, thereby suggesting that D<sub>2</sub> receptor activation induces the formation of a macromolecular signaling complex [148] as a D<sub>2</sub>/RTK type 2 receptor mosaic.

## 10.5 General Comments on Receptor Mosaics

A dimeric and high-order RM is a quaternary structure in which networks of electrostatic interactions, hydrogen bonds and van der Waals forces shape the geometry of the single receptors and of the entire RM. This aspect has been discussed in the frame of the free energy landscape and, in particular, of intravalley and intervalley motion in this landscape which can be driven by the actions of several factors such as pH, temperature, and chemical composition of the medium.

This concept allows one to analyze protein geometry and protein function. As a matter of fact, a protein can assume a large number of similar conformations that are close to but differ in some details from its average conformation. Thus, there is a landscape for single receptors that can influence the formation of RMs. The landscape of the entire RM determines the possible global conformations (quaternary structure) in which each conformational state can be associated with a particular integrative function of the RM. When discussing the electrostatic epitope–epitope interactions between receptors in RMs, like those occurring in the  $A_{2A}/D_2$  receptor–receptor interaction, it will be of interest to evaluate the influence of the slaved (“random”) motions which are proportional to the fluctuation rate of the solvent versus the nonslaved (e.g., “agonist-induced”) motions which are independent of the solvent fluctuations [151]. It has been proposed that if an agonist causes a signal associated with an increased stability of a RM, there may develop a tightening of the receptor–receptor interactions in the oligomer [152].

## 10.6 Conclusions

Unique functional DA receptor dimeric and high-order RMs exist in plasma membrane microdomains of different nerve cell populations of the basal ganglia and represent a crucial mechanism for the integration of signals especially in the dorsal and ventral striatum. By being part of horizontal and vertical molecular networks of the cell surface membrane, these DA RMs can make possible a proper tuning of multiple effector systems. These systems include GIRK channels, AC, PLC, and DAT activity in which scaffolding and adapter proteins can play an important role. Synaptic strength of ligand-gated ion channels such as GABA-A and NMDA receptors can be modulated by DA-R, e.g., in the striatal GABA output neurons through the formation of receptor mosaics mainly built up of such ion channel receptors and DA receptor subtypes and that are located both synaptically and extrasynaptically. Therefore, receptor–receptor interactions in a multitude of DA receptor-containing RMs play a major role in the “information handling” in the basal ganglia [153, 154]. In this way, the integration of information in the DA receptor-containing RMs is optimized leading to an appropriate control of ion channel activity and excitability as well as gene expression within neuronal systems regulated by DA transmission. High-order DA receptor-containing RMs could have a special role in motor learning and memory in the striatum and newly formed RMs of this type may represent

the molecular basis for motor engrams (see [38]). It is clear that the DA receptor-containing RMs represent novel molecular targets for drug development against mental and neurological diseases [20].

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# Chapter 11

## Dopamine Receptor Modulation of Glutamatergic Neurotransmission

Carlos Cepeda, Véronique M. André, Emily L. Jocoy, and Michael S. Levine

**Abstract** Dopamine (DA), a prominent neuromodulator in the brain, regulates neuronal excitability and synaptic transmission. These actions are effected through diverse DA receptor subtypes whose effects vary as a function of a number of factors including pre- or postsynaptic localization and the intracellular signaling cascades they activate. We have chosen the corticostriatal synapse as a model to study the interactions between DA and glutamate, the major excitatory neurotransmitter for striatal inputs. In the striatum, DA receptors modulate glutamate release via presynaptic mechanisms and synaptic responses mediated by activation of postsynaptic glutamate receptors through alterations in voltage-gated channels, phosphorylation of glutamate receptor subunits, as well as physical interactions with other receptors. The outcomes of these actions are diverse and can lead to opposite or synergistic effects. These multiple effects are important to keep the balance between striatal output pathways to coordinate sensorimotor integration.

**Keywords** Dopamine receptors · Glutamate · Interactions · NMDA

### 11.1 Introduction

Dopamine (DA) and glutamate receptor interactions provide a necessary and important substrate for numerous brain functions. Ionotropic glutamate receptors mediate fast excitatory neurotransmission and DA receptors modulate neuronal excitability and the actions of multiple neurotransmitter systems. Alterations in the density and/or sensitivity of these receptors occur in pathological conditions such as Parkinson's (PD) and Huntington's diseases (HD), schizophrenia, and attention deficit hyperactivity disorder, to name a few.

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M.S. Levine (✉)

Mental Retardation Research Center, David Geffen School of Medicine, University of California at Los Angeles, Los Angeles, CA, 90095, USA  
e-mail: mlevine@mednet.ucla.edu

DA and glutamate receptor interactions are complex and their outcomes depend on multiple factors including receptor subtype, site of action (i.e., pre- or postsynaptic), timing of inputs, and concentration of neurotransmitter. After the discovery of different subtypes of glutamate and DA receptors, the number of potential interactions and their mechanisms has multiplied because glutamate and DA receptor subtypes elicit their actions by using multiple signaling pathways. Thus, the outcomes of interactions between these receptor families can be very diverse.

Recently, exciting findings have added new levels of complexity to these already intricate systems. For example, in addition to intracellular interactions via second messenger transduction pathways, the presence of physical interactions between glutamate and DA receptors at the membrane and cytoplasm levels has been revealed. Furthermore, the generation of mice deficient in specific DA receptors or glutamate receptor subunits and also of mice expressing enhanced green fluorescent protein (EGFP) under the control of specific DA receptor subtype promoters has provided new tools for the study of the relationships between DA and glutamate receptors. In this chapter we have chosen the corticostriatal synapse as a model to study glutamate and DA receptor interactions because of their relative abundance and because of their important implications in normal function and in pathological states involving the basal ganglia.

## 11.2 Classification of DA and Glutamate Receptors

There is diversity among DA receptors. Five different receptor subtypes have been cloned. These have been classified into two main families: the D1-like ( $D_1$  and  $D_5$  receptor subtypes) and the D2-like ( $D_2$ ,  $D_3$ , and  $D_4$  receptor subtypes) families [1, 2]. All DA receptors are G protein coupled and primarily alter the production of 3'-5'-cyclic adenosine monophosphate (cAMP) in the cell when activated but also affect other transduction systems [3].

Glutamate receptors have been classified into two principal groups: ionotropic and metabotropic receptors. Ionotropic glutamate [ $\alpha$ -amino-3-hydroxy-5-methyl-4-propionate (AMPA), kainate (KA), and NMDA] receptors are ligand-gated cation channels, whereas metabotropic glutamate receptors are coupled to various signal transduction systems [4–6]. NMDA receptors are unique in that their activation is governed by a strong voltage dependence due to receptor-channel blockade by  $Mg^{2+}$  at hyperpolarized membrane potentials [7].  $Mg^{2+}$  block gives NMDA receptors their characteristic negative slope conductance. Also, NMDA receptors allow more  $Ca^{2+}$  influx compared to non-NMDA receptors.

## 11.3 Morphological Basis for DA and Glutamate Receptor Interactions in Striatum

The striatum is the main input structure of the basal ganglia. It is the nucleus where afferents from the cerebral cortex, thalamus, and substantia nigra converge and interact. Glutamate is released from cortical and thalamic terminals [8, 9]. DA is released

from nigrostriatal terminals [10]. Because DA and glutamate inputs terminate on the same spines of striatal medium-sized spiny neurons (MSSNs), these sites offer the potential for physiological interactions between the DA and glutamate transmitter systems [11]. Morphological evidence demonstrates the presence of synaptic complexes formed by axospinous contacts in which the dendritic spine is the target of both an asymmetric (glutamatergic) bouton and a DA-positive symmetric synapse in striatal MSSNs [12]. This arrangement provides a morphological basis for DA–glutamate receptor interactions at the synapse. These interactions in the striatum support major sensory, motor, cognitive, and motivational functions [13–16].

Although all striatal MSSNs are GABAergic, they form separate populations based on distinct anatomic projections and neuropeptide expression. There are two major output pathways. The direct pathway consists of MSSNs that predominantly express D<sub>1</sub> DA receptors [17], substance P [18], and dynorphin [19]. These neurons project to the substantia nigra pars reticulata and the internal segment of the globus pallidus [17, 20]. The indirect pathway is comprised of striatal neurons that express predominantly D<sub>2</sub> receptors [17], met-enkephalin, and neurotensin [18, 21]. These neurons project to the external segment of the globus pallidus [20, 22]. DA inputs from the substantia nigra modulate the activity of these pathways, exerting a net excitatory effect on the direct pathway and a net inhibitory effect on the indirect pathway [23]. Assuming that D<sub>1</sub> and D<sub>2</sub> receptor-expressing MSSNs are segregated, the balanced opposition of these output systems is required to produce correlated and balanced activity. The prevailing hypothesis is that direct pathway promotes desired movements [24] while the indirect pathway inhibits unwanted movements [25].

The degree of DA receptor colocalization in the striatum remains an unresolved question. In particular, the percentage of MSSNs colocalizing D<sub>1</sub> and D<sub>2</sub> receptors varies from a low of 5% to a high of 80% depending on the experimental conditions [17, 26–30]. The recent generation of mice expressing enhanced green fluorescent protein (EGFP) as a marker of D<sub>1</sub> and D<sub>2</sub> receptor-containing striatal MSSNs [31] supports the idea that these receptors are segregated to different populations. In our hands, using single-cell RT-PCR in EGFP-expressing MSSNs, colocalization occurs only in about 10% of neurons from dorsal striatum [32]. However, a recent report demonstrated that EGFP probably underestimates the numbers of D<sub>1</sub>- or D<sub>2</sub>-expressing neurons because of difficulties detecting neurons that express low titers of receptors [33]. With regard to colocalization of DA receptors with various glutamate receptor subunits, evidence has shown that a high degree of coexpression occurs in striatal neurons [29]. This provides a morphological framework for physiological interactions.

## **11.4 DA Receptors Modulate Neuronal Excitability by Altering Voltage-Gated Conductances**

For a more exhaustive examination of how DA modulates voltage-gated channels please see Chapter 7. Here we only summarize aspects that are directly relevant for DA–glutamate receptor interactions. Electrophysiological experiments have shown

that DA reduces most of the voltage-activated inward and outward currents in striatal neurons [34–36] and these reductions have complex effects on cell excitability. For example, D<sub>1</sub>-like receptor agonists reduce the amplitude of evoked Na<sup>+</sup> currents in the vast majority of cells but they also reduce a slowly inactivating K<sup>+</sup> current (favoring the transition to a depolarized membrane potential). In contrast, D<sub>2</sub>-like agonists enhance this current. In addition, D<sub>1</sub> receptor activation can produce differential effects on high-voltage-activated (HVA) Ca<sup>2+</sup> currents depending on the specific type of current activated. D<sub>1</sub>-like receptor agonists reversibly reduce N- and P-type HVA currents, probably via the cAMP–protein kinase A (PKA) transduction cascade. However, in a subset of neurons, D<sub>1</sub>-like receptor-mediated activation enhances L-type HVA current [37]. These observations imply that DA produces differential effects on D<sub>1</sub> and D<sub>2</sub> receptor-containing MSSNs, hence affecting their excitability and readiness to respond to excitatory and inhibitory inputs. MSSNs containing D<sub>1</sub> receptors will respond to phasic release of DA with depolarization and increased Ca<sup>2+</sup> through L-type channels. In contrast, D<sub>2</sub> receptor-containing neurons will remain hyperpolarized and Ca<sup>2+</sup> influx will be reduced.

## 11.5 DA Modulation of Glutamate Release

DA receptors are present on presynaptic terminals where they can modulate neurotransmitter release [38]. In the dorsal striatum, D<sub>2</sub> receptors have been found on corticostriatal terminal endings and function to decrease glutamate release by presynaptic mechanisms [39]. While early pharmacological studies provided evidence that DA is capable of altering glutamate release, probably via D<sub>2</sub>-like receptors [40–44], more recent evidence for presynaptic mechanisms was obtained using electrophysiological methods [45–48]. Studies in mice lacking D<sub>2</sub> receptors also provide compelling evidence that presynaptic D<sub>2</sub> receptors can function as gatekeepers of glutamate release, i.e., primarily preventing excessive excitation in the striatum [39]. Further, optical techniques visualizing neurotransmitter release via destaining of terminals after incorporation of FM1-43, a styryl dye, have provided definite confirmation of D<sub>2</sub> receptor modulation of glutamate release at corticostriatal synapses [49]. Interestingly, DA inhibition of glutamate release appears to be frequency dependent as it increases as the rates of stimulation of corticostriatal inputs increase. DA inhibition is minimal with low-frequency stimulation (1 Hz) but increases with higher rates of stimulation (20 Hz). Thus, DA acts as a low-pass filter selective for terminals with low probability of release [50]. In this way, DA released by salient stimuli can directly regulate striatal neurotransmission by selecting specific sets of corticostriatal projections [49].

DA–NMDA receptor interactions can also modulate glutamate release indirectly through retrograde mechanisms. For example, enhancement of NMDA receptor function by D<sub>1</sub>-like receptor activation increases adenosine release which then acts as a retrograde messenger to reduce glutamate release in nucleus accumbens neurons [51]. DA also modulates excitatory transmission by means of retrograde endocannabinoid signaling in dorsal striatum [52]. Thus, confirming previous

results [49], activation of D<sub>2</sub> receptors reduces glutamatergic transmission only when receptor activation is combined with stimulation of cortical afferents at high frequencies (20 Hz). However, for this low-pass filtering function the authors provided evidence for a retrograde signal resulting from convergent DA and glutamate inputs that cooperate to produce endocannabinoid synthesis and release from the postsynaptic cell [52]. This retrograde signal reduces glutamate release by activation of CB<sub>1</sub> receptors on presynaptic terminals.

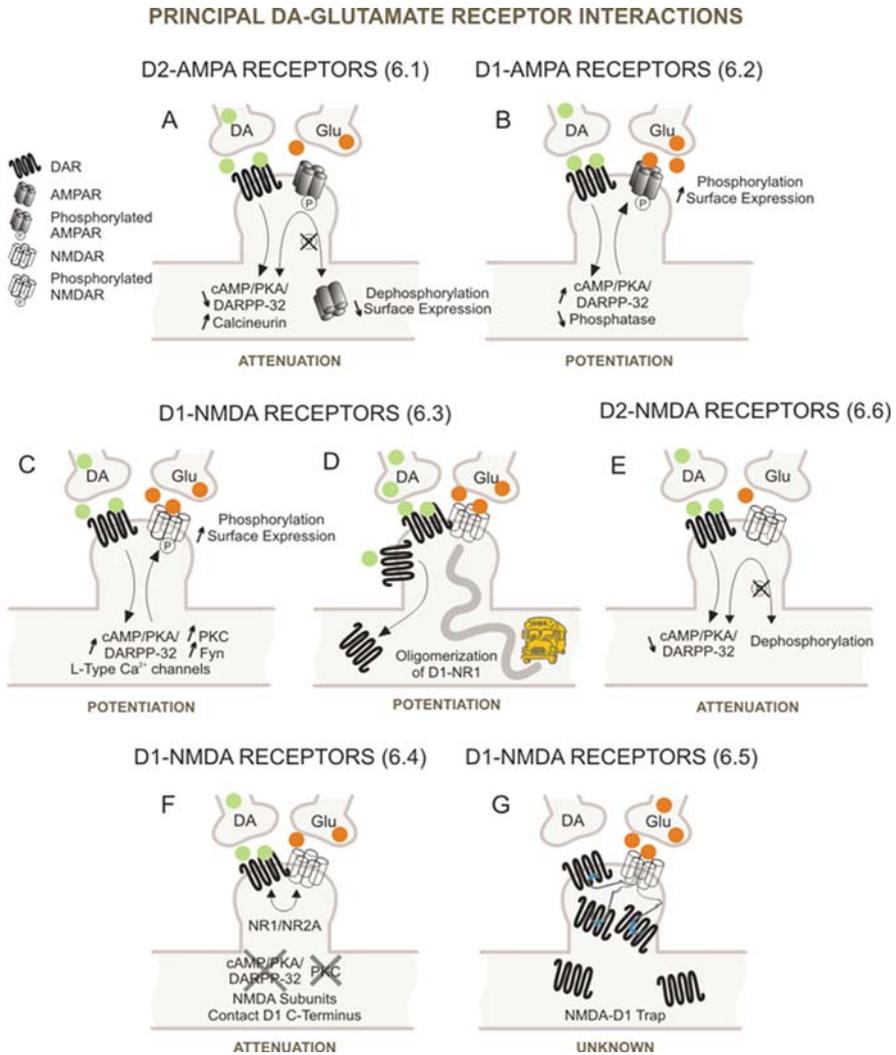
## 11.6 DA Modulation of Glutamate Receptor-Mediated Responses

The question whether or not DA is able to modulate directly excitatory postsynaptic responses, at least in dorsal striatum, remains controversial. While we and others observed clear DA modulation, other studies found no effect [53, 54]. We have provided possible explanations about why modulation was not observed [55–57]. One possibility is that the K<sup>+</sup> concentration was very low and the resting membrane potential of striatal neurons was extremely hyperpolarized. At these potentials, a number of voltage-dependent conductances may not be available for modulation. In addition, Nicola and Malenka used very young animals (<3 weeks). DA modulation at this age is minimal in the dorsal striatum. Finally, they did not use selective D<sub>1</sub>- or D<sub>2</sub>-like receptor agonists and they did not stimulate the white matter–cerebral cortex junction, the location which is more likely to produce glutamate receptor-mediated responses.

One problem involved in understanding the modulation of ligand-gated currents is how to tease apart indirect effects on voltage-gated conductances from those that are independent of these conductances [36]. This question may be difficult to resolve as DA activates multiple intracellular cascades that lead to phosphorylation of both glutamate receptor subunits and voltage-gated channels [58]. In the past we postulated that the most parsimonious explanation of DA's effects is the existence of redundant and cooperative actions involving both voltage- and ligand-gated conductances [56]. Regardless of the mechanisms, it has become clear that DA can alter glutamate receptor-mediated inputs as demonstrated in Sections 11.6.1, 11.6.2, 11.6.3, 11.6.4, 11.6.5, and 11.6.6. The main DA–glutamate receptor interactions are illustrated in Fig. 11.1.

### *11.6.1 DA and D<sub>2</sub>-like Receptors Decrease AMPA Receptor-Mediated Responses*

Early studies using extracellular recordings and iontophoresis showed that DA decreased spontaneous or glutamate-induced firing in anesthetized animals [59]. However, excitatory or mixed effects of DA were also reported [60], and these effects were hypothesized to be mediated by different DA receptors [61]. Intracellular studies *in vivo* demonstrated that iontophoretic application of DA inhibits spontaneous or glutamate-induced cell firing but concomitantly depolarizes



**Fig. 11.1** This schematic illustrates the principal DA–glutamate receptor interactions in striatum and cerebral cortex. The numbers in parenthesis indicate the section of the chapter where each interaction is explained. The *lower part* of each diagram represents a dendritic shaft and a spine, the *upper part* represents the DA- and glutamate-releasing terminals. **A–E** are interactions primarily mediated by a number of intracellular signaling cascades. **F** and **G** are physical receptor interactions. In **D**, a D1–NR1 protein complex is formed in the cytoplasm and shuttled to the membrane surface

striatal neurons, providing evidence for both excitatory and inhibitory actions of DA [62].

Results from *in vitro* preparations showed that most actions of DA were inhibitory [63]. To explain the reduction in cell firing, DA was proposed to inhibit

action potentials by reducing inward rectification mediated by sodium channels. DA also reduced excitatory postsynaptic potentials but this effect was dependent on the membrane potential [63], suggesting that some actions of DA rely on alterations in voltage-gated conductances only present at depolarized membrane potentials [64].

It remained unclear whether DA could also act on postsynaptic D<sub>2</sub>-like receptors to modulate AMPA receptor-mediated responses. More recently, activation of these receptors was indeed shown to exert inhibitory effects on AMPA responses [65, 66]. Further confirmation of direct postsynaptic modulation was obtained using an isolated cell preparation [67]. Interestingly, in these experiments the magnitude of the inhibition appeared to depend on the morphological integrity of the dendritic arbor of MSSNs and/or the amplitude of the current. Isolated cells with few and short dendrites produced small AMPA currents and modulation by the D<sub>2</sub>-like receptor agonist quinpirole was small and inconsistent. In contrast, in cells with a more intact dendritic arbor, AMPA produced larger currents and the decrement in the current in the presence of quinpirole also was greater. Cyclothiazide, by preventing AMPA receptor desensitization, increased the amplitude of the current, and the degree of modulation by the D<sub>2</sub>-like agonist was increased. In slices where most of the dendrites are present, the inhibitory effects of quinpirole are very consistent [67]. These findings suggest that the topography and/or subcellular distribution of glutamate and DA receptors plays an important role in the modulation of AMPA currents [29]. For example, it is possible that AMPA receptor density and subunit composition of somatic receptors differ from those found on the dendrites and spines. Morphological studies have shown that the density of AMPA and D<sub>2</sub> receptors is higher on spines and dendrites than on the soma [68, 69], reflecting the preferential mode of termination of cortical afferents [12].

What is the mechanism underlying D<sub>2</sub>-like receptor modulation of AMPA currents? AMPA receptor properties result from the combination of distinct subunits (GluR1–GluR4) and their state of phosphorylation [70, 71]. A balance between kinase and phosphatase activity is also an important determinant in the regulation of AMPA receptor function [72]. In MSSNs there is evidence that D<sub>2</sub>-like receptor activation affects intracellular Ca<sup>2+</sup> concentrations [73, 74] and therefore kinase and phosphatase activity. GluR1–3 subunits of the AMPA receptor are expressed in MSSNs [75–77]. The GluR1 subunit is mainly located on dendrites where asymmetrical synapses are established [75] and is phosphorylated at Ser845 by PKA following DA application [78], enhancing AMPA currents [79, 80]. Therefore, any disruption in PKA function which favors phosphatase activity may reduce AMPA currents. D<sub>2</sub>-like receptor activation reduces cAMP production through a G protein-mediated mechanism that also reduces the phosphorylation of the dopamine- and 3',5'-cyclic adenosine monophosphate (cAMP)-regulated phosphoprotein of 32 kDa (DARPP-32) [81, 82], a protein involved in AMPA receptor phosphorylation in the striatum [83]. D<sub>2</sub>-like receptor activation also could increase the activity of the protein phosphatase calcineurin, which dephosphorylates DARPP-32. Both of these processes lead to a decrease in PKA activity [82] and GluR1 phosphorylation which, in turn, could reduce AMPA currents.

### ***11.6.2 D<sub>1</sub>-Like Receptors Can Increase AMPA Receptor-Mediated Responses***

Modulation of AMPA channels by D<sub>1</sub>-like receptors is relevant to striatal function because it is another mechanism by which the efficacy of glutamatergic neurotransmission can be regulated. In our original study on DA–glutamate receptor interactions in slices, we demonstrated that AMPA receptor-mediated responses are generally potentiated by concurrent activation of D<sub>1</sub>-like receptors [65]. Activation of D<sub>1</sub>-like receptors in cultured striatal neurons also promoted phosphorylation of AMPA receptors by PKA as well as potentiation of current amplitude [84]. Similarly, in acutely isolated MSSNs, activation of D<sub>1</sub>-like receptors stabilized AMPA currents by preventing the rundown that is observed during repeated applications of the agonist [83]. This effect was explained by increased phosphorylation and decreased dephosphorylation of AMPA channels that required inhibition of PP-1 activity by phosphorylated DARPP-32 [83].

In MSSNs from nucleus accumbens, incubation with a D<sub>1</sub>-like receptor agonist increased surface expression of GluR1 subunits [85, 86]. This effect has important functional consequences as increased surface expression of AMPA receptors would enhance AMPA receptor transmission, a finding supported by *in vivo* experiments recorded from MSSNs [87].

### ***11.6.3 DA and D<sub>1</sub>-Like Receptor Activation Enhances NMDA Receptor-Mediated Responses***

DA and D<sub>1</sub>-like receptor-mediated potentiation of NMDA responses was first described in human cortex and rodent striatum 15 years ago [65, 88]. Since then, with only a few notable exceptions [53, 54], this enhancement has been verified in these and other brain structures [51, 55–57, 65, 66, 84, 88–99]. D<sub>1</sub>-like receptor enhancement of NMDA responses can be mediated by a number of redundant and cooperative signaling cascades in the striatum [55, 100]. The most prominent involve PKA and DARPP-32 [56, 89, 94], phosphorylation of NMDA receptor NR1 subunits [101], and activation of voltage-gated Ca<sup>2+</sup> channels, particularly L-type channels [90, 97]. In other cerebral regions different mechanisms may be in place. For example, in nucleus accumbens NMDA receptor potentiation by phospholipase C-coupled D<sub>1</sub>-like receptors occurs via protein kinase C (PKC) activation [93]. Similarly, in cortical pyramidal neurons intracellular application of the Ca<sup>2+</sup> chelator, calmodulin, or inhibition of PKC activity significantly reduces the potentiation of NMDA currents, indicating that this interaction can occur independent of PKA [92].

Activation of D<sub>1</sub> receptors can alter the surface distribution of NMDA receptors [78, 102]. For example, D<sub>1</sub> receptor activation produces an increase in NR1, NR2A, and NR2B proteins in the synaptosomal membrane fraction [103] that is dependent on Fyn protein tyrosine kinase but not DARPP-32 [104]. Based on the fact

that NMDA and D<sub>1</sub> receptors partially overlap in dendritic spines, protein–protein interactions might direct the trafficking of D<sub>1</sub> and NMDA receptors to the same subcellular domain.

The mechanism by which D<sub>1</sub> receptors are delivered to different spine domains has been examined in co-immunoprecipitation studies [105]. In the striatal post-synaptic density, the D<sub>1</sub> receptor selectively complexes with the NR1 subunit of the NMDA channel through its C-terminus. The physical proximity between D<sub>1</sub> receptors and NR1 subunits can be explained by the formation of constitutive protein dimers. Oligomerization with the NMDA receptor thus regulates D<sub>1</sub> receptor targeting to the plasma membrane. When the D<sub>1</sub> receptor and the NR1 subunit are coexpressed in HEK293 cells, the D<sub>1</sub> receptor is only partially targeted to the cell membrane, with the majority of D<sub>1</sub> receptor staining retained in cytoplasmic structures where it is colocalized with NR1. Coexpression of the D<sub>1</sub> receptor with both the NR1 and NR2B subunits relieves the cytoplasmic retention of the complex, allowing insertion of both the NR1 subunit and the D<sub>1</sub> receptor at the plasma membrane, where they are completely colocalized. These data suggest that D<sub>1</sub> and NMDA receptors are assembled as oligomeric units in the endoplasmic reticulum and transported to the cell surface as a preformed complex [105]. This implies that a direct protein–protein interaction with the NMDA receptor is one of the mechanisms directing the trafficking of D<sub>1</sub> receptors to specific subcellular compartments. Furthermore, this direct interaction may be crucial to recruit the D<sub>1</sub> receptor to the place where synaptic activity is occurring and to keep it in close proximity with the NMDA receptor to allow rapid cAMP–PKA–DARPP-32-mediated potentiation of NMDA transmission [105].

#### ***11.6.4 D<sub>1</sub>-Like Receptor Activation Can Depress NMDA Responses by Physical Receptor Interactions***

In specific circumstances D<sub>1</sub>-like receptor activation can lead to reduction of NMDA responses. In addition to regulating subcellular localization, the physical interactions between these receptors also allow cross talk via receptor linkages. The C-terminus of the D<sub>1</sub> receptor physically interacts with both NR1 and NR2A NMDA receptor subunits [106]. This protein–protein interaction has functional relevance because D<sub>1</sub>-like receptor activation decreases NMDA currents when PKA and PKC activations are blocked. The reduction of NMDA currents is caused by the interaction of D<sub>1</sub> receptors with the NR2A subunit and occurs through a decrease in the number of cell surface receptors [106]. The D<sub>1</sub> interaction with the NR1 subunit has been implicated in the attenuation of NMDA receptor-mediated excitotoxicity through a phosphatidylinositol 3-kinase-dependent pathway. The D<sub>1</sub>–NR1 interaction also enables NMDA receptor activation to increase membrane insertion of D<sub>1</sub> receptors [107].

The observation that physical receptor–receptor interactions reduce NMDA currents when second messenger pathways are blocked has been complicated by the demonstration that other mechanisms independent of D<sub>1</sub>-like receptor activation

can produce similar effects. A recent study revealed that one mechanism underlying reduction of NMDA currents is direct channel pore block of NMDA receptors by DA and several D<sub>1</sub>-like receptor ligands [108]. Thus, without excluding the possibility that receptor–receptor interactions may lead to functional modulation, the inhibitory effects of DA or its agonists and antagonists require further examination since they may also directly occlude the channel.

### ***11.6.5 The NMDA–D<sub>1</sub> Receptor Trap***

In primary cultures of striatal neurons, activation of NMDA receptors increases the recruitment of D<sub>1</sub> but not D<sub>2</sub> receptors into the plasma membrane [109]. This translocation is abolished in the presence of an NMDA receptor antagonist or by removing Ca<sup>2+</sup>. In addition, after NMDA treatment, a dramatic increase in the number of D<sub>1</sub> receptor-containing spines occurs. The translocation of D<sub>1</sub> receptors to the plasma membrane has been confirmed in subcellular fractionation experiments using slices of adult rat striatum. Furthermore, in organotypic cultures from rat striatum application of NMDA causes an increase in D<sub>1</sub> receptor-positive spines [110]. Surprisingly, under these conditions, this effect is independent of Ca<sup>2+</sup> and also occurs in the presence of Mg<sup>2+</sup> indicating that, in addition to the Ca<sup>2+</sup>-dependent recruitment of D<sub>1</sub> receptors by activation of NMDA receptors seen in primary cultures, other NMDA receptor-dependent mechanisms can cause redistribution of D<sub>1</sub> receptors to spines. This, according to the authors, is achieved by a diffusion-trap mechanism in which subsets of D<sub>1</sub> receptors that typically move by lateral diffusion in the plasma membrane get trapped in the spines when NMDA binds to its receptor. Exposure to NMDA reduces the diffusion rate of D<sub>1</sub> receptors and allows the formation of D<sub>1</sub>–NMDA heteroreceptor complexes. This process could be explained by the allosteric theory of receptor activation [111]. After ligand binding, one conformation of the receptor is stabilized, shifting the equilibrium toward this state, so that occupation of the binding site of the NMDA receptor favors a conformation that will bind to D<sub>1</sub> receptors and stabilizes them in spines. Thus, D<sub>1</sub> and NMDA receptor heteromers can be formed both constitutively prior to insertion of the receptors in the membrane [105] and in a NMDA receptor-regulated manner within the membranes of dendritic spines [110].

### ***11.6.6 DA, via D<sub>2</sub>-Like Receptors, Reduces NMDA Receptor-Mediated Responses***

In contrast to the enhancing effects of D<sub>1</sub>-like receptors on NMDA receptor-mediated responses, D<sub>2</sub>-like receptor activation leads to inhibitory effects [65, 66]. This may be relevant to preventing excessive activation of NMDA receptors and its consequent Ca<sup>2+</sup> accumulation which could be deleterious for the neuron. For example, DA and the D<sub>1</sub>-like receptor agonist SKF38393 increase the magnitude of

NMDA-induced cell swelling, an index of excitotoxicity [112, 113]. This effect is reduced in the presence of the D<sub>1</sub>-like receptor antagonist SCH23390 demonstrating specificity. In contrast, activation of D<sub>2</sub>-like receptors with quinpirole results in decreased cell swelling [112]. These results provide evidence that DA receptors have the potential to modulate excitotoxicity in the striatum, a process that has been suggested to be responsible for cell dysfunction and, ultimately, cell death as occurs in HD.

Compared to D<sub>1</sub>-like–NMDA receptor interactions, much less is known about the mechanisms by which D<sub>2</sub>-like receptor activation leads to reduction of NMDA currents. Decreased cAMP production and PKA activity are certainly potential mechanisms. D<sub>2</sub>-like receptors can also modulate neuronal excitability by activating the PLC–IP<sub>3</sub>–Ca<sup>2+</sup> cascade [73]. However, at least in cortical pyramidal neurons, D<sub>2</sub>-like receptor attenuation of NMDA responses does not require intracellular Ca<sup>2+</sup> or PKA inhibition but requires activation of GABA<sub>A</sub> receptors, suggesting that this effect is mediated through excitation of GABA interneurons [97].

D<sub>4</sub> receptors are abundant in the prefrontal cortex [114] and may play an important role in schizophrenia and other psychiatric disorders [115]. Mice without D<sub>4</sub> receptors show signs of hyperexcitability [116]. Application of a D<sub>4</sub> receptor agonist produces a decrease of NMDA currents via inhibition of PKA, activation of PP1, and the consequent inhibition of Ca<sup>2+</sup>–calmodulin-dependent kinase II (CaMKII) [117]. In CA1 pyramidal neurons quinpirole depresses excitatory transmission mediated by NMDA receptors by increasing release of intracellular Ca<sup>2+</sup>. This depression is dependent on transactivation of platelet-derived growth factor β by D<sub>4</sub> receptors [118]. In prefrontal cortical neurons similar effects were found but they were mediated by D<sub>2/3</sub> receptors [119].

Physical coupling between D<sub>2</sub> receptors and NR2B subunits can also reduce NMDA currents [120]. The mechanism underlying this effect involves disruption of the association between NR2B and CaMKII, thereby reducing subunit phosphorylation. It is believed that the D<sub>2</sub>–NR2B interaction plays a critical role in the stimulative effect of cocaine [120].

## 11.7 Genetic Manipulations of DA–Glutamate Receptor Interactions

The generation of mice lacking specific receptors or receptor subunits using genetic engineering marked a new era in the study of receptor function. These techniques have permitted the development of mice deficient in selective DA receptors or NMDA receptor subunits. Previous studies demonstrated that in D<sub>1</sub> receptor-deficient mice DA potentiation of striatal NMDA responses was greatly reduced [66]. Similarly, glutamate release along the corticostriatal pathway was enhanced in D<sub>2</sub> receptor knockout animals [39]. We are examining the enhancement of NMDA currents in mice lacking NR2A subunits [121]. In preliminary studies, D<sub>1</sub>-like receptor modulation of these currents is similar in MSSNs from NR2A knockout mice and their controls. Additionally we examined D<sub>2</sub>-like receptor attenuation of

NMDA responses in these mice and again found no statistically significant differences in modulation. Taken together, these results suggest that the presence or absence of the NR2A subunit does not affect D1-like or D2-like receptor modulation of NMDA receptor-mediated currents. These studies are relevant to DA–NMDA interactions as modulation of NMDA currents by DA receptors may be mediated by phosphorylation of specific receptor subunits or by physical coupling. Further, recent evidence indicates that specific NMDA receptor subunits may play different roles in synaptic plasticity and excitotoxicity [122–124].

Recently, mice that express EGFP reporter genes in a variety of cells have been generated [31]. In particular, mice that express specific DA receptor subtypes represent an important tool to differentiate neuronal subpopulations within the striatum [32]. Although in MSSNs DA or its agonists almost always modulate responses induced by NMDA receptor activation, the magnitude of this modulation varies from cell to cell. This is likely due to the fact that D<sub>1</sub> and D<sub>2</sub> receptors are largely segregated in different populations of MSSNs.

We currently are examining DA–NMDA receptor interactions in acutely dissociated D<sub>1</sub> and D<sub>2</sub> EGFP-positive MSSNs. Application of the D1-like receptor agonist SKF81297 dose-dependently and reversibly increased NMDA currents in D<sub>1</sub> but not in D<sub>2</sub> cells. NMDA current enhancement was prevented by the D1-like receptor antagonist SCH23390 (data not published). In contrast, quinpirole dose-dependently and reversibly decreased NMDA currents in D<sub>2</sub> but not in D<sub>1</sub> cells and the effect was blocked by the D2-like receptor antagonist remoxipride. At the highest concentration quinpirole also induced decreases of NMDA currents in about 25% of D<sub>1</sub> cells, suggesting colocalization of D<sub>1</sub> and D<sub>2</sub> receptors in a subset of MSSNs [125].

## 11.8 A Model of Striatal DA–Glutamate Receptor Interactions

According to the classical model, the basal ganglia in conjunction with thalamo-cortical circuits can be viewed as components of multiple parallel, segregated circuits [24]. Behavioral coordination is achieved by balanced activity within the direct and indirect pathway MSSNs that is regulated by differential actions of DA [23]. DA acting on D1-like receptors increases activity along the direct pathway but acting on D2-like receptors it reduces activity along the indirect pathway [23]. However, strong electrophysiological evidence for these actions of DA has been missing. Our findings demonstrating differential effects of DA based on the DA and glutamate receptor subtypes preferentially activated have provided a framework to begin to explain several assumptions of the model. In this framework, some interactions are highly predictable whereas others are less predictable. Inhibitory effects of DA are very predictable when high-affinity D2-like receptors are activated, as during tonic release of DA. In these conditions glutamate release is reduced and AMPA receptor-mediated responses are depressed. Such effects could induce elimination of specific behaviors. In contrast, facilitatory actions are very predictable when low-affinity D1-like receptors are activated, as occurs during phasic release of DA [126]. Under these conditions NMDA receptor-mediated responses are enhanced

and would promote synaptic plasticity and production of specific behaviors. A caveat of this model is that the segregation of D1- and D2-like receptors is not absolute and a number of MSSNs colocalize both receptors and/or send projections to the direct and indirect pathways [28, 127]. However, since the proportion of DA receptor colocalization may be very low, these caveats do not jeopardize the general validity of the model.

## 11.9 Functional Relevance of DA–Glutamate Receptor Interactions

The ultimate outcome of DA–glutamate receptor interactions will depend on a number of factors including temporal and topographic aspects [55, 100]. The outcome of activation of interacting receptors may depend heavily on the temporal sequence of neurotransmitter release. For example, activation of D1-like receptors due to DA release caused by unexpected reward can prime particular corticostriatal synapses and recruit D<sub>1</sub>–NMDA receptor complexes in a more regulated manner [105] to induce rapid potentiation of glutamatergic corticostriatal synapses. Furthermore, timing is an important requirement for this type of synaptic plasticity because DA release should occur before excitatory afferents are activated in order to induce the potentiation [128]. Massive DA release due to unexpected reward enhances the relevance of the stimulus by potentiating NMDA responses. This process is particularly important in MSSNs enriched with D<sub>1</sub> receptors that promote approach behaviors.

DA concentration and the mode of release are also important. Phasic release may produce different effects than tonic release. MSSNs are constantly bombarded by cortical and thalamic inputs, and tonic release of DA filters a sizable percentage of these glutamatergic inputs through D<sub>2</sub> receptors located on presynaptic terminals [45, 49]. Higher local concentrations of DA, which occur when it is phasically released [126], are likely to activate D1 receptors and enhance selected corticostriatal synapses.

Activation of D2-like receptors reduces glutamate release and the amplitude of the excitatory postsynaptic potential by pre- and postsynaptic mechanisms [39, 45, 46, 67]. It is plausible that D2-like receptor stimulation could counter or prevent exacerbated excitation of MSSNs induced by activation of D1-like receptors. This is important in terms of the physiological and pathological role of glutamatergic inputs in the striatum [112]. There are several lines of evidence showing that antagonists of NMDA and AMPA receptors have anti-parkinsonian effects, essentially by attenuating the imbalance between the DA and glutamate pathways within the basal ganglia network [129]. A possible function of D2-like receptor activation, both pre- and postsynaptically, could be to prevent a surge of glutamatergic activity that would otherwise be deleterious to MSSNs.

In neurodegenerative diseases DA–NMDA interactions also play an important role as unregulated enhancement of excitation, particularly excitation mediated by NMDA receptors, will cause neuronal dysfunction and disturb structural neuronal integrity. For example, the excitotoxicity hypothesis of HD posits that excessive

glutamate release at the corticostriatal terminal or altered sensitivity of postsynaptic NMDA receptors and their signaling systems can induce cell death [130]. Studies in genetic mouse models of HD have confirmed increased sensitivity of NMDA receptors in MSSNs [131–133]. However, the precise location of NMDA receptors in synaptic or extrasynaptic compartments determines the outcome of receptor activation. In hippocampal neurons, activation of synaptic NMDA receptors triggers an anti-apoptotic pathway, whereas activation of extrasynaptic NMDA receptors may cause cell death [134].

Assuming that activation of NMDA receptors recruits more functional D<sub>1</sub> receptors into the plasma membrane [107, 109, 110] and that these D<sub>1</sub> receptors in turn recruit more NMDA receptors [103], a positive feedback mechanism can be created and the outcome of these interactions can be deleterious for the neuron if it is not stopped [135]. Both D<sub>1</sub> and NMDA receptors independently exert toxic effects on striatal neurons. In addition, D<sub>1</sub>-like receptor activation also potentiates NMDA toxicity [112]. Thus, a number of protective mechanisms need to be present to prevent excessive D<sub>1</sub>-like–NMDA receptor stimulation. Activation of D<sub>2</sub>-like receptors could be neuroprotective as it reduces NMDA responses [112, 136]. Other mechanisms can also be considered. For example, the physical interaction between D<sub>1</sub> and NMDA receptors, independent of cAMP production, and the D<sub>2</sub>–NR2B interaction both reduce NMDA currents and excitotoxicity [106]. The diffusion-trap system could also represent a fast and efficient way to prevent excessive potentiation of NMDA responses if it makes the D<sub>1</sub> receptor less functional, a conclusion that remains to be verified.

Finally, DA–glutamate receptor interactions also could be important to gain a better understanding of PD. For example, a recent report indicated that loss of spines in models of PD selectively affects D<sub>2</sub> EGFP-positive MSSNs [137]. Although strong evidence was presented that this effect is due to dysregulation of postsynaptic L-type Ca<sup>2+</sup> channels, there may also be a presynaptic contribution. Previous studies had shown that DA-depleting lesions increase spontaneous glutamate-mediated synaptic activity [138, 139]. As this increase selectively affects D<sub>2</sub> receptor-containing MSSNs [32], it is likely that excessive glutamate release becomes neurotoxic and induces spine elimination. Membrane loss can then induce increases in input resistance [139], making these cells even more excitable and susceptible to deleterious effects of increased glutamate release. Supporting experimental evidence for this idea was obtained recently by the demonstration that dendritic remodeling of MSSNs seen in models of PD occurs only secondary to increases in corticostriatal glutamatergic drive [140].

## 11.10 Conclusions

It has been 15 years since a differential effect of DA on glutamate receptor-mediated responses was first observed [88]. As generally occurs with any scientific observation or hypothesis, explanations become more complex than initially assumed. The

potential mechanisms and even the outcomes of DA–glutamate receptor interactions continue to multiply. One might speculate that various interactions accomplish different functions. Some might be intended to enhance, whereas others might be designed to inhibit the outcome of receptor interactions. In the case of D1-like–NMDA receptor interactions, the traditional pathway involving D1-like receptor activation and the cAMP–PKA–DARPP-32 cascade produces various effects that enhance NMDA receptor function [141, 142].

Physical interactions between these receptors, either in the cytoplasm or in the membrane, have added new levels of complexity. In these interactions, two pathways in the formation of D<sub>1</sub>–NMDA heteroreceptor complexes are envisaged. One is G protein and Ca<sup>2+</sup> dependent, occurs in the cytoplasm, and delivers the complex to the plasma membrane, in particular the postsynaptic density [105]. The other is G protein and Ca<sup>2+</sup> independent, is membrane delimited, and could function as an inhibitory mechanism or brake to prevent and dampen continuous positive feedback [106, 109, 110]. These interactions, in conjunction with the more traditional interactions through signaling pathways, fine-tune neuronal function. Alterations in these interactions, as occur in pathological states, jeopardize functional and structural neuronal integrity. A better understanding of DA–glutamate interactions will thus provide more rational therapeutic targets in numerous diseases where these interactions are altered.

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# Chapter 12

## Unraveling the Role of Dopamine Receptors In Vivo: Lessons from Knockout Mice

Emanuele Tirotta, Claudia De Mei, Chisato Iitaka, Maria Ramos,  
Dawn Holmes, and Emiliana Borrelli

**Abstract** Dopamine exerts its action through membrane receptors that belong to the seven transmembrane domains (7TM) G protein-coupled receptor family. The dopamine receptor family is composed of five members, which have been divided into two subgroups: the D<sub>1</sub>-like family, which contains the D<sub>1</sub> receptor (D<sub>1</sub>R) and D<sub>5</sub>R, and the D<sub>2</sub>-like family containing D<sub>2</sub>R, D<sub>3</sub>R, and D<sub>4</sub>R. This subdivision is based on pharmacological, biochemical, and structural properties. Nevertheless, the close pharmacological properties together with the common anatomical site of expression of these receptors have induced the interest for generating animal models with which to assess the function of each individual dopamine receptor in vivo. To date, there exist mutants for all five receptors, in particular using the knockout technology each dopamine receptor has been independently knocked out. In this chapter we will summarize major findings related to the contribution of each dopamine receptor in the control of physiological functions regulated by dopamine. Analyses of these mutants clearly show a preponderant role for dopamine D<sub>1</sub>R and D<sub>2</sub>R receptors in most dopamine-mediated effects. At the same time these mutants are also revealing more hidden functions for D<sub>3</sub>R, D<sub>4</sub>R, and D<sub>5</sub>R very likely in the modulation of D<sub>1</sub>R- and D<sub>2</sub>R-mediated signaling.

**Keywords** Dopamine receptors · Knockout technology · Animal models · Behavior · Locomotion · Reward

### 12.1 Introduction

Understanding the mechanisms by which dopamine modulates functions as diverse as locomotion and reward or pituitary hormone production is a great scientific challenge. Since its discovery as a neurotransmitter in the 1950s, dopamine has attracted

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E. Borrelli (✉)

Department of Microbiology and Molecular Genetics, University of California Irvine,  
3113 Gillespie Neuroscience Facility, 92617, Irvine, CA, USA  
e-mail: borrelli@uci.edu

the attention of scientists from different disciplines with the common aim to unravel its mode of action *in vivo*. The presence of five dopamine receptors (DAR) [1, 2] together with their overlapping pattern of expression [3, 4] and shared signaling pathways [5] has not facilitated this task. In addition, members of the D<sub>2</sub>-like receptor subfamily are expressed into multiple isoforms generated by alternative splicing events *in vivo*; of these the best characterized are the long (D<sub>2L</sub>) and short (D<sub>2S</sub>) isoforms of the dopamine D<sub>2</sub> receptor (D<sub>2R</sub>) [5–8], although splice variants have also been reported for the D<sub>3R</sub> and D<sub>4R</sub> [9, 10]. Similarly, while it is possible pharmacologically to distinguish between D<sub>1</sub>-like and D<sub>2</sub>-like receptors, the presence of multiple members in each subfamily with similar pharmacological properties does not allow a full characterization of each receptor [1]. This promiscuity arises from the high molecular, biochemical, and pharmacological similarity existing between members of the D<sub>1</sub>-like (D<sub>1R</sub> and D<sub>5R</sub>) and D<sub>2</sub>-like (D<sub>2L</sub>, D<sub>2S</sub>, D<sub>3R</sub>, and D<sub>4R</sub>) receptor subfamilies [5], not to mention the possibility that each receptor might be able to form homo- and heterodimers/polymers and that these different conformations might modify *in vivo* responses [11], further enhancing the complexity of studying these proteins.

Thus, the possibility to genetically engineer mice [12, 13] and generate mutants lacking one particular DAR has been welcome for assessing the specific role of each receptor *in vivo*.

## 12.2 Advantages and Drawbacks of the Knockout Technology

Before discussing the results originated with DAR knockout (KO) mice, a premise needs to be made. First, KO models represent a great tool for investigating the role of specific proteins *in vivo*; however, as any other existent model, they have advantages as well as drawbacks. The advantages in the studies of the dopaminergic system have been multiple and we will mention only a few: (a) DAR KO mice have, indeed, allowed analyzing *in vivo* how absence of a specific receptor impairs well-defined dopamine-dependent functions. This would have not been possible using only pharmacological tools, due to the shared affinity for the same compound of members of each dopaminergic subfamily. In this respect, KO mice have also been used to assess the specificity of defined compounds *in vivo* [14, 15], which would not have been otherwise possible. (b) In contrast to transient analyses, KO models also enable to study the impact of loss of a specific receptor throughout the animal's life. This aspect is particularly important when analyzing proteins belonging to systems involved in neurodegenerative disorders such as the dopamine system. It has been possible, for example, to show that absence of D<sub>2</sub>-mediated signaling in D<sub>2R</sub> KO females leads to development of pituitary tumors, but only as they age [16, 17].

On the other hand, there are drawbacks of the constitutive KO technology that should not be overlooked. (a) Animals are deprived of the specific receptor as soon as the gene becomes transcriptionally active and thus even during embryogenesis (if it has an early expression pattern). This underlies the possible establishment of

homeostatic responses from the organism to adjust/cope with that loss of function/s. Therefore, phenotypes of DAR KO mice might partly result from compensatory mechanisms more than from the ablation of a specific receptor. Although this is a reasonable eventuality, results obtained from studies of the different DAR mutants suggest that it might have had very limited effects, at least based on parallels between acute pharmacological studies and phenotypes of KO mice. (b) A second debated issue is technical: most commonly KOs are generated from embryonic stem cells of a different genetic background than that of the recipient embryos. This leads to animals with mixed genetic backgrounds and the possibility that some behavioral phenotypes can be influenced by specific background contributions and not by deletion of the gene in itself. For this, littermates from heterozygote mating are used in order to have comparable wild-type (WT) and mutated mice. When possible, backcrossing KOs in the genetic background desired, for at least five generations, is advised [18, 19].

More importantly, the outcome of behavioral analyses performed with DAR KO mice has generated some controversies; this is a major issue since the behavioral settings differ in different laboratories. This is a more difficult point to address, as it would require the development of well-standardized behavioral procedures and settings common to every laboratory or at least those analyzing the same KO line.

Nevertheless, most published phenotypes have been subsequently confirmed in different laboratories using independently generated KO lines for the same receptor. Generally, the amplitude of particular impairments might increase/decrease in mixed backgrounds, but robust phenotypes are maintained whether in mixed or pure backgrounds. Despite these drawbacks, DAR KOs have contributed and will, in the future, generate important information on the physiology of these receptors that would have not been otherwise gathered.

### 12.3 Lessons from KO Mice

Since 1994 a large series of reports have been published in which DAR knockout mice were used to establish the role of individual receptors *in vivo*. Multiple KO lines have been made in particular for D<sub>1</sub>R, D<sub>2</sub>R, and D<sub>3</sub>R, while only one KO line has been generated for D<sub>4</sub>R and D<sub>5</sub>R. In this paragraph, we will highlight some of the major findings obtained through the analysis of DAR KO mice, and in particular from D<sub>2</sub>R KO mice, which well illustrate the relevance of KO studies. For instance, genetic studies have shown the importance of dopaminergic signaling not only for brain functions but also overall for the survival of the organism. Indeed, while single KO of each of the five DARs does not impact birth, growth, or reproduction of KO mice, the simultaneous KO of the two major DARs, D<sub>1</sub>R and D<sub>2</sub>R, results in a striking phenotype, which leads to death of double KO mice during the second postnatal week [20]. Notably, this phenotype strongly resembles that of tyrosine hydroxylase KO mice, in which dopamine levels are extremely reduced [21, 22]. Interestingly, lethality is observed only in the D<sub>1</sub>R/D<sub>2</sub>R double KO [20], while D<sub>2</sub>R/D<sub>3</sub>R [23, 24]

or D<sub>1</sub>R/D<sub>3</sub>R [25, 26] KO are born normally, reach adulthood, and reproduce. These findings strongly point to a preponderant physiological role of D<sub>1</sub>Rs and D<sub>2</sub>Rs in the regulation of basal body functions. At the same time, we might speculate that the principal function of D<sub>3</sub>R, D<sub>4</sub>R, and D<sub>5</sub>R is to act as sensors of dopamine activity and to modulate D<sub>1</sub>R- and D<sub>2</sub>R-dependent signaling. This view is supported by the higher affinity of the D<sub>3</sub>R, D<sub>4</sub>R, and D<sub>5</sub>R for dopamine [27] as well as by their co-localization with either D<sub>1</sub>R or D<sub>2</sub>R, for example, in striatal medium spiny neurons (MSNs) [4, 28].

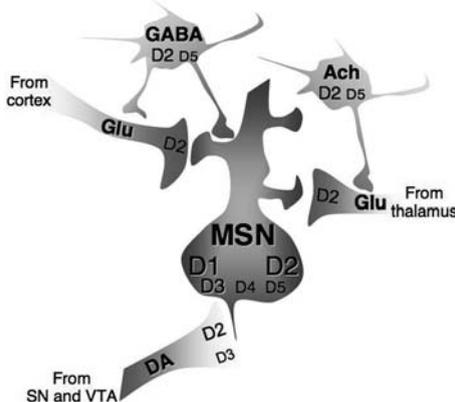
A second important finding has been the identification of D<sub>2</sub>Rs as the bona fide dopamine autoreceptor [29, 30]. This function has a critical role in the regulation and physiology of the dopaminergic system since it is responsible for the control of the synthesis and release of dopamine. Alteration or malfunction of autoreceptors strongly impairs the response of any DAR by changing inappropriately the physiological levels of the ligand in response to stimuli. Two D<sub>2</sub>-like receptors, D<sub>2</sub>R and D<sub>3</sub>R, could be anatomically responsible for such functions due to their localization in dopaminergic neurons of the substantia nigra (SN) and ventral tegmental area (VTA). Because these receptors have similar pharmacological characteristics, assessing autoreceptor function only with pharmacological tools has produced ambiguous results. The use of D<sub>2</sub>R and D<sub>3</sub>R KO has clarified that despite the presence of D<sub>2</sub>R and D<sub>3</sub>R on dopaminergic neurons, absence of D<sub>2</sub>R completely abolishes the autoreceptor regulation of dopamine release from dopaminergic neurons [30]. This indicates that D<sub>3</sub>Rs, in the absence of D<sub>2</sub>Rs, cannot compensate for the regulation of dopamine release upon challenge. Nevertheless, D<sub>3</sub>Rs might have a role in regulating dopamine levels under phasic but not tonic conditions [31] or in cooperation with D<sub>2</sub>Rs.

The third example concerns the target of antipsychotics normally used in the treatment of schizophrenia. Haloperidol, a commonly used antipsychotic, is known to exert its beneficial effect in the treatment of schizophrenia through blockade of D<sub>2</sub>-like receptors [32]. Importantly, knocking out the long isoform of the D<sub>2</sub>R, D<sub>2L</sub>, strongly impairs the property of this drug to induce catalepsy in D<sub>2L</sub> KO mice, thus identifying D<sub>2L</sub> as the major target for the postsynaptic effects of this antipsychotic [7, 8]. Furthermore, studies in which D<sub>1</sub>R, D<sub>2</sub>R, D<sub>3</sub>R, and D<sub>4</sub>R KO mice were compared to assess their involvement in modulating pre-pulse inhibition (PPI) of startle reflex have shown that only the absence of D<sub>2</sub>Rs results in disruption of PPI after amphetamine treatment [33], while D<sub>1</sub>Rs, D<sub>2</sub>Rs, and D<sub>3</sub>Rs are all involved in the disruption of PPI induced by cocaine [34].

## 12.4 Dopamine Receptors in the Control of Motor Behavior

One key role of dopamine in the CNS is the control of locomotion, as evidenced by degeneration of dopaminergic neurons in Parkinson's disease. The dopaminergic pathway involved in this control is the nigro-striatal pathway formed by fibers arising from dopaminergic neurons located in the SN, which project to the striatum.

The striatum represents the site of integration of the motor circuitry, receiving the dopaminergic fibers as well as stimuli from the cortex and thalamus [35]. The complex nature of this circuitry and co-expression of several different DARs in the same neurons make it very difficult to define the role of each receptor in this function. Indeed, DARs are present not only on striatal MSNs but also on cortical and thalamic neurons, as well as on interneurons (Fig. 12.1). It is thus very arduous to analyze how the different DARs regulate the physiology of neurons in this circuitry. Nevertheless, the development of KO mice and technical tools formed either by specific antibodies, tracers [36], or mouse models in which BAC constructs expressing fluorescent proteins, driven by the  $D_1R$  and  $D_2R$  [35, 37, 38] promoters, have been inserted in the mouse genome is starting to give useful insights into the rules that govern this circuitry.



**Fig. 12.1** This figure schematically illustrates how dopamine elicits its effects on striatal medium spiny neurons (MSNs). We aimed at representing the sites of expression of dopamine receptors on most striatal neurons and afferents.  $D_1R$ s and  $D_2R$ s are the most highly expressed neurons by MSNs, followed by  $D_3R$ s and then  $D_4R$ s and  $D_5R$ s (font size is indicative of the expression level). MSNs receive inputs from neurons originating in the SN, VTA, cortex, and thalamus as well as from striatal interneurons (i.e., striatal GABAergic and cholinergic interneurons).  $D_2R$ s have a very intricate expression pattern. Indeed, they are present on MSNs, but also presynaptically on dopaminergic fibers, as well as on cortical, thalamic, and interneuron terminals.  $D_3R$ s are both pre- and postsynaptic;  $D_1R$ ,  $D_4R$ , and  $D_5R$  expression is as indicated

Depending on which cell/region of the striatum is analyzed, different combinations of dopamine receptors are found. For example, most dorsal regions express almost exclusively  $D_1R$ s and  $D_2R$ s and are devoid of  $D_3R$  expression, while the ventral striatum expresses higher levels of  $D_3R$ s [31]. Similarly,  $D_5R$ s have very low expression levels overall in the striatum, but they are robustly expressed in cholinergic interneurons [3]. Furthermore, co-segregation of some members of the  $D_1$ -like and  $D_2$ -like receptor subfamilies in the same cells has been observed; this together with the possibility that they could physically associate in vivo [39, 40] increases

the complexity of this system. Behavioral results obtained by the study of KO mice should be interpreted keeping in mind this intricacy.

#### ***12.4.1 Motor Behavior: D<sub>1</sub>R KO***

D<sub>1</sub>R KO mice were first reported in 1994 by two independent laboratories; for clarity we will call them D<sub>1</sub>R KO-A [41] and D<sub>1</sub>R KO-B [42]. In D<sub>1</sub>R KO-A, the targeting construct contained a deletion of 95% of the D<sub>1</sub>R coding sequence, while D<sub>1</sub>R KO-B was created by deleting the region of the D<sub>1</sub>R gene encoding the putative third intracytoplasmic loop of the receptor. D<sub>1</sub>R KO-A mice were reported to present a hyperactive phenotype [41, 43, 44]; conversely, D<sub>1</sub>R KO-B mice were first reported to have decreased stereotypies, but no difference in locomotion [42]. However, more recently the D<sub>1</sub>R KO-B line has also been reported to be hyperactive in different behavioral settings [45]. Therefore, it can be concluded that loss of the D<sub>1</sub>R results in a potentiation of horizontal locomotion.

#### ***12.4.2 Motor Behavior: D<sub>2</sub>R KO***

D<sub>2</sub>R KO-A mice were first reported in 1995 [46]; in this line exon 2 of the D<sub>2</sub>R gene was deleted leading to the absence of D<sub>2</sub>Rs *in vivo*. These mice presented impairments of posture and motor activity when analyzed in an open field. In particular, a significant reduction of horizontal locomotion, stereotypies, and coordination of movements were reported [46]. A second KO line, D<sub>2</sub>R KO-B [23], was generated using a similar KO strategy as for D<sub>2</sub>R KO-A. Analyses of D<sub>2</sub>R KO-B mice supported findings obtained with D<sub>2</sub>R KO-A and confirmed motor impairments in the absence of the D<sub>2</sub>R. A third line, D<sub>2</sub>R KO-C mice, was generated using a different KO strategy, in which the 3'-region of the D<sub>2</sub>R gene containing exons 6 and 7 was deleted [47]. These mice were also reported to have motor impairments, but to a lower extent than D<sub>2</sub>R KO-A and B mice. Interestingly, ethological analyses performed by the same laboratory using D<sub>2</sub>R KO-A and C lines revealed an absence of difference in the different parameters tested between these two independent lines [48, 49]. Ethological analyses identified, in both lines, specific reductions of one type of stereotypy (total rearing) and of horizontal locomotion, although the deficits were much milder than those found when D<sub>2</sub>R KO mice were tested in the open field and rotarod. It is perhaps not surprising to obtain results from ethological analyses that differ from other behavioral tests (open field, rotarod); the first are performed in non-stressful settings (home cage), while the latter are performed under more stressful/challenging conditions. Overall, it can be concluded that loss of D<sub>2</sub>R-mediated signaling results in reduction of motor behaviors. Interestingly, deletion of the long and most abundant isoform of D<sub>2</sub>R, D<sub>2L</sub>, does not result in modifications of motor activity or coordination of movements under basal conditions [7, 8]. This indicates that the presence of only D<sub>2S</sub> is able to insure a normal D<sub>2</sub>R-dependent basal activity, very likely dependent on the still persistent control of dopamine release [7]

mediated by  $D_{2S}$ . However, challenge by  $D_1R$ -specific agonists of  $D_{2L}$  KO mice resulted in a greatly attenuated motor response as compared to their WT littermates [7]. This suggests that  $D_{2L}$  is the  $D_2R$  isoform cooperating/synergizing with the  $D_1R$  in the control of motor behavior [50].

### ***12.4.3 Motor Behavior: $D_3R$ KO***

The first reported  $D_3R$  KO-A line [51] showed increased locomotor activity. Hyperactivity in a novel environment, in the absence of the  $D_3R$ , was confirmed in a second KO line,  $D_3R$  KO-B [52]. However, the increased motor behavior was observable only during the first several minutes of assessment, but not thereafter, as  $D_3R$  KO mice habituated faster than WT to the new environment.  $D_3R$  KO-A mice were later reported to show an increase of activity only during the night phase of the light/dark cycle, but not consistently during the day [53]. The mechanism leading to hyperactivity in mice lacking  $D_3R$  was correlated with an increased dopaminergic tone [54]. Indeed, increased basal extracellular levels of dopamine, as compared to WT mice, were reported in several  $D_3R$  KO lines [54–56]. This contrasts with  $D_2R$  KO mice [57, 58] in which basal extracellular dopamine levels are normal, but dopamine release upon stimulation by drugs of abuse leads to an outstanding elevation of dopamine levels [30]. This suggests that the  $D_3R$  might regulate dopamine levels under tonic conditions.

Other groups failed to confirm the hyperactive phenotype of  $D_3R$  KO-A mice [59, 60], as well as of two independently generated lines, the  $D_3R$  KO-C [23] and  $D_3R$  KO-D [55]. The reason for this discrepancy is not clear, but very likely depends on the conditions used to perform the experiments in different laboratories. Indeed,  $D_3R$  KO-A mice also revealed reduced thigmotaxis in the open field and increased time spent in the open arms of the elevated plus maze with respect to WT mice [61], indicating a reduced level of anxiety in these mice, which might well affect other behavioral measures. Thus, absence of  $D_3R$  signaling might facilitate locomotion in conditions yet to be completely defined.

### ***12.4.4 Motor Behavior: $D_4R$ KO***

$D_4R$  KO mice have been shown to exhibit less spontaneous locomotion and rearing activity than WT in novel and familiar environments [62]. These mice, in a mixed genetic background (129SV/CS7BL/6), outperformed WT mice in the rotarod test, experiencing 50% fewer falls and remaining on the rotating rod 2.5 times longer than WT mice [62], suggesting that  $D_4Rs$  participate in the modulation of motor functions.

Interestingly, polymorphisms of the  $D_4R$  gene in humans have been correlated with variations in personality traits associated with higher novelty seeking [63, 64]. In line with these findings,  $D_4R$  KO mice show reduced exploration in the open field, emergence, and novel object tests despite an overall activity level similar to

that of WT mice. This suggests that D<sub>4</sub>R polymorphisms in humans might induce a gain of function for this receptor, which could be correlated with the decrease in novelty-related behaviors observed in mice in which the receptor is deleted [65]. However, recent studies performed in different behavioral conditions, but with the same KO line although in a pure C57BL/6 background, do not support the previously observed decrease of novelty-seeking behaviors in the absence of D<sub>4</sub>R [66]. Additional studies are requested to clarify whether or not the D<sub>4</sub>R plays a key role in motor functions and novelty seeking by testing D<sub>4</sub>R KO (C57BL/6 background) in the same experimental setting used to characterize these mutants in the mixed (F2) genetic background. To date it is possible to conclude that absence of the D<sub>4</sub>R does not appear to negatively affect locomotion and actually could even strengthen coordination of movement [62], possibly indicating an inhibitory role of D<sub>4</sub>Rs on this function.

### 12.4.5 Motor Behavior: D<sub>5</sub>R KO

Generation of D<sub>5</sub>R KO mice has shown that the influence of D<sub>5</sub>R-mediated signaling on motor behavior is very subtle. D<sub>5</sub>R KO mice responded as WT littermates in a series of behavioral tests aimed at checking most of the functions activated by dopamine signaling. Indeed, when tested in locomotor activity tests, the rotarod test, acoustic startle response, PPI [67], elevated plus maze, light/dark exploration, Morris water maze, and cued and contextual fear conditioning, no statistically relevant differences with WT mice were noted [68]. Nevertheless, more recent analyses are starting to shed some light on the function of this receptor, which appears to have facilitatory functions on motor behavior as established by pharmacological, electrophysiological [43], and ethological analyses [69].

The motor phenotype of DAR KO mice is summarized in Table 12.1.

**Table 12.1** Summary of motor phenotypes observed in DAR KO mice

| DAR KO                               | Motor phenotype: basal conditions |
|--------------------------------------|-----------------------------------|
| D <sub>1</sub> KO                    | ↑ [41, 43, 44]                    |
| D <sub>2</sub> R KO                  | ↓ [23, 46, 47]                    |
| D <sub>2L</sub> KO                   | ↔ [7, 8]                          |
| D <sub>3</sub> R KO                  | ↑ [51, 52]                        |
|                                      | ↔ [59, 60]                        |
| D <sub>4</sub> R KO                  | ↑ [62]                            |
| D <sub>5</sub> R KO                  | ↔ [68]                            |
| D <sub>1</sub> R/D <sub>2</sub> R KO | ↓↓ [24]                           |
| D <sub>1</sub> R/D <sub>3</sub> R KO | ↔ [25, 26]                        |
| D <sub>2</sub> R/D <sub>3</sub> R KO | ↓ [23]                            |

References to the phenotype are indicated. The direction of changes is indicated with respect to WT animals exposed to similar conditions.

↑: increase, ↓: decrease, ↔: no difference.

## 12.5 Dopamine Receptors and Drugs of Abuse

Converging evidence supports the implication of the mesolimbic dopaminergic pathway in the regulation of the rewarding/reinforcing properties of natural stimuli, such as food or sex [70]. This pathway is hijacked by drugs of abuse, which by different mechanisms elevate dopamine levels in the limbic system. As for other dopamine-regulated functions, pharmacological studies have shown that D<sub>1</sub>R- and D<sub>2</sub>R-mediated signaling have a major impact on the acute and chronic responses to drugs. In this respect, the behavior of KO mutants for D<sub>1</sub>R and D<sub>2</sub>R strongly supports a preponderant role of signaling mediated by these two receptors in the behavioral and cellular response to abused drugs.

### 12.5.1 The D<sub>1</sub>R and Drugs of Abuse

Interestingly, the D<sub>1</sub>R KO-A and KO-B mutant mice failed to exhibit the psychomotor stimulant effect of cocaine on motor and stereotyped behaviors as compared to wild-type littermates [71–73]. Conversely, D<sub>1</sub>R KO mice show a significant dose-dependent locomotor decrease after cocaine administration [71]. Investigations at the electrophysiological and gene expression levels of the striatum of the D<sub>1</sub>R KO mouse lines showed that this receptor plays an essential role in cocaine [71, 72], amphetamine [74], and thereby dopamine-mediated effects of drugs of abuse. Electrophysiological studies of nucleus accumbens neurons showed that the inhibitory effects of dopamine as well as those of D<sub>1</sub>R and D<sub>2</sub>R agonists were strongly reduced, whereas those of serotonin were unaffected [71]. In addition, it was later demonstrated that the cellular and behavioral effects of cocaine require intact D<sub>1</sub>R- and glutamate receptor-mediated signaling, *in vivo*, for the activation of the ERK pathway and downstream immediate early genes [75–78]. On the contrary, D<sub>2</sub>R agonists and antagonists induced functional effects in the D<sub>1</sub>R KO mice at least with respect to induction of immediate early genes (*c-fos* and *jun-b*). These results hint that D<sub>1</sub>R–D<sub>2</sub>R synergism is not obligatory for D<sub>2</sub>R function and that D<sub>1</sub>-like/D<sub>2</sub>-like receptors may interact synergistically or in opposition in striatal neurons, depending on the neural subpopulations engaged [38, 79, 80].

The rewarding properties of drugs can be evaluated by performing conditioned place preference (CPP) experiments. The D<sub>1</sub>R KO-B mouse line was used to investigate cocaine reward using this paradigm [81]. While these experiments confirmed that the D<sub>1</sub>R is involved in the stimulatory locomotor effects of cocaine, they showed that this receptor does not play a major role in the rewarding effects of this drug [81]. The reinforcing effects of food and drugs of abuse have also been analyzed in D<sub>1</sub>R KO-A. Food and opioid agonists in these mice function as positive reinforcers, whereas the effect of cocaine is affected [82]. In addition, D<sub>1</sub>R- or D<sub>2</sub>R-selective agonists do not work as positive reinforcers in D<sub>1</sub>R KO-A mice, whereas these drugs are self-administered by WT littermates [82]. Accordingly, electrophysiological studies showed that KO of the D<sub>1</sub>R abolished all DAR-mediated effects, within the nucleus accumbens, including those produced by the D<sub>2</sub>-like agonist quinpirole

[71]. These results suggest that D<sub>1</sub>Rs participate in the reinforcing effects of cocaine [82] and acquisition of self-administration of this drug. The contradictory results between CPP and self-administration studies might be due to the use of two different paradigms that measure qualitatively different aspects of cocaine effects. More recently, additional experiments have confirmed lack of motor activation upon acute cocaine administration in D<sub>1</sub>R KO mice, but a mild sensitization of these mice to the same drug after repeated administration of specific cocaine concentrations [83], indicating that absence of D<sub>1</sub>Rs does not fully prevent sensitization to this drug. It is worth mentioning that cocaine is, however, a drug affecting multiple receptor systems and thereby the contribution of other neurotransmitters/modulators in the behavioral response of D<sub>1</sub>R KO mice cannot be completely excluded.

Similar results were obtained after amphetamine administration, which, although it failed to induce locomotor behavior in D<sub>1</sub>R KO-B mice with respect to WT mice upon acute treatments, did induce a sensitized response upon chronic administration. However, the amplitude of sensitization was less pronounced in the D<sub>1</sub>R KO-B than in WT mice in agreement with their reduced acute motor response to the drug [84]. Similar results were also obtained with D<sub>1</sub>R KO-A mice [73, 74]. These results confirm earlier pharmacological studies using mice and rats that described the effects of D<sub>1</sub>R antagonists on locomotion, behavioral sensitization, and stereotyped responses to cocaine and amphetamine [85, 86]. In addition to the reduced response to cocaine and amphetamine, D<sub>1</sub>R KO-B consumed ethanol by self-administration or under forced conditions in a significantly lower amount than the WT control animals [87]. Thus, D<sub>1</sub>Rs are clearly central in signaling the rewarding/reinforcing properties of drugs of abuse.

### ***12.5.2 The D<sub>2</sub>R and Drugs of Abuse***

The contribution of D<sub>2</sub>R signaling in the motivational response to drugs of abuse has produced very interesting although complex findings. Indeed, D<sub>2</sub>R KO mice increase their locomotion upon treatment with opioids (i.e., morphine) [88], while in response to psychostimulants and alcohol they exhibit a blunted motor response [89–92]. In addition, the blunted motor response to cocaine of D<sub>2</sub>R KO-A mice was accompanied at the cellular level by absence of activation of the immediate early gene, *c-fos*, in the striatum [91]. Interestingly, absence of cellular and behavioral effects in D<sub>2</sub>R KO-A mice was specifically observed in response to cocaine, but not to D<sub>1</sub>R-specific agonists, which elicited an increased motor response and sustained *c-fos* induction in these animals [7, 91], thus indicating that the D<sub>1</sub>R-mediated signaling is overactivated in D<sub>2</sub>R KO mice, as expected by absence of D<sub>2</sub>R signaling. Consistent with this observation, cocaine in D<sub>2</sub>R KO-A mice induced increased stereotyped behaviors, which very likely contribute to the reduced forward motor response to the drug. However, loss of induction of *c-fos* expression is at odds with an overactivation of the D<sub>1</sub>R-mediated signaling. It was hypothesized that absence of *c-fos* induction in response to cocaine might be generated by lack of

D<sub>2</sub>R heteroreceptors on striatal interneurons and possibly on regulation of GABA release [93]. Increased GABA release might well explain the blunted response of immediate early gene responses to cocaine in animals lacking D<sub>2</sub>R. Alternatively, loss of the D<sub>2</sub>R might prevent the formation of heteromers with other receptors, which would be required for the induction of pathways leading to c-fos activation.

The rewarding properties of morphine were tested in D<sub>2</sub>R KO-A mice by performing CPP analyses. Strikingly, the results of these experiments showed absence of CPP to morphine in these mutants as compared to their WT siblings [88]. These results were recently confirmed and supported by absence of morphine self-administration in D<sub>2</sub>R KO-C mice [94, 95]. In addition to loss of the reinforcing properties of morphine, D<sub>2</sub>R KO mice do not self-administer ethanol [89, 96, 97]. Conversely, D<sub>2</sub>R KO-A mice performed CPP in response to cocaine [91], although the CPP response was attenuated with respect to that of WT controls. D<sub>2</sub>R KO-A mice also self-administer more cocaine than WT littermates [98], indicating that D<sub>2</sub>R-mediated signaling might be involved in mechanisms that limit rates of high-dose cocaine self-administration. Keeping in mind that the mechanism of action of psychostimulants involves the activation of multiple neurotransmitters/modulators, the possibility exists that in D<sub>2</sub>R KO mice absence of reward/reinforcement to morphine and ethanol, but presence of response to cocaine and amphetamine (although attenuated), might be generated by molecules other than dopamine. These results indicate a general role for D<sub>2</sub>R-mediated signaling in motivated responding, more than a specific effect of a particular drug in D<sub>2</sub>R KO mice. Thereby, D<sub>2</sub>R-mediated signaling appears to play an essential role in the response to drugs and ultimately in addiction [99]. Importantly, D<sub>2L</sub> KO mice have a normal motor response to cocaine and also perform as WT animals in the CPP paradigm to this drug ([91], and our unpublished data). This suggests that the presence of only D<sub>2S</sub> is sufficient to mediate responses to addictive drugs, possibly through normal modulation of dopamine release [7, 30].

### ***12.5.3 The D<sub>3</sub>R and Drugs of Abuse***

The D<sub>3</sub>R, although expressed at much lower levels with respect to the D<sub>1</sub>R and the D<sub>2</sub>R, shows a highly restricted expression in limbic regions involved in the regulation of reward, particularly in the nucleus accumbens [100–102]. This suggests that this receptor may play a prominent role in mediating reward-related behaviors [54]. Indeed, drugs acting at the D<sub>3</sub>R are potent modulators of the reinforcing effects of psychostimulants, and changes in D<sub>3</sub>R function are associated with altered responses to these drugs [54, 103].

The analysis of the D<sub>3</sub>R KO mice has provided further evidence by showing that D<sub>3</sub>R KO mice are more sensitive to the motor stimulant effects of cocaine at low doses of the drug, as compared to WT animals [52]. However, at high doses the degree of stimulation is similar in both genotypes. As for cocaine, CPP analyses in response to amphetamine demonstrated that D<sub>3</sub>R KO mice exhibited an increased response to amphetamine relative to control mice at low doses of the drug [52].

Similar results were also obtained when the D<sub>3</sub>R KO mice were assessed for presence of morphine-induced rewarding effects. Indeed, a significant CPP for the drug-associated compartment was observed in D<sub>3</sub>R KO mice at low doses of morphine (0.1–0.56 mg/kg), whereas no preference was observed in WT mice at these doses [104].

A different study [105] also reported a higher dose-dependent CPP response to morphine in D<sub>3</sub>R KO versus WT animals. D<sub>3</sub>R KO mice were more responsive than their WT littermates at the lowest dose of morphine tested while morphine-induced CPP was attenuated in response to higher concentrations of the drug.

The implication of the D<sub>3</sub>R in regulating the rewarding/reinforcing properties of drugs has also been assessed pharmacologically, using a D<sub>3</sub>R-specific partial agonist BP897 [106–108]. It has been concluded that D<sub>3</sub>R is not directly implicated in the reinforcing effects of drugs of abuse, but appears to be involved in the motivation to self-administer drugs in specific conditions (high-requirement self-administration schedules) [109, 110]. These data suggest that the D<sub>3</sub>R plays a modulatory role over dopamine-mediated responses to drugs of abuse and, in particular, that this receptor functions as a sensor in the system. This is very likely dependent on the high affinity of the D<sub>3</sub>R for dopamine with respect to other D<sub>2</sub>-like receptors.

### ***12.5.4 The D<sub>4</sub>R and Drugs of Abuse***

Polymorphisms of the dopamine D<sub>4</sub>R have been associated with novelty seeking in humans [63, 64]; this trait has been associated with risk-taking behaviors and thereby drug abuse. This hypothesis is consistent with studies showing avoidance of novel objects placed in a familiar environment and supersensitivity to the locomotor-stimulating effects of alcohol, amphetamine, and cocaine in D<sub>4</sub>R KO mice [62, 65]. More recently, it has been reported that cocaine's potency in producing discriminative stimulus and psychomotor stimulant effects is stronger in D<sub>4</sub>R KO than in WT mice. This despite the absence of appreciable novelty seeking in the testing environments in D<sub>4</sub>R KO mice, thus suggesting that the response to a novel environment plays only a marginal role in the different sensitivity to cocaine [111]. In addition, D<sub>4</sub>R KO mice demonstrated an enhanced and dose-dependent increase in amphetamine-stimulated activity; they also showed enhanced dose-dependent sensitized response to repeated amphetamine administration compared to the WT mice [112].

### ***12.5.5 The D<sub>5</sub>R and Drugs of Abuse***

In agreement with a very limited effect of absence of D<sub>5</sub>Rs on motor functions, responses to drugs of abuse and in particular to cocaine are quite similar in WT and D<sub>5</sub>R KO mice. The acute response to cocaine was found mildly attenuated in an original report [113], which has not been subsequently supported using

D<sub>5</sub>R KO in a congenic background [83]. This well illustrates the point discussed in the first paragraph of this chapter, namely that small differences found when testing KO animals in mixed backgrounds (F2) might not be maintained in pure backgrounds. Congenic D<sub>5</sub>R KO mice were also found to perform as WT littermates in cocaine discrimination stimulus effect as well as in CPP for the same drug [83].

The response to drugs of abuse of DAR KO mice is summarized in Table 12.2.

**Table 12.2** Response to drugs of abuse of DAR KO mice

| DAR KO              | Responses to drugs of abuse                                       |  |  |
|---------------------|---|--|--|
|                     | Motor activity<br>(acute doses)                                   | CPP  | Self-administration  |
| D <sub>1</sub> R KO | Cocaine: Ø [71–73]  | Cocaine: + [81]  | Cocaine: Ø [82]<br>Ethanol: Ø [87]                                 |
| D <sub>2</sub> R KO | Cocaine: ↑ [91]   | Cocaine: + [91] (only<br>at high doses)<br>Morphine: Ø [88]                                  | Cocaine: + [98]<br>Ethanol: Ø [89, 96, 97]<br>Morphine: Ø [94, 95] |
| D <sub>3</sub> R KO | Cocaine: ↑↑ [52] (more<br>sensitive to low doses<br>than WT mice) | Morphine: + [104]<br>Amphetamine: + [52]<br>(more sensitive to<br>low doses than WT<br>mice) | Implicated: [109, 110]   |
| D <sub>4</sub> R O  | Cocaine: ↑↑↑ [62, 65]   | na   | na   |
| D <sub>5</sub> R KO | Cocaine: ↑ [83]   | Cocaine: + [83]  | na   |

References to the phenotype are indicated. The direction of changes is indicated with respect to WT animals exposed to similar conditions. +: positive response, Ø: no response, ↑: hyperactivity, ↔: same as WT, ↑: minimal response, na: not assessed.

## 12.6 Dopamine and Growth

The dopaminergic mesolimbic pathway is naturally involved in the motivational and rewarding mechanisms regulating food intake, thus interfering with growth and very likely with the development of obesity [114, 115]. The generation of KO mice has clarified some aspects of dopamine signaling in the control of this key function. Interestingly, KO mice for both the D<sub>1</sub>R and the D<sub>2</sub>R have shown that absence of each of the two receptors interferes with food intake and thereby with growth. Indeed, one of the principal features observed in D<sub>1</sub>R KO-A and B animals is a reduction of body weight and smaller brain size as compared to their WT littermates [41, 42]. D<sub>2</sub>R KO-A mice were also reported to eat less and have a reduction of body weight of 10–15% [23, 46, 47] when adult. These differences in food consumption and growth, however, although relevant do not impair the animal life and indeed both D<sub>1</sub>R and D<sub>2</sub>R mutants reach adulthood and have normal life span. Nevertheless,

when D<sub>1</sub>R and D<sub>2</sub>R genes are deleted simultaneously [20] the result is deadly and animals do not survive the second week after birth. These findings clearly show that D<sub>1</sub>R- and D<sub>2</sub>R-mediated signaling is crucial to regulate food intake, not only by regulating motivation but also by regulating gastrointestinal functions [20]. In agreement with these findings, KO of either D<sub>3</sub>Rs, D<sub>4</sub>Rs, or D<sub>5</sub>Rs does not interfere with either food intake or growth. Importantly, this also shows that D<sub>1</sub>R- and D<sub>2</sub>R-specific functions cannot be compensated by the activity of any of the other DARs, at least with respect to food intake. Future analyses should be performed to evaluate the role of D<sub>1</sub>R- and D<sub>2</sub>R-mediated signaling in the escalating search for food, which leads to obesity [114].

## 12.7 Future Challenges

A decade and a half after the publication of the first DAR KO model, it is now time to move forward and generate additional animal models that would allow an even more detailed analysis of the function of these receptors *in vivo*. Novel technologies and strategies have been developed to create cell- and region-specific KOs; this surely will expand the types of questions that can be addressed *in vivo*, as well as produce further insights into the complexity of the dopaminergic system. In addition, recently developed models [35, 38] and others to come might further help the understanding of the dopaminergic system with hopeful positive outcomes not only at the basic science levels but also for the development of more specific and efficient human therapies for the treatment of dopaminergic dysfunctions.

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# Chapter 13

## Dopamine Receptors and Behavior: From Psychopharmacology to Mutant Models

Gerard J. O'Sullivan, Colm O'Tuathaigh, Katsunori Tomiyama, Noriaki Koshikawa, and John L. Waddington

**Abstract** Elucidating the relative involvement of individual dopamine receptor subtypes in the regulation of behavior has been made difficult by anomalies at the psychopharmacology–molecular biology interface; specifically, the extent to which gene cloning has revealed greater diversity in dopamine receptor typology beyond the original D<sub>1</sub>/D<sub>2</sub> classification, to include individual members of D<sub>1</sub>-like (D<sub>1</sub> and D<sub>5</sub>) and D<sub>2</sub>-like (D<sub>2Short</sub>, D<sub>2Long</sub>, D<sub>3</sub>, and D<sub>4</sub>) families, has not been matched by similar progress in developing selective agonists and antagonists for these receptors. Thus, although classical psychopharmacological approaches have been instrumental in defining dopamine-dependent behaviors at the family level, more incisive molecular genetic techniques have been required to determine the functional roles of the individual members of these families. This chapter seeks to (a) summarize the classical psychopharmacology of dopamine receptor subtype function, (b) provide an overview of recent findings in dopamine receptor subtype knockouts across several domains of behavior, and (c) interpret new insights in the context of the limitations of these techniques and prior knowledge of the regulation of behavior by dopamine receptors.

**Keywords** Dopamine receptor subtypes · Behavior · Psychopharmacology · Selective agonists and antagonists · Molecular biology · Knockouts · Knockins · Transgenics · Mutant models

### 13.1 Introduction

Over the past 50 years it has been recognized that (a) dopaminergic neurons in the brain are topographically organized in four distinct populations, known as the nigrostriatal, mesolimbic, mesocortical, and tuberoinfundibular pathways and

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J.L. Waddington (✉)

Molecular and Cellular Therapeutics, Royal College of Surgeons in Ireland, Dublin 2, Ireland  
e-mail: jwadding@rcsi.ie

(b) these anatomical distinctions are, in broad terms, reflected in modulation of motoric, motivational, cognitive, and neuroendocrine functions, respectively [1, 2]. Furthermore, disruption of dopamine signaling is associated with a number of pathological conditions including schizophrenia, Parkinson's disease, and Huntington's disease, as detailed elsewhere in this book.

Elucidating the relative involvement of individual dopamine receptor subtypes in these processes and the identification of novel dopamine-mediated behaviors has been impeded by incongruence at the psychopharmacology–molecular biology interface [3]. Specifically, the extent to which gene cloning has revealed greater diversity in dopamine receptor typology beyond the original D<sub>1</sub>/D<sub>2</sub> classification, to include individual members of D<sub>1</sub>-like (D<sub>1</sub> and D<sub>5</sub>) and D<sub>2</sub>-like (D<sub>2Short</sub>, D<sub>2Long</sub>, D<sub>3</sub>, and D<sub>4</sub>) families, has not been matched by similar progress in developing selective agonists and antagonists for these receptors. Thus, although classical psychopharmacological approaches have been instrumental in defining dopamine-dependent behaviors at the family level, more incisive molecular genetic techniques have been required to determine the functional roles of the individual members of these families [4].

The profound impact of gene targeting on dopamine research is illustrated by the fact that within 10 years of its application to the field, knockout mice were created for dopamine [5], the dopamine transporter [6], each of the cloned mammalian dopamine receptor subtypes [1, 7–10], including splice variants of the D<sub>2</sub> receptor [11, 12], and discrete intracellular signal transduction coupling proteins [4].

During this period a number of reviews have described the evolution of findings in dopamine receptor knockouts at various levels of phenotypic investigation [1–4, 13–17]. With regard to dopaminergic regulation of behavior, recent reviews have evaluated findings in dopamine receptor knockouts in the context of a specific behavioral disorder [16] or a generalized perspective of behavioral roles for each receptor subtype [1]. We have offered comprehensive reviews on how studies in knockout mice have helped to elucidate the relative involvement of individual dopamine receptors in spontaneous and drug-induced unconditioned behavior [3, 4]. This chapter aims to elaborate upon these earlier reviews by (a) providing an update of recent behavioral findings in dopamine receptor knockouts, (b) describing additional findings from studies of conditioned and cognitive behavior in these mutants, and (c) placing these developments in the context of prior knowledge of dopamine receptor function in behavior.

## 13.2 Psychopharmacological Studies

A detailed account of findings obtained to date from behavioral studies using selective dopamine agonists and antagonists in intact vs. lesioned animals is voluminous and beyond the scope of this chapter. Reviews of basic concepts in the regulation of behavior by D<sub>1</sub>-like vs. D<sub>2</sub>-like receptors and by cooperative/synergistic and

oppositional D1-like:D2-like interactions are available [18–20]. Thus, we have chosen to focus primarily on behavioral modalities and psychopharmacological agents that have undergone complementary evaluation in dopamine receptor knockouts in an effort to facilitate the appraisal of behavioral findings using both approaches and the identification of dopamine receptor-specific functional roles. For example, we have previously investigated in rats the role of D1-like vs. D2-like receptors, their interactions and associated transduction mechanisms in the regulation of orofacial movements as a model system for studying these processes [21–24]. However, only by developing more incisive assessment systems applicable to mice [25–27] have we been able to exploit the potential of dopamine receptor subtype knockouts for elucidating the role of individual receptor subtypes in the regulation of specific topographies of orofacial movement.

### ***13.2.1 D1-Like Receptors and Behavior***

An early study found that the prototypical D1-like partial agonist SKF 38393 induced contralateral rotation in rats with unilateral lesions of substantia nigra [28]. Subsequent investigations in non-lesioned rodents demonstrated that SKF 38393 potently induced grooming behavior, including intense grooming syntax: a characteristic subset of generalized grooming where the animal grooms the snout and the face with the forepaws, followed immediately by vigorous grooming of the flank/anogenital area with the snout [29]. Syntactic, intense grooming has been well described in the ethological literature and appears to be modulated by a pattern generator site within the anterior dorsolateral striatum and expressed via the globus pallidus/ventral pallidum [30]. Induction of intense grooming behavior has since become a widely accepted behavioral index of D1-like receptor activation in rodents [18, 19, 31].

Low *in vivo* potency of SKF 38393 and only partial agonist activity at D1-like receptors in terms of stimulating dopamine-sensitive adenylate cyclase prompted the search for D1-like agonists with a more desirable pharmacological profile [18, 32]. Accordingly, several analogues of SKF 38393 were developed with varying efficacy to stimulate dopamine-sensitive adenylate cyclase [33, 34]. Behavioral studies using these agonists indicate that D1-like activation can, among others, alleviate motor deficits in animal models of Parkinson's disease [35], induce discrete topographies of orofacial movement [26], and reduce the reinforcing effects of cocaine [36]. Furthermore, studies using the selective D1-like antagonist SCH 23390 have identified functional roles for D1-like receptors in the cataleptic response to dopamine depletion [37] and in reward-related learning [38].

More recent work in our laboratories using two selective D1-like agonists with distinct biochemical effects indicates that subsets of D1-like-dependent behaviors are coupled to distinct intracellular signaling mechanisms [21–24, 39]. For example, SKF 83959, which fails to stimulate adenylate cyclase but stimulates phospholipase C-mediated intracellular calcium release via heterooligomerization with D<sub>2</sub> receptors [40], readily induces grooming and vacuous chewing that is sensitive to

antagonism by SCH 23390, together with other effects typical of D1-like receptor agonists [18]. Conversely, SKF 83822 which stimulates dopamine-sensitive adenylyl cyclase, but not phospholipase C, induces prominent seizures in mice in the absence of any material effect on grooming behavior [39].

The high degree of sequence homology that exists between D<sub>1</sub> and D<sub>5</sub> receptors translates into substantial similarity in their respective pharmacological profiles. Accordingly, at present no ligands have been identified which can materially differentiate these cloned receptor subtypes in terms of ligand-binding affinity or potency to stimulate adenylyl cyclase using recombinant cell lines. Ironically, dopamine itself is the most discriminating agent within the D1-like receptor family, demonstrating approximately tenfold higher affinity for the human D<sub>5</sub> receptor. Certain antagonists, including *cis* [Z]-flupentixol and [+]-butaclamol, exhibit seven- to tenfold lower affinity for D<sub>5</sub> than D<sub>1</sub> receptors. While these ligands can be used to differentiate D<sub>1</sub> and D<sub>5</sub> receptors in radioligand-binding studies and functional *in vitro* assays, none can be used reliably to determine subtype-specific functions *in vivo* [18].

### ***13.2.2 D2-Like Receptors and Behavior***

Early experiments with selective D2-like agonists, including quinpirole and quinlorane, found that activation of D2-like receptors induced circling behavior in rats with unilateral lesions in the basal ganglia [41]. Shortly thereafter, it was reported that the induction of locomotion and rearing by apomorphine in mice was mimicked by administration of RU 24213 alone [42], consistent with a fundamental role for D2-like receptors in facilitating movement-related behavior. Indeed, proven effectiveness of D2-like agonists in counteracting motor deficits in various animal models of Parkinson's disease initiated their use clinically, and D2-like agonists remain a primary strategy in treating the disease [43]. Other findings that several D2-like antagonists, including haloperidol and YM 09151-2, could attenuate apomorphine- or amphetamine-stimulated hyperactivity in rodents [44] provided indirect evidence for a fundamental role of D2-like receptors in the regulation of such behavior. Furthermore, reports that D2-like agonists and antagonists are, respectively, anti-convulsant and pro-convulsant, in epilepsy models [45] indicate an important role for D2-like receptors in modulating seizure threshold.

Despite extensive structural homology between D<sub>2</sub> and D<sub>3</sub> receptors, a number of compounds with high affinity and moderate selectivity for D<sub>3</sub> receptors have been developed. Low doses of the D<sub>3</sub>-preferring agonists 7-OH-DPAT and PD 128907 have been reported to reduce spontaneous activity in rats, whereas higher doses stimulate non-stereotyped sniffing, locomotion, and chewing [46, 47]. More recent findings from studies with 7-OH-DPAT suggest that D<sub>3</sub> receptors are additionally involved in discrete aspects of social behavior [48], anxiety [49], and attention [50]. Furthermore, convergent evidence from studies with D<sub>3</sub> antagonists indicates an important functional role for D<sub>3</sub> receptors in facilitating drug-seeking behavior [51]. Localization of D<sub>3</sub> receptors in cortico-limbic brain regions associated with

cognitive and emotional functions has provoked considerable interest in selective D<sub>3</sub> receptor antagonists as potential antipsychotic agents devoid of the extrapyramidal side effects linked to striatal D<sub>2</sub> receptor blockade [52].

The initial observation that the second-generation antipsychotic clozapine has higher affinity for D<sub>4</sub> vs. D<sub>2</sub> receptors stimulated interest in developing D<sub>4</sub> antagonists as putative therapies in the treatment of schizophrenia. While some pre-clinical studies suggested antipsychotic effects for selective D<sub>4</sub> antagonists, others found little or no effect. Moreover, a number of clinical trials have found that selective D<sub>4</sub> receptor antagonism is ineffective in alleviating psychotic symptoms in patients with schizophrenia [53]. Studies in our own laboratory have demonstrated that the selective D<sub>4</sub> receptor antagonists L 745,870 and RO 61-6270 do not influence spontaneous or D<sub>2</sub>-like agonist-induced motor behavior [54], suggesting that D<sub>4</sub> receptors might be involved in more discrete social and cognitive processes. Indeed, D<sub>4</sub> receptor blockade has been found to improve cognitive impairments in both rodents [55] and non-human primates [56]. Furthermore, Zhang and colleagues have reported that D<sub>4</sub> antagonists are effective in an animal model of attention deficit hyperactivity disorder [57]. More recently, a role for D<sub>4</sub> receptors in emotion has been suggested by the report that infusion of L 745,870 into the medial prefrontal cortex increases the percentage of open-arm entries and open-arm time in the elevated plus maze test for anxiety [58]. Furthermore, studies with the selective D<sub>4</sub> agonists PD 168,077 and RO 10-5824 have suggested functional roles for the D<sub>4</sub> receptor in memory consolidation [59] and novelty-seeking behavior [60], respectively.

### 13.3 D<sub>1</sub>-like Receptor Family

Among the five cloned dopamine receptor subtypes, the D<sub>1</sub> receptor gene was the first to successfully undergo targeted deletion by homologous recombination [10, 61]. Despite normal gross anatomy, brain architecture, and primitive reflexes, homozygous D<sub>1</sub> knockouts are significantly growth retarded, weighing on average 20–30% less than heterozygous knockout and wild type littermates [10, 61–63]. Five years later, mice lacking functional D<sub>5</sub> receptors were reported [15]. Homozygous D<sub>5</sub> knockouts are indistinguishable from wild types on gross inspection and display intact sensory abilities and neurological reflexes [64].

#### 13.3.1 D<sub>1</sub> Knockout: Spontaneous Behavior

Initial studies using D<sub>1</sub> knockouts maintained on a hybrid (129/Sv × C57BL/6) genetic background found that horizontal and vertical activity were markedly elevated in D<sub>1</sub> knockouts in both novel and familiar environments [10, 65]. In contrast, two subsequent studies using an independently created D<sub>1</sub> knockout line maintained on a similar hybrid genetic background observed reduced rearing, but normal locomotor activity, in D<sub>1</sub> knockouts relative to wild types [61, 66]. Conversely, a more

comprehensive behavioral evaluation of the same hybrid D<sub>1</sub> knockout line [63] and a third independently created D<sub>1</sub> knockout [67] demonstrated a modest reduction in the distance traveled by D<sub>1</sub> knockouts over a short period of assessment in a novel environment; however, a prominent delay in the initiation of movement was evident in D<sub>1</sub> knockouts upon initial exposure to the test arena in one of these studies, which likely contributed to the observed locomotor effect [63]. Another group has reported that hybrid D<sub>1</sub> knockouts exhibit reduced locomotion and rearing relative to wild types over 15 min in an open field but not over 60 min in an automated activity chamber [68]. In contrast, a more recent study by these investigators, using same knockout line backcrossed to C57BL/6 for two generations, demonstrated marked hyperactivity in D<sub>1</sub> knockouts in both novel and familiar environments [69]. Spontaneous hyperactivity has also been observed in hybrid D<sub>1</sub> knockouts over a longer time frame under habituated conditions [70], consistent with an inhibitory role for D<sub>1</sub> receptors in movement-related behavior. Studies in our own laboratory have confirmed and elaborated the hyperactive phenotype in mice lacking D<sub>1</sub> receptors. Specifically, using a comprehensive ethologically based behavioral assessment technique, hybrid D<sub>1</sub> knockouts were found to display increased sniffing and locomotion together with altered grooming during an initial period of exploration in a novel environment [71, 72]. Furthermore, we have shown that habituation of sniffing, locomotion, and rearing during the course of familiarization with an environment is profoundly retarded in congenic D<sub>1</sub> knockouts [62].

D<sub>1</sub> knockouts have also been examined in a number of behavioral paradigms designed to assess learning and reward. In the Morris water maze, hybrid D<sub>1</sub> knockouts exhibit a longer latency to locate a submerged escape platform [63, 66, 68], despite having a swim speed comparable to wild types and intact locomotor coordination [61, 63, 66]. Another study has found that hybrid D<sub>1</sub> knockouts require significantly more trials than wild types to learn an operant conditioning paradigm and demonstrate reduced responding for sucrose under various reinforcement schedules. Furthermore, D<sub>1</sub> knockouts were found to have a longer extinction time and impaired reversal learning following acquisition of the task [73]. More recently, impaired learning was observed in D<sub>1</sub> knockouts when the temporal relationship between reward-oriented behavior and reward retrieval was increased. Specifically, D<sub>1</sub> knockouts performed more poorly than wild types in the "triple T" maze in which a predetermined sequence of correct left-right turns is required to obtain a distal food reward [74]. Similar to the earlier report described above [73], the magnitude of the learning deficit in D<sub>1</sub> knockouts was greater when the required turn sequence was altered following acquisition of the task [74]. However, it may be that impaired learning in D<sub>1</sub> knockouts is context dependent, as they have been reported to perform normally in spontaneous alternation, passive avoidance, fear conditioning, and two odor discrimination paradigms [63, 66]. Evidence for blunted reward-related behavior in the absence of D<sub>1</sub> receptors has been provided by the recent report that D<sub>1</sub> knockouts travel less and obtain fewer brain stimulation rewards than controls in spatial learning tasks [67]. Indeed, more intense intracranial self-stimulation of the nucleus accumbens was required in D<sub>1</sub> knockouts to achieve wild type levels of responding in this study.

Additional studies have been performed in D<sub>1</sub> knockouts at other levels of behavioral investigation. With regard to dopaminergic regulation of spontaneous orofacial movements, congenic D<sub>1</sub> knockouts have been shown to display a marked reduction in horizontal jaw movements in the absence of any material alteration in vertical jaw movements, together with lower levels of tongue protrusions and incisor chattering [75]; an additional finding, that D<sub>1</sub>-like agonist-stimulated orofacial topographies are absent in D<sub>1</sub> knockouts, provides convincing evidence that D<sub>1</sub> receptors are indeed responsible for the observed phenotypic effects. Inconsistent findings have emerged in relation to the putative role for D<sub>1</sub> receptors in the behavioral manifestation of anxiety. In particular, one study found that hybrid D<sub>1</sub> knockouts spent less time in the more aversive open arms of the elevated plus maze than wild types and executed a reduced number of transitions between the open and closed arms [76], while other studies observed no effect of genotype in this test [68] or the light–dark paradigm [77].

### ***13.3.2 D<sub>1</sub> Knockout: Drug-Induced Behavior***

Pharmacological studies using selective D<sub>1</sub>-like and D<sub>2</sub>-like ligands in D<sub>1</sub> knockouts have helped to determine the relative involvement of D<sub>1</sub> vs. D<sub>5</sub> receptors in D<sub>1</sub>-like-dependent behaviors and to identify functional D<sub>1</sub>:D<sub>2</sub>-like interactions. Initial phenotypic characterization of hybrid D<sub>1</sub> knockouts revealed that the locomotor-stimulant effects of the selective D<sub>1</sub>-like agonist, SKF 81297, are abolished in the absence of D<sub>1</sub> receptors. Furthermore, catalepsy induced by the selective D<sub>1</sub>-like antagonist, SCH 23390, in the ring test was absent in D<sub>1</sub> knockouts [10]. More recently, we elaborated these findings by demonstrating that constituent behaviors in the ethogram of congenic D<sub>1</sub> knockouts are unaltered by a D<sub>1</sub>-like agonist or antagonist [62]. Despite inconsistent findings in relation to the level of spontaneous grooming behavior in D<sub>1</sub> knockouts [71, 78], characteristic induction of grooming by SKF 83959 is reduced in these mutants relative to wild types [62, 79]. Furthermore, grooming induced by cocaine and various neuropeptides is attenuated in D<sub>1</sub> knockouts [80, 81]. Additionally, the report that haloperidol-induced catalepsy is dose dependently exaggerated in D<sub>1</sub> knockouts [82] indicates that inhibitory D<sub>1</sub>:D<sub>2</sub>-like receptor interactions are involved in mediating the cataleptic response to D<sub>2</sub>-like receptor antagonism.

A significant body of evidence has accumulated supporting a role for D<sub>1</sub> receptors in the psychostimulant effects of cocaine. Specifically, locomotor activation in response to acute and repeated cocaine administration is absent in D<sub>1</sub> knockouts [65, 69, 78, 81, 83]. Furthermore, the prominent rearing and grooming response to repeated cocaine administration is markedly reduced in hybrid D<sub>1</sub> knockouts [81]. Although two studies have reported no difference between hybrid or incipient congenic D<sub>1</sub> knockouts and wild types in the cocaine conditioned place preference paradigm [69, 83], a recent study has demonstrated that hybrid D<sub>1</sub> knockouts exhibit impaired acquisition of cocaine self-administration [84]. The latter study also found that (a) wild types, but not D<sub>1</sub> knockouts, successfully recommence cocaine

self-administration following saline-induced extinction of responding and (b) selective agonists for D1-like or D2-like receptors function as positive reinforcers in wild types, but not D<sub>1</sub> knockouts.

Additional studies have investigated a role for D<sub>1</sub> receptors in the mechanisms of action of other commonly abused psychoactive substances. Indeed, independent observers have found that hybrid D<sub>1</sub> knockouts are unresponsive to the locomotor-stimulant effects of morphine and ketamine [85, 86]. Furthermore, two groups have reported a reduction in voluntary ethanol consumption and preference over water in hybrid D<sub>1</sub> knockouts relative to wild types, despite similar overall levels of fluid consumption across the genotypes [76, 87]. A specific role for D<sub>1</sub> receptors in these effects is supported by the observation that pretreatment with a selective D1-like antagonist produced a comparable level of alcohol consumption in wild type and D<sub>1</sub> knockout mice. Additionally, the finding that a selective D2-like antagonist reduced ethanol consumption in both genotypes indicates that cooperative D<sub>1</sub>:D2-like interactions are involved in the reinforcing properties of alcohol in mice [87].

Results obtained from studies investigating D<sub>1</sub> receptor involvement in the behavioral response to amphetamine are less consistent. Specifically, some investigators have observed reduced locomotor stimulation and sensitization in response to both acute and repeated treatment with amphetamine, respectively, in hybrid D<sub>1</sub> knockouts [81, 88]. In contrast, another group has found that locomotor sensitization to repeated amphetamine administration in hybrid D<sub>1</sub> knockouts is indistinguishable from wild types across a wide range of doses [89]. More recently, a marked increase in locomotor sensitization to repeated amphetamine has been observed in hybrid D<sub>1</sub> knockouts when assessed in a novel but not familiar environment [90]. Pretreatment with a selective D1-like antagonist has been found to block the development of locomotor sensitization in wild types but not D<sub>1</sub> knockouts [89]. Collectively, these findings have led to speculation that external associative factors and endogenous compensatory mechanisms (not involving D<sub>5</sub> receptors) may be responsible for the development of amphetamine-induced behavioral sensitization in D<sub>1</sub> knockouts [89, 90].

Novel findings in D<sub>1</sub> knockouts have revealed an important role for D<sub>1</sub> receptors in modulating seizure threshold. We have previously shown that the ability of selective D1-like agonists to induce seizures is critically dependent on their intracellular signal transduction coupling effects [39]. Specifically, the D1-like agonist, SKF 83822, which selectively stimulates adenylate cyclase, induces prominent behavioral seizures in mice, whereas SKF 83959, which selectively stimulates phospholipase C, does not (see Section 13.2.1). Interestingly, we have recently found that SKF 83822-induced behavioral and EEG seizures are gene dose dependently abolished in congenic D<sub>1</sub> knockouts; in addition, EEG seizures in response to SKF 83822 are markedly reduced in knockout mice lacking the intracellular signal integration molecule, DARPP-32; furthermore, administration of SKF 83822 in wild types produced a fivefold increase in DARPP-32 phosphorylation at Thr34 in striatal slices and twofold increases in ERK1/2 and GluR1 AMPA receptor phosphorylation in both the striatum and the hippocampus [91].

### ***13.3.3 Interpretation of D<sub>1</sub> Knockout Phenotype***

A summary of the behavioral changes reported to date from studies in D<sub>1</sub> knockouts can be seen in Table 13.1. Despite uncertainty concerning the involvement of D<sub>1</sub> receptors in unconditioned psychomotor activity from early studies in hybrid D<sub>1</sub> knockouts [10, 61, 63], it is now clear that spontaneous locomotor and rearing behavior are increased in D<sub>1</sub> knockouts relative to wild types [62, 69, 92]. A hyperactive phenotype in mice lacking D<sub>1</sub> receptors is surprising given that selective D<sub>1</sub>-like receptor antagonism induces profound locomotor suppression and catalepsy in intact rodents [4]. Such incongruity between findings from pharmacological and gene knockout studies is not easily reconciled, although radioligand-binding data showing that D<sub>5</sub>- and D<sub>2</sub>-like receptor expression is essentially unaltered in D<sub>1</sub> knockouts [10, 61, 65, 93] suggests that genetic compensation is not responsible. One possibility is that normally expressed D<sub>5</sub> receptors are supersensitive in mice lacking D<sub>1</sub> receptors, as manifested in spontaneous hyperactivity; indeed, modest hypoactivity is seen in congenic D<sub>5</sub> knockouts [94] (see Section 13.3.4). Paradoxically, locomotor stimulation in wild types following challenge with a selective D<sub>1</sub>-like agonist is absent in D<sub>1</sub> knockouts [10, 62, 91]. A ceiling effect on locomotion in D<sub>1</sub> knockouts (whereby phasic drug challenge cannot further stimulate spontaneous levels of activity) is unlikely, given that periods of behavioral inactivity are seen in D<sub>1</sub> knockouts under basal conditions [83]. Thus, it appears that D<sub>1</sub> receptors are critically involved in facilitating locomotion under phasic conditions.

Classical pharmacological studies in genetically intact rodents have shown that grooming behavior, and particularly ethologically complete grooming syntax, is controlled by activity at D<sub>1</sub>-like receptors. Therefore, findings that spontaneous grooming is only modestly reduced or even elevated in D<sub>1</sub> knockouts under different environmental conditions were surprising [62, 71, 72, 78]. However, similar to unconditioned locomotor activity, results from pharmacological studies in D<sub>1</sub> knockouts have been more consistent. Specifically, induction of grooming by SKF 83959 [62, 79], cocaine [81], and various neuropeptides [78] is attenuated in D<sub>1</sub> knockouts. Furthermore, Cromwell and colleagues have shown that sequencing of discrete patterns of grooming behavior is disrupted in mice lacking D<sub>1</sub> receptors [95]. Taken together, these findings indicate that D<sub>1</sub> receptor activation is indeed necessary for the expression of grooming behavior in mice. However, it should be mentioned that considering dopamine agonist-induced grooming is reduced, but not abolished, in D<sub>1</sub> knockouts, it is likely that other receptors are also involved. Indeed, we have recently found modest modulatory roles for D<sub>4</sub> and D<sub>5</sub> receptors in grooming behavior [94, 96] (see Sections 13.3.4 and 13.4.9).

Converging evidence indicates that D<sub>1</sub> receptors have an important functional role in shaping psychostimulant-induced reward-related behavior; that this is most evident for cocaine, but less so for amphetamine, raises the possibility that novel antagonists selective for D<sub>1</sub> receptors may be efficacious in the treatment of cocaine abuse. Precise reasons underlying the differential involvement of D<sub>1</sub> receptors in mediating the behavioral effects of two psychostimulants that are

**Table 13.1** Behavioral changes identified in dopamine receptor knockout mice

| Behavior                     | D1-like receptors          |                         |                                |                          |                                  | D2-like receptors       |                         |                         |  |
|------------------------------|----------------------------|-------------------------|--------------------------------|--------------------------|----------------------------------|-------------------------|-------------------------|-------------------------|--|
|                              | D <sub>1</sub> knockout    | D <sub>5</sub> knockout | D <sub>2</sub> knockout        | D <sub>2L</sub> knockout | D <sub>3</sub> knockout          | D <sub>3</sub> knockout | D <sub>4</sub> knockout | D <sub>4</sub> knockout |  |
| <b>Locomotion</b>            |                            |                         |                                |                          |                                  |                         |                         |                         |  |
| Spontaneous                  | ↑ [10, 62, 65, 69–72]      | ↓ [94]                  | ↓ [8, 108, 110, 111, 113, 114] | ↓ [11, 12, 141]          | ↑ [7, 68, 72, 144–146, 148, 149] |                         |                         | ↓ [9]                   |  |
| <b>Drug-induced</b>          |                            |                         |                                |                          |                                  |                         |                         |                         |  |
| D1-like agonist              | ↓ [63, 67]                 | ↑ [15]                  |                                |                          |                                  |                         |                         |                         |  |
| D2-like agonist              | ↓↓ [10, 62]                | ↓ [64]                  |                                | ↓ [11]                   |                                  |                         |                         |                         |  |
| Cocaine                      | ↓↓ [65, 69, 78, 81, 83]    | ↓ [104]                 |                                | ↓ [130]                  | ↑ [145, 156]                     |                         |                         | ↑ [9, 171]              |  |
| <b>Amphetamine</b>           | ↓ [81, 88]                 |                         |                                |                          | ↓ [155]                          |                         |                         |                         |  |
|                              | ↑ [90]                     |                         |                                | ↓ [141]                  | ↑ [157]                          |                         |                         | ↑ [172]                 |  |
| <b>Methamphetamine</b>       |                            |                         |                                |                          |                                  |                         |                         |                         |  |
| Apomorphine                  |                            |                         | ↓ [126]                        |                          |                                  |                         |                         | ↑ [9]                   |  |
| Morphine                     | ↓↓ [85]                    |                         |                                | ↓ [11, 141]              |                                  |                         |                         |                         |  |
| Ketamine                     | ↓↓ [86]                    |                         |                                |                          | ↑ [149]                          |                         |                         |                         |  |
| MDMA                         |                            |                         |                                |                          | ↓ [127]                          |                         |                         |                         |  |
| Caffeine                     |                            |                         | ↓ [123, 124]                   |                          |                                  |                         |                         |                         |  |
| <b>Rearing</b>               |                            |                         |                                |                          |                                  |                         |                         |                         |  |
| Spontaneous                  | ↑ [10, 62, 65, 69, 71, 72] | ↑ [15, 94]              | ↓ [8, 111]                     | ↓ [12]                   | ↑ [7, 68, 72, 144]               |                         |                         | ↓ [9]                   |  |
|                              | ↓ [61, 66]                 | ↓ [64]                  | ↑ [114]                        |                          |                                  |                         |                         |                         |  |
|                              | ↓ [81]                     | ↑ [94]                  |                                |                          |                                  |                         |                         |                         |  |
| <b>Drug induced Grooming</b> |                            |                         |                                |                          |                                  |                         |                         |                         |  |
| Spontaneous                  | ↓ [62, 72, 78]             | ↓ [94]                  |                                |                          |                                  |                         |                         |                         |  |
|                              | ↑ [71]                     |                         |                                |                          |                                  |                         |                         |                         |  |

**Table 13.1** (continued)

| Behavior                | D1-like receptors       |                         |                            | D2-like receptors        |                         |                         |  |
|-------------------------|-------------------------|-------------------------|----------------------------|--------------------------|-------------------------|-------------------------|--|
|                         | D <sub>1</sub> knockout | D <sub>5</sub> knockout | D <sub>2</sub> knockout    | D <sub>2L</sub> knockout | D <sub>3</sub> knockout | D <sub>4</sub> knockout |  |
| Drug-induced            |                         |                         |                            |                          |                         |                         |  |
| D1-like agonist         | ↓ [62, 79]              | ↓ [94]                  |                            |                          |                         | ↓ [96]                  |  |
| Cocaine                 | ↓ [81]                  |                         |                            |                          |                         |                         |  |
| Neuropeptide induced    | ↓ [80]                  |                         |                            |                          |                         |                         |  |
| Coordination            |                         | ↑ [15]                  | ↓ [8, 111, 114]            | ↓ [12, 137]              |                         | ↑ [9]                   |  |
| Catalepsy               |                         |                         | ↑ [8, 111]                 |                          |                         |                         |  |
| Spontaneous             |                         |                         |                            |                          |                         |                         |  |
| D1-like antagonist      | ↓↓ [10]                 |                         |                            |                          |                         |                         |  |
| D2-like antagonist      | ↑ [82]                  |                         | ↓ [122, 137]               | ↓ [11, 12, 142]          |                         |                         |  |
| Learning/memory         | ↓ [63, 66-68, 73, 74]   |                         | ↓ [114, 118-120]           | ↓ [137, 138]             | ↓ [121]                 |                         |  |
| Reward                  |                         |                         |                            |                          |                         |                         |  |
| Natural stimuli         | ↓ [67]                  |                         | ↓ [117]                    | ↓ [139]                  |                         |                         |  |
| Psychoactive drugs      | ↓ [76, 84, 87]          |                         | ↓ [116, 117, 130, 132-134] | ↓ [138]                  | ↑ [145, 149]            | ↑ [171]                 |  |
| Seizures                |                         |                         |                            |                          |                         |                         |  |
| D1-like agonist         | ↓↓ [91]                 | ↓ [91]                  |                            |                          |                         | ↓ [96]                  |  |
| Non-dopamine agonist    |                         |                         | ↑ [135, 136]               |                          |                         |                         |  |
| Novelty-seeking         |                         |                         |                            |                          |                         | ↓ [166]                 |  |
| Anxiety                 |                         |                         |                            |                          | ↓ [68, 144, 152]        |                         |  |
| Antidepressant activity |                         | ↑ [64]                  |                            |                          | ↑ [153]                 |                         |  |

**Table 13.1** (continued)

| Behavior            | D1-like receptors       |                         |                         | D2-like receptors       |                          |                         |                         |
|---------------------|-------------------------|-------------------------|-------------------------|-------------------------|--------------------------|-------------------------|-------------------------|
|                     | D <sub>1</sub> knockout | D <sub>5</sub> knockout | D <sub>5</sub> knockout | D <sub>2</sub> knockout | D <sub>2L</sub> knockout | D <sub>3</sub> knockout | D <sub>4</sub> knockout |
| Orofacial movements |                         |                         |                         |                         |                          |                         |                         |
| Horizontal jaw      | ↓ [75]                  | ↓ [103]                 | ↑ [103]                 | ↑ [115]                 |                          |                         |                         |
| Vertical jaw        |                         | ↑ [103]                 |                         | ↓ [115]                 |                          |                         |                         |
| Tongue protrusions  | ↓ [75]                  |                         |                         | ↓ [115]                 |                          |                         |                         |
| Incisor chattering  | ↓ [75]                  |                         |                         | ↓ [115]                 |                          | ↓ [115]                 |                         |
| Vibrissae           |                         | ↓ [103]                 |                         |                         |                          |                         |                         |

References are in square brackets

↑ or ↓: Behavior significantly increased or decreased, respectively, in knockout relative to wild types

↑↓: Evidence supporting the specified behavioral change in knockouts is insufficient or equivocal

↓↓: Behavioral change in wild type is abolished in knockout

each indirect agonists at dopamine receptors are currently unknown and warrant further investigation.

It is well recognized that dopaminergic mechanisms in general and D1-like receptors in particular are involved in mediating orofacial movements [18, 92]. Detailed understanding of the endogenous mechanisms that control orofacial movements is important given their criticality in consumptive behavior, self-care, offensive and defensive behaviors, vocalization and, in higher mammals, verbal and non-verbal communication [4]. Additionally, in the clinical setting, orofacial dyskinesia is a common and distressing side effect of certain antipsychotic drugs that requires resolution. The study of spontaneous and D1-like agonist-induced orofacial movements in D<sub>1</sub> knockouts has identified functional roles for D<sub>1</sub> receptors in positively modulating horizontal jaw movements, tongue protrusions, and incisor chattering. Furthermore, the finding that gross head movements in response to a selective D2-like agonist are excessive in D<sub>1</sub> knockouts suggests that the inhibitory D<sub>1</sub>:D2-like receptor interactions known to modulate certain dopamine-dependent behaviors also regulate discrete topographies of orofacial movement [75].

There is now strong evidence that the ability of certain D1-like agonists to lower seizure threshold is critically dependent on their stimulation of adenylate cyclase-coupled, rather than phospholipase C-coupled, signal transduction cascades [39] that involve DARPP-32 and ERK1/2 [91]. Indeed, it has recently been reported that ERK signaling at D<sub>1</sub> receptors occurs via an adenylate cyclase/protein kinase A/DARPP-32 pathway, as the ability of amphetamine to induce ERK activation is absent in DARPP-32 mutants [97]. Future studies examining the seizure profile in D<sub>1</sub> knockouts (a) following local administration of SKF 83822 in discrete brain regions and (b) in response to convulsant agents acting on glutamatergic, GABAergic, and cholinergic systems will clarify further the precise involvement of D<sub>1</sub> receptors in seizure processes.

Genetic manipulations other than conventional gene knockout by homologous recombination in embryonic stem cells have been performed in mice to alter the expression of D<sub>1</sub> receptors in an attempt to elucidate their functional roles in vivo. The first report of a transgenic mouse over-expressing D<sub>1</sub> receptors appeared in 1999. Two heterozygote D<sub>1</sub> transgenic lines were noted to have increased D<sub>1</sub> receptor-binding sites in extra-striatal regions. Spontaneous behavior and locomotor stimulation by amphetamine or cocaine was indistinguishable between D<sub>1</sub> transgenics and controls. Surprisingly, locomotor, rearing, and climbing responses to the selective D1-like agonist SKF 81297 in wild types were reversed, not potentiated, in mice over-expressing D<sub>1</sub> receptors [98]. A similar spontaneous hypokinetic phenotype in D<sub>2</sub> knockouts led these investigators to speculate that stimulation of over-expressed D<sub>1</sub> receptors may suppress D<sub>2</sub> receptor function in this model; however, a subsequent study in D<sub>1</sub> transgenic/D<sub>2</sub> knockout mice failed to support this hypothesis [99]. These findings are not easily reconciled with data described above from pharmacological studies in intact rodents or mice with targeted gene deletion of D<sub>1</sub> receptors. However, the random integration of transgenes into the host genome using conventional transgenic techniques, leading to regional and quantitative differences in protein expression, may be responsible for

the observed phenotype in D<sub>1</sub> transgenic mice. Future development of genetically engineered mice with enhanced promoter activity of the native D<sub>1</sub> receptor gene would help to resolve this issue and may provide novel insights into D<sub>1</sub> receptor function.

In a separate study, Drago and colleagues used an elegant approach to specifically ablate D<sub>1</sub> receptor-expressing cells in mice [100]. Although most heterozygote mutants harboring activated diphtheria toxin in the D<sub>1</sub> receptor gene died in the neonatal period, those that survived were characterized by dystonic posturing, myoclonic jerks, and marked bradykinesia relative to wild types, consistent with an important role for neurons expressing D<sub>1</sub> receptors in the control of movement. More recently these investigators have used a similar approach to create a separate mutant in which progressive ablation of D<sub>1</sub> receptor-expressing cells begins in the postnatal period [101]; unlike mice with congenital loss of D<sub>1</sub> receptor-expressing cells [100, 102], these mutants survive to adulthood and have normal gait and coordination. Postnatal loss of D<sub>1</sub> receptor-expressing cells was associated with hind limb dystonia, hyperactivity in both novel and familiar environments, impaired oral behavior, and spontaneous seizures [101]. While these models are invaluable pre-clinical research tools in the study of neurological disorders characterized by loss of discrete neuronal cell populations, such as Huntington's disease, direct phenotypic comparison with D<sub>1</sub> knockouts is complicated by the concomitant loss of other cellular constituents in cell ablation mutants.

### ***13.3.4 D<sub>5</sub> Knockout: Spontaneous Behavior***

A preliminary account of D<sub>5</sub> knockouts maintained on a hybrid genetic background (129/SvJ1 × C57BL/6) first appeared in a review article of dopamine receptor function. Hybrid D<sub>5</sub> knockouts evidenced significantly higher levels of horizontal and vertical activity in an open-field environment and outperformed their wild type counterparts in the rotarod test for locomotor coordination, leading to the suggestion that D<sub>5</sub> receptors normally act to depress or inhibit spontaneous motor behavior [15]. A subsequent more comprehensive assessment of hybrid D<sub>5</sub> knockouts evidenced incongruent phenotypic effects [64]. In contrast to the earlier report outlined above, spontaneous locomotor activity was unaltered in hybrid D<sub>5</sub> knockouts, while rearing activity was reduced in one batch of knockouts, but not another. Additionally, no differences were observed between D<sub>5</sub> knockouts and wild types in a test of locomotor coordination.

Phenotypic assessments of hybrid D<sub>5</sub> knockouts have also been carried out at other levels of behavioral investigation. The finding that hybrid D<sub>5</sub> knockouts perform normally in the light–dark box and elevated plus maze argues against a functional role for D<sub>5</sub> receptors in anxiety-related behavior [15, 64]. Furthermore, in the Morris water maze, D<sub>5</sub> knockouts were found to exhibit normal learning and spatial memory capabilities. Acoustic startle responses were found to be reduced in one batch of D<sub>5</sub> knockouts but not another; however, prepulse inhibition did not differ between the genotypes in either batch suggesting that the involvement of D<sub>5</sub>

receptors in gating responses to environmental stimuli, if any, is minimal and/or complex. A gender-specific genotypic effect in D<sub>5</sub> knockouts has been identified in the Porsolt forced swim test for antidepressant activity, with male D<sub>5</sub> knockouts exhibiting lower levels of immobility compared to male wild types in this behavioral paradigm [64].

To clarify the functional involvement of D<sub>5</sub> receptors in mediating spontaneous motor behaviors, we recently examined ethologically the phenotype of congenic D<sub>5</sub> knockout mice over the course of exploration and habituation in a novel environment. During the initial period of exploration, D<sub>5</sub> knockouts evidenced a modest reduction in locomotion and a modest increase in sifting (exploratory movements of the forepaws through the cage bedding), with no change in rearing or other behaviors relative to wild types. Over the course of subsequent habituation, topographical shifts in behavior revealed additional phenotypic differences in D<sub>5</sub> knockouts, specifically an overall reduction in the level of grooming and delayed habituation of rearing [94]. Furthermore, in a recent study to evaluate the involvement of D<sub>5</sub> receptors in mediating spontaneous orofacial movement topography, congenic D<sub>5</sub> knockouts were found to exhibit an increase in vertical jaw movements, which habituated more slowly than in wild types, together with a decrease in both horizontal jaw movements and movements of the vibrissae [103].

### ***13.3.5 D<sub>5</sub> Knockout: Drug-Induced Behavior***

As part of the original behavioral characterization of hybrid D<sub>5</sub> knockouts described in Section 13.3.4 above, Holmes and colleagues examined behavioral responsiveness to the selective D1-like agonist, SKF 81297, and the selective D1-like antagonist, SCH 23390. SKF 81297-induced horizontal activity was dose dependently reduced in hybrid D<sub>5</sub> knockouts over a 15-min period of assessment, while vertical activity did not differ between the genotypes. During the dark phase of rodent diurnal cycle, SCH 23390 was found to reduce horizontal and vertical activity indistinguishably between hybrid D<sub>5</sub> knockouts and wild types [64]. Collectively, these findings led the investigators to speculate that D<sub>5</sub> receptors might be involved in facilitating phasic D1-like receptor-mediated locomotor stimulation but not tonic baseline activity.

In 2003, Elliot and co-workers used hybrid D<sub>5</sub> knockouts to investigate the functional involvement of D<sub>5</sub> receptors in the locomotor and discriminative stimulus effects of cocaine. In an automated open-field environment, cocaine dose dependently stimulated horizontal activity over a 1-h period of assessment. Horizontal activity was gene dose dependently reduced in homozygous D<sub>5</sub> knockouts relative to wild types, consistent with a facilitative role for D<sub>5</sub> receptors in mediating the locomotor-stimulant effects of cocaine. In contrast, the ability to discriminate cocaine from saline did not differ between D<sub>5</sub> knockouts and wild types; the selective D1-like antagonist SCH 39166 was found to produce saline-appropriate cocaine responding in both genotypes [104]. Taken together, these

findings are consistent with a primary role for D<sub>1</sub>, but not D<sub>5</sub>, receptors in cocaine discrimination.

Recently, we assessed congenic D<sub>5</sub> knockouts in response to a range of selective D<sub>1</sub>-like agonists with varying efficacies to stimulate adenylate cyclase and/or phospholipase C, and the selective D<sub>2</sub>-like antagonist RU 24213 [94]. Administration of SKF 83959 characteristically induced a dose-dependent topographical shift in behavior from self-directed grooming at lower doses to prominent exploratory locomotion, sifting, and rearing at higher doses [62, 79, 96]. Whereas overall levels of grooming did not differ between the genotypes, episodes of ethologically complete syntactic, intense grooming were significantly reduced in D<sub>5</sub> knockouts. Challenge with SKF 83959 produced a reciprocal increase in rearing behavior in D<sub>5</sub> knockouts relative to wild types. Unexpectedly, characteristic induction of stereotyped "ponderous" locomotion by RU 24213 was dose dependently increased in D<sub>5</sub> knockout mice, indicating that inhibitory D<sub>5</sub>:D<sub>2</sub>-like receptor interactions participate in discrete dopamine-mediated behaviors [94].

Interestingly, recent evidence has emerged to support a role for D<sub>5</sub> receptors in modulating seizure threshold. Specifically, cortical EEGs were recorded in congenic D<sub>5</sub> knockouts in response to a dose of the selective D<sub>1</sub>-like agonist SKF 83822 previously shown to readily induce behavioral seizures in mice [39]. In both heterozygous and homozygous D<sub>5</sub> knockouts, the latency to first seizure was significantly increased relative to wild types. Furthermore, the total number of EEG seizures and, particularly, the number of high amplitude, high-frequency polyspike EEG events were reduced in D<sub>5</sub> knockouts [91].

### ***13.3.6 Interpretation of D<sub>5</sub> Knockout Phenotype***

A summary of the behavioral changes reported to date from studies in D<sub>5</sub> knockouts can be seen in Table 13.1. Inconsistent behavioral phenotypes observed in D<sub>5</sub> knockouts maintained on a hybrid (129/SvJ1 × C57BL/6) genetic background between and within laboratories [15, 64] have complicated elucidating the functional roles of the D<sub>5</sub> receptor. Reduction in rearing in one batch of hybrid D<sub>5</sub> knockouts but not another within the same study [64] suggests permutational differences in 129/SvJ1 and C57BL/6 alleles between mice rather than deletion of the D<sub>5</sub> receptor may have produced the observed effect. Indeed, reduced rearing activity is characteristic of 129/SvJ mice when compared directly with the C57BL/6 inbred strain [105]. Alternatively, it might be that D<sub>5</sub> receptors are minimally involved in mediating discrete behaviors and large numbers of animals are required to resolve these subtle effects. Regardless, it is difficult to determine with confidence the relevance of isolated behavioral changes, such as increased antidepressant activity and decreased acoustic startle responses, identified to date from studies using hybrid D<sub>5</sub> knockouts alone. Replicating these studies in congenic D<sub>5</sub> knockouts would provide a more conclusive understanding of the precise behavioral roles of the D<sub>5</sub> receptor and possibly identify novel functions.

Spontaneous locomotion and locomotor stimulation to a selective D1-like agonist or cocaine are reduced in both hybrid and congenic D<sub>5</sub> knockouts [64, 94, 104], providing convincing evidence for a facilitative role of D<sub>5</sub> receptors in ambulation. In contrast, both spontaneous and D1-like agonist-induced rearing are increased in congenic D<sub>5</sub> knockouts. The latter finding combined with the reported increase in spontaneous sifting in congenic D<sub>5</sub> knockouts over an initial period of exploration in a novel environment suggest a modest inhibitory role for D<sub>5</sub> receptors in mediating complex patterned exploratory behavior [92, 94]. Collectively, these findings in D<sub>5</sub> knockouts complement localization studies demonstrating D<sub>5</sub> receptor expression in discrete areas of the basal ganglia [106], a brain region well established in processing signals relating to motor coordination and exploratory behavior.

Interestingly, D<sub>1</sub> knockouts maintained on both hybrid and congenic backgrounds exhibit a contrasting spontaneous behavioral phenotype to that observed in congenic D<sub>5</sub> knockouts (see Section 13.3.1); they demonstrate increased locomotion and decreased sifting upon initial exploration of a novel environment [62, 71]. Therefore, despite similarities in their respective pharmacological and biochemical profiles, reciprocal functional organization might exist between D<sub>5</sub> and D<sub>1</sub> receptors to regulate discrete topographies of behavior. In support of this hypothesis, opposing roles of D<sub>5</sub> and D<sub>1</sub> receptors in modulating locomotor behavior have been identified through the use of selective antisense oligonucleotide strategies in 6-OHDA-lesioned rats [107]. However, evidence from the study of orofacial movements in individual D<sub>1</sub> and D<sub>5</sub> knockout lines suggests that cooperative functional organization also exists within the D1-like receptor family. Specifically, both D<sub>1</sub> and D<sub>5</sub> receptors inhibit spontaneous vertical jaw movements and facilitate spontaneous horizontal jaw movements in mice, albeit with functional prepotency of the D<sub>1</sub> receptor [75, 92, 103]. The recent finding that characteristic induction of stereotyped “ponderous” locomotion following challenge with a selective D2-like agonist occurs to excess in congenic D<sub>5</sub> knockouts [94] indicates that D<sub>5</sub> receptors also interact functionally with D2-like receptors to modulate behavior. How such inhibitory D<sub>5</sub>:D2-like receptor interactions are organized within the brain at a molecular, cellular, or network level and the relative involvement of D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub> receptors remains to be established.

In congenic D<sub>5</sub> knockouts, spontaneous and drug-stimulated grooming behavior is reduced [94]. A critical role for D1-like receptors in regulating grooming is well recognized. Given promotion by D1-like agonists, attenuation by D1-like antagonists, and attenuation in congenic D<sub>1</sub> knockouts (see Section 13.3.2), it has traditionally been assumed that D<sub>1</sub> receptors play a primary, if not, exclusive role in regulating grooming on the basis of their dense localization relative to D<sub>5</sub> counterparts in brain regions such as the dorsolateral striatum that are known to mediate grooming [3, 4]. However, recent findings in congenic D<sub>5</sub> knockout mice indicate this conclusion to have been premature; both D<sub>1</sub> and D<sub>5</sub> receptors appear to be involved in the expression of grooming [94]. Furthermore, reduction in syntactic intense grooming, but not overall grooming events, in response to the selective D1-like agonist SKF 83959 implies a functional role for D<sub>5</sub> receptors in generating

sequential grooming movements, as distinct from grooming initiation. A comparable, more profound behavioral phenotype has also been observed in both hybrid and congenic D<sub>1</sub> knockout mice [62, 95]. Interestingly, lesion mapping studies in rats have identified the dorsolateral neostriatum as crucial for the induction of sequential grooming behavior without disrupting the ability to emit grooming actions [30]. This, together with the report that D<sub>5</sub> and D<sub>1</sub> receptor immunolocalization is found throughout the neostriatum in both rats and non-human primates [106], suggests that intact D<sub>1</sub> and D<sub>5</sub> receptor signaling within this region is necessary for the induction of sequential grooming behavior.

The recent finding in congenic D<sub>5</sub> knockouts that D<sub>5</sub> receptors participate in the induction of seizures by selective D<sub>1</sub>-like agonists [91] elaborates an earlier pharmacological study utilizing D<sub>1</sub>-like antagonists which could not determine the relative anticonvulsant properties of the individual D<sub>1</sub>-like receptors [39]. A functional role for D<sub>5</sub> receptors in the mechanisms of seizure generation by selective D<sub>1</sub>-like agonists has previously received little attention due to the well-established preponderance of D<sub>1</sub> vs. D<sub>5</sub> receptor expression in both cortical and striatal brain regions. Indeed, as the overall number of EEG seizures is reduced similarly in both heterozygous and homozygous D<sub>5</sub> knockouts, it would appear that, unlike for D<sub>1</sub> receptors (see Section 13.3.2), decreasing the level of D<sub>5</sub> receptor expression beyond 50% does not enhance the seizure protective effect. Regardless, these EEG findings in congenic D<sub>5</sub> knockouts have revealed a modest functional role for the D<sub>5</sub> receptor in mediating the convulsant effects of SKF 83822 that could not be determined using behavioral assessment alone [94].

## 13.4 D<sub>2</sub>-Like Receptor Family

Shortly after the generation of the first D<sub>1</sub> knockouts, mice lacking functional D<sub>2</sub> receptors were reported [8]. The introduction of a premature stop codon in exon 2 of the D<sub>2</sub> receptor gene prevented the expression of either short or long splice variants of the D<sub>2</sub> receptor protein. Other “complete” D<sub>2</sub> knockouts have since been created [108–110], followed by mutants with selective knockout of the long isoform (D<sub>2L</sub>) of the D<sub>2</sub> receptor protein [11, 12]. Successful deletion of the D<sub>3</sub> receptor gene in mice was reported initially in 1996 [7], while D<sub>4</sub> knockouts emerged the following year [9].

### 13.4.1 D<sub>2</sub> Knockout: Spontaneous Behavior

In 1995, the first “complete” D<sub>2</sub> knockout constructed on a hybrid (129/SvJae × C57BL/6) genetic background was found to exhibit multiple physical and movement-related abnormalities. Specifically, during a 5-min period of assessment in an open field, D<sub>2</sub> knockouts were characterized by hypoactivity and a marked reduction in exploratory rearing behavior; posture, gait, and motor coordination were also abnormal in these mutants. Furthermore, D<sub>2</sub> knockouts demonstrated less

mobility on the ring test used for the assessment of catalepsy in mice [8]. The following year, as part of a study evaluating the functional involvement of  $D_2$  receptors in regulating pituitary hormone secretion, hybrid (129/Sv  $\times$  BDF1),  $D_2$  knockouts created using a different gene targeting vector were similarly found to be hypoactive relative to wild types and to exhibit abnormal gait [110]. Consistent with these earlier reports, a third hybrid (129/Sv  $\times$  C57BL/6)  $D_2$  knockout line evidenced reduced body weight, hunched posture, and bradykinesia; surprisingly, the magnitude of these deficits was noted to improve significantly with increasing age [108]. In an experiment to investigate the effect of heterogeneity in the genetic background on mutant phenotypes, a fourth  $D_2$  knockout line [109] was examined on the original hybrid (129/SvEv  $\times$  C57BL/6) genetic background and also following multiple backcrosses to each of the parental strains. Profound deficits in motor coordination were observed in hybrid  $D_2$  knockouts and the parental 129/SvEv strain, but not incipient congenic C57BL/6  $D_2$  knockouts, leading these investigators to conclude that strain-related differences, not deletion of the  $D_2$  receptor, were responsible for the ataxia [111].

Realization that genetic background is a potential confounder in the interpretation of mutant phenotypes prompted additional studies in  $D_2$  knockouts at increasing levels of congenicity. Indeed, in contrast to previous findings in hybrid  $D_2$  knockouts [8, 110], postural abnormalities, spontaneous catalepsy, or tremor were not observed in  $D_2$  knockouts comprising mainly C57BL/6 alleles [111, 112]. A more consistent effect of  $D_2$  receptor deletion has been shown in relation to other movement-related behaviors. Specifically, we have demonstrated that, in agreement with their hybrid counterparts, incipient congenic  $D_2$  knockouts exhibit a modest reduction in spontaneous locomotion and qualitative shifts in discrete topographies of rearing relative to wild types over an initial period of exploration in a novel environment [113]. Furthermore, reduced locomotion and increased topographies of rearing have also been described in congenic  $D_2$  knockouts [114]; an additional finding that poor performance in congenic  $D_2$  knockouts on the rotarod is unrelated to parental strain indicates that absence of  $D_2$  receptors is indeed responsible for the observed deficit in motor coordination [114] and not epistasis, as previously suggested [111]. In relation to dopaminergic regulation of spontaneous orofacial movements, we have recently shown that incipient congenic  $D_2$  knockouts are characterized by increased vertical jaw movements and unaltered horizontal jaw movements, with reductions in tongue protrusions, incisor chattering, and head movements relative to wild types [115], consistent with both facilitative and inhibitory roles for  $D_2$  receptors in discrete topographies of orofacial movement.

$D_2$  knockouts have also been used to investigate the involvement of  $D_2$  receptors in learning and reward-related behavior. In relation to the latter, an early study found no difference between hybrid  $D_2$  knockouts and wild types in a conditioned place preference paradigm where food was available as a reward [116]. Conversely, in a more recent study using congenic  $D_2$  knockouts where mice were trained to self-stimulate the lateral hypothalamus, stronger electrical currents were necessary to achieve a stable level of operant responding in mutants [117]; deficits have also been identified in  $D_2$  knockouts in the acquisition of a task where intracranial

stimulation was available as a reward [118], indicating that reinforcement processes are impaired in the absence of D<sub>2</sub> receptors. A more consistent picture has emerged with regard to D<sub>2</sub> receptor involvement in associative learning. Specifically, one study has shown that congenic D<sub>2</sub> knockouts require more trials than wild types to achieve stable operant responding in a conditioned place preference paradigm [114]. More recently, impaired associative learning has been reported in congenic D<sub>2</sub> knockouts in a two-odor discrimination paradigm; in particular, whereas female, but not male, D<sub>2</sub> knockouts exhibited poor ability to discriminate between two odors to obtain a food reward [119], both genders required significantly more trials than wild types to demonstrate reversal learning of the task [120]. However, the possibility that reinforcement mechanisms are disturbed in D<sub>2</sub> knockouts renders it difficult to distinguish between the effects of D<sub>2</sub> receptor knockout on reinforcement vs. acquisition of cue value via associative learning.

In a delayed alternation paradigm, incipient congenic D<sub>2</sub> knockouts were characterized by impairments in spatial working memory, as determined by their inability to enter the correct arm on a T maze, when progressive time delays were introduced before commencing a previously learned task [121].

### ***13.4.2 D<sub>2</sub> Knockout: Drug-Induced Behavior***

A number of studies have examined D<sub>2</sub> knockouts following challenge with selective D1-like or D2-like agonists to further characterize the mechanisms through which functional dopamine receptor interactions modulate behavior and to identify additional behavioral phenotypes that might have been masked under basal conditions. In dopamine-depleted mice, combined administration of a selective D1-like and D2-like agonist but not the selective D1-like agonist alone was found to reverse locomotor deficits in wild types but not hybrid D<sub>2</sub> knockouts [111], indicating that cooperative D1-like:D<sub>2</sub> receptor interactions are necessary for the production of spontaneous ambulatory behavior. Our own finding that characteristic induction of stereotyped sniffing and ponderous locomotion in response to high doses of the selective D2-like agonist RU 24213 was markedly reduced in incipient congenic D<sub>2</sub> knockouts [113] provides additional evidence that D<sub>2</sub> receptors are involved in mediating discrete dopamine-dependent behaviors. Indeed, haloperidol-induced catalepsy is gene dose dependently abolished in both hybrid and incipient congenic D<sub>2</sub> knockouts [111, 122], indicating that among D2-like receptors, selective D<sub>2</sub> receptor blockade is responsible for the emergence of extrapyramidal side effects that frequently complicate the use of first-generation antipsychotic drugs. It also appears that D<sub>2</sub> receptors participate in inhibitory dopamine receptor processes to modulate particular behaviors. Specifically, Boulay and colleagues have shown that the D<sub>2</sub>/D<sub>3</sub> agonists 7-OH-DPAT and PD 128907 reduce locomotor activity in wild types but not incipient congenic D<sub>2</sub> knockouts in a gene dose-dependent manner [112]. Furthermore, we have found that incipient congenic D<sub>2</sub> knockouts exhibit heightened orofacial movements, termed vacuous chewing, when compared with wild types following challenge with the selective D1-like agonist A 68930 [113].

Such findings are most readily explained by the absence in  $D_2$  knockouts of  $D_2$  receptors that exert inhibitory effects on these functions. Pharmacological studies in  $D_2$  knockouts have also identified functional interactions between dopamine and other neuromodulators. Specifically, the locomotor-stimulant effects of the adenosine  $A_{2A}$  receptor antagonist caffeine are attenuated in  $D_2$  knockouts [123, 124]. Furthermore, a selective adenosine  $A_{2A}$  receptor agonist has been shown to reduce spontaneous and amphetamine-stimulated locomotion in  $D_2$  knockouts and wild types [123]. Taken together, these findings are consistent with antagonistic and independent roles for dopamine  $D_2$  and adenosine  $A_{2A}$  receptors in controlling discrete motor functions.

Generation of  $D_2$  knockout mice has enabled researchers to investigate a putative role for  $D_2$  receptors in the locomotor-modulating effects of various drugs of abuse. With regard to opiates, separate findings in hybrid [116] and congenic [125]  $D_2$  knockouts do not support a role for  $D_2$  receptors in morphine-induced hyperactivity. Conversely, the opioid antagonist naloxone has been shown to suppress spontaneous locomotor activity in wild types but not congenic  $D_2$  knockouts. Interestingly, naloxone was found to similarly reduce basal locomotion in  $\beta$ -endorphin knockouts but not in enkephalin knockouts or  $\beta$ -endorphin/enkephalin double knockouts. Collectively, these findings indicate that  $D_2$  receptors are involved in modulating spontaneous locomotor activity stimulated by the endogenous opioid enkephalin [125]. Unlike morphine, the locomotor-stimulant effects of methamphetamine and MDMA are reduced in congenic  $D_2$  knockouts [126, 127]. Furthermore, ethanol-induced ataxia is reduced in  $D_2$  knockouts of incipient congenicity on either a C57BL/6 or a 129/Sv background [128, 129]. To date, no consensus has been reached concerning  $D_2$  receptor involvement in cocaine-induced hyperactivity, with one study demonstrating reduced locomotor activity in hybrid  $D_2$  knockouts [130] and another showing no difference between congenic  $D_2$  knockouts and controls [131].

Other studies have evaluated drug-seeking behavior in  $D_2$  knockout mice. Two groups have shown that morphine-induced conditioned place preference is absent in both hybrid and congenic  $D_2$  knockouts under different reinforcement schedules [116, 132]. Furthermore, although morphine-induced conditioned place preference was unaltered in drug-naïve incipient congenic  $D_2$  knockouts, opiate withdrawal and dependent  $D_2$  knockouts did not show place preference for morphine [133]. More recently, morphine has been shown to potentiate the rewarding properties of self-administered hypothalamic brain stimulation in wild types but not congenic  $D_2$  knockout mice. Interestingly, a similar effect of  $D_2$  receptor deletion was not observed for amphetamine using identical experimental techniques [117]. In relation to cocaine, high, but not low, doses have been found to increase levels of self-administration [134] and induce conditioned place preference [130] in hybrid  $D_2$  knockouts. Furthermore, the abilities of selective  $D_2$ -like antagonists and agonists, respectively, to increase cocaine self-administration and serve as cocaine substitutes in wild types are absent in hybrid  $D_2$  knockouts [134]. Collectively, these findings suggest that although  $D_2$  receptors are not essential for cocaine self-administration, they are involved in positively modulating the rewarding effects of this drug.

Finally, additional studies in D<sub>2</sub> knockouts have evaluated the role of D<sub>2</sub> receptors in seizure processes. Interestingly, although D<sub>2</sub> knockouts do not evidence spontaneous behavioral seizures, Bozzi and colleagues have demonstrated that hybrid D<sub>2</sub> knockouts develop seizures at doses of kainic acid and pilocarpine that do not affect seizure threshold in wild types. Furthermore, seizure-related neuronal cell death in response to these agents was reduced in D<sub>2</sub> knockouts [135, 136]. These findings, when considered with recent results from seizure studies in D<sub>1</sub> knockouts [91] (see Section 13.3.2), indicate that D<sub>1</sub> and D<sub>2</sub> receptors have important functional roles in lowering and elevating seizure threshold, respectively.

### 13.4.3 *D<sub>2L</sub> Knockout*

In 2000, two reports emerged describing the spontaneous behavioral phenotype in mice with selective knockout of the long isoform (D<sub>2L</sub>) of the D<sub>2</sub> receptor [11, 12]. In the first study, no difference was found in locomotor activity between D<sub>2L</sub> knockouts and wild types over a period of exploration in a novel environment [11]. Conversely, in the second study, locomotion and rearing were reduced in both hybrid and incipient congenic D<sub>2L</sub> knockouts over 5 min of assessment in an open field. Furthermore, latency to fall from the rotarod was significantly reduced in incipient congenic D<sub>2L</sub> knockouts on the first trial but not during subsequent trials [12]. Additional evidence for movement-related abnormalities in D<sub>2L</sub> knockouts has been provided by a study comparing incipient congenic mutants and wild types at various developmental stages [137]. Interestingly, deficits in locomotion and coordination in young adult D<sub>2L</sub> knockouts mirrored those in aged, but not young, wild types, consistent with a Parkinsonian-like phenotype in D<sub>2L</sub> mutants in a manner similar to that previously suggested in “complete” knockout mice [8].

D<sub>2L</sub> knockouts have also been used to determine the relative contribution of individual D<sub>2</sub> receptor isoforms to other dopamine-dependent behaviors. In relation to associative learning, a significant impairment has been observed in incipient congenic D<sub>2L</sub> knockouts in the acquisition of a conditioned avoidance task [137, 138], suggesting that D<sub>2L</sub> receptors participate in the behavioral response to aversive stimuli. Additional evidence has emerged supporting the involvement of D<sub>2L</sub> receptors in reward-related behavior. Specifically, in the pleasurable wheel-running paradigm, incipient congenic D<sub>2L</sub> knockouts were found to perform fewer wheel turns than wild types, in the absence of any detectable difference between the genotypes on the rotarod, suggesting that blunted reward and not impaired motor coordination was responsible for the observed effect [139].

Other investigators have investigated D<sub>2L</sub> receptor involvement in the regulation of discrete emotion-driven behaviors. There were no difference between D<sub>2L</sub> knockouts and wild types in terms of general activity or open sector entries on the zero maze, indicating that D<sub>2L</sub> receptors are not involved in the behavioral manifestation of anxiety [137]. In support of this finding, a separate study found no difference in defecation between the genotypes following exposure to a stressful environment [138]. In fact, hybrid D<sub>2L</sub> knockouts have been characterized by

a lower bite frequency and shorter attack duration than wild types in the resident intruder test, consistent with attenuated stress-induced offensive aggression in these mutants [140].

Many of the pharmacological studies conducted in “complete” D<sub>2</sub> knockouts have also been performed in D<sub>2L</sub> knockouts. A low dose of the selective D<sub>2</sub>-like agonist quinpirole suppressed locomotion in hybrid D<sub>2L</sub> knockouts but not wild types [11]. Conversely, in an alternative hybrid D<sub>2L</sub> knockout line, a similarly low dose of quinpirole was not associated with an observable genotypic difference in locomotion [12]; however, methodological differences in the time between injection of the drug and commencing behavioral assessments may explain the discrepant findings between these two studies. Locomotor stimulation by the non-selective dopamine receptor agonist apomorphine and the selective D<sub>1</sub>-like agonist, SKF 81297 were also markedly reduced in D<sub>2L</sub> knockouts [11]. More recently, it has been reported that climbing behavior induced by amphetamine, apomorphine, and combined D<sub>1</sub>-like and D<sub>2</sub>-like agonists is significantly attenuated in incipient congenic D<sub>2L</sub> knockouts. In addition, a higher level of stereotyped non-offensive biting was observed in D<sub>2L</sub> knockouts than wild types in response to the combined administration of quinpirole and SKF 81297, but not when these agonists were administered individually [141] leading these authors to speculate that cooperative D<sub>1</sub>-like/D<sub>2L</sub> and D<sub>1</sub>-like/D<sub>2S</sub> receptor interactions are involved in mediating locomotor and stereotyped behavior, respectively. A number of studies have shown that catalepsy induced by the antipsychotics haloperidol and raclopride is essentially abolished in both hybrid and incipient congenic D<sub>2L</sub> knockouts [11, 12, 142]. Furthermore, locomotor suppression following challenge with these antagonists in wild types is attenuated in D<sub>2L</sub> knockouts [12, 142].

In relation to D<sub>2L</sub> receptor involvement in mediating behavioral responsiveness to drugs of abuse, one study has shown that the locomotor-stimulant effect of morphine is unaltered in incipient congenic D<sub>2L</sub> knockouts. In contrast, conditioned place preference for morphine and conditioned place avoidance induced by naloxone-precipitated morphine withdrawal was disrupted in D<sub>2L</sub> knockouts [138]. Taken together, these results suggest that while D<sub>2L</sub> receptors do not appear to participate in morphine-induced hyperactivity, they are important in the rewarding properties of morphine and aversive properties of opiate withdrawal. Interestingly, additional findings that cocaine-induced locomotor stimulation is moderately reduced [130] while cocaine conditioned place preference is unaltered in D<sub>2L</sub> knockouts [130, 138] indicate that D<sub>2L</sub> receptors may have different functional roles for individual drugs of abuse.

#### ***13.4.4 Interpretation of D<sub>2</sub> and D<sub>2L</sub> Knockout Phenotypes***

A summary of the behavioral changes reported to date from studies in D<sub>2</sub> and D<sub>2L</sub> knockouts can be seen in Table 13.1. The availability of independent knockout lines lacking both short and long isoforms of the D<sub>2</sub> receptor or selective

deletion of the latter allows systematic comparison of results obtained from studies in these mutants to identify isoform-specific D<sub>2</sub> receptor functions. Before discussing the results from studies in D<sub>2L</sub> knockouts and their contribution to our understanding of D<sub>2</sub> receptor function at the level of behavior, it should be mentioned that, as expected, northern blot analysis in both of the original D<sub>2L</sub> knockout lines revealed no difference in D<sub>2</sub> receptor mRNA between knockouts and wild types [11, 12]. Therefore, the short isoform of the D<sub>2</sub> receptor is over-expressed in D<sub>2L</sub> knockouts and may be functionally relevant. In an elegant approach to resolve this issue, Centonze and colleagues mated "complete" D<sub>2</sub> knockouts and D<sub>2L</sub> knockouts to achieve more physiological levels of D<sub>2S</sub> receptor expression [143]; however, this strategy has not been adopted in behavioral studies to date.

Initial phenotypic characterization of D<sub>2</sub> knockouts on a hybrid genetic background exhibited some of the clinical features found in Parkinson's disease, leading the originators to speculate that the D<sub>2</sub> knockout mouse constitutes a reliable model of the human neurodegenerative condition [8]. However, subsequent studies have failed to identify abnormal posture, gait, or spontaneous tremor in incipient or fully congenic D<sub>2</sub> knockouts [111, 112]. Despite these inconsistencies, converging evidence indicates that spontaneous locomotion and coordination are significantly reduced in D<sub>2</sub> knockouts [8, 108, 110, 111, 113, 114]. More detailed assessment of locomotion in D<sub>2</sub> knockouts has revealed that initiation of movement, time spent in motion, and distance traveled are all decreased in these mutants [111]. Thus it would appear that akinesia rather than bradykinesia is responsible for spontaneous hypoactivity in D<sub>2</sub> knockouts. Interestingly, similar locomotor and coordination deficits have been observed in D<sub>2L</sub> knockouts [11, 12, 137], indicating that the long isoform of the D<sub>2</sub> receptor may be responsible for movement-related phenotypes in D<sub>2</sub> knockouts.

A comparative study between congenic D<sub>2</sub> knockouts and the inbred 129/Sv and C57BL/6 parental strains has identified additional D<sub>2</sub> receptor-dependent behaviors that are unrelated to genetic background effects [114]. First, rearing directed toward the walls of the testing apparatus is significantly increased in D<sub>2</sub> knockouts. Excessive rearing confined to the perimeter of the cage together with reduced locomotion could indicate increased anxiety in D<sub>2</sub> knockouts. However, D<sub>2</sub> or D<sub>2L</sub> knockouts do not exhibit increased defecation during exploration of an unfamiliar environment [138, 144] and D<sub>2L</sub> knockouts are indistinguishable from wild types on the zero maze [137], consistent with normal levels of anxiety in these mutants. Furthermore, our finding that D<sub>2</sub> knockouts are characterized by significant shifts in multiple topographies of rearing during the course of habituation to a novel environment [113] indicates that D<sub>2</sub> receptor involvement in rearing is more complex and cannot be loosely classified as either facilitative or inhibitory. Second, D<sub>2</sub> knockouts are supersensitive to the tremor-inducing effect of the indole alkaloid, harmaline [114]. It is possible that increased tremor may be due to known learning deficits in D<sub>2</sub> knockouts [114, 118–120] in a manner where movement-induced tremor acts as an aversive stimulus in wild type mice. Alternatively, increased tremor may

represent phasic exacerbation of Parkinsonian-like abnormalities in D<sub>2</sub> knockouts that are compensated for under tonic conditions.

Induction of catalepsy in rodents is a characteristic feature of antipsychotics whose pharmacological effects are mediated via selective antagonism at D<sub>2</sub>-like receptors. It is generally accepted that antipsychotics with low potency to induce catalepsy are associated with fewer extrapyramidal side effects that frequently complicate the treatment of psychosis. Interestingly, haloperidol-induced catalepsy is markedly reduced in D<sub>2</sub> knockouts [111, 122], suggesting that, within the D<sub>2</sub>-like family, D<sub>2</sub> receptors are predominantly involved in the cataleptic response to typical antipsychotics. Similar observations in D<sub>2L</sub> knockouts [11, 12, 142] indicate that the long isoform of the D<sub>2</sub> receptor may be responsible for the induction of cataleptic behavior. It therefore remains possible that novel antagonists with preferential affinity for D<sub>3</sub> receptors may retain therapeutic efficacy in treating psychosis in the absence of motoric side effects.

The extent to which D<sub>2</sub> receptors modulate locomotor activity induced by psychostimulants is less clear. While D<sub>2</sub> receptors appear to facilitate hyperactivity induced by caffeine, methamphetamine, and MDMA [123, 124, 126, 127], they do not appear to modulate locomotor stimulation induced by morphine [116, 125] or cocaine [130, 131]. Conversely, there is convincing evidence that D<sub>2</sub> receptors are important, but not essential, in the reinforcing properties of both morphine [116, 117, 132, 133] and cocaine [130, 134]. Interestingly, D<sub>2</sub> receptors do not appear to participate in the rewarding effects of amphetamine [117] and D<sub>2L</sub> receptors appear to be differentially involved in the mechanisms of action of various drugs of abuse [130, 138], highlighting the complexity of neural processes underpinning substance abuse-related behavior. It should be noted that learning and coordination deficits in D<sub>2</sub> and D<sub>2L</sub> knockouts [8, 12, 111, 114, 118–120, 137, 138] may impair performance in operant conditioning paradigms that are frequently employed in substance abuse studies.

Pharmacological studies using selective dopamine agonists in D<sub>2</sub> and D<sub>2L</sub> knockouts have broadened our understanding of the mechanisms through which D<sub>2</sub> receptors functionally interact with their D<sub>1</sub>-like counterparts to modulate locomotor behavior. Findings that locomotor stimulation by indirect and non-selective dopamine agonists is attenuated in both D<sub>2</sub> and D<sub>2L</sub> knockouts [11, 111, 141] indicate that cooperative D<sub>1</sub>-like/D<sub>2L</sub> receptor interactions are necessary for the production of normal ambulatory behavior. How such interactions are organized within the brain is presently unclear; one possibility involves D<sub>1</sub>/D<sub>2</sub> heterodimers formed by direct protein–protein interactions (reviewed in Chapter 10). Our finding that vacuous chewing following challenge with a selective D<sub>1</sub>-like agonist occurs to significant excess in D<sub>2</sub> knockouts [113] suggests that inhibitory D<sub>1</sub>-like/D<sub>2</sub> receptor interactions also exist. Such inhibitory functional interactions may be conceptualized by the absence of pre-synaptic D<sub>2S</sub> receptors in D<sub>2</sub> knockouts causing increased dopamine synthesis and enhanced activation of D<sub>1</sub>-like receptors. Similar mechanisms might also explain excessive D<sub>1</sub>-like receptor-dependent induction of grooming following challenge with cocaine in D<sub>2</sub> knockouts [130].

The study of spontaneous orofacial movements in dopamine receptor knockouts has provided additional insight into the mechanisms by which signaling through individual dopamine receptor subtypes can influence behavioral phenotype. Specifically, D<sub>2</sub> knockouts are characterized by increased vertical jaw movements and unaltered horizontal jaw movements [115] while D<sub>1</sub> knockouts evidence reduced horizontal jaw movements and unaltered vertical jaw movements [75] (see Section 13.3.1), consistent with reciprocal roles for D<sub>1</sub> and D<sub>2</sub> receptors in regulating composite oral behavior [4, 20].

Finally, classical seizure studies using selective D<sub>2</sub>-like agonists and antagonists in rodents have suggested that D<sub>2</sub>-like receptors elevate seizure threshold under normal conditions [45]. Studies with convulsant agents in D<sub>2</sub> knockouts have elaborated these earlier findings by demonstrating that, among the D<sub>2</sub>-like family, D<sub>2</sub> receptors are primarily involved in these effects and further suggest that D<sub>2</sub> receptors prevent seizure-induced neuronal cell death [135, 136]. To date, seizure studies have not been performed in D<sub>2L</sub> knockouts so the relative importance of short and long isoforms of the D<sub>2</sub> receptor in these actions is currently unknown. Regardless, these findings raise the possibility that development of novel agonists selective for D<sub>2</sub> receptors may have therapeutic utility as anticonvulsant agents.

### ***13.4.5 D<sub>3</sub> Knockout: Spontaneous Behavior***

Generation and behavioral characterization of the first D<sub>3</sub> receptor knockout mouse was reported in 1996 [7]. Homozygous hybrid (129/SvJ1 × C57BL/6) D<sub>3</sub> knockouts displayed significant increases in both horizontal and rearing activity relative to wild types throughout 15 min of exploration in an open field, while locomotor activity was increased to a similar level in heterozygous D<sub>3</sub> knockouts in a time-dependent manner. The following year, phenotypic evaluation of a second D<sub>3</sub> knockout mouse line created using a different gene targeting construct was reported [145]. Although overall levels of spontaneous horizontal activity in these hybrid (129/Sv × C57BL/6) D<sub>3</sub> knockouts did not differ from wild types over 30 min in a novel environment, post hoc analysis revealed that D<sub>3</sub> knockouts were hyperactive during the first 5 min of the test. Subsequent assessments of locomotor activity following habituation to the testing environment were not associated with any observable genotypic effects. A similar lack of significant genotypic effect for horizontal activity and total distance traveled over 30 min in an unfamiliar environment has been reported in a third independently generated D<sub>3</sub> knockout line [108]. In the most recently constructed D<sub>3</sub> knockout mouse, non-significant increases in total distance traveled and vertical activity relative to wild types have been observed under similar experimental conditions [146]. However, analysis of the data over constituent time bins, which revealed significant time × genotype interactions for locomotion in the first two D<sub>3</sub> knockout lines [7, 145], was not documented in the latter two studies.

A number of behavioral studies incorporating phenotypic assessments of locomotion and/or rearing have since been conducted on the original D<sub>3</sub> knockout

lines. In separate studies comparing single and double dopamine receptors knockouts, hybrid D<sub>3</sub> knockouts created by Accili and colleagues evidenced significant increases in horizontal and vertical activity relative to wild types over 15 min of exploration in an unfamiliar environment [68, 144]. Backcrossing this particular hybrid D<sub>3</sub> knockout line to the C57BL/6 inbred strain for one generation produced discrepant behavioral results across two laboratories. In one study, activity levels in D<sub>3</sub> knockouts were indistinguishable from wild types over the course of exploration of and habituation to a novel environment when tested during either the light or the dark phase of the rodent diurnal cycle [147]. Conversely, in another study, although no genotypic difference was observed for spontaneous locomotor activity in a novel environment during the light phase, D<sub>3</sub> knockouts were consistently hyperactive relative to wild types over a 3-h period during the dark phase [148]. Results from more recent experiments in D<sub>3</sub> knockouts of increasing congenicity demonstrate similar incongruity. Specifically, among three studies evaluating spontaneous locomotion in a novel and/or familiar environment in incipient or fully congenic D<sub>3</sub> knockouts [69, 149, 150], only one [149] observed a significantly greater level of locomotion in D<sub>3</sub> knockout mice.

In our own laboratory, when assessed ethologically over a 1-h period of exploration in a novel environment, hybrid D<sub>3</sub> knockouts were characterized by significant increases in spontaneous sniffing, locomotion, and discrete topographies of rearing, together with a decrease in grooming relative to their wild type counterparts. Over the course of habituation to the environment, initially high levels of sniffing and rearing endured in D<sub>3</sub> knockouts but not in wild types [72]. In contrast, when evaluated using identical phenotypic assessment techniques by the same observer, congenic D<sub>3</sub> knockouts were characterized by no alteration in any topography of spontaneous behavior present in the mouse repertoire during exploration in a novel environment; continued assessment over several hours revealed only delayed habituation of rearing that was limited to females [151].

A number of studies have utilized D<sub>3</sub> knockouts to investigate the possible involvement of D<sub>3</sub> receptors in the behavioral manifestation of anxiety. Xu and colleagues noted that hybrid D<sub>3</sub> knockouts and wild types made a similar number of entries into the more aversive open arms of an elevated plus maze, leading these investigators to speculate that increased locomotion previously reported in these mutants is not secondary to a heightened state of anxiety [145]. In contrast, two subsequent studies using the original hybrid line created by Accili and colleagues found that D<sub>3</sub> knockouts made significantly more entries and spent more time in the open arms of an elevated plus maze [68, 152], consistent with an anxiolytic effect of D<sub>3</sub> receptor deletion in these mice. In support of this finding, D<sub>3</sub> knockouts were more inclined than wild types to enter the central section of an unfamiliar open field [152]. Furthermore, in a separate study characterizing the behavioral phenotype of hybrid D<sub>3</sub> knockouts over the course of exploration in a Lat maze, defecation during the test, which is another objective measure of anxiety, was reduced in heterozygous D<sub>3</sub> knockouts [144].

D<sub>3</sub> knockouts have also been investigated in other spontaneous behavioral paradigms. In relation to orofacial movement topography, we have demonstrated

that, relative to wild types, congenic D<sub>3</sub> knockouts evidence transient increases and reductions in head movements and horizontal jaw movements, respectively; vertical jaw movements, tongue protrusions, and movements of the vibrissae are unaltered in these mutants. Furthermore, habituation of incisor chattering was significantly reduced in D<sub>3</sub> knockouts in a gender-specific manner [115]. On the T maze, which is a delayed alternation paradigm used to evaluate spatial working memory, modest impairments were noted in incipient congenic D<sub>3</sub> knockouts when successive increments in retention time before commencing the next trial were introduced [121]. Finally, although a recent study found no genotypic differences in spontaneous immobility during the forced swim test for antidepressant behavior, an increase in immobility was seen following vehicle injection in wild types but not incipient congenic D<sub>3</sub> knockout mice [153]. Interestingly, other studies involving D<sub>3</sub> knockouts, including isolated findings in our own laboratory, have reported similar genotypic differences in response to vehicle injection [147, 151, 154], raising the possibility that D<sub>3</sub> receptors might be involved in the behavioral response to stress in mice.

#### ***13.4.6 D<sub>3</sub> Knockout: Drug-Induced Behavior***

As part of the original characterization of their hybrid D<sub>3</sub> knockout, Xu and colleagues found that D<sub>3</sub> knockouts exhibit locomotor supersensitivity in response to the combined administration of selective D1-like and D2-like agonists but not when these agents are administered separately [145]. In support of this finding, we have recently demonstrated that wild type locomotor responses to either the selective D1-like agonist SKF 83959 or the selective D2-like agonist RU 24213 are unaltered in congenic D<sub>3</sub> knockouts over the course of exploration and subsequent habituation to a novel environment [151]. Interestingly, the enhanced locomotion in response to the combined administration of D1-like and D2-like agonists is preserved in dopamine-depleted D<sub>3</sub> knockouts [145]. Taken together, these results suggest that D<sub>3</sub> receptors modulate ambulatory behavior by inhibiting the cooperative effects of post-synaptic D1-like and D2-like receptors.

Locomotor hyperresponsivity in hybrid D<sub>3</sub> knockouts has also been observed following acute challenge with low, but not high, doses of the indirect dopamine agonist cocaine [145]. In contrast, a subsequent experiment demonstrated that D<sub>3</sub> knockouts are characterized by a blunted locomotor response to both acute and repeated cocaine administration; however, the progressive emergence of stereotyped head-bobbing behavior associated with serial cocaine dosing in this study was markedly elevated in D<sub>3</sub> knockouts relative to wild types [155]. Similar studies investigating the behavioral effects of cocaine have also been performed in incipient congenic D<sub>3</sub> knockouts and produced inconsistent findings. Specifically, whereas repeated cocaine administration was associated with a higher level of locomotion in D<sub>3</sub> knockouts relative to wild type controls in one study [156], another group reported that locomotor stimulation and stereotyped behavior in response to acute cocaine administration did not differ between the genotypes [148]. Furthermore, in a recent study evaluating the role individual dopamine receptors and interactions

thereof in the behavioral effects of cocaine, locomotor stimulation, and conditioned place preference were unaltered in D<sub>3</sub> knockouts [69].

A number of studies in D<sub>3</sub> knockout mice have investigated the role of D<sub>3</sub> receptors in mediating behavioral responses to other psychostimulant drugs of abuse. Xu and colleagues have documented that a lower dose of amphetamine is required to produce conditioned place preference in hybrid D<sub>3</sub> knockouts than wild types [145]. In addition, low, but not high, dose amphetamine has been shown to stimulate locomotion to a greater extent in incipient congenic D<sub>3</sub> knockouts than in wild types over 3 h under partially habituated conditions [157]. A similar place preference and locomotor profile in response to morphine has been reported in incipient congenic D<sub>3</sub> knockouts. With regard to the former, an antagonist selective for  $\mu$ -opioid receptors prevented the morphine-induced place preference effect, suggesting that functional D<sub>3</sub>: $\mu$ -opioid receptor interactions mediate the reinforcing effects of this drug [149]. These findings of exaggerated locomotor responses to cocaine, amphetamine, and morphine in D<sub>3</sub> knockouts are consistent with an inhibitory role for D<sub>3</sub> receptors in psychostimulant-induced hyperactivity. Conversely, Risborough and colleagues have recently observed a modest gender-specific reduction in MDMA-induced locomotor activation in congenic D<sub>3</sub> knockouts, suggesting that D<sub>3</sub> receptors may normally facilitate the stimulant effects of this drug [127].

In addition to investigating the functional involvement of D<sub>3</sub> receptors in the locomotor and reinforcing properties of psychostimulant drugs of abuse, pharmacological studies in D<sub>3</sub> knockouts have also been performed on the basis of previous behavioral findings using preferential D<sub>3</sub> receptor ligands in intact animals. In an early study, locomotor activity in a novel environment following challenge with a range of D<sub>3</sub>-preferring agonists (7-OH-DPAT, quinelorane, and PD 128907) or a selective D<sub>3</sub> antagonist (PNU 99194A) was indistinguishable between incipient congenic D<sub>3</sub> knockouts and wild types [147]. In contrast, a subsequent study found that novelty-induced locomotor activity following challenge with either 7-OH-DPAT or PD 128907, at lower doses than those used previously, was significantly reduced in wild type but not incipient congenic D<sub>3</sub> knockouts, supporting previous pharmacological and genetic evidence that D<sub>3</sub> receptors inhibit locomotion under normal conditions [158]. Of note, higher doses of these agents, below those used in the earlier study [147], inhibited locomotion similarly between the genotypes, indicating that both D<sub>2</sub> and D<sub>3</sub> receptors are activated at these higher doses. Interestingly, there is evidence that the mechanisms through which D<sub>3</sub> receptor activation inhibits novelty-induced locomotion do not appear to operate in a familiar environment [158]. Other studies have investigated the ability of selective D<sub>3</sub> ligands to modulate the locomotor-stimulant effects of non-dopaminergic compounds in D<sub>3</sub> knockout mice. Specifically, Leriche and colleagues documented that inhibition of locomotor stimulation by the selective NMDA receptor antagonist MK-801 in wild types by a partial D<sub>3</sub> agonist or a D<sub>3</sub> antagonist is absent in incipient D<sub>3</sub> congenic knockouts [159]. More recently, the novel selective D<sub>3</sub> receptor antagonist, NGB 2904, has been shown to exaggerate amphetamine-stimulated locomotion in wild types but not incipient congenic D<sub>3</sub> knockouts. Furthermore, high doses of

NGB 2904 stimulated spontaneous locomotion in wild types but not D<sub>3</sub> knockouts [159, 160]. Thus, it appears that some newer agents are indeed highly selective for the D<sub>3</sub> receptor and may be used in intact animals and knockout mice to further elucidate the behavioral roles of the D<sub>3</sub> receptor.

Emerging evidence that dopaminergic dysregulation is present in certain mood disorders has prompted studies investigating the role of D<sub>3</sub> receptors therein. However, in the forced swim test, increased immobility in wild types following administration of the antiparkinsonian and putatively antidepressant D<sub>2</sub>-like agonist pramipexole was unaltered in either hybrid or congenic D<sub>3</sub> knockouts [150], suggesting that D<sub>3</sub> receptors are not involved in any antidepressant effect of this drug. A similar result has been observed with imipramine in hybrid D<sub>3</sub> knockouts [161]. In contrast, a recent study has demonstrated that incipient congenic D<sub>3</sub> knockouts are more sensitive to a range of antidepressant drugs in the forced swim test [153], leading these authors to speculate that elevated dopamine levels in mesolimbic pathways [146, 162] may be responsible for the observed effect in D<sub>3</sub> knockout mice.

### ***13.4.7 Interpretation of D<sub>3</sub> Knockout Phenotype***

A summary of the behavioral changes reported to date from studies in D<sub>3</sub> knockouts can be seen in Table 13.1. Numerous studies have evaluated spontaneous locomotor activity in the four available D<sub>3</sub> knockout lines in an effort to resolve inconsistent findings obtained from initial experiments in these mutants. These studies have described either modest hyperactivity [68, 72, 144, 148, 149] or no material locomotor phenotype [69, 147, 150, 151] in D<sub>3</sub> knockout mice. Methodological differences related to the novelty of or familiarity with the test environment appear to have contributed to discrepant findings across laboratories. Specifically, the transient hyperactive phenotype in D<sub>3</sub> knockouts occurs very early during the course of exploration and is not apparent following habituation to the environment [7, 145, 149, 158]. As hybrid or incipient congenic strains were used in all instances where a significant locomotor phenotype has been identified in D<sub>3</sub> knockouts, it is possible that heterogeneity in the genetic background of these mutants may have produced the observed phenotypic effects. However, considering that (a) an increase in locomotion has been observed in D<sub>3</sub> knockouts across various laboratories using differently constructed D<sub>3</sub> knockout lines, (b) in the majority of instances the hyperactivity in D<sub>3</sub> knockouts was found to dissipate over time such that post hoc analysis over constituent time bins was required to detect these differences, (c) in other studies unaltered locomotion, but not hypoactivity, has been reported in D<sub>3</sub> knockouts, and (d) D<sub>3</sub> knockouts have been repeatedly found to exhibit an exaggerated locomotor response to phasic dopaminergic stimulation, it is plausible that D<sub>3</sub> receptors have a subtle functional role in negatively modulating locomotion under normal conditions. Indeed, D<sub>3</sub> receptor-mediated inhibition of locomotor activity is supported by recent pharmacological studies in intact rodents showing that low doses of novel selective D<sub>3</sub> agonists and antagonists attenuate and increase locomotion, respectively [158, 160].

Interestingly, additional pharmacological approaches in D<sub>3</sub> knockouts indicate that the inhibitory action of D<sub>3</sub> receptors on ambulatory behavior requires the cooperative activation of D1-like and D2-like receptors. Specifically, whereas locomotor stimulation in response to administration of either a selective D1-like or D2-like agonist is unaltered in D<sub>3</sub> knockouts relative to wild types [151], combined administration of these agonists induces exaggerated locomotor activity in D<sub>3</sub> knockouts [145]. In agreement with this hypothesis, the indirect dopamine agonists cocaine and amphetamine have also been shown to induce exaggerated locomotor responses in D<sub>3</sub> knockouts [145, 156, 157]. While one study has demonstrated a reduction in cocaine-stimulated locomotion in D<sub>3</sub> knockouts [155], the high dose of cocaine used by these investigators was not associated with a heightened locomotor responses in D<sub>3</sub> knockouts in a previous study demonstrating genotypic effects at a lower dose of the drug [145]. High-dose cocaine was associated with the emergence of stereotyped head-bobbing behavior that occurred to significant excess in D<sub>3</sub> knockouts. Given that increasing doses of dopamine agonists induce a behavioral phenotype characterized by progressive locomotor stimulation and leading to the emergence of competitive motor stereotypy (see Section 13.2), the findings of Carta and colleagues [155] are also consistent with an inhibitory role for D<sub>3</sub> receptors in psychostimulant-induced locomotion. Results obtained from studies evaluating the behavior of D<sub>3</sub> knockouts in a drug-conditioned place preference paradigm indicate that D<sub>3</sub> receptors are also functionally involved in the rewarding effects of psychostimulants [145, 149]. These findings complement previous immunocytochemical studies demonstrating high levels of D<sub>3</sub> receptor expression in the nucleus accumbens, a brain area well established in mediating reinforcement processes.

Although the original characterization of the hybrid D<sub>3</sub> knockout created by Xu and colleagues found no significant genotypic effects on the elevated plus maze [145], subsequent findings in D<sub>3</sub> knockouts in this paradigm [68] and also the open field [152] and Lat maze [144] suggest a functional role for D<sub>3</sub> receptors in facilitating behavioral responses to anxiety-provoking stimuli. When evaluated in tandem with the previous finding of novelty-induced hyperactivity in D<sub>3</sub> knockouts, a phenotype consistent with reduced anxiety in these mutants raises some additional points for consideration. Specifically, in the absence of any material increase in topographies of exploratory behavior such as sifting in D<sub>3</sub> knockouts [72, 151], it is possible that increased locomotion relative to wild types during initial exploration in a novel environment is secondary to lower levels of anxiety in these mutants. Alternatively, it could be argued that increased locomotor drive and not decreased anxiety is responsible for the higher number of entries into the open arms of the elevated plus maze and the centre of an open field in D<sub>3</sub> knockouts [68, 152]; however, increased locomotor drive cannot explain the lower level of defecation by D<sub>3</sub> knockouts under anxiety-provoking conditions [144]. Furthermore, indirect evidence that D<sub>3</sub> knockouts exhibit less behavioral reactivity to stress and invasive procedures than wild types [147, 151, 154] provides additional support for a facilitative role of D<sub>3</sub> receptors in mediating behavioral responses to anxiety.

The availability of D<sub>3</sub> knockouts has enabled testing of a growing hypothesis that D<sub>3</sub> receptors have a functional role in psychotic disorders including schizophrenia [163]. NMDA receptor antagonists such as phencyclidine and ketamine can induce psychosis in healthy individuals and precipitate psychotic episodes in patients with schizophrenia. In rodents, these agents produce robust behavioral changes including marked hyperactivity that constitutes a well-established animal model of psychosis. Interestingly, Leriche and colleagues have reported that hyperactivity induced by NMDA is attenuated in D<sub>3</sub> knockouts. Furthermore, the ability of the antipsychotics haloperidol and clozapine to inhibit MK 801-induced hyperactivity in wild types was essentially unaltered in D<sub>3</sub> knockouts, leading these investigators to speculate that agents demonstrating selective D<sub>3</sub> receptor blockade may have antipsychotic activity [159].

Additional evidence linking D<sub>3</sub> receptors and schizophrenia has emerged from the assessment of spatial memory in D<sub>3</sub> knockout mice. Working memory relates to the temporary storage of external information and is known to be impaired in patients with schizophrenia. The prefrontal cortex is responsible for consolidating working memory through a mechanism that requires activation of D<sub>1</sub> receptors. A study in D<sub>3</sub> knockout mice has shown that deletion of D<sub>3</sub> receptors is associated with blunted responsivity to stimulation of D<sub>1</sub> receptors in this region [121]. Furthermore, this study demonstrated impaired working memory in D<sub>3</sub> knockouts using a spatial memory paradigm, suggesting that abnormal D<sub>3</sub> receptor function may be involved in the cognitive deficits of schizophrenia. Conversely, the finding that individual topographies of orofacial movement are essentially unaltered in D<sub>3</sub> knockouts [115] argues against a role for D<sub>3</sub> receptors in the manifestation of orofacial dyskinesias that often develop consequent to prolonged antipsychotic treatment in schizophrenia.

An enduring controversy in the interpretation of results generated from studies in D<sub>3</sub> knockouts relates to the relative importance of pre-synaptic vs. post-synaptic sites in mediating the observed phenotypic effects. Reports that (a) discrete behavioral effects in D<sub>3</sub> knockouts are preserved following depletion of endogenous dopamine [145] and (b) extracellular dopamine levels and the dopamine metabolites DOPAC and HVA are unaltered in D<sub>3</sub> knockouts [149] have led to the postulate that post-synaptic D<sub>3</sub> receptors are involved. Furthermore, the fact that electrophysiological changes in single neurons following the combined administration of D<sub>1</sub>-like and D<sub>2</sub>-like agonists are unaltered in D<sub>3</sub> knockouts [145] suggests that post-synaptic D<sub>3</sub> receptors involved are located on neuronal cells distinct from those expressing D<sub>1</sub>-like and other D<sub>2</sub>-like receptor subtypes. Indeed, D<sub>3</sub> receptor expression on inhibitory GABAergic interneurons would result in disinhibition of dopaminergic function and explain many of the results obtained to date from studies in D<sub>3</sub> knockout mice. On the other hand, microdialysis studies have found a significant increase in the level of dopamine in the striatum [146, 162], consistent with an autoreceptor role for D<sub>3</sub> receptors in dopamine release/synthesis. Elevated extracellular dopamine in mesolimbic pathways has been hypothesized to be a possible mechanism for the antidepressant behavioral phenotype observed in mice lacking functional D<sub>3</sub> receptors [153]. In reality, as immunocytochemical

studies have confirmed the presence of pre-synaptic and post-synaptic D<sub>3</sub> receptors [164], it is likely that both populations are functionally involved in modulating D<sub>3</sub> receptor-dependent behaviors.

### ***13.4.8 D<sub>4</sub> Knockout: Spontaneous Behavior***

Initial phenotypic characterization of D<sub>4</sub> knockouts maintained on a hybrid genetic background (129/OlaHsd × C57BL/6) identified multiple spontaneous behavioral abnormalities. In a novel environment, D<sub>4</sub> knockouts covered less horizontal distance, exhibited fewer rearing episodes and moved more slowly than wild type mice. Following habituation to the testing environment, D<sub>4</sub> knockouts also initiated fewer movements and spent less time in motion than controls [9], indicating that D<sub>4</sub> receptors are involved in facilitating a variety of normal locomotor behaviors. Furthermore, in a test of motor coordination, D<sub>4</sub> knockouts outperformed their wild type counterparts, experiencing 50% fewer falls on the rotarod and remaining on the apparatus 2.5 times longer; this led to the postulate that D<sub>4</sub> knockouts are more adept at complex, coordinated motor tasks, possibly due to altered dopamine metabolism in the dorsal striatum of these animals [9].

To examine the putative functional involvement of D<sub>4</sub> receptors in the personality trait of novelty-seeking suggested from genetic linkage/association studies [165], Dulawa and colleagues evaluated hybrid D<sub>4</sub> knockouts in three approach-avoidance paradigms [166]. In contrast to the original report by Rubinstein and colleagues [9], no differences were observed between D<sub>4</sub> knockouts and wild types in terms of gross spontaneous locomotor activity in the open-field environment under either novel or familiar conditions. D<sub>4</sub> knockouts did show reduced behavioral responses to novelty, as indicated by fewer entries into the center of the field; however, the total time spent in the center of the arena did not differ significantly between the genotypes. In the emergence test, a free exploration paradigm in which animals can explore the open field or retreat into a cylinder, D<sub>4</sub> knockouts displayed a longer latency to emerge from the cylinder, made fewer entries into the cylinder, and spent more time inside the cylinder. Furthermore, in the novel object test, another free exploration paradigm which allows animals to explore a novel object in a non-threatening and familiar environment, D<sub>4</sub> knockouts were found to spend proportionately less time in the center after introduction of the stimulus [166].

Reduced exploratory activity in hybrid D<sub>4</sub> knockouts in the conflict-producing environments reported above might be due to avoidance behavior associated with heightened anxiety and not a reduced response to novelty per se. Accordingly, a subsequent study used hybrid D<sub>4</sub> knockouts to investigate the functional involvement of D<sub>4</sub> receptors in unconditioned anxiety-related behaviors. In the elevated plus maze, D<sub>4</sub> knockouts made fewer open-arm entries and spent less time in the open arms [167]. The total number of entries into either the open or closed arms was similar between the genotypes, indicating that the reduced number of open-arm entries exhibited by D<sub>4</sub> knockouts was not due to a locomotor or motivational deficit. In the light–dark test, D<sub>4</sub> knockouts displayed an increase in their initial latency to

enter the light compartment and spent less time on the illuminated side compared to wild types. In both paradigms, avoidance behavior in D<sub>4</sub> knockouts was completely prevented by pretreatment with anxiolytic drugs [167].

Several genetic linkage/association studies have identified discrete polymorphisms in the dopamine D<sub>4</sub> receptor gene as conferring increased risk for developing ADHD [168, 169]. In 2004, Avale and colleagues presented evidence that neonatal 6-OHDA lesioning in wild type mice represents a valid animal model of this clinical disorder. Specifically, lesioned mice exhibit hyperactivity that wanes after puberty, paradoxical hypolocomotor responses to amphetamine and methylphenidate, poor behavioral inhibition in approach/avoidance conflict paradigms, and deficits in continuously performed motor coordination tasks. Interestingly, congenic D<sub>4</sub> knockout mice with superimposed neonatal 6-OHDA lesioning failed to develop the hyperactive phenotype. Furthermore, wild type mice lesioned with 6-OHDA exhibited behavioral disinhibition when tested in an open field and the elevated plus maze, whereas D<sub>4</sub> knockouts demonstrated normal avoidance of the unprotected areas [170]. Collectively, the results from this study are consistent with a facilitative role for D<sub>4</sub> receptors in manifesting discrete behavioral features in an animal model of ADHD.

The most recent behavioral studies involving D<sub>4</sub> knockouts have been conducted in our laboratory [96, 103]. At the level of spontaneous ethological behavior, congenic D<sub>4</sub> knockouts were characterized by only a marginal reduction in exploratory sniffing together with delayed habituation of sifting. While such phenotypic differences might be interpreted as reduced novelty seeking or heightened anxiety in D<sub>4</sub> knockouts, other related behaviors such as rearing and locomotion were unaltered. Thus, the small magnitude and topographical specificity of these phenotypic effects indicate that any functional role for D<sub>4</sub> receptors in mediating spontaneous locomotor or exploratory/anxiety-related behavior is subtle [96]. In relation to dopaminergic regulation of orofacial movement topography, congenic D<sub>4</sub> knockouts were indistinguishable from wild type mice when assessed quantitatively for vertical and horizontal jaw movements, tongue protrusions, and incisor chattering [103], arguing against any material role for D<sub>4</sub> receptors in these processes.

### ***13.4.9 D<sub>4</sub> Knockout: Drug-Induced Behavior***

Original pharmacological characterization of hybrid (129/OlaHsd × C57BL/6) D<sub>4</sub> knockouts evaluated the locomotor-stimulant effects of clozapine, ethanol, cocaine, and methamphetamine in these animals [9]. Low-dose clozapine was found to attenuate apomorphine-induced locomotion in wild type but not in hybrid D<sub>4</sub> knockouts, whereas high-dose clozapine blocked apomorphine-induced behavior in both genotypes, perhaps via antagonism at other D<sub>2</sub>-like receptor sites. In contrast to the depressant effect of D<sub>4</sub> receptor deletion on spontaneous locomotor topographies reported by these investigators (see Section 13.4.8), hybrid D<sub>4</sub> knockouts were found to be hyperreactive to the locomotor-stimulant effects of ethanol, cocaine, and methamphetamine [9].

To further characterize the involvement of D<sub>4</sub> receptors in mediating the effects of psychostimulant drugs of abuse, subsequent studies evaluated additional behavioral parameters in D<sub>4</sub> knockout mice in response to cocaine [171] and amphetamine [172]. In agreement with the earlier report of Rubinstein and colleagues, locomotor responses to cocaine were greater in hybrid D<sub>4</sub> knockouts compared to wild type controls [171]. As an extension of this work, Katz and co-workers examined the involvement of D<sub>4</sub> receptors in mediating the discriminative stimulus effects of cocaine. While lower doses of cocaine were able to initiate cocaine responding in D<sub>4</sub> knockouts relative to wild types, the observation that the D<sub>2</sub>/D<sub>3</sub> antagonist raclopride antagonized cocaine responding to a similar extent in both genotypes suggests that D<sub>4</sub> receptors are minimally and indirectly involved in mediating the discriminative effects of cocaine, possibly via inhibitory functional interactions with other D<sub>2</sub>-like receptors [171]. In response to amphetamine, locomotor activity was unaltered in congenic D<sub>4</sub> knockouts relative to wild types over a 1-h period following acute administration of amphetamine; however, post hoc analysis of activity over constituent time bins during the assessment revealed a time × genotype interaction at higher doses of the drug, characterized by a transient increase in locomotor activity in D<sub>4</sub> knockout mice. Furthermore, following a chronic administration schedule, congenic D<sub>4</sub> knockouts displayed an enhanced dose-dependent sensitized response to amphetamine compared to wild types, consistent with a functional role for D<sub>4</sub> receptors in psychostimulant-mediated neural plasticity [172].

The above pharmacological studies in D<sub>4</sub> knockout mice employed non-selective or indirect dopamine agonists, having indiscriminate activity across the five cloned dopamine receptor subtypes, to probe the functional roles of the D<sub>4</sub> receptor. Recently, we sought to elaborate these findings by evaluating the behavioral phenotype of congenic D<sub>4</sub> knockouts in response to selective D<sub>2</sub>-like and D<sub>1</sub>-like agonists using an ethologically based behavioral assessment technique [96]. The characteristic shift from normal fluid ambulation to stereotyped ponderous locomotion in response to the selective D<sub>2</sub>-like agonist RU 24213 was reduced in D<sub>4</sub> knockouts, consistent with a role for D<sub>4</sub> receptors in facilitating the expression of stereotyped locomotor topographies. Interestingly, induction of intense grooming syntax by the selective D<sub>1</sub>-like antagonist SKF 83959 was reduced in D<sub>4</sub> knockout mice. Furthermore, the ability of the structurally related but pharmacologically distinct selective D<sub>1</sub>-like agonist SKF 83822 to lower seizure threshold [39, 91, 94] was attenuated in D<sub>4</sub> knockouts in accordance with a minor facilitative role for D<sub>4</sub> receptors in mediating dopamine-dependent seizures [96].

### ***13.4.10 Interpretation of D<sub>4</sub> Knockout Phenotype***

A summary of the behavioral changes reported to date from studies in D<sub>4</sub> knockouts can be seen in Table 13.1. It is clear from the preceding sections that considerable inconsistency exists between findings relating to spontaneous locomotion in hybrid (129/OlaHsd × C57BL/6) D<sub>4</sub> knockouts. One study observed significant reductions in gross spontaneous locomotor and rearing activity in both novel

and familiar environments in D<sub>4</sub> knockouts [9], whereas a subsequent investigation reported no significant locomotor differences between D<sub>4</sub> knockouts and wild types under similar experimental conditions [166]. Furthermore, in a study evaluating the locomotor-stimulant effects of cocaine in hybrid D<sub>4</sub> knockouts, locomotor activity in saline-treated groups did not differ significantly between the genotypes [171]. Collectively, these results indicate that factors unrelated to loss of the D<sub>4</sub> receptor may have produced these phenotypic effects. In relation to genetic background, when C57BL/6 and 129/OlaHsd inbred mouse strains are compared directly, 129/OlaHsd mice are hypoactive in the open-field arena [173]. This might explain the lack of any material spontaneous locomotor phenotype in congenic D<sub>4</sub> knockouts for which the contribution of 129/OlaHsd alleles is expected to be below 0.1% [96].

Assessment of hybrid D<sub>4</sub> knockouts in targeted behavioral paradigms has identified facilitatory and inhibitory roles for D<sub>4</sub> receptors in the related traits of novelty-seeking [166] and anxiety [167], respectively, suggesting that D<sub>4</sub> receptors may be involved in the expression of certain emotionally driven behaviors. In addition, an elegant experiment utilizing a combined gene knockout and pharmacological lesioning approach has provided evidence that D<sub>4</sub> receptors are necessary to recapitulate many of the core behavioral features in an animal model of ADHD [170], a relationship supported by clinical genetic studies in humans. However, it is pertinent to mention that any putative relationship between genetically determined D<sub>4</sub> receptor-mediated phenotypes in humans and mice must be interpreted with caution given that the 48 bp repeat polymorphism in exon III of the human D<sub>4</sub> receptor gene associated with ADHD (and novelty-seeking behavior) is absent from the murine homologue [174].

Absence of D<sub>4</sub> receptors has consistently been shown to augment the locomotor-stimulant effects of various drugs of abuse including the indirect dopamine agonists cocaine and amphetamine [9, 171, 172]. In contrast, the characteristic stereotyped locomotor response to the selective D<sub>2</sub>-like agonist, RU 24213, is reduced in D<sub>4</sub> knockouts. Taken together, these findings are important at two levels. Firstly, D<sub>4</sub> receptors appear to be integral to the development of motor stereotypy, a hypothesis further supported by anatomical reports localizing D<sub>4</sub> receptors to discrete areas of the basal ganglia purported to be involved in the expression of behavioral stereotypies. Secondly, these findings provide indirect evidence that functional D<sub>4</sub>:D<sub>1</sub>-like receptor interactions are operating to produce locomotor supersensitivity in D<sub>4</sub> knockouts. Direct evidence for functional D<sub>4</sub>:D<sub>1</sub>-like receptor interactions *in vivo* has emerged from behavioral studies examining selective D<sub>1</sub>-like agonists in congenic D<sub>4</sub> knockout mice [96].

Until recently, no evidence has been reported to suggest the functional involvement of individual D<sub>2</sub>-like receptor subtypes in mediating grooming behavior. Specifically, induction of syntactic, intense grooming in response to the selective D<sub>1</sub>-like agonist SKF 83959 is conserved in congenic D<sub>3</sub> receptor knockouts [151]; SKF 83959 has yet to be tested in D<sub>2</sub> knockout mice. The finding that such SKF 83959-induced grooming is reduced in congenic D<sub>4</sub> knockouts indicates, for the first

time, that subtle D<sub>4</sub>:D<sub>1</sub>-like receptor interactions participate in mediating grooming behavior. Furthermore, the observation that induction of seizures by the selective D<sub>1</sub>-like agonist SKF 83822 is reduced in D<sub>4</sub> knockouts suggests that cooperative functional D<sub>4</sub>:D<sub>1</sub>-like receptor interactions also participate in the regulation of neuronal excitability. Behavioral indices of such functional D<sub>4</sub>:D<sub>1</sub>-like interactions are reinforced by the recent observation that D<sub>1</sub> receptor expression is up-regulated in D<sub>4</sub> knockouts [175]. However, how these interactions are organized within the brain at a molecular, cellular, or network level and the relative involvement of D<sub>1</sub> and D<sub>5</sub> receptors remains to be established.

## 13.5 Double Knockouts Involving Dopamine Receptors

### 13.5.1 D<sub>1</sub>/D<sub>2</sub> Double Knockout

The relative abundance of D<sub>1</sub> and D<sub>2</sub> receptors vis-à-vis other dopamine receptor subtypes in the brain prompted the generation of D<sub>1</sub>/D<sub>2</sub> double knockouts to investigate their involvement in functional D<sub>1</sub>-like:D<sub>2</sub>-like interactions [176]. Although the progeny from heterozygous D<sub>1</sub>/D<sub>2</sub> double knockout matings follows the expected Mendelian ratio, homozygous D<sub>1</sub>/D<sub>2</sub> double knockouts die in the early postnatal period in the absence of any identifiable macroscopic or microscopic brain abnormalities; this is most likely due to altered feeding behavior and a dysfunctional gastrointestinal system. In contrast, heterozygous D<sub>1</sub>/homozygous D<sub>2</sub> double knockouts evidence reduced body weight but survive to adulthood, while homozygous D<sub>1</sub>/heterozygous D<sub>2</sub> double knockouts develop ulcers in the small intestine and only survive if fed a semi-liquid diet. Collectively, these findings indicate that cooperative D<sub>1</sub>:D<sub>2</sub> receptor interactions are involved in feeding behavior and gastrointestinal function, with functional primacy of D<sub>1</sub> receptors in these effects. Interestingly, spontaneous locomotor behavior and coordination in homozygous D<sub>1</sub> or homozygous D<sub>2</sub> single knockouts are unaltered by concomitant deletion of one functional D<sub>2</sub> or D<sub>1</sub> receptor allele, respectively [176]. However, given that meaningful locomotor assessment cannot be performed in homozygous D<sub>1</sub>/D<sub>2</sub> double knockouts for the reasons outlined above, it would be premature to exclude a role for D<sub>1</sub>:D<sub>2</sub> receptor interactions in these behaviors based on this finding. Future development of tissue specific and/or conditional homozygous D<sub>1</sub>/D<sub>2</sub> double knockouts or studies with selective D<sub>1</sub>-like or D<sub>2</sub>-like drugs in this model may help to clarify the issue.

### 13.5.2 D<sub>1</sub>/D<sub>3</sub> Double Knockout

In situ hybridization studies have shown the D<sub>1</sub> and D<sub>3</sub> receptor mRNAs are co-localized in single neurons, suggesting that these receptors functionally interact at

a cellular level [177]. In 2000, individual  $D_1$  and  $D_3$  knockouts and  $D_1/D_3$  double knockouts maintained on a hybrid genetic background were compared in a number of behavioral paradigms [68]. No evidence was found for receptor interaction in tests of spatial memory or motor coordination. Conversely, a lower level of locomotion and rearing in  $D_1$  knockouts relative to wild types during exploration in an open field was exacerbated in  $D_1/D_3$  double knockouts, leading these authors to conclude that  $D_1$  and  $D_3$  receptors interact to modulate discrete topographies of exploratory behavior. However, it should be mentioned that abundant evidence indicates that  $D_1$  knockouts are characterized by spontaneous hyperactivity (see Section 13.3.3), and not hypoactivity as reported in this study. Indeed, a subsequent study by these investigators using incipient congenic lines reported excessive locomotion in both  $D_1$  and  $D_1/D_3$  knockouts under novel and familiar conditions [69]. Furthermore, we have shown that increased locomotion, sniffing, and rearing in  $D_1$  knockouts during exploration in a novel environment are unaltered in hybrid  $D_1/D_3$  double knockouts [72]. Interestingly, although isolated features of  $D_3$  knockout phenotype are apparent in mice lacking both  $D_1$  and  $D_3$  receptors, the overall spontaneous behavioral phenotype in  $D_1/D_3$  double knockouts mirrors considerably that of  $D_1$  knockout mice [68, 72]; this suggests that  $D_1$  receptors facilitate discrete behaviors in  $D_3$  knockout mice. In support of this hypothesis, increased anxiety in  $D_3$  knockouts is abolished in the absence of  $D_1$  receptors [68]. More recent findings in  $D_1/D_3$  double knockouts indicate that while  $D_1$  receptors are important in the locomotor-stimulant effects of cocaine (see Section 13.3.3), functional interaction with  $D_3$  receptors may be involved in the reinforcing properties of this drug [69].

### ***13.5.3 $D_2/D_3$ Double Knockout***

Within the  $D_2$ -like family, the high degree of structural homology between  $D_2$  and  $D_3$  receptors led to the early hypothesis that these receptors may have complementary functions in regions of shared expression [108]. Indeed, both  $D_2$  and  $D_3$  (but not  $D_4$ ) receptors are known to function as pre-synaptic autoreceptors to regulate dopamine synthesis/release. An initial comparative study between hybrid  $D_2$  and  $D_3$  single knockouts and derived  $D_2/D_3$  double knockouts found that impaired ambulation in mice lacking  $D_2$  receptors is more pronounced in the absence of  $D_3$  receptors. Furthermore,  $D_3$  receptor expression was increased in  $D_2$  knockouts in this study, leading these authors to postulate that cooperative  $D_2:D_3$  receptor interactions normally facilitate locomotion in mice and  $D_3$  receptors may partially compensate for  $D_2$  receptor functions in  $D_2$  knockout mice [108]. However, these findings are incongruent with other evidence from single mutants that  $D_3$  receptors normally inhibit motor behavior (see Section 13.4.7) and previous data demonstrating unaltered  $D_3$  (or  $D_4$ ) RNA expression in an independently created  $D_2$  knockout line [8]. A subsequent study has shown that in a Lat maze, locomotion and rearing frequency and duration in  $D_2$  knockouts are essentially unaltered in  $D_2/D_3$  double knockouts [144]. In addition, a recent study has found that  $D_2$  receptor-mediated

motor stereotypies are not influenced by D<sub>3</sub> receptors [178]. Thus, inconsistent findings from the small number of studies conducted to date involving D<sub>2</sub>/D<sub>3</sub> double knockouts do not support the existence of prominent functional D<sub>2</sub>:D<sub>3</sub> receptor interactions in the behaviors examined; this does not exclude (a) the possibility that methodological factors including genetic background effects may have obscured subtle interactions and (b) a role for D<sub>2</sub>/D<sub>3</sub> receptor interactions in modulating other dopamine-dependent behaviors.

### 13.6 Challenges

There are few domains of behavior for which regulation by one or more dopamine receptors has been excluded and those domains where such regulation is known to be either fundamental or an important modulatory factor are multiple and diverse. However, it is now many years since the continuing identification of new, molecular biologically defined dopamine receptor subtypes exceeded the capacity of medicinal chemists to identify selective agonists and antagonists for each of those subtypes. This psychopharmacological vacuum reflects at least two factors: difficulties in identifying chemical structures that can distinguish between receptor proteins whose amino acid sequences evidence only subtle differences and some concern in the pharmaceutical industry as to whether such selectivity is of therapeutic potential in “volume” disorders.

The adage that “nature abhors a vacuum” appears just as true in neuroscience as elsewhere; hence this psychopharmacological vacuum has been filled by an alternative approach to parcellation of function between dopamine receptor subtypes, namely mutant mice with targeted gene manipulation. This approach is a “two-edged sword”: the potential of these techniques is not yet fully realized, particularly in terms of conditional mutants that afford the investigator temporal and/or regional control over expression of the receptor mutation, and the ability to target specific cell types; yet these techniques engender their own concerns, particularly in terms of genetic background effects, compensation processes, and sex-specific phenotypes; also, concerns endure over non-replicability between laboratories that may reflect differing molecular genetic strategies for targeting the same receptor and/or differing test paradigms for targeting the same domain of behavior [4]. Nevertheless, the yield to date from mutant studies has been substantial and is likely to increase. This yield would likely be facilitated by combining studies in mutants with an enhanced psychopharmacological “toolbox,” to the extent that further selective agents are forthcoming, and systematic studies that allow more valid comparisons between laboratories. We have learned much over the past 50 years, but there is still more to understand.

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# Chapter 14

## Dopamine Modulation of the Prefrontal Cortex and Cognitive Function

Jeremy K. Seamans and Trevor W. Robbins

**Abstract** This chapter will review the basic neurobiology of the dopamine (DA) system in the prefrontal cortex (PFC) and its functional role in cognition. It will consider the properties of DA release and of DA receptors in the PFC and how they may contribute to the overall function of the mesocortical DA system. DA release in the PFC occurs in response to a variety of events that can be appetitive or aversive in nature and this release may prepare the PFC networks to deal with environmental or cognitive challenges. The amount of DA released may selectively affect the different subtypes of receptors on PFC neurons, which in turn have different modulatory actions on PFC networks. It has been proposed that the PFC DA system and especially D1 receptors are tuned according to an inverted-U dose–response function such that too much or too little DA or D1 receptor activation is detrimental to cognitive performance. At optimal levels, DA acting via D1 receptors may increase the signal-to-noise ratio to improve the efficiency of active PFC networks, while levels higher or lower levels may reduce the overall signal to noise but allow PFC networks to deal with information in a more flexible manner. The key to understanding the PFC DA system may lie in understanding how a balance is achieved to promote optimal modulation across a variety of situations.

**Keywords** Prefrontal cortex · Working memory · Response flexibility · Inverted-U · Computational models

### 14.1 Introduction

This chapter focuses on the properties of the dopamine (DA) system in the prefrontal cortex (PFC) and how these properties may contribute to higher cognitive function.

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J.K. Seamans (✉)

Department of Psychiatry and The Brain Research Centre, University of British Columbia, 2211 Wesbrook Mall, Vancouver, BC V6T 2B5, Canada  
e-mail: seamans@interchange.ubc.ca

Here we will discuss the basic anatomy, chemistry, physiology, and behavioral pharmacology of the PFC DA system. The chapter ends with an attempt to present an integrative overview of the possible function of the mesofrontal DA system.

## 14.2 Basic Anatomy of DA Release

The dopaminergic innervation of the forebrain is constituted by  $\sim 30,000$ – $40,000$  highly collateralized neurons residing in the ventral mesencephalon [1–3]. These mesencephalic cell groups are designated as A8, A9, and A10, according to the nomenclature of Dahlström and Fuxe [4], and generally correspond to the DA cells of the substantia nigra (SN, A9), ventral tegmental area (VTA, A10), and the retrorubral area (A8) [3, 5, 6].

DA neurons show two predominant patterns of firing activity termed tonic and phasic [7, 8]. Tonic activity consists of a pace-maker like firing pattern of  $\sim 1$ – $6$  Hz that DA neurons usually exhibit in the absence of salient stimuli [9–11]. Tonic firing patterns maintain basal extracellular levels of DA in afferent regions and can be affected by visceral stimuli that can moderately increase or decrease efferent DA levels to provide a “tone” on DA receptors [7].

Basal DA levels in PFC recorded using *in vivo* microdialysis are typically on the order of  $0.1$ – $0.4$  nM [12, 13]. However, when interpreting these values it is important to note that (a) the values are often not corrected for *in vitro* recovery which is on the order of  $10$ – $13\%$  [12], (b) the microdialysis probe itself may cause an  $\sim 10$ -fold drop in its vicinity as revealed by simultaneous voltammetric recordings [14], and (c) these measurements reflect extrasynaptic DA levels. Taking into account  $\sim 10\%$  recovery and the  $10$ -fold drop caused by the probe, the measured extrasynaptic concentrations of  $\sim 0.1$ – $0.4$  nM roughly correspond to extrasynaptic DA levels of  $10$ – $40$  nM in the PFC. PFC DA levels were close to this range as measured using the more accurate no-net-flux procedure [15]. If  $10$ – $40$  nM DA exists in the extrasynaptic space then based on the results of diffusion modeling, one would expect perisynaptic DA concentrations  $10$ -fold higher on the order of  $100$ – $400$  nM [16, 17] with intrasynaptic levels being an order of magnitude higher than that. Activation of the mesocortical DA system would then increase DA levels above this baseline level.

Salient environmental stimuli, particularly rewarding, aversive, and novel stimuli, all have been shown to modulate the phasic firing pattern of DA neurons [11, 18, 19]. Physiologically patterned burst stimulation of DA fibers causes DA levels in PFC to increase by  $\sim 40$ – $200$  nM while aversive stimuli increased PFC DA levels by  $100$ – $200$  nM, as measured in the prelimbic region of the PFC using carbon-fiber electrodes [20–24]. Therefore, based on the known biochemical properties of the mesofrontal system, basal perisynaptic levels of DA in the PFC are on the order of hundreds of nanomolars with extrasynaptic concentrations in the range of tens of nanomolars while phasic physiological activation increases DA by  $40$ – $200$  nM over these basal levels.

## 14.3 Behavioral Activation of the Mesocortical DA System

### 14.3.1 Aversive Events

The most studied aspect of PFC DA release is how it changes when the animal is presented with stimuli of negative emotional valence. Early studies showed that metabolic activation of the DA system in the PFC increased in association with electric footshock, conditioned fear, or swim stress [25–27]. Later studies using microdialysis reported that DA levels in the PFC were increased by a wide array of negative events such as tail pinch [28, 29], footshock or conditioned footshock [30, 32, 33], handling stress [13, 32, 34], pharmacological stressors [29, 35, 36], social defeat stress [37], and electrical stimulation of the midbrain tectum [38]. The changes in the DA signal associated with these stimuli were typically on the order of 100–200% above baseline. Again assuming a basal extrasynaptic level of  $\sim 10$ –40 nM DA, this would mean that the increase detected in these microdialysis studies was on the order of 20–120 nM. The tail pinch induced increases in extrasynaptic PFC DA levels measured in the prelimbic cortex with voltammetry were of similar magnitude and on the order of 100–200 nM [21, 23, 24].

One of the most striking aspects of the response of the PFC DA system to stress is its remarkably protracted nature. PFC DA levels can remain elevated for tens of minutes following even light handling as measured with microdialysis [13, 34]. Remarkably, aversive electrical stimulation of the inferior colliculus for 15 s when delivered at stimulation intensities that evoked escape responses in awake animals, increased PFC DA for  $>3$  h [38]. Even with voltammetry, which is able to measure evoked changes in DA levels on millisecond time scales, similar long-lasting changes have been reported. For instance, tail-pinch stress in the form of a wooden clothespin placed at the base of the tail for 15 min caused an increase in DA measured with nafion-coated carbon-fiber electrodes in the PFC that lasted from 25 min to over an hour after removal of the clothespin [21, 23, 24]. Even if the tail pinch was given for only 2 min, it caused an increase in PFC DA that again lasted tens of minutes [39]. Therefore, the protracted nature of the PFC DA response to stress appears to be a genuine property of the system and does not mask some more transient phenomenon.

The protracted nature of release may provide insights into the function of the mesofrontal DA signal. One possible explanation for these prolonged increases in PFC DA is that they may reflect or even produce emotional arousal [34, 40]. In accordance with this idea, anxiolytic agents that reduce emotional arousal also reverse stress-induced increases in DA levels and DA turnover [27, 35, 36, 41]. Accordingly, the PFC DA response also varies across rat strains that have intrinsically different levels of arousal. For instance, Roman low-avoidance rats are characterized as more fearful than Roman high-avoidance rats that show less freezing behaviors, better coping, and lower HPA activity [42]. Giorgi et al. [29] showed that tail-pinch or pharmacological stressors increased PFC DA levels of Roman high-avoidance but not low-avoidance rats, suggesting that the rise in PFC DA levels

may be related to a more effective coping strategy rather than the stress response per se. Furthermore, long-term administration of antidepressants had no marked effect on the stress-induced physiological responses (increases in neuroactive steroids or corticosterone), yet prevented the stress-induced raise in PFC DA [43], again implying that the DA response may not be related to emotional arousal per se but rather the marshalling of resources to deal with a stressor [29]. Thus, one reason why the elevations in PFC DA are so long lasting may be because the processing of the significance of environmental stressors often far outlasts their presence.

### ***14.3.2 Appetitive Events***

Food rewards also increase PFC DA release but the increases are typically less than those observed for aversive stimuli [28, 34, 41, 44, 45]. Although appetitive stimuli, like aversive stimuli, can increase PFC DA for tens of minutes, more transient changes have also been reported. Richardson and Gratton [47] observed changes in the voltammetric signal just in a short 45 s consumption period following a lever press for milk reward. When the delivery of the milk was delayed by 20–30 s, the PFC DA signal increased by a few nanomolars until the point where the milk was delivered. The DA levels also increased if the reward was unexpectedly withheld or decreased or if the response requirement was increased by changing the fixed ratio schedule. This way, the transient DA signal appeared to be related to the animal's uncertainty about how much reward it would receive. This implies that the PFC DA system may be engaged as reward contingencies change in anticipation of cognitive effort. Hence the PFC DA system may become relevant in situations requiring cognitive effort perhaps in a parallel manner to the way the mesolimbic DA system is activated in situations requiring motivation and physical effort [48].

### ***14.3.3 Cognitive Processing***

The PFC DA system is also activated during various forms of learning. Robust and sustained DA release is associated with classical appetitive or aversive conditioning to a context [30, 32] or to an auditory cue [31, 33]. In primates, DA levels were elevated on the delayed-response working memory task, but not a nondelayed task [49]. Likewise, in rats, PFC DA levels increased during and in anticipation of the performance of a delayed alternation working memory task [50]. On the delayed win-shift working memory task on a radial maze, Phillips et al. [51] showed that DA levels increased by >100% during training and test phases of the task where the trial-unique information for a given trial was acquired and used but decreased to baseline levels during the delay period. DA levels often began to rise toward the end of the delay, again suggesting that the DA signal reflected anticipation of the forthcoming cognitive challenge. When the delay period was unexpectedly increased, DA levels did not increase and task performance worsened. These data suggest that

the PFC DA system may be recruited to solve the task at hand and an inability to appropriately raise DA levels could lead to poor task performance.

DA levels were also increased in another form of executive function involving the PFC, namely response flexibility. van der Meulen et al. [52] observed a large and extended increase in DA efflux in rats performing initial reversals on a spatial 2-lever discrimination task. Stefani and Moghaddam [53] measured PFC DA levels using microdialysis during a rodent set-shifting task on a plus maze. In addition to rats performing the actual task there was a separate yoked group of rats that received intermittent unpredictable rewards and a “reward retrieval” group that was rewarded on every trial. Increases in PFC DA were observed for the first two groups but not the passively rewarded group. The increases in DA levels were on the order of 100–200% and again these increases greatly outlasted the period of the actual task. A correlation was also observed between magnitude of PFC DA and the rapidity of the shift to the new response rule. Notably however, the yoked rats exhibited the highest DA levels, suggesting that the DA system may have been recruited in a vain attempt to figure out the arbitrary response–reward mappings. Likewise, the cognitive load imposed by the set-shift task may also have raised the DA levels in that group, while the only group without a cognitive load, the passively rewarded group, showed no change in PFC DA levels. Hence although there is an extensive neural network responsible for how attentional resources are allocated during behavior, the PFC and in particular the PFC DA system may provide the attentional or cognitive resources needed to understand the meaning of stimuli and strategies to deal with them.

The PFC DA system also becomes activated on tasks specifically designed to assess attention, such as the five choice serial reaction time task (5CSRTT) which is a good rodent analogue of the continuous performance attentional task in humans [54]. In this task, rats must monitor five light ports simultaneously so that if a light comes on, a nose poke must be made to obtain reward. PFC DA and DOPAC levels are increased in the medial PFC over baseline levels during the performance of this task, as measured by in vivo microdialysis [55]. The tendency shown by some rats to respond prematurely on the attentional task – a form of impulsivity – was not correlated with individual levels of DA or the DA metabolite DOPAC, in contrast to what was found for 5-HT. However, *post mortem* analysis revealed that those rats that were the most impulsive had a higher DA turnover in the PFC. Accordingly, on a temporal discounting of reward task that specifically assesses impulsivity, DOPAC (and not 5-HT or 5-HIAA) levels increased by 200–250% during the delay period following choice [56]. These data suggest that DA turnover can also significantly increase in association specifically with attention or in response to impulsive forms of choice.

#### ***14.3.4 Release Conclusions***

DA release in the PFC is modulated in association with a variety of events and behaviors. Aversive stimuli are particularly potent in this regard and can elevate DA

levels by  $\sim 200\%$ , which based on the calculations above, would produce extrasynaptic DA levels of  $>100$  nM with presumed perisynaptic levels well over  $1$   $\mu\text{M}$ . DA release is also often extremely long lasting even when measured with techniques that have millisecond precision such as voltammetry. Finally a common conclusion across studies was that the DA signal might become activated with cognitive demands, when the animal needs to attend to a stimulus, figure out its meaning as well as the rules for attaining rewards and avoiding potentially harmful stimuli.

## 14.4 DA Receptors in PFC

Once released from presynaptic axonal terminals, DA interacts with at least five receptor subtypes:  $D_1$ ,  $D_2$ ,  $D_3$ ,  $D_4$ ,  $D_5$  receptors. Based on G protein coupling and the length of the 3rd cytoplasmic loop and the carboxy tail of the receptors, the current classification of all the cloned DA receptors subdivides them into the  $G_s$ -,  $G_q$ - or  $G_{olf}$ -coupled  $D_1$  family and  $G_{i/o}$   $D_2$  family [57–60]. For simplicity, we will refer to  $D_1/D_5$  receptors as  $D_1$  receptors and  $D_2/D_3/D_4$  receptors as  $D_2$  receptors throughout unless otherwise noted.

$D_2$  receptors exist in high ( $D_2^{\text{high}}$ ) or low ( $D_2^{\text{low}}$ ) affinity states [61] and these two affinity states have been observed in a variety of brain regions and species including rat and human PFC [62, 63]. The affinities for DA are on the order of  $5\text{--}50$  nM vs.  $1\text{--}5$   $\mu\text{M}$  for  $D_2^{\text{high}}$  versus  $D_2^{\text{low}}$  states, respectively [63–65]. The exact percentages of receptors in each state depends on a variety of factors, but for rat striatal slices, Richfield et al. [63] reported  $77\%$  vs.  $23\%$  of  $D_2$  receptors in their high and low states, respectively, while for tissue homogenates others found numbers of  $20\text{--}45\%$  vs.  $50\text{--}80\%$  for  $D_2^{\text{high}}$  and  $D_2^{\text{low}}$  respectively [62, 64–66]. Likewise,  $D_1$  receptors appear to have high and low affinity sites on the order of  $1\text{--}4$  nM and  $1\text{--}2$   $\mu\text{M}$ , respectively, although the affinity of  $D_5$  receptors is 10-fold higher [63, 67, 68]. Therefore, the affinities of these receptors based on available methods, is such that either receptor could be activated by the levels of DA released during the behaviors described above. The relative activation of each receptor may be determined mainly by the prevailing affinity state and their locations relative to sites of release.

In rodent and monkey PFC, the abundance of both  $D_1$  receptor mRNA and  $D_1$  receptor binding sites is significantly greater than the other DA receptor subtypes [69–72]. Anatomically, in the primate PFC, DA-immunoreactive terminals converge on pyramidal cells and parvalbumin-containing, DA-receptive fast-spiking interneurons [73–75]. In rodent PFC, both  $D_1$ - and  $D_2$ -like receptors are also found on pyramidal and nonpyramidal neurons [76–79].  $D_1$  receptors are located primarily on the dendritic spines and shafts of pyramidal neurons and on the dendrites and axon terminals of putative GABAergic interneurons [80, 81].  $D_1$  receptors are usually displaced to the side of the postsynaptic density of large asymmetric synapses that showed profiles not indicative of DA synapses. Likewise, Bergson et al. [80] reported that  $D_1$  and  $D_5$  receptors are usually found on asymmetric synapses and not

at DA synapses. D<sub>1</sub> receptor labeling was found more often in spines than D<sub>5</sub> receptor labeling which was found in shafts or at some distance from a specialization. There is also a high density of D<sub>5</sub> receptors in the perisomatic plasma membrane that may form a perisomatic “microdomain” [82]. Likewise, most D<sub>2</sub> immunogold labeling in dendrites and spines is associated with asymmetric synapses, but is also found outside the postsynaptic density at extrasynaptic and perisynaptic sites [83]. However, the D<sub>2</sub> receptor is likely closer to the release sites than the D<sub>1</sub> receptor [84].

Based on these biochemical and anatomical considerations, it appears that a DA terminal in the PFC does not often oppose DA receptors and that DA likely acts on its receptors mainly through volume transmission. The affinities and locations of the DA receptors in PFC probably dictate which receptor is activated under which conditions. We have argued [85–87] that D<sub>2</sub> receptors, perhaps in their low affinity state, may be closer to release sites and would be activated by the  $\mu\text{M}$  levels of DA thought to be present in the perisynaptic region. In contrast, D<sub>1</sub> receptors, which are located exclusively outside of the perisynaptic region (and perhaps other DA receptors in their high affinity state) would be activated by the hundreds of nM levels of DA present in the extrasynaptic space.

In support of this view, DA applied at concentrations of 10–500 nM increased synaptic responses in PFC neurons via D<sub>1</sub> receptors while DA at concentrations  $>1 \mu\text{M}$  decreased the same synaptic currents via D<sub>2</sub> receptors [88]. As a result, the amount of DA released and the time following a release event may differentially activate D<sub>1</sub> versus D<sub>2</sub> receptors potentially having different functional outcomes. Indeed, D<sub>1</sub> receptors appear to contribute to different cognitive processes than D<sub>2</sub> receptors in the PFC.

## 14.5 Contribution of PFC DA Receptors to Stress

As reviewed above the PFC DA system responds potently to stress. Stress (foot-shock or tailshock) has been shown to increase the density of D<sub>2</sub> dopamine receptors in the PFC and to change their relative affinity state [89]. Changes in D<sub>4</sub> receptors as a result of stress in turn have been shown to impair cognitive function [90]. The pre- and postsynaptic changes in the PFC DA system are relevant to the stress response itself. On an elevated plus maze, PFC DA depletion using 6 hydroxydopamine (6OHDA) caused a lower preference to stay on open arms, lower open arm entries and hypomobility [91]. D<sub>4</sub> knockout mice also exhibited reduced exploration of the open arms of the plus maze and longer latencies to explore the illuminated compartment of the light/dark shuttle box, again indicating an increase in anxiety [92].

One interpretation of these data may be that PFC DA is producing or modulating the physiological response to stress, thereby producing anxiety. However, a variety of DA drugs acting on D<sub>1</sub> and D<sub>2</sub> classes of DA receptors (SKF82958, SKF83566, raclopride, or quinpirole) did not affect the tail pinch evoked increase

in heart rate [93]. Rather, as argued above, the PFC DA system appears to help to evaluate the meaning of a stressor and how to deal with it. As noted above, this process would presumably occur in the period following the experience, which may explain why manipulations of the PFC DA system have a strong effect on the consolidation of fear memories. For example, 6OHDA lesions of the PFC do not affect the acquisition of conditioned fear but rather delay its extinction [94, 95]. Likewise, a D<sub>4</sub> receptor antagonist microinjected into PFC before a fear extinction paradigm reduced the memory of the extinction when tested a day later [96]. Finally, a D<sub>1</sub> receptor antagonist when delivered immediately after training on an inhibitory avoidance-learning task impaired recall 24 h later [97]. These data therefore are consistent with the idea that the PFC DA receptors do not generate an anxiety response per se, but rather are involved in the processes allowing an organism to learn about and adapt to stress-related changes in the environment.

## 14.6 Contribution of PFC DA Receptors to Cognition

### 14.6.1 DA Modulation of Working Memory

Perhaps the most notable and investigated effects of PFC DA receptor manipulation are with regards to their role in working memory. Both D<sub>1</sub> agonists or antagonists and DA depletions in the PFC are highly detrimental to working memory performance [98–104]. These studies suggested that the DA receptor activity is finely tuned in the PFC and perhaps may exhibit an inverted-U-shaped dose–response function [105, 106]. This idea arose from both pharmacological studies in the 1990s where it was reported that systemic administration of higher doses of D<sub>1</sub> agonists impaired performance of the delayed-response working memory task, while very low doses could improve performance [107, 108]. The theory of an inverted-U-shaped dose–response function for D<sub>1</sub> receptor (or more broadly DA) regulation of working memory has since been supported in a variety of studies.

The DA releaser amphetamine at a low dose (<1 mg/kg) produced a delay-dependent improvement in a discrete paired trial variable delay task or a delayed alternation task on a T-maze, while higher doses (>2 mg/kg) impaired performance [109, 110]. Rather than using amphetamine to artificially increase PFC DA levels, Romanides et al. [111] injected a  $\mu$ -opioid agonist into the VTA to selectively activate the mesofrontal pathway and showed that this manipulation also produced impairments in a delayed alternation task in a T-maze that were blocked by a D<sub>1</sub> antagonist injected into the PFC. Conversely, Mizoguchi et al. [112] chronically stressed (4 weeks) and then recovered (10 days) rats as a means to depress PFC DA transmission and found that this impaired the spatial working memory evaluated by a T-maze task. They also reported a concomitant increase in DA D<sub>1</sub> receptor density in the PFC, which may have contributed to the working memory deficits.

Analogous data have been found on a delayed win-shift working memory task. Floresco and Phillips [113] showed that infusions of a D<sub>1</sub> receptor agonist into the

PFC improved performance after a long delay but disrupted performance after a shorter delay. This result is notable because these authors also showed that DA levels measured using microdialysis on the same task were increased at short delays and decreased at long delays [51]. The interpretation of these data fit well into the inverted-U framework. Specifically, rats with either an intrinsically or an imposed decrease in performance may have a suboptimal activation of D1 receptors and therefore benefit more from D1 receptor activation. Rats performing optimally at baseline may have optimal D1 receptor activation and suffer from further exogenous D1 receptor activation.

Another situation where differential effects of DA receptor activation occur is with respect to individual levels of performance. Granon et al. [114] divided rats into two groups, with low and high baseline levels of accuracy on the five choice serial reaction time task and found that a partial D1 agonist (SKF38393) enhanced performance only in the lower baseline group. By contrast, only higher performing rats were susceptible to the detrimental effects of an intra-PFC D1 receptor antagonist (but not sulpiride, a D2 receptor antagonist). A plausible interpretation of these data is that the mesofrontal DA system is primarily engaged to optimize signal detection in this task. A follow-up study by Chudasama and Robbins [115] used a combined attention and working memory (CAM) task in which rats had to commit to working memory over a short delay the location of visual events they had successfully detected. A full DA D1 receptor agonist, SKF81297, produced dose-dependent effects on the attentional component, thereby replicating and expanding the findings of Granon et al. [114]. However, effects on the working memory component of the task were much less clear; some improvements were evident when the stimulus duration was reduced at certain doses and delays. At the highest dose, good memory at short delays was impaired whilst poor memory at longer delays was improved. Thus, D1 receptor stimulation sufficient to improve attentional accuracy could facilitate or disrupt working memory performance in a dose- and delay-dependent manner but the effect appears to depend on the individual's baseline level of performance and perhaps basal levels of DA.

Support for the inverted-U dose–function relationship has also been obtained from studies in humans with genetically determined differences in intrinsic DA levels. A functional polymorphism for COMT involves a methionine (Met) to valine (Val) substitution at codon 158 [116, 117]. The Met allele has  $\frac{1}{4}$  the enzyme activity as the Val allele [116] and therefore Met individuals should have higher DA levels specifically in PFC. The inverted-U theory would predict that Val individuals who have intrinsically lower DA levels would be off the optimal point of the inverted-U curve and therefore do poorly on tests of working memory and executive function, but would benefit from manipulations that increase PFC DA levels. In contrast Met carriers should possess near optimal levels of DA receptor stimulation at baseline, and further elevations in DA levels would be detrimental [118]. Accordingly, human COMT Val/Val genotype individuals often exhibit poorer performance on tests of working memory and executive function that involve the PFC compared to Met/Met individuals [119]. These patterns can be changed by manipulating DA levels pharmacologically: Val/Val subjects showed either improved performance on tests of

executive function when given a COMT inhibitor (Tolcapone) or amphetamine, whereas the Met/Met individuals got less efficient, consistent with moving them off the optimal point of the inverted-U curve (3-back task in [120, 121]). Therefore, although the inverted-U theory, as initially proposed, was specific for D1 receptor activation, evidence across species now provides compelling support for the idea that inverted-U dose–function relationship may hold for PFC DA signaling in general.

### ***14.6.2 How Is DA Improving Working Memory?***

Early electrophysiological investigations showed that putative D1 receptor activation produced a (relative to baseline) stronger amplification of delay- and response-related single unit activity during the delayed-response task [100]. Yet D1 agonists were also shown to diminish non-target-related activity to a much larger degree than target-related activity [105, 122]. In this way, at the appropriate activation range D1 receptors might be said to increase the gain or increase the signal and decrease the noise, as suggested by early experimental and theoretical work [123–125].

In terms of the human PFC, an explanation of what signal to noise means and how it might be modulated by DA has been provided by Winterer and Weinberger [126–132]. Their definition of “noise” is the variability in the phase relationship of evoked electroencephalic activity (event-related potentials, ERP) with respect to a stimulus. It represents increased stimulus-related variability both across time and across the PFC [126]. Noise measures, according to the definition of Winterer et al. [126–131], are significantly affected by COMT genotype. Winterer and colleagues showed that on attentional tasks frontal noise in the EEG was lower in Met/Met individuals [133] while Val/Val individuals had greater frontal noise [129]. Prefrontal noise in these individuals was also negatively correlated with performance on the N-back working memory task [134]. Therefore, these EEG data indicate that, relative to homozygous Met individuals, homozygous Val carriers with presumed lower PFC DA levels show more “noise” based on various measures. Along with the differences in noise there is also a difference in the “signal” between groups as homozygous Met/Met individuals had a peak blood-oxygen-level-dependent (BOLD) response that was stronger than that found in Val/Val carriers, indicating that Met/Met genotype may also confer an increase in signal processing [131].

How might a modulation of signal to noise occur at a cellular level? DA exerts its impact on working memory and neural activity through a multitude of effects on presynaptic release, NMDA and GABA<sub>A</sub> currents, the persistent Na<sup>+</sup> current, various Ca<sup>2+</sup> currents, the slowly inactivating K<sup>+</sup> current, and the H current [135–143]. To understand the functional implications of this intricate pattern of DA-induced cellular and synaptic changes for neural processing and PFC-dependent cognition, biophysically realistic computational models have proven useful [144–148]. Such models consist of sets of differential equations for each neuron that describe the evolution of the somatic and dendritic membrane potentials according to various

voltage-gated,  $\text{Ca}^{2+}$ -gated, and synaptically gated ionic currents. The appeal of these models is their close relation to biophysical quantities measured electrophysiologically, which allows the effects of DA measured *in vitro* to be implemented rather directly with few additional assumptions. These systems can reproduce the low and high activity states classically associated with spontaneous (baseline) activity and stimulus-specific delay activity in working memory tasks, respectively [149, 150]. Starting from a configuration that mimics certain functional characteristics of a working memory network, the models explored how the D1- or D2-receptor-mediated changes found *in vitro* could affect widespread cortical network dynamics. The results revealed that the combined effects of D1-induced conductance modulations led to a change in network dynamics that made it more difficult to switch between various high activity (active memory) states, i.e., to an increase in the “energy barrier” between different discrete states of network activity [144–148, 151]. These effects are partly rooted in the differential contribution of various D1-modulated currents to different activity regimes: The D1-induced increase in NMDA and modulation of other voltage-dependent currents, by boosting recurrent excitation within cell assemblies, increases the strength of the currently active memory state. The concomitant increase in  $\text{GABA}_A$  currents leads to fiercer competition among different active ensembles of neurons, thereby limiting the number of items maintained by recurrent excitation. At the same time, this D1 mediated enhancement of  $\text{GABA}_A$  currents and the reduction in glutamate release probability make it harder to evoke activity in cell assemblies in the first place [145]. At the *in vivo* electrophysiological level, these dynamic changes would predict an increased signal-to-noise ratio in the sense of an increased differentiation of firing rates associated with currently active memory states from those associated with nonactivated states or spontaneous activity. A related complementary idea, namely an increased signal-to-noise ratio via a DA-induced change in gain of the single neuron input/output function, had been proposed in more abstract terms within connectionist-like models more than 15 years ago by Servan-Schreiber et al. [125], and has received experimental support recently [151]. These processes provide a mechanistic basis for the putative increase in signal to noise thought to occur at the peak or the optimal region of the inverted-U curve.

## 14.7 DA Modulation of Working Memory or Working Attention?

Whilst there is considerable evidence to support a role for PFC DA in working memory, it is clear that the original concept of working memory from animal studies based on the spatial delayed response, delayed matching, or delayed saccade tasks, may require some modification to accommodate results that indicate a role for DA in attentional processing *per se* in the PFC. Thus, for example, depletion of PFC DA produced impairments in the development of an attentional set, as tested by a series of repeated intradimensional shifts in discrimination learning by marmoset monkeys [152], yet it both increased distractibility and improved the performance of

extra-dimensional shifting. This is consistent with the hypothesis that DA modulates the stability of rules for representation of responses. These data are also consistent with evidence that distraction during working memory tasks is particularly important for detecting deficits after prefrontal DA depletion [153] and with the effects of systemic or intra-PFC agents on attention and working memory in rats ([114, 115, 154, 155], see below). Therefore, as noted above, DA levels in PFC become elevated upon cognitive load and in this way may focus attentional resources to the task at hand, including focusing attention on critical aspects of working memory tasks, putatively by increasing signal-to-noise ratios.

## 14.8 DA Modulation of Response Flexibility

### 14.8.1 D2 Receptors and Response Flexibility

If the main purpose of DA is to increase signal to noise in PFC, then why have the optimal signal-to-noise ratio occur only within limited range at the midpoint of the inverted-U curve? One reason may be that the “off peak” regions of the inverted-U may create conditions that are optimal for other forms of cognition. As noted above, 6OHDA lesions can improve the performance of extra-dimensional shifting [152]. Furthermore, Met carriers are less flexible and Val carriers more flexible during reversals on a competing programs task [156]. Val carriers were also more flexible in processing emotional stimuli [157]. Behavioral and neurochemical lesioning studies have suggested a partly antagonistic nature of working memory and cognitive flexibility requirements [153, 158] and therefore response flexibility may be optimal at other portions of the curve if one assumes the inverted-U theory is based on DA concentrations and not just D1 receptor activation. More specifically, the high and low ends of the curve may be more optimal for D2 receptor activation, and D2 receptor activation may be more optimal for flexible modes of responding [85, 87]. There is some support for the idea that D2 receptors in PFC may be particularly involved in flexible modes of responding. In monkeys the D2 receptor antagonist raclopride impaired the performance of a reversal task of response flexibility [159]. In the rat, the role of PFC D2 receptors in set shifting was demonstrated clearly by Floresco et al. [155] using a 4 arm + maze task. Here the rats were trained to respond using an egocentric strategy of always going to the arm that was in the same spatial location relative to their frame of reference (i.e., always go right or left). The rule then changed, and in order to perform optimally rats now had to visit arms according to a visual cue, regardless of its egocentric location (or vice versa). Floresco et al. [155] found that a D2 antagonist but not a D1 antagonist disrupted performance and caused perseverative errors on the task. In humans, a D2 antagonist has been shown to deteriorate performance on tests of attentional set shifting and response flexibility [160]. Moreover, in a group of healthy volunteers, Mehta et al. [161] showed that the D2 antagonist sulpiride not only impaired task set-switching but actually protected against the deleterious effects of intervening task-irrelevant distractors on a spatial

working memory task, as would be expected with a blockade of D2 receptors and a shift of PFC networks into the peak of the curve optimal for D1 receptor activation. Conversely, activation of D2 receptors with the D2 agonist bromocriptine improved performance on the quintessential task of response flexibility, the Wisconsin Card-Sorting Task, in patients with traumatic brain injuries [162]. Collectively, these data provide support for the idea that PFC D1 receptor activation is optimal for working memory, while D2 receptor activation may be optimal for cognitive flexibility.

Other data provide apparent difficulties for this simple idea. For example, sulpiride a D2 receptor antagonist impaired, whilst a D2 agonist, bromocriptine, improved delayed spatial working memory performance in human studies [161, 163–165]. Furthermore, the D2 agonist bromocriptine impaired the ability to reverse a learned probabilistic discrimination, which can be considered a form of behavioral flexibility [161, 164]. These apparently contradictory findings highlight the complexity of the DA system and how multiple factors come into play in any study of DA function.

One critical factor that must be taken into account is the baseline performance of the subjects as discussed above. For instance, the improvement in aspects of spatial span memory by the D2 agonist bromocriptine [164] was notable for being baseline-dependent; those subjects with worse spans on placebo showed the largest improvements. This finding is consistent with what had been found earlier by Kimberg et al. [166] who showed that subjects with lower reading spans improved on bromocriptine on various tests of executive functioning. This also parallels the findings of Frank and O'Reilly [167] that another D2 receptor agonist, cabergoline, improved the flexible updating (i.e., switching) of working memory in healthy volunteers with low reading spans.

A similar baseline dependency has also recently been found for the effects of bromocriptine on attentional switching and working memory [168]. In this case, the effect depended on the baseline level of impulsivity, as measured by the Barratt Impulsivity Scale. Notably, the high-impulsive subjects also exhibited lower reading spans than low-impulsive individuals. These authors used a cued delayed matching to sample task in which healthy volunteers were required to retrieve either briefly-presented faces or scenes, depending on the color of the fixation cross. Distractors were also presented in the retention interval. The required category was switched in such a way as to induce switching or maintenance of the encoding “set,” switching being slower and more error prone. In this study, bromocriptine reduced behavioral switch costs as expected for a drug that activates D2 receptors and facilitates behavioral flexibility. Yet this occurred only in high-impulsive subjects, while in low-impulsive subjects, if anything, performance was impaired.

These data highlight an important point; that many cognitive functions other than working memory depend on baseline DA levels, perhaps in regions other than the PFC. Accordingly, at least in some subject populations, the level of impulsivity is correlated with genetic determinants of intrinsic DA levels [169, 170] especially in the striatum [170, 171]. Likewise, the drug-induced improvement by bromocriptine in the work of Cools et al. [168] was also accompanied by a drug-induced modulation of activity in the putamen, whereas lateral frontal activity was unaltered during

switching. Thus, impulsivity and flexibility may be determined by the intrinsic levels of DA in brain regions other than the PFC and may be optimal at other portions of the putative inverted-U curve than for working memory.

Another recent study [172] has highlighted yet another important factor in determining the effects of DA acting at receptors in PFC and striatum: genetic polymorphisms that predict effects on reward and avoidance learning. A polymorphism in the DARPP-32 gene, associated with striatal dopamine function (putatively allied to D1 receptor function), predicted relatively better probabilistic reward learning. Conversely, the C957T polymorphism of the DRD2 gene, associated with D<sub>2</sub> receptor function, predicted the degree to which participants learned to avoid choices that had been probabilistically associated with negative outcomes. The Val/Met polymorphism of the COMT gene, associated with prefrontal cortical DA function, predicted participants' ability to rapidly adapt behavior on a trial-to-trial basis – in other words utilizing working memory. Finally, a computational model was used to account for these effects based on three independent genetic effects on three parameters of a reinforcement learning-based model.

These important studies highlight a number of key points; first that D2 receptors exert effects on cognition in humans at striatal as well as prefrontal cortical sites. Notably, in human psychopharmacological studies drugs are necessarily administered systemically and may therefore affect receptors in noncortical sites, especially the striatum, which may function in a reciprocal manner to the cortex in terms of its regulation by DA. Second, in human subjects, brain imaging methodology (PET or fMRI) will probably be necessary for unraveling such effects. Thirdly, knowledge of individual differences (possibly at the level of genetic polymorphisms) will also be vital for predicting effects of DA-ergic agents. This may well prove to be a key consideration when investigating effects of DA-ergic agents on cognition for another reason; with DA D2 agents there is the possibility of low-dose autoreceptor activation, which produces opposite effects on striatal DA-ergic activity to that normally produced by agonist activity. These effects particularly afflict human studies where low doses must be employed to avoid debilitating nausea or extrapyramidal side-effects. Virtually all of the studies reviewed above are susceptible to this issue. Indeed, one of them [167] actually assumed that their effects of cabergoline and haloperidol indeed result from autoreceptor actions. One way of resolving this issue will be to perform experiments using PET to measure displacement of the PET DA ligand by DA. Mehta et al. [173] used PET with the DA D2 receptor ligand raclopride to study the effects of sulpiride on spatial working memory. They replicated the earlier finding with this task of impaired accuracy but also showed that this impairment was significantly but *inversely* related to raclopride receptor occupancy – leading them to speculate that the detrimental effects of sulpiride were actually related to presynaptic effects and that extrastriatal D2 receptors may also play a role. Clearly, the future availability of methods for visualizing cortical D2 receptors which now are very difficult to detect, will enable a more satisfactory resolution of these issues.

Collectively, these data suggest that D2 receptors both within and outside of the PFC have a preferential role in the regulation of behavioral flexibility. The effects

may be determined by the genetically regulated intrinsic levels of DA system activity. These levels in turn determine where a particular individual sits on the putative inverted-U curve for DA. Furthermore there may be multiple inverted-U-type curves for DA in various brain regions that influence not only response flexibility but also other processes such as impulsivity.

### ***14.8.2 How Is DA Modulating Response Flexibility?***

In addition to working memory, computational models based on the known biophysical effects of DA have also provided insights into the question of how DA might regulate response flexibility. As noted above, the striatal DA system contributes to a number of “PFC-mediated” behaviors and the theoretical models of Frank and O’Reilly provide an account of how D2 receptors in the striatum might influence flexible modes of responding [167, 172, 174]. In their models, information within the PFC is discarded and updated based on the preferential activation of the striatal “Go” and “no-Go” systems. Within the striatum, unlike the PFC, neurons tend to contain either D1 or D2 receptors, and the idea is that activation of neurons with D2 receptors form the “no-GO” system and promote avoidance learning. Avoidance learning is of course a key aspect of flexible responding since a behavior must first be inhibited when it is no longer rewarded. The striatal D1 containing “Go” pathway neurons then are suggested to update network ensembles in PFC that maintain information in working memory. There is currently a growing literature supporting the predictions of this model of striatal DA function.

At the level of the PFC, D2 receptors may achieve a similar function but through different biophysical means. D2 agonists tend to act oppositely from D1 receptors on NMDA and GABA<sub>A</sub> currents, as well as on pyramidal cell excitability in PFC [85, 88, 136, 141]. The collective effect of simulating the D2-mediated reduction in NMDA and GABA currents was a reduction in the “barrier” separating activity states in the model networks, i.e., the valleys of the energy landscape become so flat and so near that noise may easily push the system from one representation into the other. This resulted in spontaneous pop-out of activity states caused by noisy fluctuations, highly unstable representations, and fast and spontaneous transitions between many different activity states [87, 141, 145, 148]. The D2-state, due to the decreased energy barrier among activity states, would allow easier access to PFC networks and faster switching among different PFC activity patterns such that the network may quickly cycle through multiple representations that could become active nearly simultaneously [87, 141, 145, 148]. Therefore, the D1-mediated changes in PFC neurons and networks may explain why their activation is optimal for working memory and attention, while the D2-mediated changes may explain why these receptors are more involved in other types of cognition, such as response flexibility and impulsivity.

While the PFC DA system is activated during the various cognitive processes discussed above, recall that the most striking activation occurs in response to various

stressors. Also recall that it appeared to be mainly D2-like or more specifically D<sub>4</sub> receptors in the PFC that are the critical modulators of fear or stress-related behaviors. It is of note that the low affinity state of the D<sub>4</sub> receptor is comparable to that of the D<sub>2</sub> receptor discussed above, while the high affinity state of the D<sub>4</sub> receptor is an order of magnitude lower than the high affinity state of the D<sub>2</sub> receptor [67, 68]. Therefore, the large stress-induced increases in PFC DA may be particularly well-suited to activate PFC D2-like and especially D<sub>4</sub> receptors. Remarkably the electrophysiological effects induced by D<sub>4</sub> receptors are similar to those produced by D<sub>2</sub> receptors, including a reduction in NMDA and GABA<sub>A</sub> currents [175, 176]. As described above, modulation of these currents was the critical determinant of the D2-mediated effects in the computational models and therefore, D<sub>4</sub> receptor stimulation should produce a similar dynamic. This implies that the strong release of DA in response to stress may activate D<sub>4</sub> receptors and establish a “D2-like” dynamic in PFC, which is associated with increased flexibility characteristic of effective problem solving under stress.

## 14.9 Summary and Conclusions

Anatomical, biochemical, neuropharmacological, and electrophysiological data on the PFC DA system were reviewed. The data suggested that the PFC DA system was activated under a variety of circumstances, usually for periods that outlasted the initiating event. Across studies, a consistent theme that emerged was that the PFC DA system becomes activated in response to a cognitive challenge when the organism has to understand the meaning of a particularly salient stimuli and how to deal with it. The levels of DA evoked by stressful stimuli were either measured or extrapolated to be on the order of 200–500 nM in the extrasynaptic space, with perisynaptic levels in the low  $\mu$ M range. These levels of DA released would be sufficient to activate D1-like and/or D2-like receptors, depending on their affinity state and anatomical location. However, in terms of functional measures, such as the modulation of NMDA and GABA currents, D1-like receptors tended to modulate currents in the range of hundreds of nM while D<sub>2</sub> and possibly D<sub>4</sub> receptors tended to modulate the same currents at much higher levels. D<sub>2</sub> receptors in their high affinity state may occupy the far left side of the curve, responding to very low levels of DA and paradoxically producing a similar dynamic to that observed at high DA levels. Once activated, D1-like and D2-like receptors initiated a variety of changes that modulated both intrinsic and synaptic currents on PFC neurons, including importantly NMDA and GABA. Computational models showed that the D1-like receptor-mediated changes tended to increase the signal to noise of cortical representations and protect these representations from distraction. In contrast, D<sub>2</sub>/D<sub>4</sub> receptor-mediated changes tended to be in the opposite direction and collectively aided in avoidance learning and subsequently decreased the robustness of cortical representations by putting the PFC in a mode that could handle information in a more flexible manner.

One way in which these data could be integrated would be to suggest that DA is released in the PFC under conditions of cognitive load when cognitive resources must be dedicated to understand a stressful or rewarding stimulus and how to deal with it most effectively. D<sub>2</sub>/D<sub>4</sub> receptors closer to the sites of release may be first activated by the higher levels of prevailing DA locally and initiate a flexible mode of processing in an attempt to find solutions. As the DA diffuses away, the exclusively extrasynaptically located D<sub>1</sub>-like receptors may become active and help to protect this processing from distractors that could interfere with the cognitive search. This implies that PFC networks are processing information perhaps simultaneously in different modes so as to most effectively deal with the events at hand. Whether this interpretation of the data or another interpretation is correct, it would appear that the PFC DA system does exist in some sort of a balance and it is clear that different receptors have different functions under different conditions. Therefore, one of the greatest challenges to the field will be to understand how PFC DA maintains a balance so as to become activated in a manner that is optimal for dealing with the task at hand.

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# Chapter 15

## In Vivo Imaging of Dopamine Receptors

Anissa Abi-Dargham and Marc Laruelle

**Abstract** Positron emission tomography (PET) and single photon emission computed tomography (SPECT) have been used to study indices of dopamine transmission in schizophrenia, mood disorders, anxiety, dimensions of personality, attention deficit and hyperactivity disorder (ADHD), and addiction. This is due not only to suspected dopamine alterations in these disorders, but also to the availability of a wide array of probes to image the dopaminergic system. In this review we will summarize some of the findings that have emerged from these studies and highlight controversies and future needs.

**Keywords** PET imaging · Dopaminergic receptors · Schizophrenia · Occupancy measures · Addiction

### 15.1 Introduction

In vivo molecular imaging with positron emission tomography (PET) and single photon emission computed tomography (SPECT) can be used to measure protein molecules such as receptors, transporters, and enzymes, as well as cellular processes such as transmitter synthesis and release. An important property of PET and SPECT is that they can measure molecules present in the brain in the nanomolar to picomolar range of concentrations [1]. To date, the neurochemical system most widely studied in humans with imaging is the dopamine system. This relates to multiple factors: (1) the availability of probes for many dopaminergic targets, including  $D_{1/5}$  receptors,  $D_{2/3}$  receptors, dopamine transporters (DAT), and vesicular monoamine transporters (VMAT), (2) the recent availability of probes that are agonists, such as [ $^{11}\text{C}$ ]PHNO, which label the high-affinity sites of  $D_{2/3}$  receptors, (3) the

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A. Abi-Dargham (✉)

Division of Translational Imaging, Departments of Psychiatry and Radiology, Lieber Center, Columbia University College of Physicians and Surgeons, New York, NY 10032, USA  
e-mail: aa324@columbia.edu

availability of probes with various levels of affinity revealing receptors in areas of the brain with low receptor density, such as [ $^{18}\text{F}$ ]Fallypride or [ $^{11}\text{C}$ ]FLB457, in addition to areas of high receptor density, such as [ $^{11}\text{C}$ ]raclopride, (4) and most importantly the relevance of dopamine to many basic mental processes (cognition, reward) and many psychiatric disorders: schizophrenia, mood disorders, anxiety, dimensions of personality, attention deficit and hyperactivity disorder (ADHD), addiction. Studies using *in vivo* imaging of dopaminergic receptors and other transmission indices have been conducted comparing patients in these categories to healthy subjects. Furthermore, dopaminergic interventions have a prominent role in our treatment of psychosis, depression, ADHD, and others. For this reason, PET and SPECT have been used not only to assess the involvement of various dopaminergic indices in mental activity and psychiatric disease states, but also to assess the roles of dopaminergic receptors in the treatments for these psychiatric conditions.

In this chapter we will describe the contributions of imaging dopaminergic receptors, at baseline, after manipulation of dopaminergic levels *in vivo*, and after treatment, to the understanding of psychiatric disease and therapeutic effects.

## 15.2 Imaging Dopamine Receptors in Schizophrenia

Molecular imaging became available in the 1980s at a time when the dopaminergic hypothesis of schizophrenia had been a focus of research interest for decades, initially because of the early observations that dopamine receptors are activated by psychostimulants, that non-reserpine neuroleptics are dopamine antagonists, and that dopamine plays an important role in the extrapyramidal motor system. This interest was strengthened later by the discovery of the correlation between clinical doses of antipsychotic drugs and their potency to block DA D<sub>2</sub> receptors [2, 3] and studies confirming the psychotogenic effects of DA-enhancing drugs [4, 5]. These led to the classical dopamine hypothesis of schizophrenia, postulating an increase in dopamine transmission in this condition.

Over the years, the awareness of negative symptoms (flattening of affect, apathy, poverty of speech, anhedonia, and social withdrawal) and cognitive symptoms (deficits in attention, working memory, and executive functions) in this illness and of their resistance to D<sub>2</sub> receptor antagonism led to a reformulation of the classical DA hypothesis. Functional brain imaging studies suggested that these symptoms might arise from altered prefrontal cortex (PFC) functions [6]. A wealth of preclinical studies emerged documenting the importance of prefrontal DA transmission at D<sub>1</sub> receptors (the main DA receptor in the neocortex) for optimal PFC performance [7]. Together, these observations led to the hypothesis that a deficit in DA transmission at D<sub>1</sub> receptors in the PFC might be implicated in the cognitive impairments and negative symptoms of schizophrenia [8, 9] while the excess DA transmission may be related only to the core or “positive” symptoms (hallucinations, delusions).

The advent in the early 1980s of techniques based on PET and SPECT to measure indices of DA activity in the living human brain opened the possibility of direct investigation of these hypotheses. We will review these below.

Studies of striatal DA transmission in schizophrenia examined both post-synaptic ( $D_{2/3}$  receptors and  $D_{1/5}$  receptors, although for simplicity of notation we will refer to these as  $D_2$  receptors and  $D_1$  receptors) and presynaptic (DOPA decarboxylase activity, stimulant-induced DA release, baseline DA release, and DAT) functions.

### ***15.2.1 Striatal DA Transmission and Receptors***

#### **15.2.1.1 Dopamine Receptors**

Striatal  $D_2$  receptor density in schizophrenia has been extensively studied with PET and SPECT imaging. Studies comparing parameters of  $D_2$  receptor binding in patients with schizophrenia and healthy controls ( $n = 17$  studies) included a total of 245 patients (112 were neuroleptic naïve and 133 were neuroleptic free for variable periods of time) [10–26]. These patients were compared to 231 controls, matched for age and sex. Eleven studies used PET and six studies used SPECT. Radiotracers included butyrophenones ( $[^{11}\text{C}]\text{N-methyl-spiperone}$ ,  $[^{11}\text{C}]\text{NMSP}$ ,  $n = 4$ , and  $[^{76}\text{Br}]\text{bromospiperone}$ ,  $n = 3$ ), benzamides ( $[^{11}\text{C}]\text{raclopride}$ ,  $n = 3$ , and  $[^{123}\text{I}]\text{IBZM}$ ,  $n = 5$ ) or the ergot derivative  $[^{76}\text{Br}]\text{lisuride}$ ,  $n = 2$ .

Only 2 out of 17 studies detected a significant elevation of  $D_2$  receptor density parameters at a level  $p < 0.05$ . However, meta-analysis of the 17 studies reveals a small but significant elevation of  $D_2$  receptors in patients with schizophrenia [27]. If  $D_2$  receptor density did not differ between patients and controls (null hypothesis), one would expect approximately 50% of the studies to report lower  $D_2$  receptor levels in schizophrenics compared to controls. Instead, 13 out of 17 studies reported an increase (although not significant in 11 out of 13 cases), 2 reported no change, and only 2 studies reported a decrease in patients compared to controls. This distribution is unlikely ( $p < 0.05$ , sign test) under the null hypothesis. The average effect size (mean value in schizophrenic group – mean value in control group/SD in control group) of the 17 studies was  $0.51 \pm 0.76$  (SD), and the probability to yield such effect size under the null hypothesis is again lower than 0.05. The aggregate magnitude of this elevation is thus 51% of the SD of controls. Given an average control SD of 23%, the effect is about 12%. To detect an effect size of 0.51 at 0.05 significance level with a power of 80%, a sample of 64 patients and 64 controls would be needed. Clearly, none of the studies included enough patients to detect this small effect with appropriate power.

No clinical correlates of increased  $D_2$  receptor binding parameters have been reliably identified. Thus, the simplest conclusion from these studies is that untreated or never treated patients with schizophrenia show a modest elevation in  $D_2$  receptor density parameters (of about 12%) of undetermined clinical significance, that all studies were underpowered, and that positive results occasionally reported [10, 11] are due to a sampling effect. A similar conclusion was reached by Kestler et al. [28]

in their own meta-analysis. This conclusion is reached under the assumptions that all studies measured parameters from the “same” D<sub>2</sub> receptors population. Clearly, the aggregate D<sub>2</sub> receptor increase reported in vivo in drug-free patients is lower than that the increase reported in postmortem studies, supporting the idea that post-mortem results were significantly affected by antemortem medications. A study in unaffected monozygotic twins of patients with schizophrenia also suggested that a modest elevation of D<sub>2</sub> receptors in the caudate might be associated with genetic vulnerability to schizophrenia [29].

Studies performed with butyrophenones ( $n = 7$ ) have an effect size of  $0.96 \pm 1.05$ , while studies performed with other ligands (benzamides and lisuride,  $n = 10$ ) have an effect size of  $0.20 \pm 0.26$ , a difference that is significant ( $p = 0.04$ ). This observation suggests that the in vivo increase in butyrophenone binding might be larger than the increase in benzamide binding. Unfortunately, no studies have been reported in which the same subjects were scanned with both ligands. Such a study is warranted to directly test this proposition. Several hypotheses have been advanced to account for the existence of a differential increase in [<sup>11</sup>C]NMSP in vivo binding in patients with schizophrenia in the face of normal in vivo benzamide binding. Since [<sup>11</sup>C]raclopride and [<sup>123</sup>I]IBZM bind to D<sub>2</sub> and D<sub>3</sub> receptors while [<sup>11</sup>C]NMSP binds to D<sub>2</sub>, D<sub>3</sub> and D<sub>4</sub> receptors, this difference could reflect a selective elevation of D<sub>4</sub> receptors in schizophrenia [30]. However, this hypothesis has not been substantiated [31]. Another hypothesis derives from the observation that D<sub>2</sub> receptors, like several G-protein-coupled receptors, exist in monomers, dimers, and other oligomeric forms [32–35]. Photoaffinity-labeling experiments suggested that butyrophenones detect only monomers, while benzamides detect both monomers and dimers. Thus, increased butyrophenone binding and normal benzamide binding might reflect a higher monomer/dimer ratio in schizophrenia. This interesting hypothesis deserves further exploration. A third proposition evolved around the idea that the binding of these ligands would display different vulnerability to competition by endogenous DA [36, 37]. This proposition was based on two assumptions: (1) the concentration of DA in the proximity of D<sub>2</sub> receptors might be higher in patients compared to controls and (2) [<sup>11</sup>C]NMSP might be less affected than [<sup>11</sup>C]raclopride or [<sup>123</sup>I]IBZM binding by endogenous DA competition. It follows that D<sub>2</sub> receptor density measured in vivo with [<sup>11</sup>C]raclopride and [<sup>123</sup>I]IBZM would be “underestimated” to a greater extent in patients with schizophrenia than in control subjects. This hypothesis played an important role in bringing the endogenous competition concept to the attention of the imaging field (see below).

Regarding striatal D<sub>1</sub> receptors, several imaging studies [16, 38, 39] have confirmed the results of postmortem studies of unaltered levels of these receptors in the striatum as a whole in patients with schizophrenia.

Several lines of evidence suggest that D<sub>3</sub> receptors might play an important role in the pathophysiology and treatment of schizophrenia [40, 41]. Until recently, imaging D<sub>3</sub> receptors was not feasible: PET radiotracers commonly used to study D<sub>2</sub> and D<sub>3</sub> receptors exhibit similar affinities for both receptors and the concentration of D<sub>3</sub> receptors in the human striatum is lower than that of D<sub>2</sub> receptors.

[<sup>11</sup>C]PHNO is an agonist at D<sub>2/3</sub> receptors with higher affinity for D<sub>3</sub> versus D<sub>2</sub> [42]. A study comparing [<sup>11</sup>C]PHNO in patients with schizophrenia to healthy controls found no differences showing no alterations in the affinity for the receptors or in the D<sub>3</sub> composition [43], although a more selective tracer is needed to confirm these results.

### 15.2.1.2 Dopamine Transporter

Three imaging studies have confirmed the in vitro observation of normal striatal DAT density in schizophrenia [44, 45]. In addition, no association between amphetamine-induced DA release and DAT density was found [44], suggesting that the increased presynaptic output revealed by the studies reviewed above is not due to higher terminal density.

### 15.2.1.3 Vesicular Monoamine Transporter

Using the radiotracer [<sup>11</sup>C]DTBZ [46] Taylor et al. were not able to show any difference in vesicular monoamine transporter BP in patients with schizophrenia compared to healthy subjects.

### 15.2.1.4 Striatal Amphetamine-Induced DA Release

In addition to the small increase in striatal D<sub>2</sub> receptors, studies have shown increased rates of dopamine synthesis and release. The decrease in [<sup>11</sup>C]raclopride and [<sup>123</sup>I]IBZM in vivo binding following acute amphetamine challenge has been well validated as a measure of the change in D<sub>2</sub> receptor stimulation by DA due to amphetamine-induced DA release [47–49].

Three studies showed that the amphetamine-induced decrease in [<sup>11</sup>C]raclopride or [<sup>123</sup>I]IBZM binding is elevated in untreated patients with schizophrenia compared to well-matched controls [50, 51] [49]. A significant relationship was observed between the magnitude of this effect and the transient induction or worsening of positive symptoms. This exaggerated response of the DA system to amphetamine was observed in both first-episode/drug-naïve patients and previously treated patients [52], but was larger in patients experiencing an episode of illness exacerbation than in patients in remission at the time of the scan [52]. This exaggerated DA reactivity did not appear to be a nonspecific effect of stress, as higher self-reports of anxiety before the experiments were not associated with larger effect of amphetamine on [<sup>123</sup>I]IBZM binding. Furthermore, non-psychotic subjects with unipolar depression, who reported levels of anxiety similar to the schizophrenic patients at the time of the scan, showed normal amphetamine-induced displacement of [<sup>123</sup>I]IBZM [53].

### 15.2.1.5 Baseline Occupancy of Striatal D<sub>2</sub> Receptors by DA

In rodents, acute depletion of synaptic DA is associated with an acute increase in the *in vivo* binding of [<sup>11</sup>C]raclopride or [<sup>123</sup>I]IBZM to D<sub>2</sub> receptors [54]. The increased binding is observed *in vivo* but not *in vitro*, indicating that it is not due to receptor upregulation [55], but to removal of endogenous DA and unmasking of D<sub>2</sub> receptors previously occupied by DA. A similar acute DA depletion technique paired with D<sub>2</sub> receptor imaging in humans using alpha-methyl-para-tyrosine, αMPT, an irreversible inhibitor of tyrosine hydroxylase, the rate-limiting step in dopamine synthesis, has been developed to assess the degree of occupancy of D<sub>2</sub> receptors by DA [55]. In schizophrenia, there was a higher occupancy of D<sub>2</sub> receptors by DA in patients experiencing an episode of illness exacerbation, compared to healthy controls [24]. Higher synaptic DA levels in patients with schizophrenia were predictive of good therapeutic response of these symptoms following 6 weeks of treatment with atypical antipsychotic medications [24].

Both sets of findings, stimulated and baseline DA release, shown to be higher in drug naïve patients with schizophrenia than in controls [56], have generally been interpreted as reflecting an increase in synaptic DA in the schizophrenic group. Another interpretation of these observations would be that schizophrenia is associated with increased affinity of D<sub>2</sub> receptors for DA, but this was shown not to be the case recently by using a D<sub>2/3</sub> agonist radiotracer [43]. Furthermore, the increased release is consistent with the findings of presynaptic increased synthesis as shown by [<sup>18</sup>F]DOPA or [<sup>11</sup>C]DOPA studies.

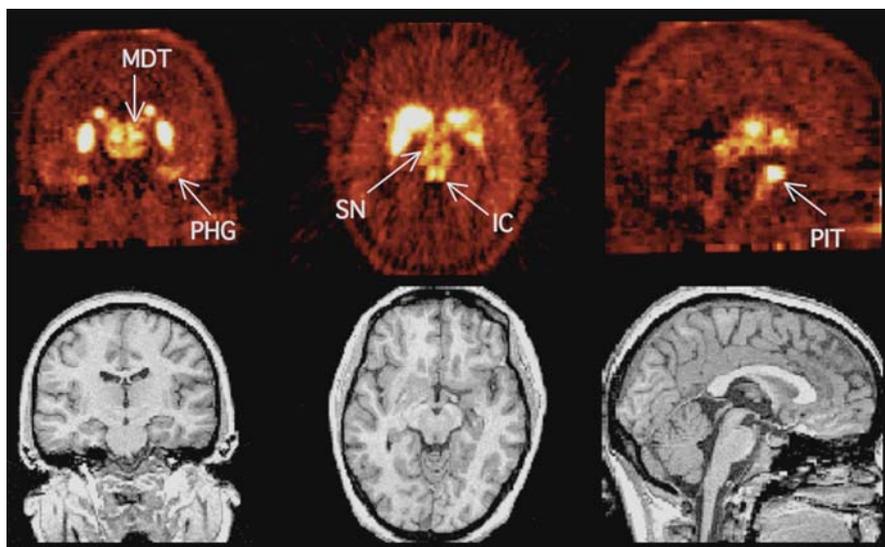
### 15.2.1.6 Striatal Aromatic Amino Acid Decarboxylase Activity

Eight studies have reported rates of DOPA decarboxylase in patients with schizophrenia, using [<sup>18</sup>F]DOPA or [<sup>11</sup>C]DOPA. Six out of the eight studies reported increased accumulation of DOPA in the striatum of patients with schizophrenia [57–64], one reported no change [57], and one study reported reduced [<sup>18</sup>F]DOPA striatal uptake [58]. All three studies that involved first-episode schizophrenia showed an increase of DOPA in the striatum [59–61]. Increased uptake of radiolabeled DOPA reflects both increased DOPA decarboxylase activity and increased vesicular accumulation of the radiolabeled DOPA product, dopamine. Interestingly, a recent study observed a relationship between poor prefrontal activation during the Wisconsin Card Sorting task and elevated [<sup>18</sup>F]DOPA accumulation in the striatum, suggesting a link between alteration of the dorsolateral prefrontal cortex function and increased striatal DA activity in schizophrenia [63]. In rats as in anesthetized pigs, increases in AADC activity *in vitro* and *in vivo* have been reported following acute treatment with dopamine antagonists [65–67]. Conversely acute treatment with the dopamine agonist apomorphine decreases <sup>11</sup>C-DOPA influx in monkeys [68]. Evidence for such effects in humans, however, is extremely limited. Thus, in the only comprehensive study to date Grunder et al. recently reported a decrease in [<sup>18</sup>F]DOPA uptake in nine patients with schizophrenia following subchronic treatment with haloperidol [69], suggesting that chronic neuroleptic

administration will tend to decrease AADC activity and hence dopamine synthesis. Interestingly, acute administration of antipsychotics increases DA neurons firing whereas chronic administration decreases the number of spontaneously active DA neurons in the rat substantia nigra [70], suggesting that the different effects of antipsychotics on AADC activity in the living brain could reflect such phenomena.

### 15.2.2 Extrastriatal $D_2$ Receptors

The recent availability of high-affinity  $D_2$  radiotracers allowed the study of  $D_2$  receptors in low-density regions such as the substantia nigra, thalamus, and temporal cortex in patients with schizophrenia compared to controls (Fig. 15.1). Lower  $D_2$  receptor density has been described in untreated schizophrenia in the thalamus [71–75], as well as in the midbrain [76], temporal cortex [71], and cingulate cortex [75, 77]. One study showed an increase in  $D_2$  receptors in the substantia nigra [78]. A very recent large study using similar methodology did not confirm any of these alterations in extrastriatal  $D_2$  receptors [79]. Additional studies are needed to resolve the discrepancies and expand beyond measuring levels of  $D_2$  receptors to assess alterations of the transmitter itself in extrastriatal areas. As in striatum,



**Fig. 15.1** Coronal, transaxial, and sagittal views of PET images acquired 50–80 min following injection of 2.5 mCi [ $^{18}\text{F}$ ]Fallypride, a high-affinity  $D_{2/3}$  radiotracer, in a 30-year-old female, with coregistered MRI. Slices were chosen to illustrate extrastriatal regions with detectable specific-binding signal, such as the thalamus including the medio-dorsal nucleus (MDT), the parahippocampal gyrus (PHG), the substantia nigra (SN), the inferior colliculi (IC), and the pituitary (PIT)

alterations in levels of neurotransmitter may mask potential differences in receptor density between patients and controls.

### ***15.2.3 Prefrontal DA Receptors***

The majority of DA receptors in the PFC are of the D<sub>1</sub> subtype [80, 81]. Cortical D<sub>1</sub> receptors have been studied in schizophrenia using [<sup>11</sup>C]SCH 23390 [82] and [<sup>11</sup>C]NNC 112 [83, 84]. In humans, [<sup>11</sup>C]NNC 112 provides higher specific to non-specific ratios compared to [<sup>11</sup>C]SCH 23390 [84, 85], a property that is important for quantification of cortical D<sub>1</sub> receptors. It should be noted that both ligands display only moderate in vivo selectivity for D<sub>1</sub> relative to 5-HT<sub>2A</sub> receptors, and that 20–30% of cortical binding of both radiotracers correspond to binding to 5-HT<sub>2A</sub> receptors [86, 87].

PET studies with [<sup>11</sup>C]SCH 23390 reported decreased [16] or unchanged [88] prefrontal D<sub>1</sub> receptor availability in untreated patients with schizophrenia. In contrast, a study using [<sup>11</sup>C]NNC 112 reported increased D<sub>1</sub> receptor availability in the dorsolateral PFC (DLPFC) of patients with schizophrenia [39]. Interestingly, increased [<sup>11</sup>C]NNC 112 binding was associated with poor performance on the “n-back” test of working memory [39]. The reason for the discrepancy in the results obtained with [<sup>11</sup>C]SCH 23390 and [<sup>11</sup>C]NNC 112 remains to be elucidated, but it is interesting to note that the binding of both radiotracers is differentially affected by endogenous DA competition and receptor trafficking [54]. For example, chronic DA depletion in rodents is associated with decreased and increased in vivo binding of [<sup>11</sup>C]SCH 23390 and [<sup>11</sup>C]NNC 112, respectively [89]. Thus, the contradictory observations of decreased [<sup>11</sup>C]SCH 23390 binding [16] and increased [<sup>11</sup>C]NNC 112 binding [39] observed in the PFC in patients with schizophrenia might in fact both represent consequences of sustained deficit in prefrontal DA function. Much work remains to be done to validate this hypothesis. This point illustrates that the in vivo binding of radiotracers is affected by several factors that are not present in the typical in vitro situation, such as the impact of receptor trafficking on ligand affinity [54]. This situation represents both a challenge, because the interpretation of the results is less straightforward, and an opportunity, because more information can be gained on the functions of the living neurons. However, more selective tracers are needed to pursue this line of investigation.

### ***15.2.4 Antipsychotic Drug Occupancy Studies***

An important use of neuroreceptor imaging in schizophrenia over the last two decades has been the assessment of receptor occupancy achieved by typical and atypical antipsychotic drugs [90, 91]. The main focus has been on D<sub>2</sub> receptor occupancy, but 5HT<sub>2A</sub> and D<sub>1</sub> receptors have also been investigated. Studies have

repeatedly confirmed the existence of a threshold of occupancy of striatal D<sub>2</sub> receptors (about 80%) above which extrapyramidal side effects (EPS) are likely to occur [92] with the exception of the most recently approved antipsychotic, aripiprazole, which functions as a partial agonist [93]. A relationship between the degree of D<sub>2</sub> receptor occupancy and clinical response has not been observed [94, 95] at doses achieving more than 50% occupancy; however, two recent studies that included a wider range of receptor occupancies showed a relationship between striatal D<sub>2</sub> receptor occupancy and treatment of positive symptoms [93, 96]. Two studies performed with low doses of relatively selective D<sub>2</sub> receptor antagonists (haloperidol and raclopride) suggested that 50–60% occupancy was required to observe a rapid clinical response [97, 98]. Clozapine, at clinically therapeutic doses, has been found to achieve only 40–60% D<sub>2</sub> receptor occupancy [92, 95, 99], which, in conjunction with its anticholinergic properties, may account for its low liability for EPS. Occupancy of 5-HT<sub>2A</sub> receptors by “5-HT<sub>2A</sub>/D<sub>2</sub> balanced antagonists” such as risperidone does not confer protection against EPS, since the threshold of D<sub>2</sub> receptor occupancy associated with EPS is not markedly different between these drugs and drugs devoid of 5HT<sub>2A</sub> antagonism [100–103]. Studies with quetiapine suggest that, at least with this agent, transient high occupancy of D<sub>2</sub> receptors might be sufficient to elicit clinical response [104, 105].

An interesting question relates to putative differences in the degree of occupancy achieved by antipsychotic drugs in striatal and extrastriatal areas. Pilowsky et al. [106] initially reported lower occupancy of striatal D<sub>2</sub> receptors compared to temporal cortex D<sub>2</sub> receptors in seven patients treated with the atypical antipsychotic drug clozapine, using the high-affinity SPECT ligand [<sup>123</sup>I]epidepride. In contrast, typical antipsychotics were reported to achieve similar occupancy in striatal and extrastriatal areas, as measured with [<sup>11</sup>C]FLB 457 [107] or [<sup>123</sup>I]epidepride [108]. It should be noted, however, that these very high-affinity ligands do not allow accurate determination of D<sub>2</sub> receptor availability in the striatum [109]. Conversely, [<sup>18</sup>F]fallypride enables accurate determination of D<sub>2</sub> receptor availability in both striatal and extrastriatal areas [110]. Occupancy studies using [<sup>18</sup>F]fallypride confirmed that clozapine and quetiapine, but not olanzapine or haloperidol, achieved higher D<sub>2</sub> receptor occupancy in temporal compared to striatal regions [111–113]. Occupancy studies performed with [<sup>76</sup>Br]FLB457 also reported higher occupancies in cortex compared to striatum for a number of antipsychotic drugs, including typical antipsychotic drugs [114]. Conversely, a study combining [<sup>11</sup>C]FLB 457 imaging for extrastriatal D<sub>2</sub> receptor receptors and [<sup>11</sup>C]raclopride imaging for striatal D<sub>2</sub> receptors suggested similar occupancy of D<sub>2</sub> receptors in both regions for both typical and atypical antipsychotic drugs [115]. Our own study showed a small difference with higher EC<sub>50</sub> for aripiprazole in extrastriatal regions compared to striatal regions [93]. This difference may have been too small to detect consistently, conferring discrepant findings across studies. Thus, at this point in time, there is a strong suggestion that many, if not most, antipsychotic drugs achieve higher occupancies in extrastriatal regions compared to striatum, although this phenomenon has not been universally observed. Factors underlying this difference remain to be elucidated.

Finally, it is important to point out that D<sub>2</sub> receptor occupancy levels in striatum has been showed to be more predictive of therapeutic response than in temporal cortex [93, 96]. Thus, the observation that, in a restricted dose range, D<sub>2</sub> receptor occupancy by antipsychotic drugs is higher in temporal cortex than in striatum does not necessarily imply that the temporal cortex is the therapeutic site of actions of these agents.

## 15.3 Dopamine Receptors in Affective Disorders

### 15.3.1 Major Depressive Disorder

The critical role of DA in brain reward systems, the reports of low cerebrospinal fluid homovanillic acid levels in depressed patients, the association of major depression with Parkinson's disease, and the enhancement of dopaminergic activity by several antidepressant treatments suggest that a deficiency of dopaminergic function might be associated with major depression [116–119]. Five studies compared striatal D<sub>2</sub> receptor availability with [<sup>123</sup>I]IBZM and SPECT in patients with major depression and control subjects. Two of the five studies reported higher [<sup>123</sup>I]IBZM-specific binding in the striatum of depressed subjects compared to controls [120, 121], whereas three studies reported no changes [122–124]. Using [<sup>11</sup>C]raclopride and PET, one study reported elevated D<sub>2</sub> receptor availability in putamen in patients with depression with motor retardation [125]. Amphetamine-induced DA release was also assessed in patients with major depression and found to be unchanged [124].

Two studies examined [<sup>123</sup>I]β-CIT striatal binding to the dopamine transporter (DAT) in patients with major depression and yielded conflicting results: one study reported normal levels of striatal DAT in patients with major depression [126], while the other one reported increased DAT levels [127]. One study reported decreased DAT density in depression using [<sup>11</sup>C]RTI-32 [128]. SPECT studies conducted with [<sup>99m</sup>Tc]TRODAT-1 also reported conflicting results, with studies reported increased [129] or unchanged [130] striatal [<sup>99m</sup>Tc]TRODAT-1 uptake in patients with major depression.

Finally, [<sup>18</sup>F]DOPA uptake in the left caudate was observed to be significantly lower in depressed patients with psychomotor retardation than in depressed patients with high impulsivity and in comparison subjects [131]. Thus, major depression per se does not appear to be consistently associated with alteration of the dopaminergic parameters at the level of the whole striatum. However, DA might play a role in the neurobiology underlying some clinical features of depression, such as psychomotor retardation.

### 15.3.2 Bipolar Disorder

Because of the relationship between mania and psychosis, a number of PET studies have investigated the DA system in bipolar disorders. D<sub>1</sub> receptor binding in

the frontal cortex was reported to be decreased in a study of ten symptomatically heterogeneous, drug-free bipolar patients [132]. Increases in D<sub>2</sub>-like (i.e., D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub>) receptor density in the striatum were found in 7 psychotic patients with bipolar disorder when compared to 7 non-psychotic patients with bipolar disorder and 24 control subjects. The authors concluded that an increase in D<sub>2</sub>-like receptors is associated with the state of psychosis rather than with a diagnosis of bipolar disorder [133]. As part of the same studies, Gjedde and Wong also reported findings consistent with an elevated concentration of synaptic DA in bipolar patients with psychosis, but not in non-psychotic bipolar patients [134]. On the other hand, amphetamine-induced DA release was reported to be normal in euthymic patients with bipolar disorders [135].

In conclusion, few investigations have been reported using PET molecular imaging techniques in patients with bipolar disorders, and the findings reported so far might be related to clinical states (depression, mania with psychosis) rather than to the bipolar condition per se.

## 15.4 Social Phobia (Social Anxiety Disorder)

Neurobiological mechanisms underlying social phobia, including neuroimaging findings, have been reviewed recently [136–138]. One SPECT study using [<sup>123</sup>I]β-CIT to label DAT in the striatum reported that densities were markedly lower in patients with social phobia than in age- and gender-matched controls [139]. Another study using [<sup>123</sup>I]IBZM reported a significant decrease in D<sub>2</sub> receptor binding potential in patients with social phobia compared to controls [140]. However, this was not replicated by the same group using PET and examining D<sub>2</sub> receptor and DA release as well as DAT with a SPECT tracer, [<sup>123</sup>I]β-CIT [141]. These inconsistencies, often described in the imaging literature, may result from heterogeneity of the disorders.

## 15.5 Personality Disorders and Traits

Personality disorders (PD) are characterized by stable patterns of maladaptive behavior. Some, such as paranoid, schizoid, schizotypal, avoidant, and obsessive-compulsive PD, have stable patterns of behavior reminiscent of their corresponding clinical disorders but do not reach a sufficient severity and their response to medication is generally poor. It might therefore be expected that some personality disorders might be associated with neurobiological abnormalities similar to, but less marked than, the disorders described in this chapter. Functional imaging studies have now begun to address the issue of how neurochemical brain functions may be associated with normal and pathological personality traits.

A number of studies have investigated differences within the normal range of personality traits or temperaments in healthy subjects. Most receptor PET studies have

so far investigated dopaminergic neurotransmission. Studies using [ $^{11}\text{C}$ ]raclopride report that the traits of depression and personal detachment are related to low  $\text{D}_2$  receptor density in the striatum [142, 143]. However, the relationship is not evident on all measures of detachment [143, 144]. Detachment was also found to be associated with low DAT binding in the putamen [145]. These findings are also interesting in view of the association between social phobia and low DAT and  $\text{D}_2$  receptors [139, 140], and it has been argued that these neurobiological findings might underlie a commonality between detachment and social phobia [146].

In schizotypal personality disorder, similar alterations in dopamine transmission have been reported as in schizophrenia, albeit in a smaller magnitude [147].

## 15.6 Attention Deficit Hyperactivity Disorder

Interesting findings have been reported in the study of attention deficit hyperactivity disorder (ADHD), a condition treated with psychostimulants. In a preliminary study of six adult subjects with ADHD, Dougherty et al. [148] observed a large increase in DAT availability (70%) compared to controls. This finding was replicated in a larger samples of adults with ADHD by Dresel et al. [149], using [ $^{99\text{m}}\text{Tc}$ ]TRODAT-1, by Larish et al. [150], using [ $^{123}\text{I}$ ]FP-CIT, and by Spencer et al. [151], using [ $^{18}\text{F}$ ]altropane. In these subsequent studies, the magnitude of DAT elevation was considerably lower than in the original study. Elevated DAT availability was also replicated in children with ADHD [152]. On the other hand, this finding has not been replicated in several studies carried out by other groups [153–155] using [ $^{123}\text{I}$ ]β-CIT SPECT, [ $^{11}\text{C}$ ]PE2I PET, and [ $^{11}\text{C}$ ]cocaine PET, respectively. Here again, the heterogeneity of this condition might account for the discrepant results.

The DAT blocker methylphenidate is the treatment of choice of ADHD, and oral therapeutic doses induce significantly decreased [ $^{11}\text{C}$ ]raclopride binding [156], presumably due to increased synaptic DA levels. This method might provide a tool to monitor the biological effectiveness (increased synaptic DA) of the treatment and be useful in the evaluation of non-responders.

## 15.7 Substance Abuse

Molecular imaging investigations yielded important information about the mode of action of addictive substances and neurochemical abnormalities associated with addictions. Given the central role of DA in mediating the rewarding effects of drugs of abuse [157–162], it is not surprising that many imaging studies focused on this transmitter system. In general, studies demonstrated that acute administration of addictive drugs is associated with increased DA transmission in the limbic striatum, and that the pleasurable effects of these drugs are associated with the magnitude of DA system stimulation. In patients suffering from addiction, studies demonstrated

deficits of both pre- and post-synaptic DA function, a finding not readily predicted from animal data.

### ***15.7.1 Cocaine***

Cocaine abuse has been extensively studied using molecular imaging techniques. Most of the work has focused on changes in striatal DA that occur with chronic cocaine use. The studies have generated a remarkably consistent set of data and illustrate admirably the ability of molecular imaging to unravel neurochemical abnormalities in the human brain associated with pathological conditions.

#### **15.7.1.1 D<sub>2</sub> Receptors**

A reduction in striatal DA D<sub>2</sub> receptors has been demonstrated by Volkow et al. using both [<sup>18</sup>F] N-methylspiroperidol and [<sup>11</sup>C] raclopride [163–166], a finding that has been independently replicated [167]. Volkow et al. [164] also noted that this decrease in striatal D<sub>2</sub> receptor availability correlated with years of use. This deficit appears to be long lasting in a group of subjects re-scanned after 3 months of inpatient rehabilitation [164]. PET studies also revealed reduction in striatal D<sub>2</sub> receptor availability in heroin abuse [168], methamphetamine abuse [169], and alcoholism [170–172], suggesting that decreased striatal D<sub>2</sub> receptor availability might be a general feature of the addicted brain.

The results of these studies raise the question of whether a decrease in D<sub>2</sub> receptors is the result of years of drug abuse or represents a neurochemical risk factor for developing substance abuse. Two observations suggested that low D<sub>2</sub> receptor availability might constitute a risk factor for the development of addiction. First, studies in healthy subjects suggested that low striatal D<sub>2</sub> receptor availability was predictive of a pleasurable experience following administration of the psychostimulant methylphenidate [173, 174]. Second, studies in nonhuman primates demonstrated that low striatal D<sub>2</sub> receptor availability was predictive of increased propensity to self-administer cocaine [175]. It should be noted, however, that low D<sub>2</sub> receptor availability is not predictive of a pleasurable experience following amphetamine in healthy subjects [176–178] nor in cocaine abusers [167]. Thus, while the association between low striatal D<sub>2</sub> receptor availability and history of chronic cocaine abuse is well established, the direction of causality in this relationship remains to be clarified.

#### **15.7.1.2 Stimulant-Induced DA Release**

As described above, PET and SPECT studies can be used to measure changes in subcortical DA transmission in the human brain following psychostimulant administration [54]. In healthy subjects, a number of independent studies have shown that the percentage decrease in radioligand binding (i.e., the increase in DA release) is

positively correlated with the pleasurable subjective effects induced by psychostimulant administration [176, 178–182]. This observation is consistent with the preclinical body of evidence indicating that DA transmission in the ventral striatum mediates the reinforcing effects of drugs of abuse [183, 184]. PET studies showed a greater decrease in [ $^{11}\text{C}$ ]raclopride binding in the ventral versus dorsal striatum in healthy controls in response to an amphetamine challenge [167, 180], and in response to a monetary reward [185]. Collectively, these studies suggest that strong DA response would correlate with increased reward value, might mediate the reinforcing effects of drugs of abuse, and might therefore constitute a risk factor toward the development of addiction.

However, cocaine abusers have been shown to have a blunted DA response to psychostimulants. A study of Volkow et al. [166] used [ $^{11}\text{C}$ ]raclopride to measure the change in  $\text{D}_2$  receptor availability before and after an i.v. dose of 0.5 mg/kg methylphenidate in healthy controls and cocaine abusers who had been abstinent for 3–6 weeks. The authors reported a 9% decrease in [ $^{11}\text{C}$ ]raclopride binding in the cocaine abusers compared to a 21% decrease in healthy controls. Malison et al. [186] performed a similar study in abstinent cocaine abusers and controls using [ $^{123}\text{I}$ ]IBZM and an amphetamine challenge (0.3 mg/kg i.v.) and reported a 1% change in binding in the cocaine abusers compared to a 10% decrease in controls. Similarly, Martinez et al. [167] showed that the effect of amphetamine on (0.3 mg/kg i.v.) on [ $^{11}\text{C}$ ]raclopride binding is markedly blunted in cocaine abusers in all striatal subregions. In the ventral striatum, this response was completely blunted. Furthermore, blunted dopamine transmission in the ventral striatum and anterior caudate was predictive of the choice for cocaine over money, suggesting that this deficit might confer vulnerability to relapse [167].

### 15.7.1.3 DOPA Decarboxylase

The findings above of blunted presynaptic DA function in cocaine abusers are supported by the study of Wu et al. [187] showing a reduction in the rate of uptake of [ $^{18}\text{F}$ ]6-FDOPA in abstinent cocaine abusers.

### 15.7.1.4 DAT

Imaging studies of the DAT in cocaine abusers have been published, and this body of work has failed to provide a clear picture of the status of the DAT in cocaine abusers. Using [ $^{11}\text{C}$ ]cocaine, no changes in DAT were observed in detoxified (>1 month) cocaine abusers [188]. In contrast, Malison et al. [189] showed a significant upregulation of DA transporters, measured with SPECT and [ $^{123}\text{I}$ ] $\beta$ -CIT, in the striatum of recently detoxified (<96 h) cocaine abusers. Such upregulation was not observed following prolonged abstinence.

*DAT occupancy by cocaine.* Studies of DAT occupancy by cocaine have generated valuable information. Volkow et al. [190] reported that a DAT occupancy of about 50% or more is needed to produce the subjective effects of cocaine. These data suggest that any treatment approach to cocaine abuse in which the transporter

is blocked would need to produce somewhere between 60 and 90% occupancy of the transporters. This issue was addressed in an occupancy study of mazindol, a non-selective catecholamine reuptake inhibitor [191]. This study showed that the clinical dosage generally used produced only a modest occupancy of 16–23% and would therefore not be expected to have sufficient efficacy to block the reinforcing effects of cocaine.

While the magnitude of DAT blockade is important for the experience of the rewarding effect, the rate of occupancy is an important feature of the addictive process [192, 193]. Thus, cocaine exhibits very rapid association and dissociation from the DAT and is highly addictive. The reinforcing effects of methylphenidate are stronger after i.v. compared to p.o. administration, due to faster access to the DAT after i.v. administration. Antidepressants like bupropion or radafaxine associated with moderated and sustained DAT occupancy due to slow peripheral clearance are devoid of abuse liability [194].

*Cue-induced cocaine craving.* Two studies showed that cue-induced cocaine craving is associated with acute decrease in [ $^{11}\text{C}$ ]raclopride availability, presumably related to acute changes in synaptic DA [195, 196]. Interestingly, craving intensity is associated with DA release in the dorsal rather than the ventral striatum suggesting the involvement of this region in the habituation process associated with craving and addiction.

Overall, the studies in cocaine abuse demonstrate a clear and pronounced dysregulation of the DA system in this disorder. The findings of decreased [ $^{18}\text{F}$ ]DOPA accumulation, decreased amphetamine- and methylphenidate-induced DA release, and decreased  $\text{D}_2$  receptor density suggest a functional deficit in  $\text{D}_2$  receptor transmission at the level of the whole striatum in this population. This alteration in DA transmission might contribute to the addictive process and the relapse risk.

### ***15.7.2 Methamphetamine***

Two imaging studies in methamphetamine abusers have demonstrated a significant decrease in DAT density using PET [197, 198]. The authors also found that the decrease in DAT availability correlated with years of abuse and with impairment in motor and memory tasks. Both studies are in agreement with a postmortem report of reduced DA transporter density in the striata of chronic methamphetamine abusers, as well as decreases in DA and tyrosine hydroxylase [199]. Evidence from studies in Parkinson's disease support the hypothesis that the reduction in DAT availability reflects a loss of DA neurons which is detectable with functional imaging [200–202]. Based on this interpretation, these studies raise the issue of whether this decrease is reversible or whether methamphetamine abuse results in neurotoxicity to the dopaminergic neurons. PET and postmortem studies in nonhuman primates have shown that methamphetamine exposure results in decreased DAT and other markers of dopaminergic transmission, suggesting a frank loss of dopaminergic neurons [203, 204]. However, one study suggested that this reduction might be reversible

after prolonged abstinence [205]. Overall, the PET data demonstrate that methamphetamine abuse in humans results in a reduction in the DAT and raise concerns about the DA neurotoxicity associated with this addiction.

### 15.7.3 *Nicotine*

Relative to the impact of smoking on public health, relatively few molecular imaging studies have been carried out to understand the impact of smoking on brain chemistry.

Molecular imaging of nicotinic receptors demonstrated that typical cigarette smoking results in rapid and sustained near saturation of the  $\alpha_2\beta_4$  nicotinic receptors measured with 2- $^{18}\text{F}$ ]85380 [206]. One SPECT study in nonhuman primates suggested that this was associated with significant and prolonged upregulation of these receptors [207].

Several studies evaluated the effect of nicotine on striatal DA release, as measured with the  $^{11}\text{C}$ ]raclopride-binding reduction method. In rhesus monkeys, i.v. nicotine doses ranging from 0.01 to 0.06 mg/kg caused a significant albeit small reduction (5%) in  $^{11}\text{C}$ ]raclopride availability [208]. In humans, a first study [209] failed to detect a significant effect of cigarette smoking in regular smokers on striatal  $^{11}\text{C}$ ]raclopride binding, but detected a relationship between the hedonic response to nicotine and decreased  $^{11}\text{C}$ ]raclopride binding. Another study in nicotine-dependent subjects demonstrated a 30% reduction in  $^{11}\text{C}$ ]raclopride binding in the ventral striatum following one cigarette [210]. The magnitude of this effect was surprising, as it exceeded the magnitude of the  $^{11}\text{C}$ ]raclopride reduction observed in the same region following i.v. amphetamine 0.3 mg/kg i.v. (15–20%) [180, 181]. In a subsequent study in a larger group of subjects, this group reported a much lower decrease in  $^{11}\text{C}$ ]raclopride striatal binding following cigarette smoking (8%) [211]. Finally, Montgomery et al. [212] failed to detect changes in  $^{11}\text{C}$ ]raclopride binding in regular smokers following intranasal nicotine administration, while relationships were reported between positive subjective effects of the drug and decrease  $^{11}\text{C}$ ]raclopride binding in striatal subregions. Together, these studies demonstrated that nicotine exposure in human smokers is associated with increases in synaptic DA and that this effect is generally of lower magnitude than the one observed with psychostimulants [54] and close to the detection limit associated with this imaging method. As previously described for stimulants [176, 178, 180–182, 213], the subjective effects of the drugs are associated with the extent of DA release.

Fowler et al. [214–217] investigated levels of monoamine oxidase (MAO) A and B in smokers and showed marked and global decreases in both enzymes. MAO A and B exist in neurons and glial cells and both enzymes degrade DA. MAO B activity was measured using  $^{11}\text{C}$ ]L-deprenyl [218]. Smokers were found to have a 42% decrease in global MAO B activity compared to controls [214, 217]. Interestingly, a study in former smokers showed that levels of MAO B activity returned to baseline after smoking cessation [216]. In a later study, this same group demonstrated a

decrease in MAO A activity in the brains of cigarette smokers using [ $^{11}\text{C}$ ]clorgyline [215]. In this study smokers had an average reduction of 28% in MAO A activity across brain regions, with a 22% decrease in the basal ganglia [215]. Decreased activities of MAO A and B are expected to be associated with increased DA availability.

Salokongas et al. [219] used [ $^{18}\text{F}$ ]fluorodopa to measure presynaptic DA and reported higher uptake in the striatum in smokers, a finding which could be explained by an increase in DOPA decarboxylase activity or a decrease in MAO activity. A study by Dagher et al. [220] reported a reduction in  $\text{D}_1$  receptor availability using [ $^{11}\text{C}$ ]SCH23390 in the striatum. Lastly, Staley et al. [221] investigated DAT and SERT density in the striatum and midbrain, respectively, in smokers and healthy controls using [ $^{123}\text{I}$ ] $\beta$ -CIT. No difference was seen in DAT availability between these groups but there was a trend toward an increase in [ $^{123}\text{I}$ ] $\beta$ -CIT binding in the midbrain.

Overall, these findings are consistent with the hypothesis of alterations of the DA system in nicotine smokers, but much work remains to be done to better understand the potential role of this dysregulation in the maintenance of nicotine addiction.

#### **15.7.4 Alcohol**

The DA system has been the most investigated neurochemical system using SPECT and PET in alcohol research, due to the wealth of preclinical data suggesting a role for DA in the reward system and clinical data suggesting alterations in DA function in alcoholic patients.

Acute effects of alcohol on DA release in humans have been studied with the [ $^{11}\text{C}$ ]raclopride reporting method. Similarly to results reported with nicotine, alcohol administration in humans is not associated with major changes in [ $^{11}\text{C}$ ]raclopride binding, but the pleasurable effects of the drugs are associated with reduced [ $^{11}\text{C}$ ]raclopride binding [222].

A number of well-controlled and independent studies have consistently demonstrated a reduction in  $\text{D}_2$  receptor availability in recently detoxified alcoholics [170, 172, 223, 224], an alteration that does not appear to be reversible following early sustained abstinence for 4 months [225]. The majority of preclinical data do not indicate that chronic alcohol exposure affects  $\text{D}_2$  receptor density [226–230], but conflicting results have been published suggesting that the effects of chronic alcohol on DA receptors might vary according to the dose and duration of exposure [231–234]. Such differences in duration of exposure, as well as inter-species differences in the response of  $\text{D}_2$  receptors to alcohol, may undermine the relevance of rodent studies in answering the question of whether decreased  $\text{D}_2$  receptor binding potential (BP) measured with PET in chronic alcoholics is a risk factor for, or an effect of, chronic alcohol intake. Another important question is whether the alterations in  $\text{D}_2$  receptor density in recently detoxified alcoholics are transient or permanent, i.e., if this abnormality persists with a prolonged period of abstinence

even beyond the initial 4 months of abstinence. Interestingly, recent data suggest that low D<sub>2</sub> receptor availability might be associated with high relapse risk [235]. Studies reporting DAT measurements in chronic alcoholics have failed to detect consistent alterations of DAT binding in alcoholism [223, 236–239].

Alcoholism is also associated with reduced amphetamine-induced DA release in the ventral striatum [172]. Together with the evidence of reduced D<sub>2</sub> receptor availability, these findings suggest that alcoholism, like cocaine and maybe other addictions, is associated with a significant decrease in DA transmission at D<sub>2</sub> receptors. Interestingly, a recent study [240] in nonalcoholic offspring from families with a positive history of alcohol dependence failed to detect alteration of DA transmission (D<sub>2</sub> receptor availability and amphetamine-induced DA release) compared to nonalcoholic subjects without a family history of alcohol dependence. Therefore, one might conclude that these alterations are a consequence rather than a risk factor of alcoholism. However, it could also be argued that a normal DA transmission in these subjects might provide protective effects, counterbalancing other genetically mediated risks. Short of a long-term prospective study, the status of these DA alterations as risk factors or consequences of addiction is likely to remain unsolved. A recent study assessing D<sub>2</sub> receptors and amphetamine-induced dopamine release in family history positive versus family history negative subjects showed no difference between groups [240].

## 15.8 Conclusions

This chapter has reviewed key findings from PET and SPECT molecular imaging of dopaminergic receptors, transporters, enzymes, and the transmitter that have contributed to our understanding of the pathophysiology and treatment of psychiatric disorders. Since 1986, the year of publication of the seminal paper of Wong et al. [10] describing the use of PET imaging to detect elevated D<sub>2</sub> receptor density in antipsychotic drug-naïve schizophrenics, this field has undergone a major expansion. So far, it is clear that these techniques have already provided unique insights into the neurochemical imbalances underlying some of these conditions and the pharmacological mechanisms involved in their treatment. It is foreseeable that this contribution will continue to expand in the near future.

Psychiatric conditions are generally characterized by clinical heterogeneity. It is likely that a number of illnesses with different etiologies and neurobiological mechanisms are currently subsumed under the same name by our diagnostic classifications. Despite this, a number of findings have been remarkably consistent and replicated across studies, suggesting that the clinical commonality underlying our diagnostic syndromes might be associated with unique and perhaps specific final common pathophysiological pathways. Furthermore, the examination of the biological processes involved in clinical conditions with nuclear medicine techniques also provides an opportunity for redefining illnesses [241].

For example, one study reported that elevated DA synaptic levels in acute schizophrenia were predictive of rapid symptomatic response to antipsychotic (i.e., antidopaminergic) treatment [24]. A subgroup of patients showed no detectable abnormality of striatal DA function despite frank psychotic symptoms and failed to respond to treatment. It is possible that, in these patients, the psychotic state is not driven by excess DA activity, and that the antidopaminergic treatment fails because the problem being treated does not exist in these patients. This result has led to the concept of dopaminergic versus non-dopaminergic driven psychotic states in schizophrenia [24]. This biological, rather than clinical, classification might prove to be useful in evaluation of non-dopaminergic antipsychotic pharmacological strategies.

Another example is the constellation of conditions that have been reliably shown to be associated with low D<sub>2</sub> receptor availability in the striatum. This finding has been associated with a personality trait (detachment), anxiety disorder (social phobia), and addiction to a variety of substances, including cocaine, heroin, alcohol, and even food. These conditions are not similar but are frequently overlapping or comorbid. Therefore, imaging studies might reveal common biological processes across conditions that were hitherto unsuspected and might help to delineate psychopathological features more directly related to altered biological brain functions than our current diagnostic classifications.

Despite these successes, a substantial number of studies yielded discordant results, and it is important to examine potential sources of discrepancies. An important drawback of this literature is the generally low number of subjects included in studies (typically less than 20 per group). In conditions characterized by marked heterogeneity, such as major depressive disorders, this factor is bound to yield divergent results across studies. Small samples are obviously due to the cost of these investigations, but also, in some instances, to the difficulty in recruiting appropriate clinical subjects (such as drug-free patients with schizophrenia). Another source of discrepancy is the variety of technical approaches to data acquisition and analysis. For example, analytical methods range from “empirical” or “semi-quantitative” methods (typically a region of interest to a region of reference ratio measured at one time point) to model-based methods using an arterial input function. The limitations associated with empirical analytical methods have been discussed elsewhere [242] and might account for artifactual results, especially when the effect size of the between-group difference and the number of subjects are small [243].

In addressing these limitations it will be important to increase the availability of these techniques beyond a few academic centers, to promote multi-center studies in well-characterized populations, and to standardize analytical methods. Until recently, SPECT was the only widely available technique, and SPECT studies have so far provided a substantial contribution to this field. With the current increase in PET camera availability, the development of <sup>18</sup>F-based molecular imaging probes will provide unique opportunities for further dissemination of these techniques.

The greatest challenge facing this field is to develop molecular imaging probes suitable for imaging neurochemical processes beyond neurotransmission itself, to

examine growth factors or intracellular signaling pathways. A sustained collaboration between industry and academic institutions will be required to expand the study of brain biomolecular processes beyond our current, and still relatively limited, arsenal.

In conclusion, the chapter has reviewed seminal findings obtained with PET and SPECT molecular imaging of DA transmission in psychiatric conditions. These techniques do not yet play a major role in the diagnosis and treatment of these disorders, and at present remain essentially as research tools. However, the results produced by this field so far suggest that PET will significantly contribute to unraveling the biological bases of these conditions and might play an increasing role in their clinical management. Moreover, it is foreseeable that PET will become more and more involved in the development of new psychiatric medications. Expanding the availability of PET and the current radiopharmaceutical portfolio will be critical for these predictions to become reality.

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# Chapter 16

## Dopamine Receptors and the Treatment of Schizophrenia

Nathalie Ginovart and Shitij Kapur

**Abstract** Schizophrenia is a most disabling psychiatric disorder characterized by a myriad of symptoms. While the delusions and hallucinations are the most iconic symptoms of schizophrenia, patients also exhibit negative and cognitive symptoms. It is thought that these symptoms arise, at least in part, through a cortical–subcortical imbalance of dopamine function and pharmacological approaches that reduce dopaminergic neurotransmission through dopamine receptor blockade, and in particular through the D<sub>2</sub> receptor, have antipsychotic action in humans. However, D<sub>2</sub> antagonists are not optimally effective against the full spectrum of schizophrenia symptoms and induce side effects that limit their use. Research to enhance the therapeutic benefits of antipsychotics while diminishing their side effects has led to the development of atypical antipsychotics (D<sub>2</sub> antagonists with activity at other receptors) and, more recently, a new strategy using dopamine partial agonists to reduce dopaminergic neurotransmission has proven to be successful. This chapter reviews the pharmacological effects of typical and atypical antipsychotics on the different dopamine receptor subtypes, as well as on non-dopaminergic receptor targets, and on the prominent role of D<sub>2</sub> receptor blockade as the primary site of their action in brain. In addition, we discuss current theories on the mechanisms of antipsychotic action, including the role of combined action at the dopamine and serotonin receptors, transient dopamine D<sub>2</sub> blockade, preferential blockade of limbic D<sub>2</sub> receptors, or combined blockade of D<sub>1</sub> and D<sub>2</sub> receptors. Some critical clinical considerations with regard to the speed of onset action and the occurrence of relapse and supersensitivity psychosis on withdrawal are discussed with special relevance to their relationship to the dopamine system. While the D<sub>2</sub> receptor-based treatments seem to have dominated the field till now, drugs that reduce dopamine-mediated transmission through action at presynaptic sites and of drugs providing D<sub>1</sub> signaling augmentation in prefrontal cortex may provide novel therapeutic avenues for the treatment of schizophrenia.

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N. Ginovart (✉)

Neuroimaging Unit, Department of Psychiatry, University of Geneva, Geneva, Switzerland  
e-mail: nathalie.ginovart@unige.ch

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## 16.1 Schizophrenia

Schizophrenia is a chronic disabling disease that afflicts 0.5–0.8% of the world's population [1]. Symptoms usually begin in late adolescence or early adulthood and are typically classified as positive (hallucinations and delusions), negative (amotivation, flattened affect, and social withdrawal), and cognitive (disorganized thoughts, deficits in attention, working and verbal memory, social cognition, and executive function) [2, 3].

The course of schizophrenia is characterized by periods of symptom exacerbation (i.e., relapse) alternating with periods of relative remission, with a different pattern of exacerbation/remission episodes between the three psychopathology dimensions and between different individuals [4, 5]. Such findings have led several researchers to theorize that positive, negative, and cognitive symptoms reflect separate pathophysiological processes [6, 7], though that still remains to be proven beyond doubt. Nonetheless, there is little doubt that schizophrenia is a disorder with strong biological underpinnings, some of it genetically determined (though the precise genes have not as yet been confirmed) and the rest influenced by the environment and interactions.

Not surprisingly then, there are several hypotheses that explain different aspects of the illness. The major thinking in the field regarding the development of the illness is that it is a neurodevelopmental disorder. In other words, the biological determinants of the disorder manifest themselves often years in advance of the cardinal symptoms. While neurodevelopmental deficits may lead to the disorder, there is little doubt that when the disease manifests itself, there is a significant neurochemical aberration. And it is this aspect of the illness, with special attention to the dopamine receptors, that is the focus of this chapter.

While the major focus of this chapter is the role of dopamine receptors vis-à-vis treatment, to provide the appropriate background for this we first review the dominant neurochemical hypotheses regarding schizophrenia. We then explain the classification of typical vs. atypical antipsychotics and then focus on the different dopamine receptors and their roles in antipsychotic action.

### 16.1.1 *The Dopamine Hypothesis*

The “classical” dopamine (DA) hypothesis of schizophrenia proposed that subcortical hyperactivity of DA transmission in brain is responsible for the positive symptoms of the illness [8]. This hypothesis was initially based on several lines of indirect evidence. First, exposure to DA-enhancing drugs, such as amphetamine, induces

psychosis in normal individuals and worsens psychotic symptoms in schizophrenia patients [9]. Second, drugs alleviating psychotic symptoms of schizophrenia were suspected to act through blockade of central DA receptors. Indeed, in 1963, Carlsson and Lindqvist [10] reported an increase in DA metabolites following chlorpromazine and haloperidol administration and proposed that this increase was the result of dopaminergic blockade, resulting in an increased rate of turnover. Further evidence for a central role of a DA dysregulation in schizophrenia came from research on the mechanism of antipsychotic action. Indeed, all drugs with a proven efficacy at relieving the positive symptoms of schizophrenia block DA D<sub>2</sub> receptors to some extent. Moreover, there is a tight correlation between the clinical doses of antipsychotic drugs needed to achieve therapeutic efficacy and their potency at blocking D<sub>2</sub> receptors [11]. This led to the dominant theory that the abnormal psychotic ideation observed in schizophrenia is largely due to an abnormally high DA transmission. Extensive research efforts have been made to determine whether the expression of DA receptors, and in particular D<sub>2</sub> receptors, is altered in schizophrenia. Early postmortem studies showed increased D<sub>2</sub> receptor levels in the striatum of patients with schizophrenia [12, 13]. However, the finding that antipsychotic drug treatment increased D<sub>2</sub> receptor density in experimental animals [14, 15] raised concerns that the D<sub>2</sub> elevation observed in schizophrenia could be related to prior drug treatment. In support of this view, some reports showed that D<sub>2</sub> receptors were only increased in patients treated with antipsychotic drugs up until death [16–18]. However, other postmortem studies in patients who were apparently drug free still showed elevated D<sub>2</sub> receptor density [19, 20]. The interpretation of D<sub>2</sub> elevation obtained postmortem thus remained controversial and imaging studies in never-medicated patients were critical to determine whether or not D<sub>2</sub> receptors were increased in schizophrenia. Initial *in vivo* brain imaging studies in drug-naïve patients yielded conflicting results, with some studies showing elevation [21, 22] and others no change in striatal D<sub>2</sub> receptors [23, 24]. Many factors have been proposed to account for this discrepancy, most of all being related to the chemical class and different pharmacokinetic properties of the radioligands employed between studies (review in [25]). Since these initial reports, there have been many other studies in this field and those generally failed to detect significant increase in striatal D<sub>2</sub> receptor in drug-naïve schizophrenic patients [26–31]. It has been proposed that while there may not be an absolute change in D<sub>2</sub> receptor number in schizophrenia, a shift toward a greater population in the D<sub>2</sub><sup>High</sup> state (D<sub>2</sub> receptors with functional high affinity for DA) may explain hyperdopaminergia [32]. However, a recent clinical study to investigate levels of D<sub>2</sub><sup>High</sup> found no difference between schizophrenic patients and controls [33]. *In vivo* studies of D<sub>1</sub> receptors in never-medicated patients showed unaltered receptor density in striatum [34, 35] but are conflicting with regard to their density in frontal cortex, with studies showing decreased [36], unaltered [34], or increased [35] D<sub>1</sub> receptor binding in this brain region. Thus far, *in vivo* study of D<sub>3</sub> receptors has been hampered by the lack of radioligands with sufficient selectivity for D<sub>3</sub> over D<sub>2</sub> receptors and by the partially overlapping distribution of these two receptor subtypes in brain. The only study performed in the field was postmortem and reported elevated striatal density of D<sub>3</sub> receptor in drug-free

patients with schizophrenia [37], a finding that remains to be confirmed in other studies. As for the D<sub>3</sub>, in vivo measures of the D<sub>4</sub> receptor have not been possible yet due to the lack of specific radioligand for this receptor subtype. Using an indirect subtraction binding method, elevated striatal density of D<sub>4</sub> receptors has been reported in schizophrenic patients postmortem [38–40], but this finding was not replicated in other studies [41–44]. Thus despite extensive efforts over the past 40 years, no convincing evidence has emerged yet that unequivocally points to a DA receptor abnormality in schizophrenia. In contrast, converging lines of evidence point to an elevated presynaptic DA function in schizophrenia. An accumulating body of in vivo imaging studies indicates that schizophrenia is associated with an increased subcortical capacity of DA synthesis [45–47], an increased DA turnover [48], and increased subcortical levels of endogenous DA at baseline [49] together with an increased subcortical release of DA following an amphetamine challenge [50–53]. Moreover, it seems that some of these DA alterations may confer susceptibility to schizophrenia as increased striatal presynaptic DA synthesis capacity is correlated to the risk of developing schizophrenia and other psychoses [54]. All together, these data suggest that psychosis is related, at least in part, to an excessive subcortical DA presynaptic function rather than to abnormalities in the levels of postsynaptic DA receptors.

Since its first formulation, the DA hypothesis of schizophrenia has been revised to account for both the positive and the negative symptoms of the disease [55]. Indeed, while administration of amphetamine worsens the positive symptoms of the illness, it may partly improve negative symptoms [56]. The revised theory proposes that the positive and negative symptoms of schizophrenia arise from an imbalance between the brain DA pathways mediating D<sub>2</sub> and D<sub>1</sub> receptor signaling. A subcortical excess of DA, leading to hyperstimulation of D<sub>2</sub> receptors, would give rise to the positive symptoms, while a concomitant cortical deficit of DA, leading to hypostimulation of D<sub>1</sub> receptors, would give rise to the negative and cognitive symptoms. There is indeed robust evidence that DA hypofunction and altered D<sub>1</sub> receptor signaling within the prefrontal cortex (PFC) play a central role in the induction of working memory deficits, suggesting that a reduced D<sub>1</sub> receptor neurotransmission might cause cognitive impairments in schizophrenia (review in [57]). Interestingly, reduced prefrontal activity has been shown to predict exaggerated striatal DA function in schizophrenia [58]. Both hypofunctioning and hyperfunctioning DA systems thus likely coexist in schizophrenia, albeit in different brain regions.

### ***16.1.2 The Glutamate Hypothesis***

The second dominant pathophysiological hypothesis of schizophrenia postulates a hypofunctional glutamate system in this disorder and, more specifically, a decreased neurotransmission at the *N*-methyl-D-aspartate (NMDA) glutamate receptor. Glutamate is the major excitatory neurotransmitter in the brain. It acts on two families of receptors: the metabotropic receptors, which include the mGlu1

to mGlu8 subtypes, and the ionotropic receptors, which include the kainate, the AMPA, and the NMDA subtypes. Some mGlu receptors, in particular the mGlu<sub>2/3</sub> and mGlu<sub>5</sub> subtypes, interact closely with NMDA receptors and may directly modulate the function of the NMDA receptor channel [59]. The idea of a glutamatergic abnormality in schizophrenia was first proposed by Kim and colleagues in 1980 [60] based on their findings of low cerebrospinal fluid (CSF) glutamate levels in patients with schizophrenia. Moreover, subanesthetic doses of NMDA receptor antagonists, such as ketamine and phencyclidine (PCP), can produce a spectrum of responses in normal subjects that partially resemble the positive, negative, and cognitive symptoms of schizophrenia [61, 62]. Ketamine and PCP can also precipitate psychoses in schizophrenic patients [63, 64]. Finally, a number of postmortem studies indicate abnormalities in NMDA receptor expression in the temporal cortex, cingulate cortex, hippocampus, and thalamus in schizophrenia [65]. Recent *in vivo* imaging studies confirmed reduced NMDA receptor binding in hippocampus [66, 67] and abnormal concentrations of glutamate in hippocampus and PFC of schizophrenic patients [68–70]. These observations thus give support to the theory that a NMDA receptor hypofunction might be involved in the pathophysiology of schizophrenia [71, 72].

### ***16.1.3 Integration of the Dopamine and Glutamate Hypotheses***

There is substantial evidence of reciprocal interactions between the DA and the glutamatergic systems. The acute administration of NMDA antagonists such as PCP and ketamine has consistently been reported to increase the firing rate of midbrain DA neurons [73–76] and to selectively increase DA release in PFC and in nucleus accumbens [76–79]. Subchronic administration of NMDA antagonists also leads to a profound dysregulation of the mesocorticolimbic DA system. Specifically, mesocortical DA neurons which largely project to the PFC show a profound loss of burst firing with decreased DA release, whereas mesolimbic DA neurons, which mainly project to the ventral striatum, show an increased firing with increased DA release [80, 81]. One mechanism to account for the subcortical DA hyperfunction proposes that the corticostriatal glutamate pathway may indirectly (via  $\gamma$ -aminobutyric acid [GABA]) inhibit DA function in the ventral striatum [82]. Therefore, protracted NMDA receptor hypofunction can produce the cortical DA hypoactivity and limbic DA hyperactivity postulated in schizophrenia and associated with the negative and positive symptoms, respectively.

## **16.2 Classification of Antipsychotic Drugs**

### ***16.2.1 Typical Antipsychotics***

Antipsychotic medications are the cornerstone treatments for reducing psychotic symptoms and relapse rates in schizophrenia. The first antipsychotic drug used for schizophrenia, chlorpromazine, was introduced in 1952 [83] and, in the late 1950s,

several other antipsychotics were subsequently introduced, including haloperidol, thioridazine, trifluoperazine, and loxapine. These first-generation antipsychotics, termed typical antipsychotics, are effective against the positive symptoms but have limited efficacy and may even exacerbate the negative and cognitive symptoms of schizophrenia. Moreover, some 30% of patients with schizophrenia show little or no response of their positive symptoms to typical antipsychotic therapy [84, 85]. Besides this, typical drugs are associated with a wide spectrum of side effects, including sedation, acute extrapyramidal symptoms (EPS), hyperprolactinemia and, although rarely, the neuromalignant syndrome. Acute EPS are dose-dependent and manifest as dystonia, akathisia, and pseudoparkinsonism [86]. The most worrisome form of EPS, tardive dyskinesia (TD), develops on long-term utilization with an incidence of about 5% a year and can be irreversible [3]. These side effects are often severe and disabling and are a leading cause of patient noncompliance [87, 88] which, in turn, leads to relapse [89]. Efforts to minimize EPS have revealed that lowering the dose indeed decreases side effects and still achieves therapeutic efficacy in many patients with schizophrenia [90, 91]. However, lower doses also carry additional risk of relapse as the doses required for efficacy are only slightly lower than the doses that cause side effects [92, 93]. Despite their clear benefits for the treatment of schizophrenia, the limited tolerability and narrow therapeutic index of typical antipsychotic drugs pointed out the need for better treatment options.

### ***16.2.2 Atypical Antipsychotics***

Research to enhance the therapeutic benefits of antipsychotics while diminishing their side effects has led to the development of a new class of antipsychotic agents, the atypical antipsychotics. Clozapine was introduced in Europe in 1975 and marked a turning point in schizophrenia therapy. Clozapine appeared to be effective with a minimal incidence of EPS, thus challenging the dogma that antipsychotic efficacy required high levels of EPS (review in [94]). Interestingly, this drug demonstrated benefits in cases of patients refractory to typical antipsychotics and was found to be somewhat more effective against the negative and cognitive symptoms [95]. However, its use is limited because of major side effects including potentially lethal agranulocytosis [96]. It was not until the late 1980s that a second atypical drug, amisulpride, was introduced. The following decade saw the introduction of a multiplicity of new drugs, including olanzapine, risperidone, sertindole, and quetiapine, with ziprasidone and aripiprazole following in the early 2000s.

Although atypical drugs improve positive symptoms with a similar efficacy [97–99], they differ from typical ones by their lower incidence of EPS and TD [100–102] and with the exception of risperidone and amisulpride have only transient effect on serum prolactin levels [103, 104]. These reduced side effects result in better tolerance and may enhance compliance [3, 97] and decrease relapse rates [89, 105, 106] when compared with high-dose typical drugs. Atypical drugs are, however, associated with other distressing non-EPS side effects which may limit their

use in clinical settings. Those include sedation, weight gain, and severe metabolic disturbances [107, 108].

Rather than their efficacy against the positive symptoms, it is thus their side effect profile and efficacy against the negative and cognitive symptoms that are generally considered to differentiate typical and atypical antipsychotics. Such a clear dichotomy between the two classes of drugs may not be as absolute as originally thought. For instance, while clozapine and quetiapine do not produce significant EPS, risperidone, olanzapine, and ziprasidone can produce them when used at higher therapeutic doses [109, 110]. Similarly, recent studies comparing atypical drugs to low doses of typical antipsychotics showed clinical benefits on negative and cognitive symptoms for typical drugs, although perhaps not as pronounced as that found after treatment with atypical drugs [111–114]. It has therefore been suggested that the superior motor side effect profile of atypicals is largely owing to excessive dosing of the typical drug used as comparator as well as to their wide therapeutic index [91, 115]. Clearly though, the newer atypical agents have emerged as a good long-term treatment option because of their wide therapeutic index and improved control of motor side effects.

### 16.3 Neuropharmacology of Antipsychotics

Antipsychotic drugs have a multitude of effects on various physiological variables through their actions on different neurotransmitter systems. Antipsychotics interact mainly at four neurotransmitter receptor systems in brain: the DA type 1 ( $D_1$  and  $D_5$ ) and type 2 receptor ( $D_2$ ,  $D_3$ , and  $D_4$ ) families, serotonin receptors ( $5HT_{1A}$ ,  $5HT_{2A}$ ,  $5HT_{2c}$ ), muscarinic cholinergic receptors ( $m_1$  and  $m_2$ ), and  $\alpha$ -adrenergic receptors ( $\alpha_1$  and  $\alpha_2$ ).

There have been a number of hypotheses on the mechanisms underlying antipsychotic atypicality. Most of the hypotheses postulate that the different side effect profile of typical and atypical drugs mainly results from differences in their receptor-binding profile. Indeed, while typical neuroleptics are usually preferential for  $D_2$ -like receptors, atypical neuroleptics usually bind to a larger spectrum of receptor types (Table 16.1). For instance clozapine exerts its action through  $D_2$  receptors but also through  $D_1$ , serotonin, muscarinic, and adrenergic receptors and this multireceptor action has been proposed to be the main determinant for atypicality. However, if this concept of multireceptor action stands for clozapine, it does not for other atypical drugs such as amisulpride, which is a highly selective  $D_2$ -like blocker with no other receptor interaction. Moreover, chlorpromazine displays affinity for  $D_2$  like but also for serotonin and adrenergic receptor subtypes and still is a typical agent with high EPS liability.  $D_2$  receptor affinity seems to be the only common denominator among all the presently available antipsychotics. Action at this receptor thus appears the most relevant marker for understanding some key actions of these drugs in humans. As developed in the following paragraphs, the weight of the evidence indicates that DA receptor blockade is essential to clinical antipsychotic

**Table 16.1** In vitro receptor-binding profile ( $K_I$  values, nM) of various typical and atypical antipsychotic drugs

|                      | CPZ              | HDL                | CZ               | AMS                  | RIS              | OLZ              | QUE                | ZIP               | ARI   |
|----------------------|------------------|--------------------|------------------|----------------------|------------------|------------------|--------------------|-------------------|-------|
| D <sub>1</sub>       | 112              | 83                 | 189              | >1,000 <sup>a</sup>  | 60.6             | 58               | 712                | 30                | 387   |
| D <sub>2</sub>       | 2                | 2                  | 431              | 2.8 <sup>a</sup>     | 4.9              | 72               | 567                | 4.0               | 0.95  |
| D <sub>3</sub>       | 5                | 12                 | 646              | 3.2 <sup>a</sup>     | 12.2             | 63               | 483                | 17                | 4.5   |
| D <sub>4</sub> *     | 24               | 15                 | 39               | >1,000 <sup>a</sup>  | 18.6             | 19               | 1,202              | 105               | 514   |
| D <sub>5</sub>       | 133              | 147                | 235              | na                   | 16               | 90               | 1,738              | 152               | 1,676 |
| 5-HT <sub>1A</sub>   | 3,115            | 1,202              | 105              | >10,000 <sup>a</sup> | 427              | 2,063            | 431                | 76                | 5.6   |
| 5-HT <sub>2A</sub> * | 3.2              | 73                 | 13               | 2,000 <sup>a</sup>   | 0.19             | 3                | 366                | 2.8               | 4.6   |
| 5-HT <sub>2C</sub> * | 26               | >10,000            | 29               | >10,000 <sup>a</sup> | 94.9             | 24               | 1,500              | 68                | 181   |
| $\alpha_1$ *         | 2.6 <sup>c</sup> | 7.3 <sup>b</sup>   | 3.7 <sup>b</sup> | na                   | 0.7 <sup>b</sup> | 7.3 <sup>b</sup> | 4.5 <sup>b</sup>   | 1.9 <sup>b</sup>  | na    |
| $\alpha_2$ *         | na               | 1,600 <sup>b</sup> | 51 <sup>b</sup>  | 1,600 <sup>a</sup>   | 1.8 <sup>b</sup> | 140 <sup>b</sup> | 1,100 <sup>b</sup> | 390* <sup>b</sup> | na    |
| m <sub>1</sub> Ach   | 47               | >10,000            | 14               | na                   | >10,000          | 79               | 858                | >10,000           | 6,776 |
| m <sub>2</sub> Ach   | 433              | >10,000            | 14               | na                   | >10,000          | 24               | 1,339              | >10,000           | 3,507 |

Data represent mean  $K_I$  values obtained from the National Institute of Mental Health's Psychoactive Drug Screening Program (PSPD)  $K_I$  database except where indicated. PSPD  $K_I$  values are for cloned human or cloned rat (as indicated by \*) receptors. PSPD-binding assays were performed using [<sup>3</sup>H]SCH23390 for the D<sub>1</sub>- and D<sub>5</sub>-receptors, [<sup>3</sup>H]NMSP for D<sub>2</sub>-, D<sub>3</sub>-, and D<sub>4</sub>-receptors, [<sup>3</sup>H]-8-OH-DPAT for the 5HT<sub>1A</sub>-receptor, [<sup>3</sup>H]ketanserin for the 5HT<sub>2A</sub>-receptor, [<sup>3</sup>H]Mesulergine for the 5HT<sub>2C</sub>-receptor, and [<sup>3</sup>H]QNB for the muscarinic acetylcholine m<sub>1</sub> and m<sub>2</sub> receptors.

AMS: amisulpride; ARI: aripiprazole; CPZ: chlorpromazine; CZ: clozapine; HDL: haloperidol; OLZ: olanzapine; QUE: quetiapine; RIS: risperidone; ZIP: ziprasidone;

na = not available

<sup>a</sup> adapted from [331].

<sup>b</sup> adapted from [378].

<sup>c</sup> adapted from [379].

activity, especially for controlling hallucinations and delusions, while interaction with serotonin receptors may rather be involved in alleviation of EPS.

## 16.4 Dopamine Receptors Involved in Antipsychotic Drug Action

DA exerts its pharmacological action through multiple membrane-spanning proteins of the G protein-coupled receptor (GPCR) superfamily. These may be divided into two subfamilies of receptor subtypes based on their structures, their linkage to adenylate cyclase, and their pharmacological properties: the D<sub>1</sub>-like (D<sub>1</sub>, D<sub>5</sub>) and the D<sub>2</sub>-like receptor subtypes (D<sub>2</sub>, D<sub>3</sub>, D<sub>4</sub>).

D<sub>1</sub> receptors are positively coupled to adenylate cyclase. They are mainly located postsynaptically on the primary dopaminergic projections of the ventral tegmental area (VTA) and substantia nigra (SN) such as the nucleus accumbens (NAcc), cortex, and striatum. In addition, D<sub>1</sub> receptors have also been detected in amygdala, globus pallidus, and hippocampal formation [116]. The D<sub>5</sub> receptors are poorly

expressed in the human brain when compared to D<sub>1</sub> receptors and are mainly localized in the SN pars compacta, hypothalamus, striatum, cerebral cortex, NAcc, and olfactory tubercle [117]. D<sub>2</sub> receptors are located both presynaptically and postsynaptically. Their expression largely overlaps with D<sub>1</sub> receptor expression in DA-rich regions such as the striatum, NAcc, SN, and VTA [116]. D<sub>3</sub> receptors are expressed in high levels in limbic brain regions such as the NAcc, the ventral putamen, and the Islands of Calleja but also to some extent in the striatum, SN, and thalamus [118]. D<sub>4</sub> receptors are located mainly in cortical regions (temporal, entorhinal, cingulate) and hippocampus with low-density levels being found in the caudate/putamen [119].

### ***16.4.1 Role of D<sub>2</sub> Receptor Blockade***

Antipsychotic drugs have a multitude of effects on various physiological variables through their antagonistic actions on different neurotransmitter systems. The antipsychotic effects of these agents are believed to occur primarily through antagonism of D<sub>2</sub>-type DA receptors. Historically, blockade of D<sub>2</sub> receptors was believed to be indispensable for the treatment of psychosis, although the efficacy of weak D<sub>2</sub> blockers such as clozapine called this theory into question. The major therapeutic as well as adverse effects of D<sub>2</sub> antagonism have been conceptualized in the context of the major DA tracts in brain, which include the mesocortical, mesolimbic (A10), nigrostriatal (A9), and tuberoinfundibular (A12) tracts. Although the effects of D<sub>2</sub> blockade on the mesocortical and mesolimbic systems are believed to represent the putative mechanism of action of antipsychotics, excessive blocking of these tracts is also believed to result in their adverse cognitive and behavioral side effects.

#### **16.4.1.1 In Vitro Evidence for an Antipsychotic Action at the D<sub>2</sub> Receptors**

A central role of DA receptor blockade in the mechanism of action of antipsychotics was first anticipated by Carlsson and Lindqvist [10] and later studies of the neuropharmacology of antipsychotics revealed their specifically high affinity for dopamine D<sub>2</sub> receptors and provided strong support for the dopamine hypothesis of schizophrenia [120]. The antipsychotic potency of a compound was found to be directly related to its D<sub>2</sub> receptor affinity. That is, a highly significant correlation exists between the dissociation constant of the D<sub>2</sub> receptor–antipsychotic complex and the average clinically effective dosage [121]. No such correlation exists between dosage and dissociation constant for the D<sub>1</sub>, D<sub>3</sub>, or D<sub>4</sub> receptors [122].

#### **16.4.1.2 Preclinical Evidence for an Antipsychotic Action at the D<sub>2</sub> Receptors**

A number of animal models have been used to explore antipsychotic action and to investigate the mechanisms underlying the differences between the actions of typical and atypical drugs. Some models are used to predict antipsychotic efficacy (i.e., inhibition of amphetamine-induced hyperactivity, disruption of conditioned avoidance responding, and induction of c-fos expression in the shell region of the NAcc), while

others are used to predict their motor side effect liability (i.e., induction of catalepsy, blockade of apomorphine-induced sniffing, and induction of c-fos expression in the dorsolateral striatum).

### Antipsychotic Effect on Indirect DA Agonist-Induced Behavior

Reversal of amphetamine-induced hyperactivity in rodents is one classical animal model used to screen antipsychotic drugs. Indirect DA agonists such as amphetamine or methylphenidate induce a strong increase in locomotor activity when injected into rodents. There is evidence that this increased locomotor activity is due to an increased DAergic activity in the mesolimbic system, mainly within the NAcc [123]. For instance, rats with lesion of this structure do not show hyperactivity after amphetamine administration [124]. While lacking in face validity, blockade of amphetamine-induced hyperactivity is considered as one of the better preclinical predictors of antipsychotic activity. Accordingly, both typical and atypical antipsychotic drugs reduce the hyperactivity produced by amphetamine and this effect has been linked to D<sub>2</sub> receptor blockade [125]. Here again, the potency of antipsychotics to antagonize amphetamine-induced hyperlocomotion correlated with their affinity at D<sub>2</sub> receptors [126]. The similar action of typical and atypical antipsychotics in the amphetamine model is consistent with their similar blockade of D<sub>2</sub> receptors and their similar antipsychotic effect in schizophrenia patients.

### Antipsychotic Effect on Direct DA Agonist-Induced Behaviors

In addition to characterize antipsychotic action on the effects of indirect DA agonists, another classical model consists of studying antipsychotic action on the behavioral effects of direct DA agonists. The most studied compound in this regard is the mixed D<sub>1</sub>/D<sub>2</sub> receptor agonist, apomorphine, which binds directly to each DA receptor subtype. When administered to rodents, apomorphine induces climbing behavior (i.e., the mice climb on the wire lids of their cages for extended periods of time) as well as stereotyped sniffing. The climbing behavior produced by apomorphine is believed to be mediated by excessive DA activity in the mesolimbic pathway, while the stereotyped sniffing is believed to reflect excessive DA activity in the nigrostriatal pathway. Reversal of apomorphine-induced climbing is predictive of efficacy against the positive symptoms of psychosis [127], while reversal of sniffing is predictive of EPS liability ([128]; see also [129] for review). As with the amphetamine model, both typical and atypical antipsychotics such as clozapine, olanzapine, and risperidone are very effective in these models [130], largely to the extent that they block the DA D<sub>2</sub> receptors. Indeed, a correlation analysis based on affinities at rat striatal D<sub>2</sub> sites has shown that the ability of antipsychotics to inhibit apomorphine-induced climbing and sniffing correlated positively with their affinity at D<sub>2</sub> receptors [131]. Typical antipsychotics though tend to be equipotent at reducing both apomorphine-induced climbing and sniffing, whereas most atypical drugs block apomorphine-induced climbing at doses lower than those blocking

apomorphine-induced sniffing (see [129] for review). These models thus demonstrate *in vivo* antagonist activity of all antipsychotics at D<sub>2</sub> receptors and suggest that a lower D<sub>2</sub> action of atypical drugs in the nigrostriatal system may explain their lower propensity to cause EPS when compared to typical.

#### Antipsychotic Effect on Conditioned Avoidance Response

Conditioned avoidance response (CAR) is an important preclinical animal model in the study of antipsychotic drugs [132]. In this paradigm, rats are placed in a two-compartment shuttle box and are trained to avoid an aversive stimulus on presentation of a neutral stimulus that immediately precedes it. All antipsychotics produce a dose-dependent suppression of the avoidance response to the neutral stimulus while the incidence of escapes to the aversive stimulus itself is relatively unaffected, indicating that the effects of antipsychotic on CAR are not due to general sedative effects. In fact, suppression of CAR represents a behavioral effect that is shared by all effective antipsychotics, including the novel compound aripiprazole [133], and potencies in the CAR test have been found to be highly predictive of therapeutic efficacy in schizophrenia [134, 135]. Since the CAR does not help to distinguish between typical and atypical drugs, it suggests that both classes of compounds exert their antipsychotic action through a common mechanism. From a neurochemical perspective, a number of receptor systems have been implicated in the CAR model, including DA D<sub>1</sub>, adrenergic, glutamnergic, muscarinic, and serotonergic receptors. However, it has been suggested that the ability of antipsychotics to selectively suppress CAR is due to their ability to block DA D<sub>2</sub> neurotransmission in the mesolimbic system [136]. Indeed, local application of the DA D<sub>2</sub> receptor antagonist (–)sulpiride into the shell portion of the NAcc, but not into the dorsolateral striatum, suppresses CAR [136]. Furthermore, a direct dose-dependent relationship has been established between the blockade of D<sub>2</sub> receptors and the disruption of CAR [126, 137, 138], indicating that D<sub>2</sub> receptor blockade is an important mechanism of antipsychotic action.

#### Antipsychotic Effect on Catalepsy

The catalepsy test is a common and widely used preclinical screening test for the propensity of an antipsychotic drug to induce EPS in humans [139]. Antipsychotics such as haloperidol and risperidone, which have a dose-dependent propensity to induce EPS in humans, dose-dependently induce catalepsy in animals. In contrast, atypical drugs such as clozapine and aripiprazole, which do not produce EPS in humans do not produce catalepsy in animals [133, 140]. The cataleptic behavior seems primarily to involve D<sub>2</sub> antagonism in the DA nigrostriatal pathway that mediate extrapyramidal motor function and a direct relationship has been established between the blockade of striatal D<sub>2</sub> receptors and catalepsy [137].

Both cataleptic potential and blocking of CAR in animals are often used in combination for predicting antipsychotic action in humans. By studying the dose effects of a given antipsychotic on catalepsy (which is related to striatal function) and CAR

(which is related to limbic function), it is possible to differentiate typical and atypical antipsychotic drugs. Indeed, whereas typical antipsychotics tend to be equipotent at inducing catalepsy and at blocking CAR, most atypical drugs are more potent at blocking CAR than at producing catalepsy [141]. Presumably drugs that are more active against limbic function than striatal function will have antipsychotic activity at doses that will not produce motor side effects [128].

#### Antipsychotic Effect on *c-fos* Expression

Immediate early genes, such as *c-fos*, have proven to be useful markers of changes in neuronal activity, and *c-fos* immunohistochemistry has been used to examine the effects of antipsychotic drugs in the brain [142–146]. These studies have shown that typical and atypical antipsychotic drugs differentially affect *c-fos* expression in various regions of the brain. Haloperidol induces *c-fos* expression in the NAcc, the lateral septum, and the dorsolateral striatum, whereas clozapine increases *c-fos* expression in the NAcc, the lateral septal nucleus, and the medial PFC. Although both typical and atypical antipsychotics increase *c-Fos* expression in the NAcc, they have different effects within the two subdivisions of the nucleus: the shell, which is allied with limbic circuits, and the core, which is allied with the extrapyramidal system. Typical drugs increase *c-fos* in both the shell and the core of the NAcc, whereas atypical drugs increase *c-fos* in the shell but not in the core. This regional specificity of antipsychotic-mediated *c-Fos* expression is thought to reflect different patterns of neuronal activation and consequently differences in the clinical profile between typical and atypical drugs. Since all antipsychotics act on the shell of the NAcc and improve positive symptoms, the shell of the NAcc is probably associated with improvement of positive symptoms. *C-fos* expression in the dorsolateral striatum is associated with motor side effects, and low or no *c-fos* production in this region is predictive of a low potential for producing EPS. The exact mechanism underlying antipsychotic drug-induced *c-fos* expression is unclear but a number of findings support the view that it is the direct result of D<sub>2</sub> blockade. Indeed, the administration of a D<sub>2</sub> receptor agonist prevents the induction of *c-fos* by haloperidol in the dorsal striatum [147] and indirect DA agonists such as cocaine and *d*-amphetamine decrease antipsychotic-induced striatal *c-fos* expression [148, 149].

#### 16.4.1.3 Clinical Evidence for an Antipsychotic Action at the D<sub>2</sub> Receptors

The last decades of research have produced unquestionable evidence for the central role of DA neurotransmission in the pathogenesis of schizophrenia and the mechanism of action of antipsychotic drugs. All currently available antipsychotics are antagonists at the DA D<sub>2</sub> receptor and the primary mechanism through which they achieve their therapeutic effect is through a blockade of these receptors in the mesolimbic DA system. Unfortunately, a concurrent blockade of the D<sub>2</sub> receptor in the nigrostriatal pathway can produce extrapyramidal symptoms (EPS), while D<sub>2</sub> receptor blockage in the tuberoinfundibular tract results in hyperprolactinemia. In

an effort to minimize EPS, positron emission tomography (PET) studies have investigated the doses of antipsychotic used to treat schizophrenics and their relations to side effects and therapeutic efficacy. A number of PET imaging studies in patients with schizophrenia showed that typical antipsychotics are most likely to be effective in a therapeutic window in which 65–78% of D<sub>2</sub> receptors are blocked [150]. Occupancies below 65% are usually associated with a lack of antipsychotic effect, whereas occupancies above 78% are associated with EPS [151]. On the basis of these findings, an optimal window for D<sub>2</sub> receptor occupancy between 65 and 78% has been suggested. D<sub>2</sub> occupancy is thus thought to be the central determinant for the therapeutic efficacy and propensity to cause EPS and prolactin elevation of antipsychotic medication.

However, the efficacy of weak D<sub>2</sub> blockers such as clozapine and quetiapine called this theory into question. Indeed, a key difference between typical and these two atypical antipsychotics is that the two latter drugs achieve robust antipsychotic activity at doses producing D<sub>2</sub> receptor occupancy that are clearly lower than those produced by typical agents. For example, treatment with clozapine and quetiapine induced D<sub>2</sub> receptor occupancies in the 20–68% and 20–64% range, respectively, whereas treatment with typical drugs such as haloperidol led to D<sub>2</sub> receptor occupancies that are rather in the 70–90% range [109, 152–156]. These low levels of striatal D<sub>2</sub> receptor blockade have been proposed as a condition for what was referred as to atypicality, that is, low incidence of EPS and TD. However, some recent evidence weakens this theory. First, some atypical drugs such as sulpiride and amisulpride do not induce EPS or TD despite inducing D<sub>2</sub> occupancies higher than 80% [152, 153, 157]. These studies thus argue against the view that modest D<sub>2</sub> antagonism alone is a valid explanation for the low incidence of EPS and TD associated with atypical drugs. Second, as observed with typical drugs, D<sub>2</sub> antagonism can predict therapeutic efficacy and incidence of EPS even for atypical drugs. Indeed, remoxipride, olanzapine, and risperidone induce D<sub>2</sub> receptor occupancies that range from modest (50–60%) to high (80–90%) depending on the dose used, but therapeutic efficacy is achieved only at doses which exceed the 65% D<sub>2</sub> occupancy level [109, 152, 158–161]. When higher doses are used and D<sub>2</sub> occupancy crosses the 80% level, “atypicality” is sometimes lost, leading to EPS and hyperprolactinemia [162, 163]. In summary, the primary mechanism through which both typical and atypical antipsychotics achieve their therapeutic effect is through a blockade of D<sub>2</sub> receptors.

#### ***16.4.2 Role of D<sub>2</sub> Receptor Partial Agonism***

Differences in regional DA function and observations of DA agonists’ therapeutic effects in schizophrenia [164] led to the development of D<sub>2</sub> partial agonists as a new class of atypical antipsychotic agents. DA D<sub>2</sub> partial agonists have high affinity for D<sub>2</sub> receptors but reduced intrinsic activity when compared to the naturally occurring full agonist ligand DA, that is, they will produce less D<sub>2</sub> receptor activation than DA. As a consequence, D<sub>2</sub> partial agonists can act as agonists or antagonists depending on the local concentration of endogenous DA: in the presence of high

DA levels, partial agonists will act as antagonists by blocking DA access to the D<sub>2</sub> receptor, whereas they will act as agonists in the presence of low DA levels [165]. In theory, this means that partial DA agonists could alleviate the positive and negative symptoms of schizophrenia by counteracting DA transmission in hyperdopaminergic mesolimbic regions and by enhancing it in hypodopaminergic mesocortical regions. Partial DA agonists are therefore thought to stabilize dopaminergic tone in schizophrenia and are thereby often referred to as “dopamine stabilizers.” On the other hand, a low intrinsic activity at the D<sub>2</sub> receptors prevents complete blockade of D<sub>2</sub> activity in the striatum and would confer a low propensity to cause EPS and prolactin elevation.

Dopamine D<sub>2</sub> autoreceptors may also be involved in the therapeutic action of partial agonists in schizophrenia. D<sub>2</sub> autoreceptors are localized on the presynaptic aspect of DA neurons and exert a negative feedback on DA release and/or synthesis. A dysregulated control of DA release/synthesis by these autoreceptors could contribute to the postulated imbalance of cortical and subcortical DA neurotransmission in schizophrenia. For instance, a reduced activity of the D<sub>2</sub> autoreceptors could lead to an increased DA release and thus contribute to the subcortical DA hyperactivity postulated in this disorder. Hence, D<sub>2</sub> partial agonists with high affinity for the presynaptic autoreceptors are particularly valuable antipsychotics as they can reduce DA synthesis and release through an agonist action at the presynaptic autoreceptors and block the response to DA through an antagonist action at the postsynaptic receptors.

Several D<sub>2</sub> partial agonists have been evaluated in schizophrenia. Preclamol, also known as (–)-3-(3-hydroxyphenyl)-*N*-n-propylpiperidine or (–)-3PPP, is a D<sub>2</sub>-like partial agonist with high selectivity for the autoreceptor [166, 167]. A placebo-controlled trial indicated that preclamol improved both the positive and the negative symptoms of schizophrenia with no occurrence of motor side effects [168]. However, tolerance occurred over the course of a week, presumably because of a D<sub>2</sub> autoreceptor desensitization, and thus limited its usefulness for the treatment of schizophrenia. Other DA partial agonists that have undergone trials in schizophrenia include talipexole (B-HT 920), roxindole (EMD 49980), terguride, and SDZ-HDC 912. Despite their favorable preclinical profile, these compounds were not successful antipsychotic agents as they either failed to improve positive symptoms [169–171] or were associated with significant motor side effects [172]. Differences in clinical effects of these partial agonists may be due to their differential intrinsic activity at D<sub>2</sub> receptors [165].

The first successful D<sub>2</sub> partial agonist to come into practice is aripiprazole (see [173, 174] for review). Aripiprazole has high affinity for the D<sub>2</sub> receptor and behaves both as a potent D<sub>2</sub> autoreceptor agonist and as a postsynaptic D<sub>2</sub> antagonist [175]. It also exhibits high affinity and partial agonism at the D<sub>3</sub> and serotonin 5HT<sub>1A</sub> receptors and antagonism at the serotonin 5HT<sub>2A</sub> receptors. In animal models, aripiprazole inhibits amphetamine-induced locomotion, CAR, and apomorphine-induced stereotypy without causing catalepsy and produces an increased expression of *c-fos* in the shell of the NAcc but not in the striatum [130, 133, 176]. Thus, aripiprazole has preclinical and receptor-binding profiles that predict therapeutic

efficacy with a low risk of side effects. Concordant with this, aripiprazole is active against both the positive and the negative symptoms of schizophrenia, has a low propensity for EPS, and produces no elevation in serum prolactin levels [177, 178]. At clinically effective doses (10–30 mg/day), aripiprazole occupies 85–95% of the striatal D<sub>2</sub> receptors but still has a low incidence of EPS [179, 180]. The threshold for aripiprazole antipsychotic response thus appears to be higher than the 65% conventional threshold observed for D<sub>2</sub> antagonists, and EPS appear to be uncommon even at occupancies that exceed the extrapyramidal side effects threshold of 78% [180]. Aripiprazole thus does not conform to the conventional relationship between D<sub>2</sub> receptor occupancy and occurrence of motor side effects. Based on the magnitude of the upward shift of this relationship, the intrinsic activity of aripiprazole has been estimated to be approximately 25% [180]. Such a small intrinsic activity limits excessive DA stimulation and D<sub>2</sub> receptor blockade and preserves dopaminergic function in presynaptic and postsynaptic neurons, thereby conferring aripiprazole its favorable clinical profile. Interestingly, the principle active metabolite of clozapine, *N*-desmethylclozapine (NDMC), was recently identified as a partial agonist at D<sub>2</sub> receptors [181], and higher ratios of NDMC to clozapine levels in plasma have been found to predict better improvements in clinical response [182]. The unique clinical profiles of aripiprazole and clozapine, which are both distinguished even from other atypical antipsychotics by their much lower propensity to induce EPS and TD, suggest that partial agonism at D<sub>2</sub> receptors is a desirable feature of an antipsychotic drug.

### ***16.4.3 Role of D<sub>1</sub> Receptor Blockade***

In the search for new leads for the development of novel antipsychotic drugs with atypical properties, D<sub>1</sub> receptor antagonists have been thought as particularly promising. Indeed, D<sub>1</sub> antagonists have often met criteria for antipsychotic potential and low EPS liability in both rodents and nonhuman primates. For instance, the potent and selective D<sub>1</sub> antagonist SCH39166 inhibits apomorphine-induced climbing at lower doses than it inhibits apomorphine-induced sniffing in mice, it inhibits CAR response in both rat and squirrel monkey, but it does not cause catalepsy or increase plasma prolactin levels [183]. The relatively high affinity of clozapine for D<sub>1</sub> receptors as compared to D<sub>2</sub> receptors points to the same direction and has been regarded as a potential reason for its unique clinical profile (high antipsychotic efficacy with low EPS). At therapeutic dose, clozapine produces stronger blockade of D<sub>1</sub> receptors as compared to typical antipsychotics (40–60% vs. 0–40%) and lower blockade of D<sub>2</sub> receptors (maximum 50% blockade vs. 70–80%) [152, 184, 185], thus providing support to the view that D<sub>1</sub> antagonism might be a potential ground to atypicality. However, several findings do not support a role for D<sub>1</sub> receptor as a primary target of antipsychotic action. First, and opposed to the predictions from animal models, efforts to improve psychosis with selective D<sub>1</sub> antagonists have failed [186–188]. Second, therapeutic doses of various typical and atypical drugs occupy low or negligible levels of D<sub>1</sub> receptors. For instance, drugs such

as haloperidol, sulpiride, perphenazine, and even quetiapine, despite being effective antipsychotic agents, occupy less than 10% of the D<sub>1</sub> receptors [152, 184, 189]. These data thus suggest that D<sub>1</sub> antagonism by itself does not significantly contribute to the therapeutic effect of antipsychotics.

However, the D<sub>1</sub> receptor may be an important target for improving cognitive function in schizophrenia. Indeed, DA neurotransmission in the PFC strongly modulates working memory performance. Microiontophoretic applications of DA into the PFC facilitate whereas 6-hydroxydopamine PFC lesions disrupt working memory processes in primates [190–193]. This beneficial effect of DA on working memory processes appeared to be primarily mediated by D<sub>1</sub> receptors as it was mimicked by local injection of D<sub>1</sub> agonists, while local injection of D<sub>1</sub>, but not D<sub>2</sub> antagonists, disrupts working memory in primates [194–196]. Interestingly, long-term treatment with a typical antipsychotic induced working memory deficits in nonhuman primates that can be reversed by brief treatment with a D<sub>1</sub> full agonist [197]. D<sub>1</sub> receptors are thus critically important in working memory function. It seems, however, that an optimal level of D<sub>1</sub> receptor “tone” in the PFC is required for adequate working memory performance. If DA levels are low, increasing D<sub>1</sub> receptor stimulation is beneficial for improving working memory while if DA levels are high, D<sub>1</sub> receptor activation could have the exact opposite effects (i.e., disrupting instead of improving working memory) [198, 199]. D<sub>1</sub> receptor activation thus follows an inverted “U”-shape function regarding performance on working memory, with too much or too little D<sub>1</sub> agonist stimulation both disrupting performance [200].

Considering the central role of D<sub>1</sub> receptors in memory function, the cognitive deficits observed in schizophrenia have long been thought to relate, at least in part, to a reduced D<sub>1</sub> signaling in the PFC. PET studies have, however, produced conflicting findings in this regards, with studies showing decreased [36], unaltered [34], or increased [35] D<sub>1</sub> receptor binding in the PFC of unmedicated patients as compared to control subjects. Despite this, D<sub>1</sub> receptor agonism, when combined with D<sub>2</sub> antagonism, should be of importance in the clinical efficacy of an atypical antipsychotic drug. The favorable profile of clozapine on cognitive functioning in schizophrenia is of particular interest. Clozapine indeed shows D<sub>1</sub> agonist properties in some animal models [201–203]. When combined with D<sub>2</sub> blockade, D<sub>1</sub> agonism rather than D<sub>1</sub> antagonism thus seems a promising option for the treatment of schizophrenia.

#### ***16.4.4 Role of D<sub>3</sub> Receptor Blockade***

The D<sub>3</sub> receptor shares a high degree of homology with the D<sub>2</sub> receptor subtype and both are negatively coupled to adenylyate cyclase. In contrast to D<sub>2</sub> receptors, which are prominently localized in projection areas of the motor nigrostriatal DA system (e.g., dorsolateral striatum), the D<sub>3</sub> receptor is preferentially localized in projection areas of the mesocorticolimbic dopaminergic system (e.g., NAcc, ventral putamen, PFC). This preferential localization of D<sub>3</sub> receptors in limbic vs. motor regions of the brain has sparked great interest in the D<sub>3</sub> receptor as a potential

target of antipsychotic action. Antipsychotic drugs generally have similar affinities for D<sub>2</sub> and D<sub>3</sub> receptors (Table 16.1). However, the relative contribution of D<sub>3</sub> vs. D<sub>2</sub> antagonism to antipsychotic efficacy is difficult to establish in humans due to the lack of selective D<sub>3</sub> compounds and to the partially overlapping distribution of D<sub>2</sub> and D<sub>3</sub> receptors. Preclinical studies have produced mixed results regarding the potential antipsychotic activity of D<sub>3</sub> antagonism. When administered repeatedly to rodents, SB-277011-A, a high affinity and highly selective D<sub>3</sub> antagonist [204], has been shown to selectively decrease the number of spontaneously active DA neurons in VTA [205]. This electrophysiological model is postulated to predict antipsychotic activity as both typical and atypical agents such as haloperidol and clozapine alter the activity of midbrain DA neurons, whereas drugs with no antipsychotic activity do not have such an effect [206, 207]. According to this model, selective D<sub>3</sub> receptor blockade using SB-277011-A is thus predicted to be associated with antipsychotic efficacy. On the other hand, this compound was found to be ineffective for blocking the amphetamine-induced hyperlocomotion, another putative animal model for antipsychotic activity [204]. Clinical trials of selective D<sub>3</sub> receptor antagonists in humans have not been reported yet and are needed to better understand the significance of D<sub>3</sub> receptors as targets for the treatment of schizophrenia.

### ***16.4.5 Role of D<sub>4</sub> Receptor Blockade***

The observation that clozapine has a high affinity for D<sub>4</sub> receptors as compared to D<sub>2</sub> receptors has sparked enormous interest in the D<sub>4</sub> receptor as a potential target for the treatment of schizophrenia [208]. This interest was further strengthened by postmortem studies showing elevated densities of D<sub>4</sub> receptors in the striatum of schizophrenic patients [38–40], although this finding has not been consistently confirmed [41–44]. However, D<sub>4</sub> receptor blockade does not appear essential for mediating antipsychotic action or for conferring low EPS liability. Indeed, several atypical drugs (e.g., amisulpride, quetiapine, aripiprazole) have very little D<sub>4</sub> receptor blocking activity, and several typical (e.g., chlorpromazine, haloperidol) and some atypical drugs (i.e., olanzapine, clozapine, risperidone) have high D<sub>4</sub> affinities (Table 16.1; see also [209]). Finally, clinical trials with two D<sub>4</sub> selective antagonists, L745870 [210, 211] and sonepiprazole [212], have failed to demonstrate antipsychotic efficacy.

## **16.5 Considerations Critical for Understanding Receptor Involvement in Antipsychotic Action**

### ***16.5.1 Speed of Onset and Implications for Mechanism***

It has long been held that onset of antipsychotic effect on psychotic symptoms is delayed by 2–3 weeks after initiation of treatment. One widely accepted hypothesis for this delayed onset of action is that of depolarization block [213]. According to

that hypothesis, the acute blockade of D<sub>2</sub> receptors initially leads to an increased firing of ventral tegmental DA neurons. However, over successive administrations this subsides, and after 2–3 weeks of chronic treatment antipsychotics ultimately produce a reversible cessation of firing of midbrain DA neurons, known as depolarization block. The delayed onset of antipsychotic action is thus thought to correlate with the delayed induction of depolarization blockade of mesolimbic DA neurons [206, 207]. Another hypothesis postulates that antipsychotic-induced changes in the synthesis or degradation of critical “effector” protein synthesis could also explain the delayed onset of antipsychotic action [214]. Although the molecular mechanism underlying the delayed improvement of psychotic symptoms is unclear, the idea of a “delayed onset” of antipsychotic action is at odds with the immediate effect of antipsychotics on D<sub>2</sub> receptor blockade, which occurs within the first few hours of antipsychotic treatment [215, 216]. This dissociation between early D<sub>2</sub> blockade and delayed therapeutic gain thus speaks against a central role of D<sub>2</sub> blockade in the mechanism of action of antipsychotic drugs. However, an emerging body of evidence suggests that antipsychotics have an earlier onset of efficacy than previously thought. In 2003, Agid et al. [217, 218] conducted a meta-analysis of 42 double-blind, comparator-controlled studies (>7000 patients) of patients treated with the common typical (haloperidol, chlorpromazine) and atypical (risperidone and olanzapine) antipsychotics. Without significant difference across antipsychotics, they found – contrary to expectations under the delayed onset hypothesis – that psychosis improved within the very first week of treatment. In fact, a larger reduction of symptoms occurs during the first 2 weeks than during the second 2 weeks of treatment. This observation of early onset of symptom response has subsequently been extended to other agents, including quetiapine [219, 220] and amisulpride [221]. Interestingly, early trials with ziprasidone [222] and aripiprazole [223] also showed detectable onset of effects on positive symptom scores within the first 2 weeks of treatment. In a double-blind placebo-controlled study comparing intramuscular olanzapine to intramuscular haloperidol in patients experiencing a psychotic exacerbation, Kapur et al. [224] reported that onset of therapeutic response occurred within the first 24 h. Abi-Dargham [49] also observed rapid improvement (i.e., within 72 h) in psychotic symptoms upon DA depletion with  $\alpha$ -methyl-para-tyrosine. These observations thus support a direct role for DA in the mediation of psychosis and further indicate that the mechanism of antipsychotic action may be more proximally related to the blockade of D<sub>2</sub> receptors than originally thought.

### ***16.5.2 Relapse on Withdrawal and Supersensitivity***

Withdrawal or decreased dosing of long-term antipsychotic treatment can induce relapse of the psychotic symptoms in some schizophrenic patients. This effect, usually called supersensitivity psychosis or rebound psychosis, has been observed after withdrawal from antipsychotic drugs such as quetiapine [225], clozapine [226, 227], olanzapine [228], haloperidol [229], chlorpromazine [230], and fluphenazine

enanthate [231, 232]. As supersensitivity psychosis can be accompanied by the development or worsening of latent TD [231, 232], both clinical manifestations are thought to arise from a DAergic supersensitivity. Supports for this hypothesis come from behavioral experiments in rodents showing that withdrawal from chronic antipsychotic treatment results in an increased responsiveness to direct or indirect DA agonists, such as apomorphine [233–238], amphetamine [239–241], and DA injected into the striatum [242]. There is evidence that postsynaptic processes contribute to this antipsychotic-induced behavioral supersensitivity. Indeed, chronic treatment with typical drugs such as haloperidol and chlorpromazine as well as atypical drugs such as remoxipride, olanzapine, and risperidone has been consistently shown to increase D<sub>2</sub> receptor density in the dorsal striatum and NAcc [243–249]. This finding led to the proposal that long-term treatment with antipsychotic drugs in humans could lead to a compensatory D<sub>2</sub> receptor upregulation, causing receptor supersensitivity and resulting in the onset of TD and supersensitivity psychosis upon withdrawal [232, 250–252]. More specifically, the development of TD is thought to reflect an increased density of D<sub>2</sub> receptors in the striatum leading to a functional supersensitivity of the nigrostriatal system, whereas receptor supersensitivity occurring in mesolimbic system would result in the development of supersensitivity psychosis [14, 250, 251, 253, 254]. It is noteworthy that besides the D<sub>2</sub> receptor supersensitivity hypothesis, other hypotheses have been proposed to explain TD. These include a deficiency of the GABA neurotransmitter system or excitotoxic neuronal damages induced by dopamine release, glutamate release, or oxidative stress [255–257]. Yet, depleting DA brain levels with tetrabenazine or reserpine constitute a most effective treatment for TD [258–260], thus indicating an important role for excessive DA signaling, likely supersensitive DA D<sub>2</sub> system, in the pathophysiology of TD.

Although D<sub>2</sub> receptor upregulation seems to be a central mechanism in mediating the long-term, and potentially irreversible, consequences of chronic exposure to most antipsychotic drugs, several lines of evidence suggest that DA supersensitivity and D<sub>2</sub> receptor upregulation can be dissociated. Indeed, the two atypical antipsychotics most often associated with supersensitivity psychosis are quetiapine and clozapine [225–227]. Both drugs also induce a supersensitive psychomotor response to DA agonists in animals [238, 261] but still, they do not induce striatal D<sub>2</sub> receptor upregulation [249, 262, 263]. This lack of striatal D<sub>2</sub> receptor upregulation has been proposed to underlie the low propensity of clozapine to induce TD in humans [264]. Therefore, increase in D<sub>2</sub> receptor density is not sufficient to explain DA supersensitivity. However, a lack of D<sub>2</sub> upregulation does not necessarily preclude the involvement of D<sub>2</sub> receptor mechanisms in the DA supersensitized state seen upon clozapine and quetiapine withdrawal. For instance, alterations at the level of G proteins that couple D<sub>2</sub> receptors to adenylyl cyclase can also result in an increased D<sub>2</sub> signaling and supersensitivity despite the lack of D<sub>2</sub> upregulation [265–267]. Such a mechanism may be involved in the DA supersensitivity seen after clozapine and quetiapine as both drugs induce elevation in D<sub>2</sub><sup>High</sup> (D<sub>2</sub> receptors with functional high affinity for DA) despite the absence of any elevation in total D<sub>2</sub> receptors [32]. Interestingly, a functional coupling of D<sub>2</sub> receptors with G proteins also appears

to be involved in the action of atypical drugs, as indicated by a larger proportion of  $D_2^{\text{High}}$  [32, 268], an increased efficacy of DA to stimulate [ $^{35}\text{S}$ ]GTP $\gamma$ S binding [233], and an increased activity of the  $D_2$  receptor– $G_i$  protein system after repeated haloperidol administrations [266, 269–271]. Moreover, as observed with clozapine and quetiapine, withdrawal from low doses of typical antipsychotics also reveals a dissociation between increased DA-mediated behavior and  $D_2$  upregulation [272, 273]. For instance, Samaha et al. [273] recently showed that chronic low doses of haloperidol enhanced amphetamine-induced locomotion with no increase in  $D_2$  densities and only higher doses lead to concomitant  $D_2$  upregulation. Low doses of haloperidol though increased  $D_2^{\text{High}}$ , indicating that elevation in  $D_2^{\text{High}}$  rather than elevation in the total population of  $D_2$  sites best predicted behavioral DA supersensitivity. Thus, there may be two types of  $D_2$  receptor-mediated supersensitivity: one associated with increased  $D_2^{\text{High}}$  and leading to supersensitivity psychosis and the other associated with increased  $D_2$  density and leading to TD. Relatively low levels of  $D_2$  blockade induced by either weak  $D_2$  antagonists or low doses of potent  $D_2$  antagonists may lead to an increased population of functionally coupled  $D_2$  receptors (i.e.,  $D_2^{\text{High}}$ ) and this may be sufficient to induce DA supersensitivity. On the other hand, stronger  $D_2$  blockade induced by typical drugs or by high doses of atypical drugs would further result in  $D_2$  upregulation, which would in turn lead to TD.

### ***16.5.3 Antagonist vs. Inverse Agonist***

It is generally assumed that antipsychotic drugs are acting as antagonists at the  $D_2$  receptor. In recent years, this picture of antipsychotic action has been modified to include inverse agonism. Inverse agonism at  $D_2$ -like receptors was first noted for haloperidol, which increased prolactin production and cyclic AMP formation in pituitary cell lines [274]. Subsequently, several other antipsychotic drugs were identified as  $D_2$  inverse agonists using a variety of techniques [275–277]. In fact, with the exception of aripiprazole, all antipsychotics tested so far are inverse agonists at the  $D_2$  receptor, independently of their typical or atypical profile [181, 278].  $D_2$  inverse agonist activity thus appears to be a common feature of antipsychotic drugs although different antipsychotics exhibit different degrees of inverse agonism, ranging from high (e.g., haloperidol, pimozide) to very low inverse agonist activity (e.g., quetiapine) [181]. From a mechanistic perspective, the way  $D_2$  inverse agonists work is not clearly established. Based on the ternary complex model of G protein-coupled receptor action [279], it has been proposed that  $D_2$  receptors may exist in an inactive state, which can isomerize to a partially active state that can ultimately couple to G proteins to form a fully active state of the receptor [280]. The fully active state of the receptor is believed to give rise to constitutive activity, leading to a tonic inhibition of adenylate cyclase even in the absence of DA. Inverse agonists would reduce this basal spontaneous  $D_2$  receptor activity by stabilizing the uncoupled forms to the detriment of the coupled, fully active, form of the receptor

[281]. Although intrinsic constitutive D<sub>2</sub> receptor activity and D<sub>2</sub> inverse agonism properties of antipsychotic drugs have been demonstrated *in vitro*, it is still unclear whether this has any relevance *in vivo*. Inverse agonism will be relevant to the effects of antipsychotics only if there is a spontaneous agonist-independent activity of the D<sub>2</sub> receptors *in vivo*. If there is no such spontaneous activity, then an inverse agonist will be indistinguishable from an antagonist.

### ***16.5.4 Fast Dissociation and Transient Occupancy of D<sub>2</sub> Receptors***

In contrast to the multireceptor hypothesis, which postulates that the atypical features of antipsychotics are conferred by binding to receptors other than D<sub>2</sub>, another theory postulates that atypicality can be produced by appropriate modulation of the D<sub>2</sub> receptor alone. Indeed, Kapur and collaborators [150, 282, 283] have proposed that the lower liability of atypical vs. typical drugs to induce EPS is related to their fast dissociation from D<sub>2</sub> receptors. Typical antipsychotics bind tightly to and dissociate slowly from D<sub>2</sub> receptors, whereas atypical drugs bind more loosely and dissociate fast from the receptors [284]. As a consequence, atypical drugs may block the receptors but be more responsive to phasic surges of DA transmission and hence may normalize transmission, rather than suppress it. In addition to molecular considerations (of fast or slow dissociation) is also the systemic issue of occupancy kinetics. *In vivo* PET studies have shown that typical drugs such as haloperidol give rise to sustained high levels of D<sub>2</sub> receptor blockade through the day [215], while certain atypical drugs such as quetiapine give rise to only transiently high levels of D<sub>2</sub> receptor blockade (up to 64% at 2 h; 0% at 12–14 h) with no incidence of EPS and prolactin elevation [156, 285]. Transient D<sub>2</sub> blockade may thus be sufficient to induce antipsychotic response while minimizing the risks of EPS and hyperprolactinemia. It is thus predicted that a low affinity and fast dissociation from D<sub>2</sub> receptors, along with administration of the drug in doses that lead to appropriate levels of D<sub>2</sub> blockade, are the most important requirements for atypicality [282]. A transient duration of action may also explain the lack of D<sub>2</sub> receptor upregulation reported following treatment with atypical drugs such as clozapine, loxapine, or thioridazine in rats [249, 263, 286–289] and the low propensity of atypical drugs to induce TD in humans [264]. Indeed, recent studies indicate that the pattern of D<sub>2</sub> occupancy kinetics achieved by chronic haloperidol has an important influence on D<sub>2</sub> upregulation and on the development of vacuolar chewing movements (VCMs), an animal model for TD. While continuously high levels (>70–80% for 24 h/day) of D<sub>2</sub> receptor blockade produced by continuous infusion of haloperidol lead to a robust upregulation of striatal D<sub>2</sub> receptors and to an increased risk for the development of VCMs in experimental animals, transiently high levels (>80% for a few hours/day) of D<sub>2</sub> receptor blockade produced by daily bolus injections of the same drug did not produce any of these effects [290, 291]. Thus, converging evidence suggests that the pharmacokinetics of D<sub>2</sub> receptor blockade during chronic treatment with haloperidol is an important determinant for the induction of D<sub>2</sub> receptor upregulation and for the development of VCMs, and potentially TD. The reason

why transiently high D<sub>2</sub> receptor blockade resulted in no receptor alteration is not clear. However, it can be postulated that blocking receptors only transiently during the day would preserve some access of endogenous DA to the receptors and that this pulsatory agonist stimulation could be sufficient to prevent a compensatory D<sub>2</sub> receptor upregulation.

### ***16.5.5 Preferential Limbic D<sub>2</sub> Receptor Blockade***

Another theory to account for atypicality is the preferential action of antipsychotics with low EPS liability on the limbic DA system. Several lines of evidence indicate that, in contrast to typical antipsychotics, atypical antipsychotics selectively target the mesolimbic DA system, while leaving the nigrostriatal system relatively unaffected. For instance, while the acute administration of haloperidol increases the number of spontaneously active DA neurons in both the SN and VTA, clozapine and olanzapine selectively increase the number of firing cells in the VTA only [207, 292, 293]. Consistent with these electrophysiological data, atypical drugs have been shown to preferentially increase DA output in the NAcc as compared to the striatum, whereas the opposite was observed after acute administration of haloperidol [294]. This regional specificity (often called limbic selectivity) of atypical agents is also observed on chronic treatment as drugs such as clozapine, quetiapine, olanzapine, and sertindole produce depolarization inactivation of VTA DA neurons, sparing those in the SN, whereas haloperidol inactivates DA neurons in both the SN and the VTA [206, 207, 292, 293, 295, 296]. Consequently, in those animal models, atypical antipsychotics can be differentiated from typical drugs on the basis of their preferential effect on DA transmission in limbic regions. Some evidence indicates that such a limbic selectivity may also exist in clinical settings. Indeed, in vivo receptor imaging studies have shown that, at clinically useful doses, several atypical antipsychotics including clozapine, olanzapine, quetiapine, risperidone, and sertindole demonstrate preferential blockade of D<sub>2</sub> receptors in limbic cortical regions than in striatum [297–301]. These studies suggest that preferential blockade of cortical and/or limbic D<sub>2</sub> receptors may be sufficient to mediate the therapeutic efficacy and low extrapyramidal symptom profile of atypical antipsychotic drugs. However, other studies report similar levels of striatal and cortical D<sub>2</sub> receptor blockade with atypical drugs [302–305]. The reason for this discrepancy between groups reporting similar striatal–extrastriatal occupancy and those showing much higher extrastriatal occupancy is not entirely clear and may be related to methodological differences between studies. However, the concept of limbic selectivity as a possible mechanism of atypical action is called into question. This is further emphasized by recent data showing that striatal rather than extrastriatal D<sub>2</sub> receptor blockade is predictive of improvement in positive symptoms as well as occurrence of motor side effects associated with antipsychotic treatment [305]. Clearly, more clinical investigations are needed to determine the exact role of limbic D<sub>2</sub> receptors in the treatment of schizophrenia.

## 16.6 Other Receptors Involved in Antipsychotic Drug Action

### 16.6.1 Role of 5HT<sub>2A</sub> Receptor Blockade and 5HT<sub>1A</sub> Receptor Activation

The therapeutic efficacy of atypical drugs such as clozapine prompted researchers to examine how their actions on various neurotransmitter receptors differ from those of typical antipsychotics. In this respect, serotonin (5-HT) receptors have received particular attention in the treatment of schizophrenia as several antipsychotic drugs exhibit high affinities for these receptors, especially for the 5-HT<sub>2A</sub>, 5-HT<sub>2C</sub>, and 5-HT<sub>1A</sub> receptor subtypes (Table 16.1).

The finding that clozapine is a potent 5-HT<sub>2A</sub> receptor antagonist has generated great interest in the potential role of these receptors in antipsychotic drug actions. As a matter of fact, most currently approved atypical antipsychotic drugs are relatively potent 5-HT<sub>2A</sub> antagonists (Table 16.1). Moreover, subchronic treatment with clozapine but not haloperidol decreased 5-HT<sub>2A</sub> mRNA and the density of [<sup>3</sup>H]ketanserin binding in frontal cortex, Nacc, and striatum [306–308], suggesting that modulation of 5-HT<sub>2A</sub> receptor levels may be important in atypical action. Several lines of evidence indicate that 5-HT<sub>2A</sub> antagonism per se does not confer antipsychotic effects. First, MDL 100,907, a compound largely lacking D<sub>2</sub> antagonism but which is a potent 5-HT<sub>2A</sub> antagonist, while showing promising antipsychotic properties in preclinical studies, was not found to be as effective as haloperidol in the treatment of schizophrenia [309]. Similarly, fananserin, a potent 5-HT<sub>2A</sub>/D<sub>4</sub> antagonist lacking D<sub>2</sub> antagonism, does not show antipsychotic activity [310]. Second, amisulpride does not occupy any 5-HT<sub>2A</sub> receptors in humans even when used at high doses but still is a highly effective atypical antipsychotic [311]. Third, 5-HT<sub>2A</sub> receptor blockade is not necessary for, nor does it alter, the D<sub>2</sub> receptor occupancy required for clinical effectiveness [150]. Indeed, PET studies have consistently showed that, at clinically relevant doses, atypical agents such as risperidone and olanzapine have higher occupancy of 5-HT<sub>2A</sub> than D<sub>2</sub> receptors [158, 303, 312–314]. However, these drugs become effective only at doses which cross the conventional 65% level of D<sub>2</sub> occupancy. Doses below this D<sub>2</sub> occupancy threshold, although saturating 5-HT<sub>2A</sub> receptors, are not therapeutic [312]. Thus, a minimal level of D<sub>2</sub> receptor blockade is a necessary condition for an antipsychotic drug to be effective independent of any action on the 5-HT<sub>2A</sub> receptor.

Although 5-HT<sub>2A</sub> antagonism does not seem to constitute a primary mechanism for antipsychotic action, it has been suggested that a high affinity for 5-HT<sub>2A</sub> receptors combined with a relatively lower affinity at the D<sub>2</sub> receptors, producing a high 5-HT<sub>2A</sub>/D<sub>2</sub> affinities ratio, is critical for conferring atypical activity [315]. Current hypotheses suggest that serotonin 5HT<sub>2A</sub> receptor mechanisms may improve cognitive function and negative symptoms and limit EPS by increasing DA release [316, 317]. Serotonin 5-HT<sub>2A</sub> receptors are indeed uniquely positioned to modulate central DA transmission. These receptors are expressed on midbrain DA neurons of the VTA [318] as well as on cortical and pallidal afferents in the dorsal striatum [319]. They are also abundant in the frontal cortex where they are localized

postsynaptically on pyramidal neurons [320, 321] and, albeit to a smaller extent, presynaptically on DA terminals [322]. Atypical antipsychotics have been reported to preferentially increase DA efflux in the mPFC compared with the NAcc in rats [323–325]. This action is due, in part, to blockade of cortical 5-HT<sub>2A</sub> receptors combined with weaker blockade of D<sub>2</sub> receptors, since it can be mimicked by the combination of potent 5-HT<sub>2A</sub> antagonism and weak blockade of D<sub>2</sub> receptors [326–328] whereas it does not occur with the selective 5-HT<sub>2A</sub> antagonist MDL 100,907 [329]. The 5-HT<sub>2A</sub>/D<sub>2</sub> model [316, 317] suggests that by blocking presynaptic 5-HT<sub>2A</sub> receptors in the DA mesocortical and nigrostriatal pathways, atypical antipsychotics locally increase DA release. This effect would lessen the action of the drugs at D<sub>2</sub> receptors, thereby improving cognitive deficits and/or negative symptoms and decreasing the incidence of EPS. In contrast, with the sparse distribution of 5-HT<sub>2A</sub> receptors in NAcc, D<sub>2</sub> blockade would still prevail in the DA mesolimbic pathways, thus preserving antipsychotic activity of these drugs. Thus, the differential distribution of D<sub>2</sub> and 5HT<sub>2A</sub> receptors may explain why atypical antipsychotic drugs exert opposite action on DA transmission in cortical and limbic brain regions.

While an anti-5HT<sub>2A</sub> effect of atypical drugs may contribute to their ability to improve cognitive function and/or negative symptoms, it is unclear whether such a mechanism is necessary for their lower EPS propensity. Indeed, atypical drugs such as remoxipride [330] and amisulpiride [311, 331] have negligible affinities for 5-HT<sub>2A</sub> receptors and still do not induce EPS at clinical dose. The reverse situation is encountered with some typical drugs, such as chlorpromazine and loxapine, which produce high 5-HT<sub>2A</sub> occupancies [311, 332] but still induce EPS at clinical dose.

Although research on the role of serotonergic mechanisms in antipsychotic drug action has mainly focused on 5HT<sub>2A</sub> receptors, 5HT<sub>2C</sub>, 5HT<sub>1A</sub>, 5HT<sub>6</sub>, and 5HT<sub>7</sub> receptors may also be of some significance [316]. For instance, another mechanism that has been proposed to modulate the DA system and prevent or reduce the motor effects of D<sub>2</sub> blockade is 5HT<sub>1A</sub> receptor agonism. Serotonin 5HT<sub>1A</sub> receptor agonism, in combination with D<sub>2</sub> receptor antagonism, facilitates DA release in PFC and NAcc but not in striatum [333] and attenuates the EPS-like side effects of D<sub>2</sub> blockade [334, 335]. Recent observations indicate that the increase in DA output produced by atypical antipsychotics such as clozapine, ziprasidone, and aripiprazole in the PFC is dependent on the activation of 5-HT<sub>1A</sub> receptors as it is partly or totally antagonized by the 5-HT<sub>1A</sub> receptor antagonist WAY-100635 [324, 336–338] and by the genetic deletion of 5-HT<sub>1A</sub> receptors [339]. Given the central role of prefrontal DA in cognitive function, the increase in PFC DA release may underlie the superior effects of clozapine and other atypical antipsychotic drugs on the negative and cognitive symptoms by normalizing a putative cortical hypodopaminergic transmission.

### ***16.6.2 Role of Drugs Acting on the Glutamate System***

The NMDA receptor hypofunction hypothesis of schizophrenia has provided a theoretical framework for investigating the effects of drugs acting on the glutamatergic

system in schizophrenia. Examples of new “glutamate-based” agents are agonists of the glycine recognition site of the NMDA receptor (e.g., glycine, D-serine, D-cycloserine), glycine reuptake inhibitors, glutamate release inhibitors (e.g., LY-354740 and lamotrigine), AMPA agonists and antagonists (e.g., LY-293558 and GYKI 52466), ampakines (e.g., CX-516), and mGlu receptor agonists (for review, see [340]). A recent meta-analysis [341] of randomized double-blind trials indicated that D-cycloserine seemed to be ineffective in treating schizophrenia whereas glycine and D-serine appeared to be effective in reducing negative symptoms of schizophrenia when added to ongoing antipsychotic treatment. The beneficial effects of glycine and D-serine on cognitive impairment were less robust and null on the positive symptoms. In the case of glutamate release inhibitors, evidence is not robust regarding the efficacy of lamotrigine for reducing the symptoms of schizophrenia, with some studies showing a beneficial effect and others being equivocal [342–344]. The use of the ampakine allosteric modulator CX-516 was also disappointing as it showed no clear beneficial effects as monotherapy [345], although it was found to be effective when added to clozapine, olanzapine, or risperidone [346]. Until recently, the usefulness of glutamatergic agents thus appeared somewhat limited for the treatment of schizophrenia. However, in a recent randomized, double-blind, parallel fixed-dose study, Patil et al. [347] reported a significant improvement of the positive and negative symptoms of schizophrenia following a 4-week treatment with the mGlu2/3 agonist LY2140023. If replicated, this finding is potentially important as LY2140023, and mGlu2/3 agonists in general, might be the first class of antipsychotic not acting through the D<sub>2</sub> receptor. However, given the functional interactions between the glutamatergic and the DA systems, their effects might still be ultimately mediated through the DA system.

### ***16.6.3 Role of CB<sub>1</sub> Receptor Blockade***

Another approach to the development of antipsychotic drugs has been to evaluate compounds acting through the brain cannabinoid-1 (CB<sub>1</sub>) receptor as a dysregulation of the endogenous cannabinoid system has been proposed to underlie some of the symptoms of schizophrenia [348]. Support for this hypothesis comes from studies showing that cannabinoids can lead to acute psychotic episodes in some individuals [349] and can produce short-term exacerbation or recurrences of pre-existing psychotic symptoms [350, 351]. Moreover, an overactivity of the endocannabinoid system has been revealed in schizophrenia by studies showing increased levels of endogenous cannabinoids in the cerebrospinal fluid [352] as well as increased brain densities of CB<sub>1</sub> receptors in schizophrenia patients [353, 354]. Finally, there is substantial evidence showing that agonist stimulation of CB<sub>1</sub> receptors increases DA neuron firing in the VTA and SN [355, 356] and, as a consequence, increases extracellular DA levels in their projection areas [357–361]. These observations have suggested that CB<sub>1</sub>

receptor antagonists may have antipsychotic properties. However, a clinical trial with the selective CB1 receptor antagonist, SR141716 (rimonabant), showed no antipsychotic efficacy [362].

#### ***16.6.4 Role of $\alpha_1$ and $\alpha_2$ Adrenergic Receptor Blockade***

The  $\alpha_1$  and  $\alpha_2$  adrenergic receptors received much attention when it was found that clozapine binds with higher affinity to these receptors than to the D<sub>2</sub> receptor [363]. In fact, many antipsychotics, whether typical or atypical, are relatively strong antagonists at the  $\alpha_1$  and/or  $\alpha_2$  adrenergic receptors. Although  $\alpha_1$  adrenergic antagonism per se does not confer antipsychotic activity [364], it may still be of some importance in the mechanism of action of antipsychotic drugs. Svesson [365] has suggested that  $\alpha_1$  adrenergic blockade by antipsychotics may contribute to suppress positive symptoms of schizophrenia by inhibiting striatal hyperdopaminergia, whereas  $\alpha_2$  adrenergic blockade may be involved in relief of negative and cognitive symptoms by enhancing DA function in cortex. This hypothesis is consistent with studies showing that blockade of  $\alpha_1$  adrenergic receptors with prazosin blocks the hyperactivity and midbrain DA release induced by the NMDA antagonists MK-801 and PCP [366, 367]. Similarly, it blocks the acute locomotor effects of amphetamine and reduces the behavioral sensitization induced by repeated injections of the drug [368, 369]. Moreover, raclopride-induced activation of VTA DA neurons has been found to be suppressed by prazosin [370], suggesting a modulatory effect of  $\alpha_1$  adrenergic receptors on mesolimbic DA transmission. A number of studies also indicate that  $\alpha_2$  adrenergic antagonism may be relevant to atypicality. Alpha<sub>2</sub> blockers have been shown to increase DA levels in the rat PFC [371, 372] and to improve cognitive functioning in aged rats [373] and in patients with frontal dementias [374]. Co-medication with the  $\alpha_2$  adrenergic antagonist idazoxan has been found to enhance the antipsychotic efficacy of the atypical drug fluphenazine in treatment-resistant schizophrenic patients, comparing favorably with clozapine [375]. Recent experimental findings also indicate that  $\alpha_2$  blockade enhances the efficacy of both typical and atypical antipsychotic drugs as it enhances the suppression of CAR seen with haloperidol and olanzapine in rodents and reverses haloperidol-induced catalepsy [372]. All together,  $\alpha_1$  and  $\alpha_2$  antagonist properties of antipsychotic drugs may improve their efficacy and contribute to the reduction of their motor side effects.

#### ***16.6.5 Role of NK<sub>3</sub> Receptor Blockade***

Neurokinin 3 (NK<sub>3</sub>) receptors have recently become of interest with regard to the treatment of schizophrenia as those receptors play a key role in the regulation of midbrain DA function [376, 377]. Indeed, agonist-induced stimulation of NK<sub>3</sub> receptors has been shown to activate DA neurons in the ventral mesencephalon and to enhance DA release in NAcc, dorsal striatal, and PFC. These effects, which can be

prevented by selective NK<sub>3</sub> receptor blockade, have motivated the development of NK<sub>3</sub> receptor antagonists as potential new antipsychotic drugs. The NK<sub>3</sub> antagonist SR142801 (onasetant) has been evaluated in schizophrenia but showed a relatively modest antipsychotic efficacy that was intermediate between placebo and haloperidol [362] and since the future development of this line of compounds has been stopped, there may be limited information on this issue in the near future.

## 16.7 Conclusion and Future directions

Thus, over half a century after the discovery of the compound that revolutionized the treatment of schizophrenia, we are still tied to the same basic principle – blockade of the dopamine D<sub>2</sub> receptors. The intervening 50 years of science have added remarkably to our understanding of how the drugs work – the differentiation and localization of D<sub>2</sub> receptors, the visualization in humans, the identification of an occupancy–outcome relationship, and the introduction of compounds with more complex pharmacologies. Yet, the fundamental principle has remained unchanged – D<sub>2</sub> blockade remains necessary and sufficient for good antipsychotic activity.

Yet, there remain several unsolved questions and several future directions. Clozapine still remains uniquely effective in patients in whom standard typical and atypical antipsychotics do not work. The mechanism of this superior efficacy is not known. Deciphering it may provide a lead to a potentially very useful new mechanism in schizophrenia. Most of the current drugs are dopamine D<sub>2</sub> blockers; yet, no pathology in the dopamine D<sub>2</sub> receptors has been conclusively identified even after nearly a dozen such studies. The definitive abnormality of the DA system in schizophrenia lies presynaptically. This opens up a new therapeutic option. Rather than just blocking the aftereffects of inappropriately released DA, the field could focus on factors that could modulate the presynaptic release of DA. Finally, the focus on dopamine D<sub>2</sub> receptors draws away from the critical role of D<sub>1</sub> receptors in the cortex and their potential relationship with cognition and negative symptoms. A plausible hope remains that enhancing D<sub>1</sub> transmission in the prefrontal cortex may lead to superior symptomatic improvement in domains untouched by current drugs. The next decade will tell whether the DA system has delivered all it can for the treatment of schizophrenia or whether there are further opportunities to harness it for the benefit of our patients.

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# Chapter 17

## Dopamine Receptor Subtypes in Reward and Relapse

David W. Self

**Abstract** With the advent of subtype-selective ligands and dopamine receptor knockout mice, the last two decades have seen an explosion in research on the role of dopamine receptor subtypes in reward and relapse to drug-seeking behavior. This chapter represents a relatively comprehensive review of this literature, beginning with the ability of D<sub>1</sub>-like and D<sub>2</sub>-like receptor agonists to support self-administration behavior and produce conditioned preference, and followed by the modulation of natural reward, brain stimulation reward, and conditioned reward with subtype-selective ligands and dopamine receptor knockout mice. Subsequent sections describe the modulation of drug and alcohol self-administration by dopamine receptor subtypes, and role of dopamine receptor subtypes in relapse to drug and alcohol seeking in animal models. Finally, down-regulation in dopamine receptors following chronic drug self-administration is discussed in reference to differential changes in dopamine receptor-mediated behavior, suggesting that better integration between biological and behavioral data is needed in future studies.

**Keywords** D<sub>1</sub> · D<sub>2</sub> · D<sub>1</sub>-like · D<sub>2</sub>-like · D<sub>3</sub> · D<sub>4</sub> · D<sub>5</sub> · Reinforcement · Reinstatement · Cocaine · Amphetamine · Heroin · Nicotine · Alcohol

### 17.1 Introduction

Dopamine involvement in natural and drug reward is well established, but the role of specific dopamine receptor subtypes in reward processes remains a topic of intensive investigation. The most common approach to investigate dopamine receptor function in reward employs pharmacological ligands with relatively good selectivity for D<sub>1</sub>-like and D<sub>2</sub>-like receptor classes, although their potential actions at other

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D.W. Self (✉)

Department of Psychiatry, The Seay Center for Basic and Applied Research in Psychiatric Illness, University of Texas Southwestern Medical Center, Dallas, Texas, 75390-9070, USA  
e-mail: David.Self@UTSouthwestern.edu

neurotransmitter receptors (e.g., serotonergic or noradrenergic) are often neglected. Unfortunately, there have been far fewer studies targeting specific D<sub>1</sub>-like (D<sub>1</sub> and D<sub>5</sub>) or D<sub>2</sub>-like (D<sub>2</sub>, D<sub>3</sub> and D<sub>4</sub>) receptor subtypes due to a lack of selective ligands, and promising candidates that exhibit good selectivity under artificial conditions *in vitro* are notorious for their lack of selectivity *in vivo* with further scrutiny. The ability to differentiate between related dopamine receptor subtypes is even more difficult when they play similar roles in behavior, but enhanced when related subtypes mediate different behavioral effects. Another potential caveat is that opposing behavioral effects are often mediated by pre- and post-synaptic receptors in the mesolimbic dopamine system, leading to biphasic dose–effect curves for behavioral responses. Given these considerations, recent advances in antagonist selectivity profiles, especially in differentiating the effects of D<sub>2</sub> and D<sub>3</sub> receptor blockade, have yielded compelling evidence for distinct receptor subtype actions in reward and reward-seeking behavior.

Genetic deletion generally is more definitive for assessing dopamine receptor involvement in natural and drug reward, although developmental compensation must be considered especially when negative results are found. Another important consideration is that behavioral responses in mice can differ substantially from rats and primates, a caveat highlighted by uniformly inhibitory effects of D<sub>2</sub>-like agonists on psychomotor behavior in mice over a wide dose range [1]. Dopamine receptor knockout mice can be used to demonstrate definitive selectivity of novel and putative subtype-selective ligands *in vivo*, most notably when their behavioral effects are completely attenuated with the deletion of a specific dopamine receptor subtype. However, the interpretation of behavioral changes that result from brain-wide receptor deletion can be complicated by competing effects of dopamine receptors in different brain regions on neural circuits regulating natural and drug reward. The recent advent of inducible and localized genetic deletion strategies in mice is a powerful approach that circumvents problems relating to developmental compensation, and provides anatomically discrete loss of specific dopamine receptor subtypes, but this approach has yet to be applied to studies on natural and drug reward. Conversely, transgenic approaches to investigate gain of dopamine receptor function have not been widely used due to the need to limit expression to cells that naturally express the dopamine receptor subtypes. Recent advances in D<sub>1</sub> and D<sub>2</sub> promoter-driven transgenics will be pivotal to modulate dopamine receptor function in the appropriate cell types in future studies.

Using anatomically discrete microinfusion of dopaminergic ligands, studies have found that dopamine receptors play different roles in mediating or modulating reward processes in different brain regions. For example, dopamine receptors in ventral striatal regions mediate primary rewarding effects. Thus, transient dopamine receptor activation in these regions is sufficient to support self-administration behavior when receptor activation is a consequence of the behavior. In contrast, dopamine receptors in neocortical or amygdala regions can modulate reward evaluation, choice, or the formation of conditioned environmental (Pavlovian) associations that acquire their own rewarding properties secondary to the role of dopamine receptors in primary reward. These regional effects, in turn, are determined by dopamine

receptor localization on specific neuronal subpopulations such as interneurons or projection neurons, and differential coupling to G protein signaling pathways, further illustrating the complexities of delineating the mechanism of dopamine receptor subtypes in reward.

In addition to reward, dopamine receptors play a prominent role in eliciting appetitive or approach behavior, a phenomenon distinguishable from reward itself by the fact that behavioral responses follow rather than precede dopamine receptor stimulation. The seminal work of Schultz and colleagues [2, 3] found that environmental predictors of reward availability activate midbrain dopamine neurons, and other studies have shown that dopamine release in forebrain regions is sufficient to elicit appetitive behavior directed at obtaining reward. This behavior often is referred to as reward-seeking behavior, and is widely studied in animal models of drug and alcohol addiction to simulate craving and relapse in humans. Thus, dopamine receptors mediate two crucial aspects of addictive behavior: (1) they mediate primary reward when stimulated consequential to self-administration behavior and (2) they elicit reward-seeking behavior during periods of forced abstinence.

This chapter reviews the role of dopamine receptor subtypes in reward and reward-seeking behavior. Initial sections review earlier work establishing that dopamine receptor agonists serve as primary rewards in self-administration studies. Other studies that use dopamine receptor agonists to induce a conditioned place preference are described; a more commonly used but indirect measure of drug reward. Subsequent sections discuss the role of dopamine receptor subtypes in natural reward, brain stimulation reward, conditioned reward, and self-administration of abused drugs and alcohol. In each section, intracranial studies that elucidate regional sites of dopamine receptor action and genetic deletion of specific receptor subtypes are reviewed where available with an emphasis on differential roles for D<sub>1</sub>-like and D<sub>2</sub>-like receptors. In later sections, the role of dopamine receptor subtypes in relapse to drug- and alcohol-seeking behavior is discussed. In a final section, alterations in dopamine receptors produced by chronic drug self-administration are highlighted together with discrepant changes in dopamine receptor-mediated behavior, suggesting the need for better integrative models of biological and behavioral change in drug addiction. Clearly, dopamine receptors play a role in several other aspects of reward-related behavior that are beyond the scope of this chapter.

## **17.2 Dopamine Receptor Subtypes that Mediate Primary Reward**

The fact that selective and directly acting dopamine receptor agonists will support self-administration behavior indicates that dopamine receptors mediate a primary rewarding stimulus. The earliest study supporting this notion found that drug-naïve female rats will learn to perform a novel lever-press response to receive intravenous injections of the direct dopamine receptor agonist apomorphine, and will

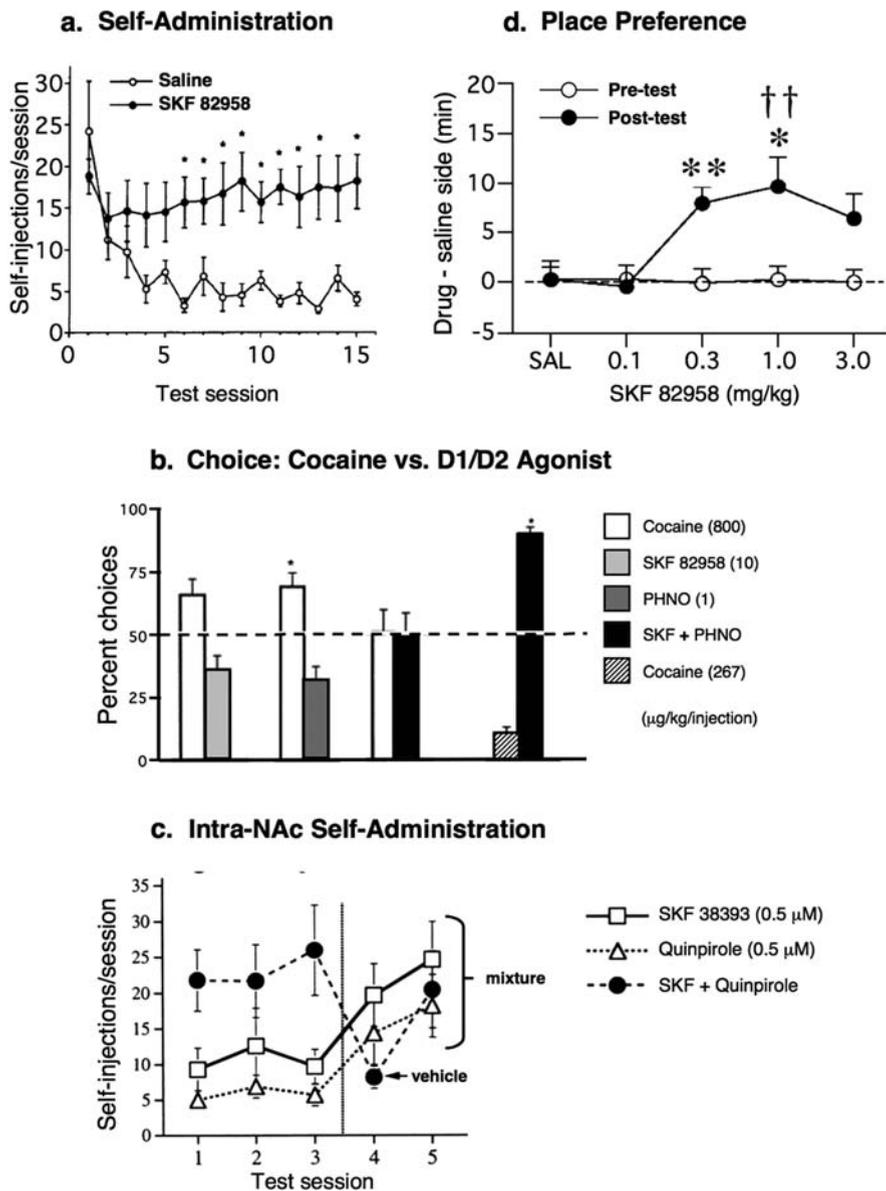
maintain stable dose-dependent responding for several weeks after acquisition [4]. Apomorphine self-administration is abolished by pretreatment with the dopamine receptor antagonist pimozone. A subsequent study found that depletion of endogenous brain catecholamines with alpha-methylparatyrosine treatment has no effect on apomorphine self-administration, but attenuates self-administration of the indirect agonist amphetamine [5]. These early studies clearly established a role for dopamine receptor stimulation in mediating primary reward and are often overlooked in more modern theoretical formulations of dopamine receptor function in reward-related behavior. Thus, in addition to serving as a primary reward, various other functions ascribed to dopamine include signaling reward prediction error [6], increasing incentive salience or wanting [7], enhancing the impact of conditioned environmental stimuli on instrumental responding [8], and reducing psychological effort requirements to obtain rewards [9]. These and other attributes suggest a complex multi-functional role for dopamine in reward processing and execution of instrumental behavior, but they do not belie the fact that dopamine receptor stimulation is in itself sufficient to mediate primary rewarding events.

### 17.2.1 Self-Administration of D<sub>1</sub>-Like and D<sub>2</sub>-Like Receptor Agonists

In addition to apomorphine, animals will self-administer intravenous injections of agonists selective for either D<sub>1</sub>-like or D<sub>2</sub>-like receptors. Early studies with the prototypical but partial D<sub>1</sub>-like receptor agonist found that intravenous infusions of SKF 38393 fail to support self-administration behavior [10]. Subsequent studies found that higher efficacy D<sub>1</sub>-like agonists such as SKF 82958 and SKF 81297 will support self-administration in rats, mice, and monkeys, and even in drug-naïve animals (Fig. 17.1a) [11–16]. Similarly, several studies found that D<sub>2</sub>-like

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**Fig. 17.1** (continued) of the D<sub>1</sub>- and D<sub>2</sub>-like agonists to a lower dose of cocaine (267 µg/kg/injection). \*Significantly different from 50%,  $P < 0.05$ . (c) Intranucleus accumbens (NAc) shell self-administration of D<sub>1</sub>- and D<sub>2</sub>-like agonists. Groups of rats self-administered 100 nl infusions containing 0.5 mM of the D<sub>1</sub>-like agonist SKF 38393, the D<sub>2</sub>-like agonist quinpirole, or a mixture during the first three sessions. The SKF and quinpirole groups were switched to the mixture for sessions 4 and 5, while the group initially trained on the mixture self-administered vehicle in session 4. During sessions 1–3, rats receiving SKF + quinpirole obtained more infusions than did rats receiving either drug alone ( $P < 0.001$ ). The SKF and quinpirole groups exhibited higher levels of self-administration in session 5, when SKF + quinpirole was given in place of SKF or quinpirole alone, than in session 3 ( $P = 0.01$ ). The replacement of SKF + quinpirole with vehicle in session 4 diminished self-administration ( $P = 0.02$ ). (d) The D<sub>1</sub>-like agonist SKF 82958 induces dose-dependent conditioned place preferences with minimal pairings (2 drug, 2 saline). Data are expressed as mean ± S.E.M. difference in preference for the drug- minus saline-paired side. Symbols indicate post-test scores differ from saline/saline pairing (SAL; \* $P < 0.05$ , \*\* $P < 0.01$ ), or from pretest scores († $P < 0.01$ ). Reproduced with permission from (a) Self and Stein [11], (b) Manzardo et al. [21], (c) Ikemoto et al. [25], and (d) Graham et al. [43]



**Fig. 17.1** (a) Self-administration of the D<sub>1</sub>-like agonist SKF 82958 in drug-naïve rats. Data points show the mean daily number of self-injections ( $\pm$  S.E.M.) of groups self-administering SKF 82958 at a dose of 10  $\mu$ g/kg/injection or saline over 15 consecutive test sessions (\*SKF 82958 differs from saline,  $P < 0.05$ ). High response rates in the initial test sessions are due to lever-press training for food pellets prior to self-administration testing. (b) In choice tests, rats prefer to self-administer a moderate dose of cocaine (800  $\mu$ g/kg/injection) to either the D<sub>1</sub>-like agonist SKF 82958 (10  $\mu$ g/kg/injection) or the D<sub>2</sub>-like agonist (+)-PHNO (1  $\mu$ g/kg/injection), but exhibit a similar preference for cocaine and a mixture of the D<sub>1</sub>- and D<sub>2</sub>-like agonists. Rats prefer the mixture

receptor agonists are self-administered intravenously by rats, mice and monkeys (reviewed by [17]), including highly D<sub>2</sub>-like selective agonists such as quinpirole, 7-OH-DPAT, and (+)-PHNO [10, 18–22]. In contrast to the self-administration of D<sub>1</sub>-like agonists in drug-naïve animals, D<sub>2</sub>-like agonists are self-administered only when substituted for drugs such as cocaine in animals with extensive prior self-administration training. Whether drug-naïve animals will learn to self-administer D<sub>2</sub>-like agonists has not been systematically studied, and there are no reports of experimentally or drug-naïve animals acquiring D<sub>2</sub>-like agonist self-administration, but studies have found that quinpirole and 7-OH-DPAT generally fail to support self-administration in monkeys without prior cocaine self-administration training [23, 24]. These findings indicate that D<sub>1</sub>-like receptor stimulation is sufficient to mediate primary rewarding effects, but it is not clear whether selective D<sub>2</sub>-like receptor stimulation is capable of mediating primary reward. One possible explanation is that D<sub>2</sub>-like agonists maintain self-administration behavior once acquired by enhancing the conditioned rewarding properties of lever-press behavior associated with primary rewards during previous training (see Section 17.3.3). Furthermore, D<sub>2</sub>-like receptors apparently can augment the magnitude of reward mediated by D<sub>1</sub>-like receptor stimulation, since rats prefer to self-administer co-injections of D<sub>2</sub>-like with D<sub>1</sub>-like receptor agonists over cocaine, but cocaine is preferred over injections of D<sub>1</sub>-like receptor agonists alone (Fig. 17.1b) [21]. Moreover, genetic deletion of D<sub>1</sub> receptors abolishes the reinforcing effects of a D<sub>2</sub>-like agonist in mice [16], further indicating that D<sub>2</sub>-like receptors fail to independently mediate primary reward.

Intracranial self-administration studies indicate that the ventral striatum contains D<sub>1</sub>-like and D<sub>2</sub>-like receptors that are important for mediating primary rewarding effects. Rats will learn to self-administer a cocktail containing both D<sub>1</sub>-like and D<sub>2</sub>-like receptor agonists into the nucleus accumbens shell (Fig. 17.1c), but not the core subregion [25]. While neither agonist alone supports self-administration behavior, only the partial D<sub>1</sub>-like receptor agonist SKF 38393 has been tested, and so it is possible that high efficacy and selective D<sub>1</sub>-like receptor agonists would support self-administration behavior in the nucleus accumbens shell. Interestingly, infusion of cocaine into more ventral olfactory tubercle regions more effectively supports self-administration behavior than infusion in the nucleus accumbens shell, an effect blocked by co-infusion with either D<sub>1</sub>-like or D<sub>2</sub>-like antagonists [26]. Dopamine receptors in the medial prefrontal cortex also support self-administration behavior, since rats will self-administer dopamine (or cocaine) into this region, and the effects are blocked by co-infusion with a D<sub>2</sub>-like but not a D<sub>1</sub>-like antagonist [27–29]. Whether animals would self-administer selective D<sub>1</sub>-like or D<sub>2</sub>-like agonists directly into the medial prefrontal cortex or other brain regions is unknown. Other studies found that cocaine is self-administered directly into the dopamine cell body region of the posterior ventral tegmental area in mice and rats, which may be mediated by D<sub>1</sub>-like receptor modulation of serotonergic excitation of dopamine neurons [30, 31].

Some studies suggest that the hedonic impact of rewards may be dissociable from dopamine receptor stimulation and its role in goal-directed behavior. Thus,

for example, depletion of central dopamine has no effect on hedonic responses to natural reward in animals [7]. In humans, indirect dopamine agonists such as cocaine and amphetamine induce euphoria, but the dopamine receptor agonist apomorphine produces nausea and dysphoria, an effect that may involve peripheral dopamine receptor activation [32]. The D<sub>2</sub>-like receptor agonist bromocriptine produces little subjective effects on its own [33], and neuroleptic drugs that block D<sub>2</sub>-like receptors fail to consistently attenuate subjective reports of euphoria with amphetamines or cocaine in humans [34, 35]. In contrast, however, acute blockade of D<sub>1</sub>-like receptors with ecopipam (SCH 39166) attenuates cocaine-induced euphoria in human cocaine addicts [36], although chronic blockade of D<sub>1</sub>-like receptors actually enhances cocaine euphoria potentially due to compensatory changes [37]. These findings suggest that the primary rewarding effects of direct dopamine receptor stimulation may be dissociable from hedonic responses in animals and that D<sub>1</sub>-like, but not D<sub>2</sub>-like, receptors may play a role in drug-induced euphoria in humans.

### ***17.2.2 Conditioned Place Preference with D<sub>1</sub>-Like and D<sub>2</sub>-Like Receptor Agonists***

Conditioned place preference has been widely used as an indirect measure of the rewarding properties of dopamine receptor agonists. In conditioned place preference, animals will prefer an environment associated with primary rewarding stimuli over those paired with neutral stimuli. The environmental context acquires conditioned rewarding properties that reflect the primary rewarding properties of the dopamine receptor agonists. Several decades of research has shown differential abilities of D<sub>1</sub>-like and D<sub>2</sub>-like receptor agonists to produce conditioned place preference [17, 38]. Early studies found that systemic administration of high doses of the partial D<sub>1</sub>-like agonist SKF 38393 actually produces a place aversion [39, 40], reflecting dysphoric effects, and this effect is blocked by a D<sub>1</sub>-like but not a D<sub>2</sub>-like antagonist [39, 41]. However, subsequent studies found that the higher efficacy D<sub>1</sub>-like agonists SKF 82958 (Fig. 17.1d), SKF 81297, and the non-benzazepine agonist ABT-431 will produce a conditioned place preference [42, 43]. Interestingly, the long-acting full D<sub>1</sub>-like agonist A-77636 produces a place aversion potentially due to profound receptor internalization [43, 44]. In this sense, place aversions with A-77636 and the partial D<sub>1</sub>-like agonist SKF 38393 resemble strong place aversions that are found with D<sub>1</sub>-like receptor blockade [45], suggesting that a loss of D<sub>1</sub>-like receptor tone produces dysphoria in animals. Together, these studies generally agree with self-administration studies indicating that selective D<sub>1</sub>-like receptor stimulation is sufficient to mediate primary rewarding effects.

Systemic treatment with D<sub>2</sub>-like agonists such as quinpirole, 7-OH-DPAT, or bromocriptine can produce a conditioned place preference, a place aversion, or have no effect depending on rat strain, dose, and other experimental conditions. Systemic administration of quinpirole at doses thought to activate post-synaptic receptors produces a weak conditioned place preference in Wistar [39, 41], Lister-hooded [46],

and Long–Evans rats [40], while it is ineffective in Sprague Dawley rats unless they have received repeated cocaine injections prior to conditioning [43]. Similarly, 7-OH-DPAT has been shown to produce a conditioned place preference in Wistar [47] and Sprague Dawley rats [48, 49] in some studies, but no effect in Swiss Webster mice or Wistar rats in other studies [50, 51]. Place conditioning with low doses that are thought to selectively activate D<sub>2</sub>-like autoreceptors actually produce conditioned place aversions [52, 53]. The less selective D<sub>2</sub>-like agonist bromocriptine has been shown to produce place preference in both rats and mice [54, 55]. Similarly, certain full efficacy and putative D<sub>3</sub>-selective ligands produce either a place preference [56] or an aversion [52], while a novel D<sub>4</sub> agonist is without effect [57]. Together these discrepancies highlight the impact of strain differences, intralaboratory variability in place conditioning procedures, or the potential differential influences of D<sub>2</sub> and D<sub>3</sub> receptors on reward substrates.

When infused into the nucleus accumbens, both D<sub>1</sub>-like and D<sub>2</sub>-like agonists produce conditioned place preferences [40], whereas negative findings have been found in the hippocampus and amygdala. However, dopamine receptors in the hippocampus and amygdala can modulate place conditioning with other drugs of abuse [58, 59], suggesting that dopamine receptors in these regions can alter associative learning between rewarding stimuli and conditioned environments. Results with place conditioning differ from self-administration studies by suggesting that either D<sub>1</sub>-like or D<sub>2</sub>-like receptors in the nucleus accumbens can produce rewarding effects in drug-naïve animals.

### **17.3 Modulation of Natural and Endogenous Reward by Dopamine Receptor Subtypes**

Given the fact that natural rewards, including highly palatable foods, water, and sexual interaction, all increase dopamine levels in terminal regions, it is not surprising that dopamine receptors play a role in natural reward. Moreover, the rewarding effect of electrical brain stimulation, or brain stimulation reward, also is mediated by dopamine receptors to a major extent. While both D<sub>1</sub>-like and D<sub>2</sub>-like receptors are implicated in natural reward, D<sub>1</sub>-like receptors in particular play an important role in reward-related learning during initial establishment of stimulus–response associations, whereas D<sub>2</sub>-like receptors play a prominent role in augmenting the motivational salience of conditioned rewards after learning has occurred. These differences suggest that D<sub>1</sub>- and D<sub>2</sub>-like receptors are involved in different phases of acquisition and expression of rewarded behavior.

#### ***17.3.1 Modulation of Food, Water, and Sexual Reward by Dopamine Receptor Subtypes***

Pretreatment with either dopamine agonists or antagonists can reduce instrumental responding for food rewards (e.g. [60]), but these effects usually reflect performance or other rate-altering effects unrelated to reward impact. In sham-fed rats,

where sucrose is ingested without instrumental requirements but prevented from remaining in the stomach, both D<sub>1</sub>- and D<sub>2</sub>-like antagonists reduce preference for rewarding sucrose [61–63]. Pretreatment with either D<sub>1</sub>- and D<sub>2</sub>-like agonists also reduces food intake, but only D<sub>1</sub>-like agonists reduce sucrose-sham feeding, consistent with a role for D<sub>1</sub>-like receptor stimulation in satiety mechanisms for highly palatable reward [64]. In contrast, instrumental responding for high sucrose content food pellets is increased by the D<sub>2</sub>-like antagonist raclopride, consistent with an antagonist-like effect on reward processes surmountable by increased self-administration behavior [65].

Water intake in thirsty mice is not affected by D<sub>1</sub>-like antagonists [66], while it is reduced by both D<sub>1</sub>-like and D<sub>2</sub>-like antagonists in rats [67]. However, the conditioned place preference to water availability in deprived rats is blocked by either the D<sub>1</sub>-like antagonist SCH 23390 or the D<sub>2</sub>-like antagonist raclopride at doses that have no effect on water intake during conditioning [67]. These findings suggest that both D<sub>1</sub>- and D<sub>2</sub>-like receptors could play a role in primary water reward, although blockade of Pavlovian learning processes independent of alterations in primary reward strength also could account for these results.

In addition, dopamine receptors are implicated in the rewarding effects of sexual interaction. Dopamine D<sub>2</sub>-like agonists promote while antagonists reduce motivational indices of copulatory behavior in male rats [68]. In contrast, the partial D<sub>1</sub>-like agonist SKF 38393 does not influence copulation [69]. When male rats perform an instrumental response to gain access to a receptive female, non-selective blockade of D<sub>1</sub>- and D<sub>2</sub>-like receptors impairs this response [70], and the pursuit of receptive females is reduced by systemic pretreatment with either D<sub>1</sub>- or D<sub>2</sub>-like antagonists [71]. In female rats, high doses of the D<sub>2</sub>-like agonist quinpirole elicit sexual behavior (lordosis) in non-receptive rats, while lower (presumably autoreceptor doses) are effective in receptive rats [72], suggesting that receptivity disrupts the sensitivity to post-synaptic D<sub>2</sub>-like stimulation. D<sub>1</sub>-like ligands are ineffective at modulating this behavior. Many sexual responses in female rats may reflect actions in brain regions unrelated to brain reward and motivational systems. However, a recent study found that the preference for male pheromones in female mice is not blocked by D<sub>1</sub>-like or D<sub>2</sub>-like antagonists, but is blocked by the D<sub>1</sub>-like agonist SKF 38393 [73], potentially reflecting a masking of the pheromone reward stimulus by tonic D<sub>1</sub>-like receptor stimulation.

D<sub>1</sub>-receptor knockout mice are capable of acquiring instrumental responding for sucrose or sweetened food reward, but acquire self-administration more slowly despite no difference in sucrose intake when freely available [16, 74]. Thus, these decrements may reflect performance rather than motivational deficits. In female D<sub>5</sub> knockout mice, the ability of apomorphine to facilitate sexual receptivity is blocked, whereas male D<sub>5</sub> knockout mice show an impaired conditioned place preference to environments paired with intromission, but not ejaculation [75]. D<sub>2</sub> receptor knockout mice show impaired acquisition of instrumental response for sweetened milk most likely due to Parkinson-like effects [76], but another study found no effect on water self-administration [77]. D<sub>3</sub> receptor knockout mice show no changes in responding for food or water rewards [78]. The inability to regulate the degree of

dopamine receptor inactivation, or to localize effects to specific brain regions, probably accounts for behavioral impairment and makes it difficult to assign a role for specific dopamine receptor subtypes in natural reward in these knockout studies.

Dopamine levels in the nucleus accumbens are elevated by unfettered sucrose consumption, but reverse microdialysis of either D<sub>1</sub>- or D<sub>2</sub>-like antagonists into the nucleus accumbens fails to alter this behavior [79]. In contrast, microinfusions of both D<sub>1</sub>- or D<sub>2</sub>-like antagonists into the nucleus accumbens core, but not shell, reduce instrumental responding for normal chow pellets under more demanding progressive ratio schedules, which could reflect performance rather than motivational effects [80]. Putative D<sub>3</sub> and D<sub>4</sub> antagonists are ineffective. When regular chow is available under free-feeding conditions in food-deprived rats, neither D<sub>1</sub>- nor D<sub>2</sub>-like receptor blockade in the nucleus accumbens impairs food intake, but the number of feeding bouts is reduced [81], consistent with a role for nucleus accumbens dopamine receptors in incentive motivational responses, but not the regulation of food intake. Kelley and colleagues found that a low dose of a D<sub>1</sub>-like antagonist that does not impair instrumental performance will attenuate acquisition of responding rewarded by sucrose pellets when infused into the nucleus accumbens, but only when co-infused with a similar low dose of an NMDA glutamate receptor antagonist [82]. These results suggest that coincident activation of D<sub>1</sub>-like and NMDA receptor signals are needed for reward-related learning. Post-trial infusions of the D<sub>1</sub>-like and NMDA antagonists fail to alter acquisition of sucrose self-administration, but post-trial infusion of a protein kinase A inhibitor (PKA) does impair acquisition, suggesting that prior D<sub>1</sub>-like receptor activation of cAMP is important for consolidating these learned stimulus–response associations [83]. A similar relationship for coincident D<sub>1</sub>-like and NMDA receptor activation and dependence on protein kinase A is found in the medial prefrontal cortex [84]. Blockade of intra-amygdala D<sub>1</sub>-like receptors also impairs acquisition of instrumental responses for sucrose reward without affecting performance, suggesting that amygdala D<sub>1</sub>-like activity is important in reward-related learning [85].

### ***17.3.2 Modulation of Brain Stimulation Reward by Dopamine Receptor Subtypes***

Electrical stimulation of several brain regions will support self-stimulation behavior, including the ventral tegmental area where dopaminergic cell bodies are located, and the lateral hypothalamus where descending fibers of the medial forebrain bundle activate dopamine neurons through direct and indirect pathways [86]. Forebrain regions including the medial prefrontal cortex also support self-stimulation behavior potentially through activation of dopamine neurons in the ventral tegmental area [87]. The magnitude of brain stimulation reward can be determined in a response rate-independent manner by measuring stimulus frequency (or intensity) thresholds, or by parallel shifts in stimulus–response curves, valuable procedures given that dopaminergic ligands can produce substantial effects on performance. Systemic administration of either D<sub>1</sub>- or D<sub>2</sub>-like antagonists attenuate the rewarding impact

of electrical brain stimulation (e.g.[88, 89]), whereas D<sub>3</sub> antagonists are ineffective [48, 90]. The rate–frequency curve is shifted rightward in D<sub>1</sub> receptor knockout mice [91], and D<sub>2</sub> knockout mice require 50% more stimulus intensity to support self-stimulation [92]. Together these studies suggest that both D<sub>1</sub> and D<sub>2</sub> receptor subtypes play a necessary role in the rewarding effects of electrical brain stimulation.

In contrast to antagonists, systemic administration of D<sub>1</sub>- and D<sub>2</sub>-like receptor agonists produces differing effects on brain stimulation reward. Thus, the prototypical but partial D<sub>1</sub>-agonist SKF 38393 is without effect [89] or inhibits brain stimulation reward [93], although the facilitation of ventral tegmental self-stimulation by SKF 38393 has been reported [94]. The full efficacy D<sub>1</sub>-agonist SKF 81297 elevates brain stimulation reward thresholds in rats [95], while the less selective D<sub>1</sub>-agonist SKF 82958 reduces thresholds in mice [96]. Pretreatment with the non-benzazepine D<sub>1</sub>-agonist A-77636 also lowers thresholds in rats [97]. Given the differential ability of these compounds to support self-administration behavior and produce a conditioned place preference (SKF 81297 and SKF 82958), or fail self-administration tests and produce a conditioned place aversion (SKF 38393 and A-77636), the relationship between facilitation of brain stimulation reward and inherent rewarding properties of these compounds is unclear.

In contrast, pretreatment with the D<sub>2</sub>-like agonist quinpirole lowers the threshold of brain stimulation reward [89, 98], while lower presumably autoreceptor doses increase thresholds [98]. Although the D<sub>1</sub>-like agonist SKF 38393 is without effect, co-administration with quinpirole augments the threshold lowering effects of quinpirole alone, while the D<sub>1</sub>-like antagonist SCH 23390 attenuates this facilitation, consistent with synergistic and enabling interactions between D<sub>1</sub>- and D<sub>2</sub>-like receptors [99]. Pretreatment with the D<sub>2</sub>-like agonist 7-OH-DPAT has inconsistent or biphasic effects [48, 95, 98, 100], with low doses attenuating and high doses facilitating brain stimulation reward, consistent with biphasic activation of pre- and post-synaptic D<sub>2</sub>-like receptors with increasing dose [101]. Similarly, 7-OH-DPAT produces biphasic effects using a progressive ratio schedule of brain stimulation reward that measures the amount of effort animals will exert to obtain brain stimulation; low doses reduce and high doses increase the amount of effort exerted [102]. The less selective D<sub>2</sub>-like agonist bromocriptine also lowers self-stimulation thresholds [103]. These results clearly indicate that stimulation of post-synaptic D<sub>2</sub>-like receptors enhances the rewarding effects of electrical brain stimulation.

Intracranial infusion studies have identified the nucleus accumbens as a major site for modulation of brain stimulation reward by D<sub>1</sub>- and D<sub>2</sub>-like receptors. Nucleus accumbens infusions of either the D<sub>1</sub>-like antagonist SCH 23390 or the D<sub>2</sub>-like antagonist raclopride attenuate brain stimulation reward, while the D<sub>3</sub> antagonist (+)-UH232 and the D<sub>4</sub> antagonist clozapine are ineffective [104, 105]. In contrast, agonist infusion studies have found that intra-accumbens infusions of SKF 38393 (D<sub>1</sub>-like) enhance but infusions of quinpirole (D<sub>2</sub>-like) attenuate brain stimulation reward, whereas medial prefrontal cortex infusions are ineffective [106]. Similarly, infusions of the D<sub>1</sub>-like agonist A-77636 into more caudal nucleus accumbens regions lower stimulation thresholds, while quinpirole

infusions elevate thresholds [97]. Another study found that nucleus accumbens infusions of the D<sub>2</sub>-like agonist 7-OH-DPAT have no effect on brain stimulation reward thresholds unless co-infused with AMPA glutamate receptor antagonists to remove glutamatergic tone [107]. While the effect of D<sub>2</sub>-like agonists differs from systemic administration, it is possible that local effects mediated by D<sub>2</sub>-like autoreceptors on dopamine terminals in the nucleus accumbens reduce dopamine release in response to brain stimulation reward. Given the reliance of D<sub>2</sub>-like receptor-mediated reward on D<sub>1</sub>-like receptor tone in the nucleus accumbens, local inhibition of dopamine release and D<sub>1</sub>-like tone could explain a lack of facilitation with direct activation of post-synaptic D<sub>2</sub>-like receptors in the nucleus accumbens.

In this regard, infusions of either D<sub>1</sub>- or D<sub>2</sub>-like agonists into the dopamine cell body region of the ventral tegmental area attenuate self-stimulation of the ventral tegmental area, but not self-stimulation of the lateral hypothalamus [106]. Local D<sub>1</sub>-like receptor stimulation in the ventral tegmental area induces GABA release that inhibits dopamine neurons [108], while D<sub>2</sub>-like autoreceptors directly inhibit dopamine neuron firing. Infusions of D<sub>1</sub>- or D<sub>2</sub>-like agonists into the frontal cortex or caudate-putamen are ineffective at modulating the rewarding effects of ventral tegmental area stimulation [97]. However, infusions of the D<sub>2</sub>-like antagonists spiperone and pimozide into the medial prefrontal cortex will decrease self-stimulation of the same site [109]. Together these studies implicate both D<sub>1</sub> and D<sub>2</sub> receptors, especially in the nucleus accumbens, in mediating the rewarding effects of electrical stimulation of midbrain dopamine neurons, while a role for D<sub>3</sub> receptors awaits further testing in D<sub>3</sub> knockout mice or the availability of more selective ligands. D<sub>4</sub> and D<sub>5</sub> receptors are not highly expressed in the nucleus accumbens [110–112], but these receptors in other brain regions may play a role in modulating brain stimulation reward.

### ***17.3.3 Modulation of Conditioned Reward by Dopamine Receptor Subtypes***

The repeated temporal pairing of hedonically neutral and temporally discrete environmental stimuli (e.g., tones and lights) with response-independent delivery of primary rewards (natural or drug) leads to the formation of conditioned reward. Through Pavlovian conditioning, these stimuli acquire rewarding properties of their own, and animals subsequently will learn to perform a novel instrumental response when rewarded by presentation of the conditioned stimulus. The phenomenon has major implications for control over behavior exerted by conditioned cues in drug addiction, since these cues can trigger craving and relapse to drug use. Studies by Robbins and Taylor showed that psychostimulants greatly enhance conditioned reward by elevating dopamine levels in the nucleus accumbens and potentially other regions [113–115].

The facilitation of conditioned reward by amphetamine is blocked by systemic treatment with either D<sub>1</sub>- or D<sub>2</sub>-like antagonists [116]. When given alone, low doses of D<sub>2</sub>-like antagonists can potentiate conditioned rewards, probably due to

enhanced dopamine release with autoreceptor blockade, while higher post-synaptic doses of D<sub>1</sub>-like and D<sub>2</sub>-like antagonists attenuate responding [117]. Systemic administration of D<sub>1</sub>-like agonists also attenuate responding for conditioned reward, potentially due to masking of temporally discrete reward-related signals with presentation of the conditioned reward [118]. In contrast, responding for conditioned rewards is markedly enhanced by systemic pretreatment with D<sub>2</sub>-like agonists [119]. Interestingly, the opposite effects of D<sub>1</sub>- and D<sub>2</sub>-like agonists on conditioned reward are remarkably similar to their effects on drug-seeking behavior as discussed in Section 17.5.1. The facilitation of conditioned reward by the D<sub>2</sub>-like agonist bromocriptine is blocked by pretreatment with the D<sub>1</sub>-like antagonist SCH 23390 [120], indicating the necessary role for D<sub>1</sub>-like receptor tone on the expression of D<sub>2</sub>-like receptor-mediated effects.

However, when directly infused into the nucleus accumbens, either the D<sub>1</sub>-like agonist SKF 38393 or the D<sub>2</sub>-like agonist quinpirole facilitates conditioned reward [121, 122], suggesting that the attenuation of conditioned reward by D<sub>1</sub>-like receptor stimulation involves multiple or other brain regions. In any event, a necessary role for both D<sub>1</sub>- and D<sub>2</sub>-like receptors in the nucleus accumbens is indicated by the fact that antagonists for either receptor will block conditioned reward when infused in this brain region [121]. Interestingly, infusions of the D<sub>2</sub>-like agonist 7-OH-DPAT into the amygdala during the conditioning phase prevent the subsequent expression of conditioned reward in a drug-free state [123], potentially due to D<sub>2</sub>-like autoreceptor inhibition of reward-related dopamine release in the amygdala. Similarly, blockade of either D<sub>1</sub>- or D<sub>2</sub>-like receptors in the amygdala during conditioning prevents the formation of conditioned reward for cocaine-associated cues [124]. These latter results suggest that stimulation of dopamine receptors in the amygdala is important for establishing enduring learned associations between primary and conditioned rewards, whereas the former results suggest that the expression of conditioned reward requires stimulation of dopamine receptors in the nucleus accumbens.

## 17.4 Modulation of Drug Self-Administration by Dopamine Receptor Subtypes

Many studies have utilized dopaminergic ligands to study the role of dopamine receptors in the rewarding effects of abused drugs. Given this vast literature, this section will focus on drug self-administration studies, arguably the most pertinent animal model of human drug abuse available. The schedule requirements for drug delivery in self-administration studies are an important consideration when modeling distinct symptoms of addictive behavior. In studies where each drug injection requires a low fixed number of instrumental responses (fixed ratio), an animal's preferred level of drug intake is not encumbered by performance demands or by prolonged intervals of drug unavailability. Under these circumstances, animals titrate their preferred level of drug intake in a highly stable and dose-sensitive

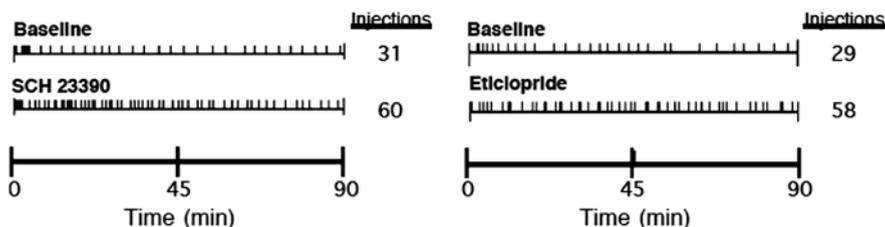
manner. For example, animals will compensate for a lowering in the injection dose by increasing the rate of self-administration, and decrease self-administration rates when the injection dose is increased. This relationship is reflected by an inverted U-shaped self-administration dose–response curve, spanning subthreshold doses that are too low to support self-administration, moderate but short acting suprathreshold doses that are self-administered at increased rates, and higher doses that are self-administered at reduced rates due to prolonged effects of the drug injections. Systemic pretreatment with dopaminergic agonists such as apomorphine reduces the rate of amphetamine self-administration by prolonging the interval between successive self-injections [18]. Since this reduction resembles the effect of increasing the injection dose of amphetamine, it is thought that generalized dopamine receptor stimulation potentiates the satiating or other rate limiting effects of self-administered amphetamine in an additive manner. Conversely, blockade of post-synaptic dopamine receptors with systemic neuroleptic treatment increases the rate of cocaine intake by shortening the time interval between successive self-injections [125], similar to the effect of lowering the cocaine injection dose. Thus, dopamine receptor blockade is thought to antagonize the impact of the cocaine injections in a manner surmounted by volitional increases in cocaine intake, and a similar effect is produced when animals transit to more addicted biological states [126]. An advantage of this approach is that the performance degrading effects of dopamine receptor blockade are negated by increases in self-administration behavior.

While the stability of fixed ratio drug self-administration has its advantage, self-administration rates on these schedules are not directly related to the magnitude of reward. For assessing reward magnitude, self-administration studies often employ progressive ratio schedules, where the degree of effort (e.g., lever pressing) an animal will exert to obtain drug is used as an index of reward, rather than the actual amount of drug consumed. In progressive ratio testing, the response demands for each successive drug injection increase progressively during active self-administration, and the highest ratio of lever presses/injection achieved before animals quit responding (break point) measures a drug's rewarding efficacy. Thus, while dopamine receptor blockade can increase drug self-administration on fixed ratio schedules (Fig. 17.2a), the same treatment can decrease self-administration on progressive ratio schedules (Fig. 17.2b). The use of both schedules of drug reward is a powerful combination for clarifying the contribution of specific dopamine receptor subtypes in the regulation of drug intake (fixed ratio) and the motivation for drugs when obtaining reward is more demanding (progressive ratio).

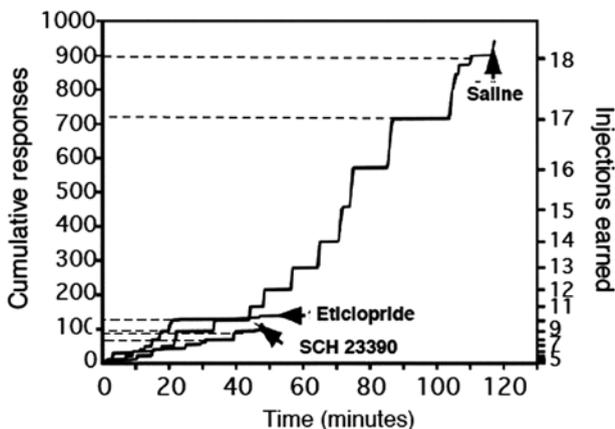
#### ***17.4.1 Modulation of Psychostimulant Self-Administration by Dopamine Receptor Subtypes***

The rewarding effects of psychostimulants such as cocaine and amphetamine involve their ability to function as indirect dopamine receptor agonists. Given that

**a. Fixed Ratio Cocaine Self-Administration**



**b. Progressive Ratio Cocaine Self-Administration**



**Fig. 17.2** (a) Intranucleus accumbens shell infusions of the D<sub>1</sub>-like antagonist SCH 23390 (3.0 μg/side) or the D<sub>2</sub>-like antagonist eticlopride (10.0 μg/side) increase stabilized cocaine self-administration (0.5 mg/kg/injection) on a fixed ratio 1:timeout 15 s schedule of reward. Representative self-administration records for individual animals during baseline self-administration one day prior to tests with intranucleus accumbens antagonist treatment. Upward hatchmarks denote times of self-injection. (b) Similar intranucleus accumbens shell infusions of SCH 23390 (1.25 μg/side) or eticlopride (10.0 μg/side) reduce cocaine self-administration on a progressive ratio self-administration schedule. Individual cumulative response records show that a saline-treated control achieves a ratio of almost 200 responses per injection (vertical distance between dotted lines on left) before quitting self-administration behavior, whereas animals treated with SCH 23390 or eticlopride achieve less than 40 responses per injection. Adapted with permission from (a) Bachtell et al. [157] and (b) Bari and Pierce [80]

both D<sub>1</sub>- and D<sub>2</sub>-like receptors play a role in mediating or modulating reward processes, it is not surprising that systemic pretreatment with either D<sub>1</sub>- or D<sub>2</sub>-like selective antagonists leads to compensatory increases in cocaine intake on fixed ratio self-administration schedules in rats [127–130], and monkeys [131]. These findings suggest that both D<sub>1</sub>- and D<sub>2</sub>-like receptors contribute to negative feedback regulation of cocaine intake. Conversely, both D<sub>1</sub>- and D<sub>2</sub>-like receptor antagonists decrease the amount of effort animals will exert to obtain cocaine or amphetamine

when self-administered on a progressive ratio schedule [130, 132–134]. Since these treatments increase self-administration rates on fixed ratio schedules, decreased self-administration on progressive ratio schedule is likely due to reduced motivational rather than performance effects. In contrast, systemic pretreatment with putative D<sub>3</sub> and D<sub>4</sub> antagonists fails to increase cocaine intake on fixed ratio schedules [135–138], but the D<sub>3</sub> antagonists NGB 2904 and SB-277011A attenuate cocaine reward on progressive ratio schedules [137, 138]. This differential sensitivity to D<sub>3</sub> antagonists with fixed and progressive ratio cocaine self-administration distinguishes these compounds from generalized D<sub>2</sub>-like receptor antagonists. Thus, D<sub>3</sub> receptors may play a necessary role along with D<sub>1</sub>- and D<sub>2</sub> receptors in cocaine reward, while D<sub>1</sub>- and D<sub>2</sub> (but not D<sub>3</sub>) receptors may be preferentially involved in negative feedback regulation of cocaine intake.

Genetic deletion of D<sub>1</sub> receptors dramatically decreases the number of mice that will acquire cocaine self-administration [16]. In contrast, D<sub>2</sub> receptor knockout mice acquire cocaine self-administration, and show increased cocaine intake on fixed ratio schedules similar to the effect of D<sub>2</sub>-like receptor antagonists [135]. However, the ability of the D<sub>2</sub>-like receptor antagonist eticlopride to further elevate cocaine intake is absent in D<sub>2</sub> receptor knockout mice, indicating the effect primarily reflects blockade of D<sub>2</sub> and not D<sub>3</sub> or D<sub>4</sub> receptors as indicated by antagonist studies in rats. These results support the notion that D<sub>1</sub> receptors play a major role in the primary rewarding properties of cocaine, while D<sub>2</sub> receptors contribute to cocaine's rate-reducing effects.

In contrast to antagonist pretreatment, pretreatment with full efficacy D<sub>1</sub>- or D<sub>2</sub>-like receptor agonists reduces cocaine self-administration on unrestricted fixed ratio schedules, but the qualitative aspects of this reduction differ. Thus, pretreatment with D<sub>1</sub>-like agonists suppress the initiation of cocaine self-administration, and produce downward shifts in the inverted U-shaped dose–response function in rats and monkeys [139–142]. In contrast, pretreatment with D<sub>2</sub>-like agonists prolongs the time interval between successive cocaine injections (post-injection pause), similar to the effect of increasing the unit cocaine dose/injection, and produces a leftward shift in the dose–response curve [20, 140, 141, 143–145]. As suggested above, these results are consistent with the idea that tonic D<sub>1</sub>-like receptor stimulation suppresses cocaine self-administration by supplanting and occluding the primary rewarding effects of cocaine, whereas tonic stimulation of D<sub>2</sub>-like receptors potentiates the rewarding effects of self-administered cocaine. Systemic pretreatment with the D<sub>2</sub>-like agonist quinpirole has no effect on amphetamine self-administration on a progressive ratio schedule [134]. However, when D<sub>1</sub>- or D<sub>2</sub>-like agonists are combined with cocaine injections in monkeys self-administering on a progressive ratio schedule, a situation where agonists are delivered in a discrete response-contingent manner, both D<sub>1</sub>-like and D<sub>2</sub>-like agonists produce leftward shifts in the dose–response curve compared to cocaine alone, indicating that either receptor contributes to cocaine reward [146].

While studies with D<sub>3</sub>-selective antagonists have been informative, studies with putative D<sub>3</sub>-selective agonists have been complicated by the fact that the behavioral profile often resembles that of general D<sub>2</sub>-like agonists on fixed ratio cocaine

self-administration, i.e., a prolonging of the interval between successive cocaine injections consistent with an additive interaction with cocaine [136, 147]. Previous studies suggested that the potency for this effect *in vivo* correlates with activity at D<sub>3</sub> but not D<sub>2</sub> receptor activation *in vitro* using a bioassay in cells expressing D<sub>2</sub> or D<sub>3</sub> receptors [148, 149]. However, other evidence suggests that D<sub>3</sub> receptors actually would oppose cocaine effects by opposing D<sub>1</sub> receptor function when co-localized on similar striatal neurons [150–152]. Furthermore, the ability to study the functional effects of D<sub>3</sub> receptors using partial D<sub>3</sub>-preferring agonists such as BP 897 is complicated by their agonist/antagonist profiles at D<sub>2</sub> and D<sub>3</sub> receptors [153].

Intracranial infusion studies suggest that D<sub>1</sub>- and D<sub>2</sub>-like receptors in multiple brain regions contribute to the modulation of psychostimulant self-administration by dopamine receptor ligands. Infusions of either D<sub>1</sub>- or D<sub>2</sub>-like antagonists into the nucleus accumbens mimic the rate-increasing effects of systemic antagonist administration on fixed ratio cocaine and amphetamine self-administration [154–157], an effect illustrated in Fig. 17.2a. However, local stimulation of nucleus accumbens D<sub>1</sub>- or D<sub>2</sub>-like receptors fails to recapitulate the reduction in cocaine intake produced by systemic agonist administration [157], although infusion of dopamine itself does reduce cocaine intake on fixed ratio self-administration schedules [158]. These results may suggest that D<sub>1</sub>- and D<sub>2</sub>-like receptors in the nucleus accumbens are saturated with dopamine during cocaine self-administration, or that co-activation of both receptor classes and possibly in multiple brain regions is needed to produce an additive interaction with cocaine to reduce self-administration rates. However, viral-mediated over-expression of D<sub>2</sub> receptors in the nucleus accumbens effectively reduces the rate of fixed ratio cocaine self-administration [159], suggesting that the amount of D<sub>2</sub> receptors in the nucleus accumbens plays an important role in regulating preferred levels of cocaine intake.

Increases in fixed ratio cocaine self-administration produced by local blockade of nucleus accumbens D<sub>1</sub>- or D<sub>2</sub>-like receptors are paralleled by decreases in the motivation for cocaine (but not food) on progressive ratio schedules (Fig. 17.2b) [80, 160]. The motivational effects are selective for cocaine when infused in the shell subregion, but responding for both rewards is blocked when antagonists are infused in the core subregion potentially reflecting performance deficits [80]. Nucleus accumbens infusions of the D<sub>3</sub> antagonist U99194A or the D<sub>4</sub> antagonist L-750,667 have no effect on cocaine reward in progressive ratio testing.

Fixed ratio cocaine self-administration is increased by infusing the D<sub>1</sub>-like antagonist SCH 23390 into several other dopamine terminal regions, including the medial prefrontal cortex [161], insular cortex [162], bed nucleus of the stria terminalis [163], and amygdala [156, 160, 162, 164]. Similar infusions of SCH 23390 in medial prefrontal cortex reduce cocaine reward on progressive ratio schedules [161], but not when infused in the amygdala [160]. These results illustrate that regulation of cocaine intake and the motivation for cocaine are distinct behavioral phenomena mediated by separate neural substrates. Interestingly, infusions of SCH 23390 in the dopamine cell body region of the ventral tegmental area also increase cocaine intake on fixed ratio schedules, and decrease the motivation for cocaine on progressive ratio schedules [165], presumably acting on D<sub>1</sub>-like receptors located on the

axons of GABAergic, serotonergic, or glutamatergic input to dopamine neurons. Local blockade of D<sub>2</sub>-like receptors in the arcuate nucleus of the hypothalamus increases fixed ratio cocaine intake potentially due to attenuation of cocaine-induced  $\beta$ -endorphin release in the nucleus accumbens [166]. Together, these findings suggest that dopamine receptors in multiple brain regions regulate cocaine reward through vastly different mechanisms.

#### ***17.4.2 Modulation of Opiate and Nicotine Self-Administration by Dopamine Receptor Subtypes***

Like most drugs of abuse, opiate drugs including heroin and morphine, along with nicotine, stimulate mesolimbic dopamine release that plays a major role in their rewarding properties, although dopamine-independent mechanisms also exist for opiate reward [167, 168]. Opiate and nicotine self-administration on fixed ratio schedules can show compensatory increases in drug intake when the primary receptors (opioid and nicotinic cholinergic) are blocked with antagonists in a surmountable manner. However, the positive effects of dopamine receptor blockade on opiate and nicotine self-administration, where present, generally show reductions rather than increases in drug self-administration on fixed ratio schedules. This difference in the response may reflect an insurmountable blockade produced by blocking dopamine receptors downstream from the primary opioid and nicotinic receptors in reward pathways. Reductions in fixed ratio drug self-administration with dopamine receptor blockade also are found when the rewarding effects are relatively weak, and exhibit shallow inverted U-shaped dose–response curves as found with nicotine compared cocaine or heroin self-administration. Thus, it is important to control for possible impairments in response performance by dopamine antagonists in these studies. Given these caveats, there are far fewer reports of the modulation of opiate or nicotine self-administration with subtype-selective dopamine receptor ligands than with psychostimulant self-administration, which also could suggest that many negative effects have not been reported.

The D<sub>1</sub>-like receptor antagonist SCH 23390 blocks the acquisition of heroin self-administration in rats when given as a systemic pretreatment prior to daily acquisition trials, but this treatment also reduces motor behavior and so performance deficits are a consideration [169]. However, similar pretreatments with SCH 23390 infused directly into the nucleus accumbens fail to impair acquisition of heroin self-administration despite decreases in motor behavior, suggesting that D<sub>1</sub>-like receptors in the nucleus accumbens do not mediate opiate reward in self-administration paradigms (but see [170]). Interestingly, D<sub>1</sub> receptor knockout mice readily self-administer the opioid receptor agonist remifentanyl similar to wild-type controls, despite impairments in cocaine self-administration [16]. Discrepancies between pharmacological blockade and D<sub>1</sub> receptor knockout could suggest a role for D<sub>5</sub> receptors, or involve species differences or compensatory changes with a total loss of D<sub>1</sub> receptors. Regarding the latter, chronic blockade of dopamine receptors causes a compensatory sensitization in dopamine-independent opiate reward in rats self-administering heroin [171].

In contrast, D<sub>2</sub> receptor knockout eliminates intravenous morphine self-administration on either fixed or progressive ratio schedules, without affecting acquisition of water self-administration [77]. Since dopamine-dependent opiate reward is mediated by disinhibition of dopamine neurons in the ventral tegmental area, the loss of both pre- and post-synaptic D<sub>2</sub> receptors complicates the interpretation of these findings. A loss of autoreceptor inhibition of dopamine neurons could occlude disinhibition by opiates. Pre- rather than post-synaptic sites of action are supported by the finding that systemic administration of the D<sub>2</sub>-like receptor antagonist sulpiride leads to extinction of intracranial morphine self-administration directly into the ventral tegmental area, but sulpiride fails to alter morphine self-administration directly into the nucleus accumbens [172]. The acquisition of morphine self-administration infused directly into the lateral septum is prevented by systemic administration of either D<sub>1</sub>- or D<sub>2</sub>-like receptor antagonists using a spatial discrimination Y-maze task less sensitive to performance issues [173].

The ability of D<sub>1</sub>-like receptor stimulation to augment heroin reward is indicated by the fact that co-injections of D<sub>1</sub>-like agonists with heroin cause an additive leftward shift in the self-administration dose–response curve on a progressive ratio schedule in monkeys, similar to their effect on cocaine self-administration [146]. However, in contrast to cocaine self-administration, heroin co-injected with D<sub>2</sub>-like agonists causes a rightward shift of the dose–response curves, again, potentially due to D<sub>2</sub>-like autoreceptor stimulation counteracting heroin's ability to disinhibit midbrain dopamine neurons. Together, these findings suggest that while dopamine-dependent opiate reward may involve post-synaptic D<sub>1</sub>-like receptors similar to psychostimulant reward, dopamine-independent opiate reward may play a major role especially when dopamine systems are chronically compromised.

Intravenous nicotine is self-administered at modest rates by animals, but inhibition of monoamine oxidase, as produced by compounds found in tobacco, dramatically enhances nicotine self-administration in rats [174]. The enhanced nicotine self-administration is blocked by systemic pretreatment with D<sub>1</sub>-like receptor antagonist SCH 23390. When nicotine is self-administered directly into the ventral tegmental area, self-administration is reduced by systemic administration of SCH 23390 [175], or by co-infusion with the D<sub>2</sub>-like receptor agonist quinpirole [176], the latter reflecting autoreceptors counteracting the ability of nicotine to excite dopamine neurons. A high dose of the D<sub>3</sub> antagonist SB-277011A reduces nicotine but not food self-administration on a more demanding progressive ratio schedule, even though this dose also impairs motor activity [177]. Another study found that SB-277011A has no effect on stable fixed ratio nicotine self-administration at doses that block nicotine-primed relapse to nicotine seeking in the absence of reward [178]. Oral nicotine self-administration is increased by clozapine but not haloperidol, potentially reflecting surmountable blockade of D<sub>4</sub> receptors [179]. Together, these studies suggest that both D<sub>1</sub>-like and D<sub>3</sub> receptors play a role in the rewarding efficacy of nicotine, although the role of D<sub>2</sub>, D<sub>4</sub>, and D<sub>5</sub> receptors remains undetermined.

### ***17.4.3 Modulation of Alcohol Self-Administration by Dopamine Receptor Subtypes***

Studies on alcohol self-administration also support a role for dopamine receptors in modulating alcohol intake and reward. Most studies measure volitional but freely available alcohol consumption in a choice over water or sucrose, but some investigators employ instrumental responses rewarded by alcohol presentation. Previous studies have found that either D<sub>1</sub>- or D<sub>2</sub>-like receptor blockade with SCH 23390 or raclopride can reduce alcohol consumption, but with the caveat that similar doses also reduce water intake [180]. Another study found that SCH 23390 and spiperone (D<sub>2</sub>-like) reduce water but not alcohol consumption [181]. Other studies using alcohol-preferring rats found that D<sub>2</sub>-like blockade with spiperone slightly increases alcohol intake, while the D<sub>1</sub>-like receptor antagonist SCH 23390 reduces consumption [182]. The D<sub>1</sub>-like receptor antagonist SCH 31966, devoid of serotonergic receptor activity, also reduces intake in alcohol-preferring rats, and at doses that reduce sucrose but not water intake [183]. In contrast, the D<sub>2</sub>-like antagonist remoxipride fails to affect alcohol intake when instrumental responses are required, even at doses that reduce appetitive responding in non-rewarded sessions [184]. Thus, studies in rats suggest that D<sub>1</sub>- rather than D<sub>2</sub>-like receptors may be necessary for alcohol reward.

In mice, pretreatment with either the D<sub>1</sub>-like agonist SKF 38393 or the D<sub>2</sub>-like agonist bromocriptine reduces alcohol consumption, but the effect of bromocriptine is reduced after mice are sensitized to alcohol exposure [185]. In alcohol-preferring rats, SKF 38393 reduces alcohol intake similar to the D<sub>1</sub>-like antagonist SCH 23390, potentially reflecting the partial agonist properties of SKF 38393 or satiating effects with D<sub>1</sub>-like stimulation [182]. Pretreatment with the D<sub>2</sub>-like agonist quinpirole also reduces alcohol intake via dopamine autoreceptor effects as discussed below. However, pretreatment with the D<sub>2</sub>-like agonist 7-OH-DPAT at very low presumably autoreceptor doses increases alcohol drinking [180]. The putative D<sub>3</sub> antagonist U99194A fails to alter preference for alcohol in mice [186], while a high dose of the D<sub>3</sub> antagonist SB-277011A reduces alcohol intake in rats [187, 188]. It is interesting that both D<sub>1</sub> and D<sub>2</sub> receptor knockout mice actually show an aversion to alcohol [189, 190]; while loss of pre-synaptic D<sub>2</sub> autoreceptors could occlude the rewarding effects of alcohol that otherwise disinhibit dopamine neurons, post-synaptic D<sub>2</sub> receptor responses also could be involved in D<sub>2</sub> receptor knockout mice. In any event, findings in knockout mice strongly implicate dopamine in the rewarding effect of alcohol.

When alcohol is self-administered directly into the ventral tegmental area, co-infusion with quinpirole reduces self-administration to control levels, reflecting the ability of direct autoreceptor stimulation to oppose alcohol-mediated disinhibition of dopamine neurons [191]. However, blockade of D<sub>1</sub>-like receptors in dopamine terminal region of the nucleus accumbens with SCH 2390 also decreases alcohol intake without altering the overall rate of instrumental responding [192]. Nucleus accumbens infusions of the D<sub>2</sub>-like receptor antagonist raclopride reduce both intake and instrumental response rates [192, 193], potentially due to motor

impairment. In the bed nucleus of the stria terminalis, D<sub>1</sub>- but not D<sub>2</sub>-like receptor blockade reduces instrumental responding for alcohol while producing lesser reductions in responding for sucrose [194].

Conversely, in a free choice procedure, intranucleus accumbens infusions of SCH 23390 have little effect on alcohol preference in alcohol-preferring rats, while the D<sub>2</sub>-like antagonist sulpiride dose dependently increases consumption of alcohol without altering intake of sucrose or saccharine [195]. Microinfusion of sulpiride into the ventral pallidum also increases alcohol intake under free choice conditions, while SCH 23390 has little effect, although both antagonist treatments elevate extracellular dopamine levels [196]. These findings suggest that alcohol intake is differentially sensitive to blockade of dopamine receptors under free choice or instrumental response procedures. D<sub>1</sub>-like receptors in the nucleus accumbens and bed nucleus of the stria terminalis may play a necessary role in regulating alcohol reward when instrumental responses are required. In contrast, D<sub>2</sub>-like receptors in the nucleus accumbens and ventral pallidum may mediate inhibitory feedback regulation of alcohol intake under free choice conditions.

Stimulation of nucleus accumbens D<sub>2</sub>-like receptors with quinpirole infusions increases instrumental responding for alcohol at low doses, opposite to the effect of receptor blockade, but decreases responding at high doses [193, 197]. Infusions of the D<sub>1</sub>-like agonist SKF 38393 have no effect. The increase in self-administration with low dose quinpirole is prevented by co-infusion of either SKF 38393 or SCH 23390 [197], suggesting that D<sub>1</sub>-like receptor tone is important for the expression of post-synaptic D<sub>2</sub>-like-mediated increases in alcohol self-administration. In contrast to instrumental responding for alcohol, viral vector-mediated increases in nucleus accumbens D<sub>2</sub> receptors decrease both alcohol preference and intake in preferring and non-preferring rats [198], indicating that the D<sub>2</sub> receptor itself is sufficient to regulate alcohol reward. Together these findings suggest that while stimulation of D<sub>2</sub>-like receptors in the nucleus accumbens is sufficient to facilitate instrumental responding for alcohol, increases in the amount of D<sub>2</sub> receptors reduce alcohol intake under free choice conditions consistent with negative feedback regulation of intake discussed above.

## 17.5 Dopamine Receptor Subtypes in Relapse to Drug-Seeking Behavior

In addition to playing a critical role in drug reward, the mesolimbic dopamine system is a major neural substrate for drug-seeking behavior. The mesolimbic dopamine system is activated by exposure to drug-related environmental cues, stress, and other pharmacological stimuli that trigger relapse to drug seeking during withdrawal [199–204]. Dopamine release in forebrain regions such as the nucleus accumbens is sufficient to trigger relapse to drug seeking. Moreover, in some but not

all cases, such dopamine release is necessary for environmental or pharmacological stimuli to trigger drug-seeking behavior.

Relapse to drug seeking is reflected by approach behavior aimed at performing responses that delivered drug injections on prior occasions during self-administration. Like self-administration on progressive ratio schedules, most studies measure the level of effort animals will exert to obtain drug when reward is withheld as an index of drug-seeking behavior, and this behavior is thought to reflect wanting or craving that would precipitate relapse to drug use in humans [7, 205]. An important distinction from self-administration behavior is that responding is measured in the non-rewarded or drug-free state either without or before reward delivery.

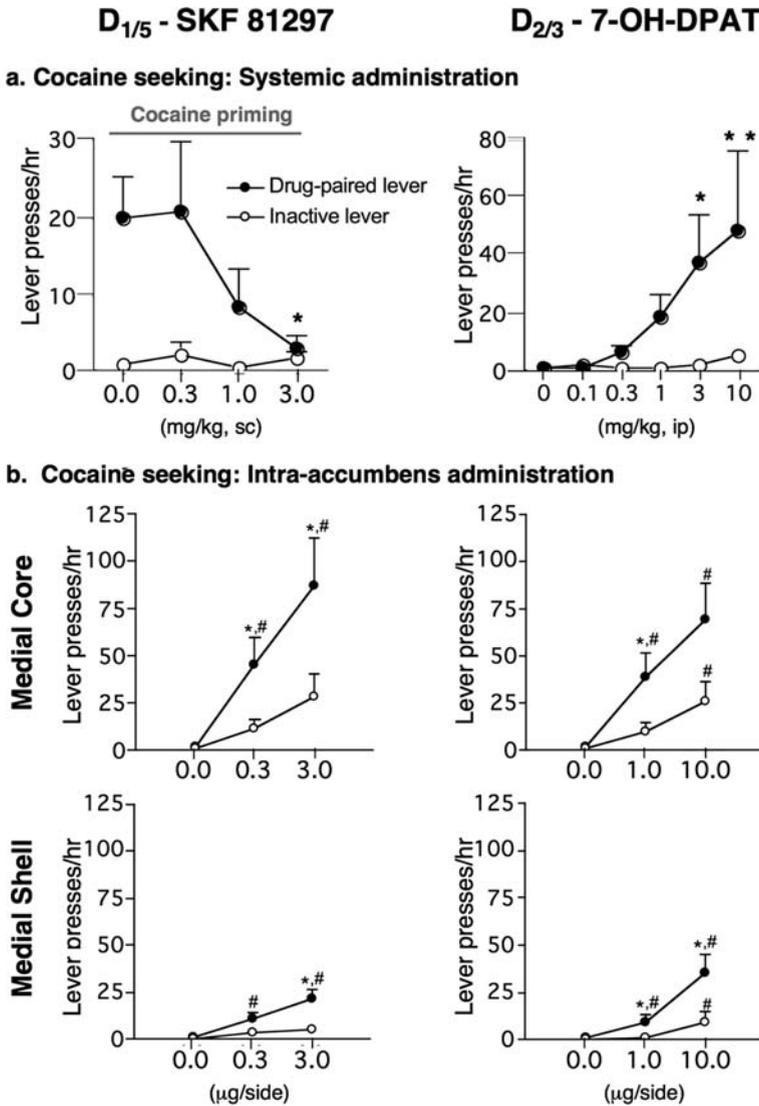
The most commonly used method to model the propensity for relapse to drug seeking is the extinction/reinstatement paradigm. The paradigm has face validity because environmental and pharmacological stimuli that reinstate drug seeking in animals also trigger drug craving in humans [206–208]. In the extinction phase of this procedure, drug-seeking behavior is elicited by environmental and contextual cues associated with drug use in the self-administration test chambers, and ultimately diminishes with repeated training in the absence of drug reward. Following extinction of drug-seeking behavior, the ability of specific experimenter-delivered stimuli to elicit or “reinstatement” drug-paired lever responding is measured. The reinstatement of drug-seeking behavior can be induced by priming injections of drugs, presentation of discrete or environmental cues associated with drug injections, and by brief exposure to moderate intermittent footshock stress. There are numerous extinction/reinstatement studies in rats and monkeys. However, there are very few reports in mice, since commonly used strains do not exhibit effective reinstatement of drug seeking with non-contingent priming injections of drugs [209, 210], although alcohol-primed reinstatement of alcohol seeking has been reported in mice [188]. More recently, the reinstatement paradigm has been adapted to the Pavlovian conditioned place preference model of drug reward, but it is difficult to conceive that conditioned place preference reflects drug-seeking behavior without volitional drug self-administration on prior occasions. Furthermore, the role of dopamine receptor subtypes in the reinstatement of volitional drug seeking markedly differs from their role in the reinstatement of a drug-induced conditioned place preference [43, 139].

Another model of drug-seeking behavior involves the use of second-order schedules of drug self-administration, where initial responding is rewarded by discrete cues predictive of ultimate drug availability. The second-order schedule illustrates the powerful control over drug seeking exerted by these cues. However, since this cue-rewarded drug seeking declines without ultimate delivery of the drug reward, it has been used less extensively to model long-term drug withdrawal. Reinstatement paradigms, on the other hand, suffer from the fact that drug seeking is triggered after extinction of the behavior, a situation vastly different from human drug abuse where craving and relapse occur without extinction experience.

### ***17.5.1 Modulation of Cocaine Seeking by Dopamine Receptor Subtypes: Systemic Administration***

Most work on the role of dopamine receptors in drug-seeking behavior has been conducted in animals self-administering cocaine. As discussed above, cocaine self-administration is reduced by systemic pretreatment with either D<sub>1</sub>- or D<sub>2</sub>-like receptor agonists, suggesting that both receptors provide inhibitory feedback regulation of cocaine intake during self-administration. Cocaine seeking in the absence of reward also is strongly regulated by both D<sub>1</sub>- and D<sub>2</sub>-like dopamine receptor classes, except that they mediate opposite effects on this relapse behavior (Fig. 17.3a). Thus, selective stimulation of post-synaptic D<sub>2</sub>-like receptors is a powerful trigger of cocaine-seeking behavior during or after responses extinguish [19, 139, 211–216]. Conversely, selective D<sub>1</sub>-like receptor stimulation is virtually without effect, even when locomotor activation is similar to D<sub>2</sub>-like receptor stimulation [139, 211, 214, 215]. In addition, pretreatment with full efficacy D<sub>1</sub>-like receptor agonists will block the ability of a single cocaine priming injection, or the presentation of cocaine-associated cues, to reinstate cocaine seeking in the absence of increased stereotypy [139, 142, 216–218]. Conversely, pretreatment with D<sub>2</sub>-like agonists facilitates cocaine-primed reinstatement [139]. A similar D<sub>1</sub>-/D<sub>2</sub>-like dichotomy regulates cocaine seeking in monkeys [219, 220] and also has been shown in some studies to suppress and stimulate craving responses in humans, respectively [221, 222]. The D<sub>3</sub>-preferring agonist PD 128,907 fails to mimic the reinstating effects of D<sub>2</sub>-like agonists in monkeys [219]. Together, these studies suggest that D<sub>2</sub> receptors play a major role in eliciting relapse to cocaine seeking when environmental stimuli such as cocaine-related cues or stress activate the mesolimbic dopamine system [223], while high D<sub>1</sub> receptor tone may provide inhibitory regulation over cocaine seeking by satiating primary reward processes.

While systemic administration of D<sub>2</sub>-like but not D<sub>1</sub>-like receptor agonists is sufficient to trigger cocaine-seeking behavior, both receptor types are necessary for the expression of cocaine seeking. Thus, systemic pretreatment with either D<sub>1</sub>- or D<sub>2</sub>-like receptor antagonists attenuates cocaine-seeking behavior elicited by priming injections of cocaine [217, 219, 224], discrete cues associated with prior cocaine injections [217, 225], cues predictive of cocaine availability [213, 226], or exposure to a cocaine-associated environmental context [227]. In monkeys, cocaine-primed reinstatement is not reduced by the D<sub>3</sub>-preferring antagonists UH 232 and AJ-76 [219]. In rats, however, the D<sub>3</sub> antagonist SB-277011-A reduces cocaine seeking during initial extinction conditions [228], and reduces responding maintained by cocaine-associated but not sucrose-associated cues with a second-order self-administration schedule [229]. Similarly, the D<sub>3</sub> antagonists SB-277011A and/or NGB 2904 dose dependently attenuate cue-primed [230], cocaine-primed [138, 231], and footshock stress-primed [232] reinstatement of cocaine seeking following extinction, without altering reinstatement of sucrose-seeking behavior [232]. Since these compounds also reduce cocaine self-administration on progressive ratio self-administration schedules, but fail to increase cocaine intake on fixed ratio schedules



**Fig. 17.3** (a) *Left*, systemic subcutaneous (sc) pretreatment with the highly selective D<sub>1</sub>-like dopamine agonist SKF 81297 attenuates the ability of intravenous cocaine (2.0 mg/kg) priming to reinstate cocaine-seeking behavior (non-rewarded responding on the drug-paired lever) in rats. The priming injections of cocaine were given 30 min after pretreatment with SKF 81297 following extinction of cocaine-seeking behavior in the reinstatement paradigm. *Right*, intraperitoneal (ip) priming injections with the D<sub>2</sub>-like agonist 7-OH-DPAT trigger cocaine-seeking behavior (\**P* < 0.05 compared to vehicle pretreatment). (b) When infused directly into the nucleus accumbens, both D<sub>1</sub>- and D<sub>2</sub>-like agonists reinstate cocaine-seeking behavior in rats, with greater effects in the medial core than medial shell subregions of nucleus accumbens (\**P* < 0.05 compared to inactive lever responses or vehicle-infused controls #*P* < 0.05). Reinstatement of non-rewarded lever-press responding at the drug-paired lever is thought to model relapse behavior. Adapted with permission from (a) Self et al. [139] and (b) Bachtell et al. [157]

(unlike general D<sub>2</sub>-like antagonists), D<sub>3</sub> receptors may play a distinct role in the motivation for cocaine independent of regulation of cocaine intake as discussed in Section 17.4.1.

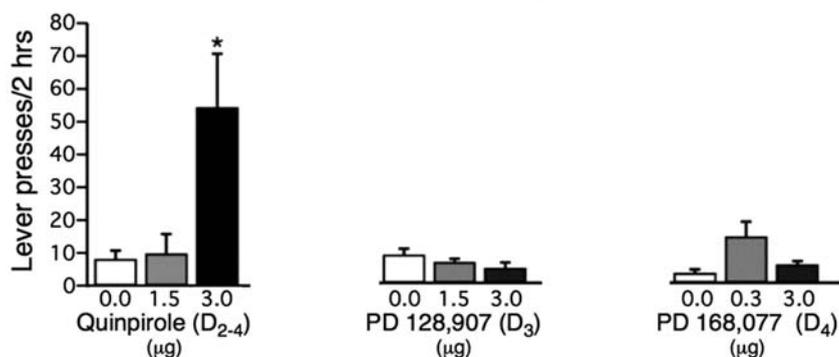
### ***17.5.2 Modulation of Cocaine Seeking by Dopamine Receptor Subtypes: IntraCranial Administration***

Although systemic D<sub>1</sub>-like agonist administration attenuates cocaine-seeking behavior, infusion of SKF 81297 directly into the nucleus accumbens actually triggers cocaine seeking in reinstatement paradigms [157, 233]. This effect involves D<sub>1</sub>-like modulation of calcium/calmodulin-mediated kinase II and activation of L-type calcium channels [234]. Nucleus accumbens infusions of D<sub>2</sub>-like agonists also reinstate cocaine seeking [157, 233], an effect that may involve D<sub>2</sub>-like receptor-mediated inhibition of cyclic AMP-protein kinase A signaling [235]. In both cases, D<sub>1</sub>- and D<sub>2</sub>-like agonists induce more robust cocaine seeking when infused into the medial core rather than the shell subregion as shown in Fig. 17.3b, while lateral core infusions are ineffective [157, 233]. Such enhanced sensitivity of dopamine receptor responses in the medial nucleus accumbens core may be important for cocaine seeking elicited by cocaine-associated cues, since unanticipated cues elevate dopamine levels in the core rather than shell [203, 236].

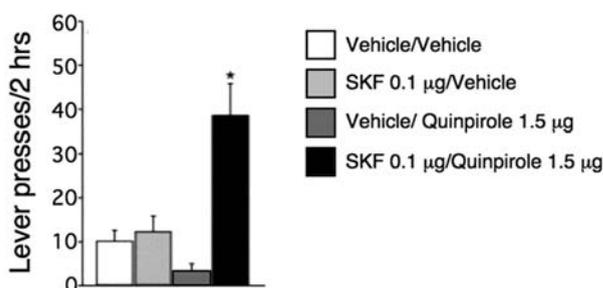
As shown in Fig. 17.4a, the reinstating effects of D<sub>2</sub>-like agonists in the nucleus accumbens probably involve the D<sub>2</sub> subtype, since the D<sub>3</sub> agonist PD 128,907 and the D<sub>4</sub> agonist PD 168,077 fail to mimic reinstatement of cocaine seeking elicited by the D<sub>2</sub>-like agonist quinpirole [233]. Synergistic interactions between D<sub>1</sub>- and D<sub>2</sub>-like receptors are demonstrated by the ability of subthreshold doses of SKF 81297 and quinpirole to elicit far greater cocaine-seeking behavior when co-infused in the nucleus accumbens than when infused alone (Fig. 17.4b) [237]. Similarly, cooperativity between D<sub>1</sub>- and D<sub>2</sub>-like receptors and a role for endogenous dopamine receptor tone is indicated by the ability of the D<sub>1</sub>-like antagonists to block cocaine seeking induced by D<sub>2</sub>-like agonists, while D<sub>2</sub>-like antagonists block cocaine seeking induced by D<sub>1</sub>-like agonists, when co-infused in the nucleus accumbens (Fig. 17.4c) [157, 237].

In contrast to direct activation of dopamine receptors, systemic priming injections of cocaine preferentially elevate dopamine levels in the shell subregion of the nucleus accumbens [238, 239]. Blockade of either D<sub>1</sub>- or D<sub>2</sub>-like receptors in the nucleus accumbens shell attenuates cocaine seeking elicited by systemic cocaine priming injections [157, 240, 241]. Nucleus accumbens infusions of the D<sub>3</sub> antagonist U99194A and the D<sub>4</sub> antagonist L-750667 are ineffective [241]. However, nucleus accumbens infusion of the D<sub>3</sub> antagonist SB-277011A is effective at blocking reinstatement of cocaine seeking induced by footshock stress [232], but SB-277011A fails to block cue-maintained cocaine seeking on a second-order self-administration schedule [242]. Since response-contingent cue presentation in second-order schedules does not increase dopamine levels in the nucleus accumbens [236], it is not clear whether local D<sub>3</sub> blockade would attenuate reinstatement of cocaine

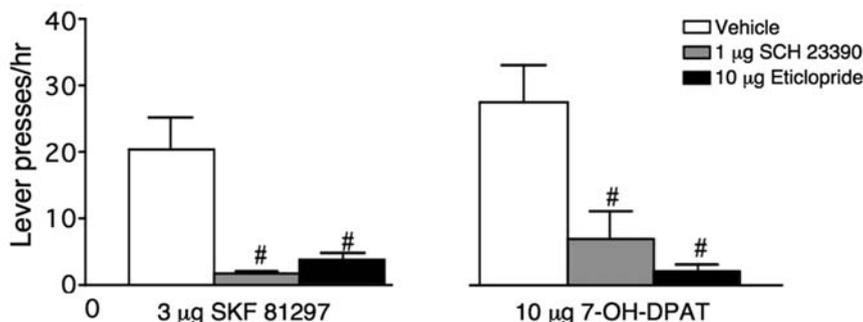
### a. Cocaine seeking: Intra-accumbens D<sub>2</sub>-like agonists



### b. Synergistic interactions of D<sub>1</sub> and D<sub>2</sub>-like agonists



### c. Cooperative interactions of D<sub>1</sub> and D<sub>2</sub>-like receptors



**Fig. 17.4** (a) Intranucleus accumbens shell infusions of the D<sub>2</sub>-like agonist quinpirole, but not the D<sub>3</sub> agonist PD 128,907 or the D<sub>4</sub> agonist PD 168,077, elicit cocaine-seeking behavior in a reinstatement paradigm in rats. Total number of responses (mean  $\pm$  S.E.M.) on the drug-paired lever differs from saline ( $*P < 0.05$ ). (b) Co-infusion of subthreshold doses of SKF 81297 and quinpirole into the nucleus accumbens shell reinstates cocaine seeking. Total number of drug-paired lever responses differs from either SKF 81297 or quinpirole alone ( $*P < 0.05$ ). (c) Cross blockade of reinstatement induced by intra-accumbens D<sub>1</sub>- and D<sub>2</sub>-like agonists by D<sub>1</sub>- and D<sub>2</sub>-like antagonists. Co-infusion of SCH 23390 or eticlopride in the nucleus accumbens blocks SKF 81297- and 7-OH-DPAT-induced reinstatement of cocaine seeking. # $P < 0.05$  compared to vehicle/agonist co-infused controls. Adapted with permission from (a) Schmidt et al. [233], (b) Schmidt and Pierce [237], and (c) Bachtell et al. [157]

seeking induced by unanticipated cues that do elevate nucleus accumbens dopamine. In any event, it appears that D<sub>1</sub>- and D<sub>2</sub>-like receptor stimulations in the nucleus accumbens is both sufficient and in most cases necessary for induction of cocaine-seeking behavior. Given the ability of systemic D<sub>3</sub> antagonist administration to block cocaine- and cue-mediated cocaine seeking, these findings suggest that D<sub>3</sub> receptors in other brain regions may be involved, while D<sub>3</sub> receptors in the nucleus accumbens could play a role in stress-induced relapse. Conversely, the failure to block cue- and cocaine-primed cocaine seeking with nucleus accumbens infusions of D<sub>3</sub> antagonists indirectly implicates D<sub>2</sub> receptors in these behaviors, since D<sub>4</sub> receptors are only marginally expressed in the nucleus accumbens [110, 111]. Clearly, further investigation with multiple and selective D<sub>3</sub> ligands is needed.

Reinstatement of cocaine seeking by response-contingent cues is blocked by local infusion of the D<sub>1</sub>-like receptor antagonist SCH 23390 in the amygdala, while the D<sub>2</sub>-like antagonist raclopride is ineffective [243]. However, amygdala infusions of the D<sub>3</sub> antagonist SB-277011A reduce cue-maintained responding using a second-order self-administration schedule [242]. These results suggest that D<sub>1</sub>-like and D<sub>3</sub> receptors in the amygdala may be critical for the expression of conditioned reward mediated by cocaine-associated cues, similar to their role in the formation of these associations during conditioning as discussed in Section 17.3.3. Cocaine-primed reinstatement of cocaine seeking also is blocked by amygdala infusions of the D<sub>1</sub>-like antagonist SCH 23390 [162].

Modulation of neocortical dopamine receptors also regulates cocaine-seeking behavior. Local blockade of D<sub>1</sub>- or D<sub>2</sub>-like receptors in the medial prefrontal cortex with SCH 23390 and eticlopride, respectively, attenuates cocaine-primed relapse to cocaine seeking without affecting food self-administration [244]. Another study found no effect when specifically targeting the prelimbic subregion with SCH 23390 and raclopride [245]. However, this study found that blockade of D<sub>1</sub>-like, but not D<sub>2</sub>-like, receptors in the medial prefrontal cortex attenuates relapse to cocaine seeking induced by footshock stress. Cocaine- and cue-primed reinstatement of cocaine seeking also is attenuated by D<sub>1</sub>-like blockade in the insular cortex [162]. Interestingly, stimulation of D<sub>1</sub>-like receptors in the agranular insular area of prefrontal cortex with SKF 81297 actually reduces cocaine seeking maintained by cues on a second-order schedule of cocaine self-administration [246]. In this sense, the agranular insular subregion of cortex represents the only brain site known to date where a D<sub>1</sub>-like agonist attenuates cocaine seeking in a manner consistent with systemic administration. However, focal D<sub>1</sub>-like receptor stimulation in regions such as the nucleus accumbens may have different effects on limbic circuits than when the same accumbens D<sub>1</sub>-like receptors are stimulated concomitant with brain-wide D<sub>1</sub>-like receptor activation. For example, D<sub>1</sub>-like receptor stimulation of prefrontal cortical afferents to nucleus accumbens alters the physiological response to coincident D<sub>1</sub>-like receptor stimulation in nucleus accumbens neurons, producing excitatory rather than inhibitory effects [247]. If so, the behavioral responses of such isolated and localized receptor activation could be epiphenomenal to more natural situations.

### ***17.5.3 Modulation of Heroin, Nicotine, and Alcohol Seeking by Dopamine Receptor Subtypes***

Far fewer studies have been conducted on dopamine receptor involvement in relapse behavior with other drugs of abuse. As found with cocaine-trained animals, reinstatement of heroin-seeking behavior is induced by systemic administration of the D<sub>2</sub>-like receptor agonist quinpirole, but only as long as animals remain sensitized to D<sub>2</sub>-like receptor stimulation in withdrawal [19, 248]. Similarly, the D<sub>1</sub>-like agonist SKF 82958 is ineffective and tends to reduce heroin seeking [211]. Systemic pretreatment with the D<sub>1</sub>-like antagonist SCH 23390 or the D<sub>2</sub>-like agonist raclopride blocks reinstatement induced by non-contingent heroin priming injections, but fails to block relapse elicited by footshock stress [249]. However, generalized blockade of both D<sub>1</sub>- and D<sub>2</sub>-like receptors with flupenthixol effectively blocks this behavior [249], suggesting a role for dopamine in stress-induced relapse. Systemic administration of SCH 23390, but not raclopride or the D<sub>3</sub> antagonist NGB 2904, attenuates reinstatement of heroin seeking induced by food deprivation [250], indicating a specific role for D<sub>1</sub>-like receptors in the motivational effects of hunger on heroin-seeking behavior. However, stimulation of D<sub>2</sub>-like receptors with 7-OH-DPAT effectively reinstates food-seeking behavior in animals self-administering food pellets, although D<sub>2</sub>-like antagonists fail to block food seeking elicited by non-contingent priming with food pellets [251]. These results suggest that D<sub>2</sub>-like receptor activation may underlie a fundamental mechanism for reward-seeking behavior in the absence of primary reward, whereas both D<sub>1</sub>- and D<sub>2</sub>-like receptors are necessary for expression of heroin seeking induced by heroin priming and footshock stress.

Blockade of D<sub>1</sub>-like receptors in the nucleus accumbens shell reduces reinstatement of heroin seeking induced by environmental contextual cues, whereas heroin seeking elicited by discrete cues paired with prior heroin injections is reduced by blockade of D<sub>1</sub>-like receptors in the nucleus accumbens core [252], consistent with the ability of discrete cocaine-associated cues to induce dopamine release in the core but not in the shell [236]. Cues that predict food availability will reinstate food-seeking behavior, and this effect is blocked by local D<sub>1</sub>-like receptor blockade in the nucleus accumbens [253].

Systemic administration of a novel D<sub>3</sub> antagonist or SB-277011A attenuates nicotine-primed reinstatement of nicotine seeking in rats, without affecting cue-primed reinstatement or fixed ratio nicotine self-administration [178, 254]. Since D<sub>3</sub> antagonists also reduce nicotine self-administration on a progressive ratio schedule (see Section 17.4.2), D<sub>3</sub> receptors may be critical for the incentive motivational effects of nicotine. Pretreatment with SB-277011A also blocks alcohol- and cue-primed reinstatement of alcohol seeking in rats and mice [188, 255], and the withdrawal-induced binge in alcohol consumption known as the alcohol deprivation effect [255]. More generalized D<sub>2</sub>-like receptor blockade with remoxipride reduces alcohol-seeking behavior under initial extinction conditions at doses that have no effect on instrumental responding for alcohol [184]. The effects of systemic remoxipride on alcohol seeking are recapitulated by infusions of raclopride

directly into the nucleus accumbens at doses that have no effect on alcohol consumption [256, 257]. D<sub>1</sub>- and D<sub>2</sub>-like antagonists also attenuate alcohol seeking induced by cues that predict alcohol availability in rats [258], and the D<sub>1</sub>-like antagonist SCH 23390 blocks renewal of alcohol seeking elicited by an environmental context associated with alcohol self-administration [259]. These findings suggest that both D<sub>1</sub>- and D<sub>2</sub>-like receptors, potentially in the nucleus accumbens, are important for relapse to nicotine- and alcohol-seeking behavior, similar to cocaine relapse. A role for D<sub>3</sub> receptors in the motivation for nicotine and alcohol during withdrawal also is strongly indicated.

## 17.6 Future Directions

With the advent of subtype-selective ligands and knockout mice, a vast body of work on dopamine receptor function in natural and drug reward and in relapse to drug-seeking behavior has accumulated in the past two decades. An equally expansive literature has shown that chronic drug and alcohol use can change the amount of D<sub>1</sub>- and D<sub>2</sub>-like receptors in specific brain regions in animals and more recently, in humans using neuroimaging procedures. A major challenge for future work will involve integrating observed changes in the amount of dopamine receptors in specific brain regions with changes in dopamine receptor regulation of reward and relapse. The breadth of our current knowledge will facilitate this integration, but it is important for future research to track changes in the biochemical, physiological, and behavioral responses mediated by D<sub>1</sub>- and D<sub>2</sub>-like receptors as animals transit from initial drug self-administration to more addicted biological states. It is also important to identify premorbid alterations in D<sub>1</sub>- and D<sub>2</sub>-like receptors that predispose individual vulnerability to drug and alcohol addiction.

For example, decreases in the amount of D<sub>2</sub>-like receptors in the nucleus accumbens of rats are predictive of impulsive behavior and early escalation of cocaine self-administration [260], whereas increases in D<sub>2</sub>-like receptors that accompany social dominance in monkeys are associated with resistance to initial propensity for cocaine self-administration [261]. After self-administration is initiated, prolonged daily access to drugs leads to profound escalation in drug intake, along with a greater propensity for relapse to drug seeking [126, 262, 263]. Animals that escalate cocaine self-administration also show enhanced sensitivity to the rate-altering effects of generalized dopamine receptor blockade on a fixed ratio self-administration schedule [264] suggesting a loss of D<sub>1</sub>- and/or D<sub>2</sub>-like dopamine receptor function with the transition to addiction. These results are consistent with enduring reductions in cortical and striatal D<sub>2</sub>-like receptors that are found in human cocaine, methamphetamine, heroin, and alcohol addicts [265–268].

These decreases in D<sub>2</sub>-like receptors are intriguing given that D<sub>2</sub>-like receptor stimulation triggers relapse to drug-seeking behavior as discussed above. Furthermore, animal data clearly show that chronic cocaine or heroin self-administration [211, 216, 248], and opiate withdrawal [269], increases sensitivity

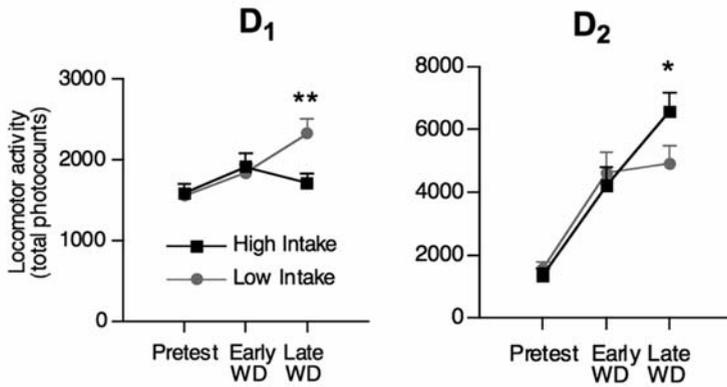
to D<sub>2</sub>-like receptor-mediated behaviors. Similarly, rats with higher preferred levels of cocaine intake are more sensitive to D<sub>2</sub>-like agonist-induced relapse to cocaine seeking [216], consistent with the development of greater sensitization in D<sub>2</sub>-like receptor responses in more addicted biological states. Conversely, rats with lower preferred levels of cocaine intake are more sensitive to the ability of a D<sub>1</sub>-like agonist to suppress cocaine-primed relapse to cocaine-seeking behavior [216], potentially reflecting a compensatory neuroadaptation that prevents low intake animals from developing a more addicted phenotype. These opposing differences in D<sub>1</sub>- and D<sub>2</sub>-like receptor regulation of cocaine seeking are paralleled by changes in the unconditioned locomotor response to D<sub>1</sub>- and D<sub>2</sub>-like receptor challenge after 4 weeks withdrawal, where both D<sub>1</sub>- and D<sub>2</sub>-like receptors mediate directionally similar behavioral effects (Fig. 17.5a–b). Furthermore, higher levels of cocaine intake are positively correlated with sensitization in D<sub>2</sub>-like receptor responsiveness after 4 weeks withdrawal from self-administration, and negatively correlated with changes in D<sub>1</sub>-like receptor responsiveness (Fig. 17.5c).

Thus, a challenge for future work will be to relate changes in the amount of D<sub>1</sub>- and D<sub>2</sub>-like receptors in human drug abusers or in animal studies to seemingly discrepant changes in behavioral responses mediated by dopamine receptors in animal models of drug addiction. One possible explanation for these discrepancies could involve the finding that chronic drug administration increases the amount of high affinity (G protein-coupled) D<sub>2</sub>-like receptors in striatal regions, despite decreases in the total amount of D<sub>2</sub>-like receptors [270–273]. Thus, drug-induced neuroadaptations that reduce the total amount of D<sub>2</sub>-like receptors often are associated with increases in the amount of functional D<sub>2</sub>-like receptors. It would be interesting to determine whether the amount of functionally coupled D<sub>2</sub>-like receptors parallels or diverges from sensitization in D<sub>2</sub>-like receptor-mediated relapse in the same study. In this regard, decreases in the amount of total D<sub>2</sub>-like receptor binding in striatal subregions in human cocaine abusers fail to correlate with cocaine-induced euphoria or cocaine-primed self-administration [274], which could reflect an inability to measure functionally coupled D<sub>2</sub>-like receptors in vivo.

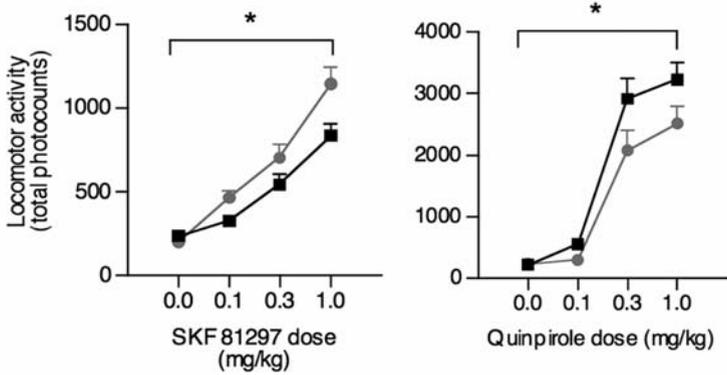


**Fig. 17.5** Differential development of D<sub>1</sub>- and D<sub>2</sub>-like receptor sensitization in low and high intake rats during withdrawal from chronic cocaine self-administration. **(a)** Low intake animals develop D<sub>1</sub>-like receptor sensitization from early to late withdrawal, whereas high intake animals develop greater D<sub>2</sub>-like receptor sensitization. Data in *top panels* show changes in cumulative locomotor responses for dose–response tests (0.1–1.0 mg/kg) with the D<sub>1</sub>-like agonist SKF 81297 and the D<sub>2</sub>-like agonist quinpirole conducted before self-administration (pretest) and at early (2–3 days) and late (28–29 days) withdrawal (WD) times. **(b)** Locomotor dose–response data for low and high intake animals challenged with the D<sub>1</sub>-like and D<sub>2</sub>-like agonists at late withdrawal. Asterisks indicate that high differ from low intake animals \* $p < 0.05$ , \*\*  $p < 0.01$ . **(c)** Average daily cocaine intake during the last 6 days of acquisition training is negatively correlated with the change ( $\Delta$ ) in D<sub>1</sub> responsiveness from early to late withdrawal ( $r = -0.507$ ,  $p = 0.001$ ), but positively correlated with the change in D<sub>2</sub> responsiveness ( $r = 0.686$ ,  $p < 0.001$ ) among individual animals based on cumulative locomotor responses in dose–response tests. Reproduced with permission from Edwards et al. [216]

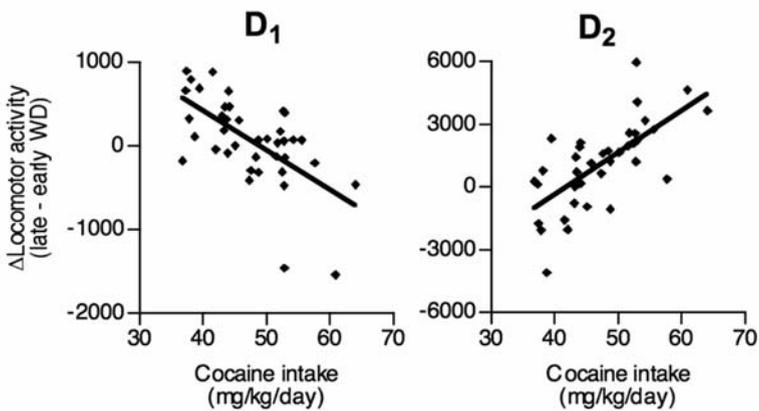
**a. Locomotor sensitization**



**b. Dose-response (late WD)**



**c. Δ in receptor responses**



Given that D<sub>1</sub>- and D<sub>2</sub>-like receptors play such integral roles in reward and relapse behavior, alterations in these receptors due to genetic or environmental factors will remain a major focus for addiction research. It is increasingly apparent that changes in the amount of D<sub>1</sub>- and D<sub>2</sub>-like receptors in drug and alcohol addiction belie a straightforward interpretation that integrates these findings with their functional roles in reward and relapse phenomena. More work is needed to compare changes in the amount of receptors with changes in D<sub>1</sub>-like and D<sub>2</sub>-like receptor function using biochemical and physiological measures. It is imperative that findings from multiple approaches ultimately converge with changes in behavioral responses mediated by D<sub>1</sub>- and D<sub>2</sub>-like receptors before an unambiguous understanding of alterations in dopamine receptor function in drug and alcohol addiction can be appreciated.

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# Chapter 18

## Dopamine Receptors and the Treatment of Parkinson's Disease

Eugenia V. Gurevich and Vsevolod V. Gurevich

**Abstract** Parkinson's disease is a devastating disorder caused by progressive degeneration of dopaminergic neurons in the substantia nigra and the consequent loss of dopamine in the striatum. Dopamine replacement therapy with the dopamine precursor levodopa (L-DOPA), introduced in the 1960s, remains the most effective treatment. Unfortunately, L-DOPA, upon long-term administration, gradually loses its efficacy and eventually leads to severe motor complications, including dyskinesia. The data from numerous studies on Parkinson's patients and animal models of the disease show a complex pattern of changes in multiple signaling pathways in the striatum induced by dopamine depletion. These include modulation of the expression and activity of several subtypes of dopamine receptors, G proteins, effectors, multiple protein kinases, components of the machinery for desensitization and trafficking of G protein-coupled receptors, ionotropic glutamate receptors, and transcription factors. Dopamine replacement therapy reverses many of these changes. However, select signaling effects are exacerbated and/or induced de novo by chronic treatment with L-DOPA. The L-DOPA-induced dyskinesia appears closely associated with selective increases in the activity of specific D<sub>1</sub> receptor-dependent pathways. The contribution of D<sub>2</sub> and D<sub>3</sub> receptor-mediated signaling to dyskinesia development remains largely unexplored. The mechanisms underlying the further enhancement by L-DOPA of signaling pathways already made supersensitive by dopamine depletion need to be elucidated. The recently introduced long-lived dopamine agonists cause less dyskinesia than L-DOPA but are also less efficacious as antiparkinsonian agents. The clinically used DA agonists, which target D<sub>2</sub>-like receptors and often show preference for the D<sub>3</sub> over D<sub>2</sub> subtype, in addition to their antiparkinsonian action, may protect surviving dopaminergic neurons. Continuous delivery of L-DOPA or dopamine agonists, which mimics the physiological tonic stimulation of dopamine receptors, holds the promise of providing therapeutic benefits with minimal side effects. A much better understanding of the molecular

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E.V. Gurevich (✉)

Department of Pharmacology, Vanderbilt University, Nashville, TN 37232, USA  
e-mail: eugenia.gurevich@vanderbilt.edu

processes underlying the therapeutic action of dopaminergic drugs and the development of dyskinesia is necessary in order to modify existing treatments and/or devise new approaches to maximize the beneficial effects of dopamine replacement and minimize the side effects.

**Keywords** Parkinson's disease · L-DOPA · Dyskinesia · Motor complications · Sensitization · Receptor supersensitivity

## 18.1 Dopamine Receptors in the Pathology of Parkinson's Disease

Parkinson's disease (PD) is a progressive neurodegenerative disorder characterized by bradykinesia or akinesia, resting tremor, and muscle rigidity. These symptoms are often accompanied by changes of posture, gait, and sleep; autonomous disturbances; cognitive decline; and depression as the disease progresses. The main underlying pathology in PD is the death of dopaminergic neurons in the substantia nigra pars compacta. These neurons project to the striatum, and their demise results in the loss of dopamine (DA) in the striatum. DA exerts a critical modulatory influence over the striato-thalamo-cortical circuit. DA depletion in the striatum enhances overall striatal output, bringing about excessive inhibition of the excitatory thalamo-cortical projections. As a result, the motor cortical output is reduced, leading to the paucity of voluntary movements in PD patients [1]. This model is applicable to akinesia. Another major symptom of PD, rest tremor, has a somewhat different, and poorly understood, pathophysiology. Tremor is caused by nigrostriatal deficits, but its generation involves extrastriatal areas such as the cerebellum and thalamus [2]. Due to difficulties of reliably modeling tremor in animals [3], no studies have yet been performed addressing the molecular mechanisms of parkinsonian tremor. Therefore, we will confine the discussion to the mechanisms of akinesia.

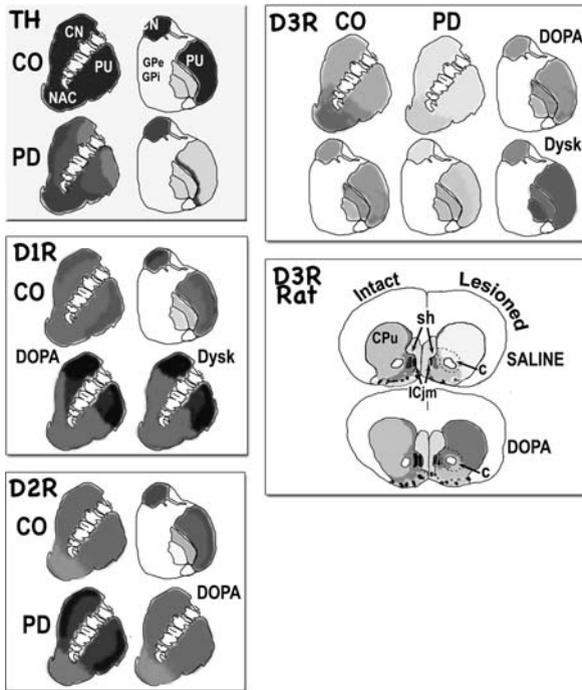
Obviously, the best treatment of PD would be prevention of the degeneration of dopaminergic neurons, or, at least, an arrest of their loss at early stages. Unfortunately, no means to achieve these goals are available at the moment. Some of the DA agonists used to alleviate parkinsonian features have shown neuroprotective properties improving survival of dopaminergic neurons in culture and animal models of PD. Currently, though, attempts to compensate for the diminishing production of endogenous dopamine are the prevailing therapeutic strategy. Although DA receptor agonists are used for this purpose, the most common and effective replacement is achieved with the dopamine precursor levodopa (L-DOPA). Two problems develop over the years as a result of L-DOPA treatment: (1) its therapeutic effectiveness gradually decreases and (2) patients develop severe motor complications. Attempts to alleviate these unwanted effects simply by varying the doses and delivery regimens of L-DOPA and/or DA agonists do not appear to solve these problems. To design effective therapies with minimum side effects, we need a detailed understanding of the molecular mechanisms of dopaminergic

signaling in the normal brain, as well as of the changes in DA-driven signaling pathways induced by DA depletion in PD and by different types of DA replacement therapy. Therefore, here we primarily focus on DA-mediated signaling and its modulation in PD, with the objective of reconstructing a coherent picture from the rather fragmentary information and identifying gaps in our knowledge that need to be filled.

### ***18.1.1 Expression Pattern of DA Receptors in the Forebrain of Rodents and Primates***

DA acts via five subtypes of G protein-coupled DA receptors. Two of the receptors belong to the D1-like subfamily ( $D_1$  and  $D_5$ ) and three to the D2-like subfamily ( $D_2$ ,  $D_3$ , and  $D_4$ ). D1-like receptors couple to  $G\alpha_s/G\alpha_{olf}$  and induce accumulation of cyclic adenosine monophosphate (cAMP), whereas D2-like receptors couple to  $G\alpha_i/G\alpha_o$  and inhibit cAMP production. The  $D_1$  subtype is the main D1-like receptor expressed at a very high level in the striatum (Fig. 18.1).  $D_1$  receptors are largely localized on the striatal medium spiny neurons, projecting to the internal segment of the globus pallidus and the substantia nigra pars reticulata (direct striatal output pathway), which also express the neuropeptides substance P and dynorphin [4–6].  $D_1$  receptors are also expressed at moderate levels throughout the cortex [7, 8].  $D_2$  receptors are highly abundant in the caudate nucleus, putamen, and nucleus accumbens (Fig. 18.1). In the striatum, they are located on a different population of medium spiny neurons than those expressing  $D_1$  receptors.  $D_2$  receptors are found on neurons expressing enkephalin and projecting to the globus pallidus external (indirect pathway) [4, 9, 10].  $D_2$  receptors are also localized presynaptically on nigrostriatal dopaminergic terminals and on the substantia nigra neurons [11–14].  $D_2$  receptors are found at low levels throughout the cortex [7].  $D_2$  receptors located on presynaptic corticostriatal terminals inhibit striatal glutamate release [7, 15, 16].

The experimental support for the model of segregated localization of the two major DA receptor subtypes is somewhat mixed. Double in situ hybridization labeling studies invariably demonstrate practically exclusive expression of  $D_1$  receptors in substance P/dynorphin-positive neurons and expression of  $D_2$  receptors in enkephalin-positive neurons [5, 9, 17, 18]. However, physiological, histochemical, and single cell PCR studies demonstrate co-expression of  $D_1$  and  $D_2$  subtypes [19, 20], although the estimates of the degree of co-expression vary from 10–25 to 100%. It is equally unclear whether the direct pathway neurons express only substance P and dynorphin and whether the indirect pathway neurons express exclusively enkephalin. Another source of controversy is that the segregation of the direct and indirect pathways is incomplete. Most striatal output neurons in both the rodent and the primate brain extensively collateralize, often sending collateral projections to all striatal output targets [10, 21, 22]. Thus, it is no longer possible to adhere to the simplistic model of complete segregation of  $D_1$  and  $D_2$  DA receptors. Nonetheless, in situ hybridization experiments convincingly demonstrate that  $D_1$  receptor mRNA is present at a high level in approximately half of striatal medium



**Fig. 18.1 Changes in the dopamine receptor number in Parkinson's disease.** Schematic illustrations of alterations in dopamine receptors in the primate, including human, brain following dopamine depletion or in Parkinson's disease. The concentrations of the proteins are color-coded: darker colors denote higher density of the proteins. *TH box* (top left): The density of dopaminergic terminals in the striatum in the normal brain (CO) and loss of dopaminergic innervation in Parkinson's disease (PD) at the rostral (left) and caudal (right) levels. The expression of the D<sub>1</sub> (*D1R box*), D<sub>2</sub> (*D2R box*), and D<sub>3</sub> (*D3R box*) dopamine receptors in the normal primate striatum (CO) is shown at different rostro-caudal levels. The alterations in the receptor densities specific for PD, chronic L-DOPA treatment (regardless of the presence of dyskinesia), or overt dyskinesia (Dysk) are also shown. *D3R Rat box*: The expression of the D<sub>3</sub> receptor in the brain of the hemiparkinsonian rat is shown (upper image): Intact – the intact hemisphere; Lesioned – the hemisphere depleted of dopamine with 6-hydroxydopamine. Lower image – alterations in the D<sub>3</sub> receptor density induced by chronic L-DOPA treatment (in comparison with the saline treatment; upper image).

Abbreviations: c – the core subdivision of the nucleus accumbens (dashed outline); CN – caudate nucleus; CO – control subjects; CPu – caudatoputamen; DOPA – the group chronically treated with L-DOPA; Dysk – the group of subjects displaying overt dyskinesia; GPe – external segment of the globus pallidus; GPi – internal segment of the globus pallidus; ICjm – island of Calleja magna; NAC – nucleus accumbens; PD – subjects with Parkinson's disease or drug-naïve animals following dopamine depletion by toxins; PU – putamen; sh – the shell subdivision of the nucleus accumbens.

spiny neurons, whereas the remaining half shows no detectable signal. Similarly, a non-overlapping population of striatal neurons expresses high levels of D<sub>2</sub> mRNA. Since there is no reason to disregard these findings, an explanation consistent with all available data would be that the D<sub>1</sub> and D<sub>2</sub> receptors are expressed at a high

level by substance P/dynorphin- and enkephalin-positive neurons, respectively, but many neurons express the “wrong” receptors at lower levels. This explanation would account for single cell PCR data as well as for physiological data showing that most striatal neurons respond to both D<sub>1</sub> and D<sub>2</sub> agonists [19, 20, 23]. The D<sub>1</sub> and D<sub>2</sub> receptors co-expressed on the same striatal neurons may have differential subcellular distribution resulting in the subtype-specific role in the striatal function [23]. It is important to remember that most of these data come from studies of the rodent brain. There is evidence that a similar distribution exists in the brain of non-human primates [4, 10], but no direct evidence has been produced so far for the human brain. D<sub>2</sub>, but probably not D<sub>1</sub>, receptors localize to cholinergic striatal interneurons [11, 24, 25] in both the rodent and the primate brains and may play an important regulatory role via these neurons in the normal and diseased brain [26]. D<sub>2</sub> receptors are also found throughout the neocortex and hippocampus [7, 8, 27].

The D<sub>3</sub> DA receptor is another member of the D<sub>2</sub>-like subfamily. It is often said that it has a more restricted distribution than the D<sub>2</sub> receptor. Indeed, in the rodent brain, D<sub>3</sub>-binding sites and mRNA are detectable in a limited number of brain regions: the nucleus accumbens, mostly rostral pole and shell subdivisions, the islands of Calleja, the olfactory tubercle, the ventral pallidum, and at low levels in the striatum [11, 28, 29]. However, the pattern of D<sub>3</sub> receptor expression in the primate brain is quite different from that in the rodent (Fig. 18.1). In primates, including humans, D<sub>3</sub> receptors are seen throughout the striatum, although they are most abundant in the nucleus accumbens [8, 11, 30–32]. D<sub>3</sub> receptors are also detected in the globus pallidus, particularly the internal segment (where they are undetectable in rodents), anterior thalamus, amygdala, and throughout the cortex and hippocampus [11, 32]. The concentration of D<sub>3</sub> receptors in the striatum in the human brain is approximately 30% of that of D<sub>2</sub> receptors, whereas in the rodent brain it is barely 5% [11, 31]. In the rat and human brain, D<sub>3</sub> receptors colocalize with both D<sub>1</sub> and D<sub>2</sub> receptors [11, 20, 33]. Functional importance of the D<sub>3</sub> receptor stems from its high affinity to most D<sub>2</sub> agonists, including the endogenous agonist DA [29]. Thus, many DA agonists used in the treatment of PD are D<sub>3</sub>-preferring drugs targeting the D<sub>3</sub> receptor more than the D<sub>2</sub> [34].

Pharmacological properties of the D<sub>3</sub> receptor are peculiar. In contrast to the D<sub>2</sub> receptor, the D<sub>3</sub> receptor is not converted into the low-affinity state by GTP and there is little difference in the affinity of agonists to the D<sub>3</sub> receptor in the presence or absence of GTP [35]. This feature has been extensively used to achieve selective labeling of the D<sub>3</sub> receptor in radioligand-binding experiments [11, 12, 31, 35]. Originally, when the receptor was first cloned, this phenomenon gave rise to the idea that the D<sub>3</sub> receptor is not functional. Indeed, it proved difficult to define the signal transduction pathways activated by the D<sub>3</sub> receptor and attribute specific functions to it. However, D<sub>3</sub> certainly plays a functional role, which is yet to be understood. An interesting feature of the D<sub>3</sub> receptor is its expression in the proliferative zones during prenatal and early postnatal development [12, 36, 37] and the transient expression in the primary sensory cortical areas during postnatal development [38, 39]. This expression pattern suggests a role for the D<sub>3</sub> receptor in neurogenesis and brain maturation.

Much less is known about the distribution of the other two DA receptors in the brain. The D<sub>2</sub>-like D<sub>4</sub> receptor is largely found in extrastriatal areas, the septum, thalamus, cortex, and hippocampus [8, 27]. D<sub>4</sub> receptors are present in both populations of the striatal output neurons at a modest level [20, 40, 41] but are not detectable in striatal interneurons [40]. The D<sub>1</sub>-like D<sub>5</sub> receptor has been detected in the striatum, where it has a somewhat different subcellular distribution than its closest relative the D<sub>1</sub> receptor, localizing more to dendritic shafts, whereas the D<sub>1</sub> subtype is found more often on dendritic spines [24, 42]. D<sub>5</sub>, but not D<sub>1</sub>, receptors are expressed by most cholinergic striatal interneurons [24, 25, 43, 44] as well as by parvalbumin-positive [43] and nitric oxide-positive [45] interneurons. The D<sub>5</sub> receptor is also found in the hippocampus and cortex of the human brain, as well as in the substantia nigra, thalamus, and cerebellum [24, 27, 44].

### ***18.1.2 Changes in Dopamine Receptor Expression in Parkinson's Disease***

In PD, when dopaminergic neurons degenerate and the brain is deprived of DA, DA receptors undergo multiple plastic changes (Fig. 18.1). One type of alteration that is easy to measure and that has been studied extensively is the change in receptor expression. D<sub>2</sub> receptors located on nigrostriatal terminals are obviously lost when the terminals degenerate, which leads to a reduction in the D<sub>2</sub> receptor concentration in the striatum. However, most studies found that the concentration of D<sub>2</sub> receptors increases in the striatum of patients with PD (detected by live imaging methods) [46–54] or at postmortem [55–58], as well as in animal models of PD [59–62]. These data suggest compensatory up-regulation of postsynaptic D<sub>2</sub> receptors (and, possibly, presynaptic receptors on the remaining nigrostriatal terminals). The magnitude of this increase is quite modest (20–50%). With less severe DA depletion in MPTP-treated monkeys, a down-regulation of D<sub>2</sub> receptors is detected, apparently reflecting the loss of presynaptic D<sub>2</sub> receptors, which in this case is not masked by the up-regulation of postsynaptic receptors observed after extensive DA depletion [63]. There have been conflicting reports regarding changes in the expression of striatal D<sub>1</sub> receptors in the parkinsonian brain, but most studies found no significant changes or a slight decrease in the D<sub>1</sub> receptor number [46, 52, 56, 59, 62, 64]. In the rat, D<sub>3</sub> receptors in the nucleus accumbens and striatum decrease following DA depletion [60, 65–67]. Most studies found a similar decrease in the striatum of monkeys depleted of DA by treatment with the neurotoxin 1-methyl 4-phenyl 1,2,3,4-tetrahydropyridine (MPTP) [30, 68] and parkinsonian patients at postmortem [57, 58]. No information is currently available about changes in the concentration of striatal D<sub>4</sub> or D<sub>5</sub> receptors induced by DA depletion.

The striatum receives the bulk of dopaminergic projections, and striatal neurons express DA receptors at high levels. In PD, there is a strict pattern of degeneration of dopaminergic cells, with neurons of the ventral tier of the substantia nigra pars compacta projecting to the dorso-lateral striatum being the most vulnerable

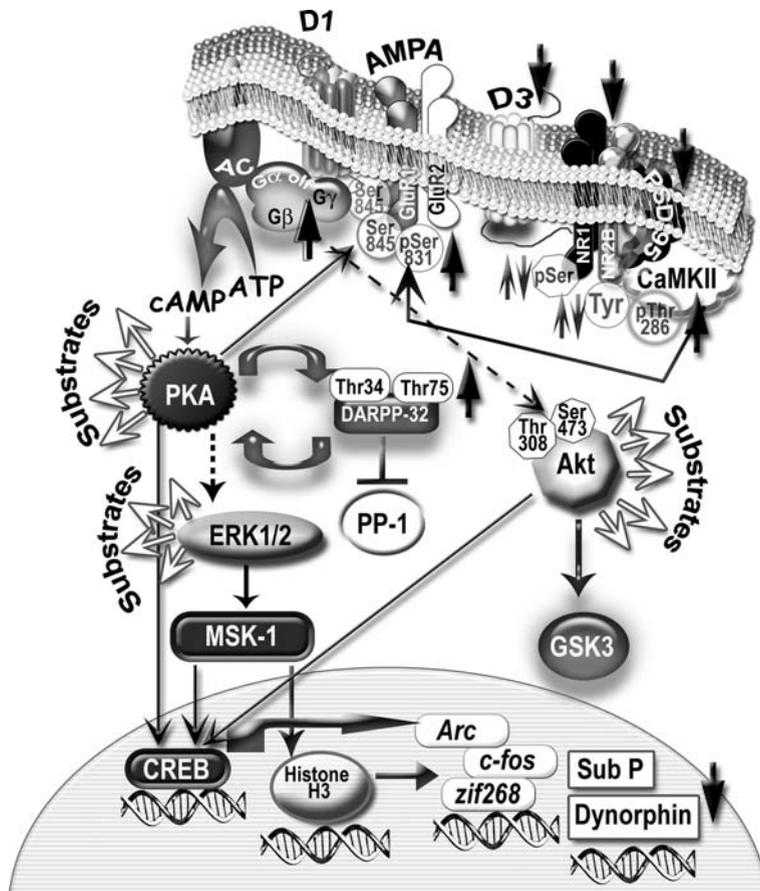
[69–71]. Thus, the highest degree of DA depletion is seen in the dorso-lateral putamen [72, 73], and DA receptors are most likely to change in this region (Fig. 18.1). The dopaminergic neurons of the mesolimbic and mesocortical systems are relatively spared in PD, resulting in less pronounced or minimal loss of DA in other brain regions. Among cortical regions, only the prefrontal cortex has relatively dense dopaminergic innervation, and it is unknown how much it is affected by dopaminergic degeneration in PD. Human postmortem studies found no changes in the concentration of DA receptors in extrastriatal regions of the basal ganglia [55, 58]. Imaging studies detected reduced densities of D<sub>2</sub> receptors in selected cortical areas [74].

### ***18.1.3 Modifications of Dopamine Receptor Signaling in Parkinson's Disease***

The most striking change in the function of DA receptors brought about by the loss of DA is their supersensitivity. This supersensitivity, first described by Ungerstedt [75], in rats unilaterally lesioned with the dopaminergic toxin 6-hydroxydopamine (6-OHDA), manifested itself as rotations induced by dopaminergic drugs at doses 10–100 times lower than those required to cause noticeable behavioral effects in intact animals. This model, the hemiparkinsonian rat, was to become the most important animal model of PD for molecular and signaling studies, since it allowed for the comparison of signaling events between the intact and the dopamine-depleted striatum in the same animal. When hemiparkinsonian animals are injected with direct DA agonists such as apomorphine or the DA precursor L-DOPA, they rotate contralaterally to the lesioned side, but the animals rotate ipsilaterally upon injection of the indirect agonist amphetamine, which induces the release of endogenous DA. The widely accepted interpretation for these observations is that dopaminergic drugs induce activation seen as rotations due to the imbalance in dopaminergic activity between the intact and the lesioned hemispheres. Thus, the animals rotate away from the side of stronger stimulation. The DA releaser amphetamine stimulates the intact side, where endogenous DA is present, whereas direct DA agonists stimulate the lesioned side, where DA receptors are supersensitive. Similarly, the locomotor response to dopaminergic stimulation is supersensitive in DA null mice (in which the gene of tyrosine hydroxylase, the rate-limiting enzyme in the DA biosynthesis, is inactivated) [76].

#### **18.1.3.1 Changes in the Responsiveness of Signaling Pathways Caused by DA Depletion**

The stimulation of DA receptors in the DA-depleted striatum produces exaggerated molecular responses, which presumably underlie the supersensitive behavioral response (Fig. 18.2). Multiple reports showed enhanced DA-induced activity of adenylyl cyclase and suggested that elevated accumulation of cAMP underlies the



**Fig. 18.2 Alterations in the dopamine D<sub>1</sub> receptor signaling following dopamine depletion.** Schematic representation of the putative mechanisms of the D<sub>1</sub> receptor supersensitivity induced by dopamine depletion. Loss of D<sub>1</sub> receptor stimulation following DA depletion results in specific alterations of the expression of multiple proteins. *Short black arrows* pointing up or down next to the protein symbols indicate an increase or decrease in the basal expression; arrows next to the phosphorylation sites indicate changes in the basal phosphorylation level at the sites; pairs of up and down arrows indicate that there are published reports of up- as well as down-regulation. Many pathways with unaltered basal activity respond with a stronger signal to acute dopaminergic challenge. Known stimulatory signaling connections are indicated by *solid arrows* (the arrow between Akt and GSK3 depicts the Akt-mediated phosphorylation of GSK3, which inhibits the GSK3 activity); the inhibitory connection between DARPP-32 and PP-1 is indicated; *dashed arrows* indicate hypothetical connections. Since all signaling proteins have multiple substrates, the possibilities for the propagation of supersensitivity are indicated by *open arrows*. Note that there is no direct evidence that changes in NMDA receptors occur in D<sub>1</sub>-bearing neurons. They are shown here because they follow the same general pattern as other D<sub>1</sub> receptor-mediated changes

circling behavior in hemiparkinsonian rats [77–83]. Elevated DA-stimulated accumulation of cAMP was found in the striatum of PD patients [81, 84]. Downstream targets of cAMP-dependent phosphorylation are also affected (Fig. 18.2). In 6-OHDA-lesioned rodents, the phosphorylation level of the DA- and cAMP-regulated phosphoprotein 32 kD (DARPP-32) at Thr34, which is the substrate of protein kinase A (PKA), in response to acute dopaminergic stimulation by L-DOPA is dramatically increased in the lesioned striatum without changes in the basal level of DARPP-32 phosphorylation [85]. The level of phosphorylation of another PKA substrate, the GluR1 subunit of the AMPA receptor, is also increased at the PKA site Ser845 in response to acute dopaminergic challenge without changes in the phosphorylation level at the calcium/calmodulin-dependent protein kinase II (CaMKII) site Ser831.

DARPP-32 is an important component of the DA signaling, particularly in the striatum, where it is expressed at a high level in medium spiny neurons [86]. DARPP-32 activity is regulated by phosphorylation at multiple sites. It is phosphorylated by PKA at Thr34, which converts it into an inhibitor of protein phosphatase-1 [87, 88]. By inhibiting the dephosphorylation of proteins phosphorylated by PKA, DARPP-32 creates positive feedback for the D<sub>1</sub> receptor-mediated signaling. Stimulation of D<sub>1</sub> receptors enhances DARPP-32 phosphorylation at Thr34, and deactivation of DARPP-32 blunts the D<sub>1</sub>-mediated signaling and suppresses the D<sub>1</sub> behavioral effects [88]. The DARPP-32-based positive feedback loop for the D<sub>1</sub> receptor signaling includes an additional component aimed at promoting PKA function. DARPP-32 is phosphorylated at Thr75 by cyclin-dependent kinase 5 (cdk5), which converts it into an inhibitor of PKA [89]. DA acting via D<sub>1</sub> receptors and PKA reduces DARPP-32 phosphorylation at Thr75 [90], thus removing the inhibition and promoting PKA-mediated signaling. In the DA-depleted striatum, the basal level of DARPP-32 phosphorylation at Thr75 is elevated [91], as should be expected. These data suggest that in the DA-depleted striatum the D<sub>1</sub> receptor-mediated signaling is enhanced at many levels, leading to exaggerated behavioral responses to D<sub>1</sub> drugs. D<sub>2</sub> receptor activation reduces the level of DARPP-32 phosphorylation at Thr34 via inhibition of PKA and activation of calcium/calmodulin signaling [92]. Loss of DARPP-32 results in a reduction in D<sub>2</sub> receptor-mediated behavioral effects, such as raclopride-induced catalepsy [88]. The fact that in the denervated striatum challenged with dopaminergic drugs the level of DARPP-32 phosphorylation is enhanced suggests that the D<sub>1</sub> supersensitivity predominates, outweighing the D<sub>2</sub> signaling, at least within this specific molecular pathway.

Dopaminergic activation induces a 2–3 times higher level of phosphorylation of extracellular signal-regulated kinases 1 and 2 (ERK1/2) in the DA depleted as compared to the intact striatum [18, 60, 76, 85]. L-DOPA does not alter ERK1/2 phosphorylation in the intact striatum but strongly activates it following dopaminergic denervation [60, 76, 85]. The supersensitive ERK1/2 response in the denervated striatum has been shown to be mediated by D<sub>1</sub> receptors [18, 93] and, presumably, by PKA. The ERK1/2 activation is influenced by DARPP-32, since ERK1/2 supersensitivity to acute L-DOPA is attenuated in DARPP-32 null mice [85]. The

dopaminergic denervation results in elevated phosphorylation of Akt (at both Thr34 and Ser375) and its substrate glycogen synthase kinase 3 $\alpha$  and  $\beta$  (GSK3 $\alpha,\beta$ ) in response to acute administration of the D<sub>1</sub>/D<sub>2</sub> agonist apomorphine in the 6-OHDA rat model of PD [60].

The denervation-induced supersensitivity of DA receptors can be demonstrated easily and reliably in the hemiparkinsonian rat model of PD. However, it is much more difficult to detect in other animal models of PD, and next to impossible in human patients. In the MPTP monkey model of PD, the lesion produced by systemic administration of the dopaminergic neurotoxin MPTP is bilateral and results in akinesia similar to that seen in advanced PD patients. Dopaminergic stimulation alleviates akinesia, thus producing an antiparkinsonian effect. Monkeys with unilateral lesions produced by a single injection of MPTP into the carotid artery exhibit contralateral circling behavior in response to L-DOPA or DA agonists [94] indicative of functional DA receptor supersensitivity on the lesioned side. Increased DA-stimulated adenylyl cyclase activity has been reported in patients with PD at postmortem [81, 84], but since all patients come for the autopsy after having been treated with L-DOPA for years or even decades, it cannot be ascertained whether this enhancement is due to denervation, L-DOPA treatment, or the combination of both. The degree of enhancement is usually not impressive, hovering around 50–60%.

In the MPTP monkey model, it is possible to separate the effects of L-DOPA treatment from those caused by DA denervation. Denervation leads to an enhanced stimulation of adenylyl cyclase activity by DA in L-DOPA-naïve MPTP-lesioned primates [81] and enhanced [<sup>35</sup>S]GTP $\gamma$ S binding induced by the D<sub>1</sub> agonist SKF38393 [95] indicative of an increased D<sub>1</sub> receptor coupling to G protein. Similarly to the rodent data, ERK phosphorylation and expression is increased in the striatum of MPTP-treated monkeys [96], possibly as a result of receptor supersensitivity. In common marmosets unilaterally lesioned with 6-OHDA, L-DOPA elicits strong activation of *c-fos* and *c-jun* expression in the lesioned hemisphere, which is undetectable on the intact side [97]. However, the experiments necessary to detect DA receptor supersensitivity, such as acute injection of dopaminergic drugs and rapid detection of changes, are rarely performed in monkeys for practical reasons. Therefore, the supersensitivity of the multiple signaling pathways known to be super-responsive in hemiparkinsonian rats remains unproven in the parkinsonian primate brain, although there is no compelling reason to suppose that the situation there is substantially different than in the rodent.

### 18.1.3.2 The Effects of Dopamine Depletion on Transcription Factors

The lesion-induced supersensitivity of DA receptors causes strong activation of multiple genes in the striatum in response to acute dopaminergic stimulation. Many of these genes are transcription factors belonging to the *fos* (*c-fos*, *FosB*,  $\Delta$ *FosB*, *fra-1*, *fra-2*) and *jun* (*c-jun*, *JunB*, *JunD*) gene families. The protein products of these genes, Fos and Jun, heterodimerize to form Fos/Jun, or homodimerize forming Jun/Jun complexes, collectively known as activator protein-1 (AP-1) transcription factors, which can bind to AP-1 consensus sites on target genes and regulate their

transcription [98]. The transcriptional activity of AP-1 depends heavily on the actual composition of the complex, posttranslational modifications, and interactions with regulatory proteins [99]. Many of these genes are termed *immediate early genes* (IEG) because their transcription is rapidly induced by acute challenges and just as rapidly deactivated within a few hours. The activation of these genes can be easily detected by in situ hybridization or immunohistochemistry and has been extensively used as a general indicator of neuronal activation following various stimuli. It was found that the level of activation of the gene expression in the DA-deprived striatum of hemiparkinsonian rats is many times stronger than on the intact side [97, 100–102].

The cAMP response element-binding protein (CREB) is a transcription factor activated via cAMP- or  $\text{Ca}^{2+}$ -dependent phosphorylation at Ser133 by multiple protein kinases [103, 104]. Acute L-DOPA injection induces a substantially higher level of CREB phosphorylation in the lesioned than in the intact striatum [105, 106] indicative of supersensitivity. The supersensitive CREB response to L-DOPA is reproduced by  $\text{D}_1$  but not  $\text{D}_2$  agonist and blocked by  $\text{D}_1$  antagonist, demonstrating the supersensitivity of  $\text{D}_1$  receptors in the DA-depleted striatum [106]. The increased transcription of *c-fos* in the lesioned striatum induced by dopaminergic stimulation may reflect increased activation of CREB, since CREB activation has been shown to regulate drug-induced *c-fos* expression [104, 105, 107]. At the same time, it has been reported that in the lesioned striatum, in contrast to the intact brain, CREB does not participate in the induction of *c-fos* transcription [108], which would leave supersensitive *c-fos* induction unaccounted for. Interestingly, knockdown of CREB exacerbated the behavioral effects of L-DOPA in hemiparkinsonian rats [108], suggesting that supersensitive CREB activation is not the cause of behavioral supersensitivity but rather its negative regulator.

### 18.1.3.3 Changes in the Basal Activity or Expression of Signaling Proteins

In addition to the lesion-induced supersensitivity, which requires acute dopaminergic challenge to be revealed, the loss of DA causes changes in the basal level of activity or expression of various proteins. The increased level of DARPP-32 phosphorylation at Thr75 [91] is possibly mediated by loss of stimulation of the  $\text{D}_1$  receptor, which normally inhibits Thr75 phosphorylation via activation of protein phosphatase 2A (PP2A) [90]. In the lesioned striatum, the basal level of autophosphorylation of calcium-, calmodulin-dependent protein kinase II (CaMKII) at Thr286 is elevated [91, 109]. The autophosphorylation of CaMKII at Thr286 enhances autonomous kinase activity and eventually leads to increased basal phosphorylation of the GluR<sub>1</sub> subunit of the AMPA receptor at the CaMKII substrate Ser831, although this effect does not occur until months after the dopaminergic denervation [91]. The increase in CaMKII autophosphorylation is mimicked by a  $\text{D}_1$ , but not  $\text{D}_2$ , antagonist and by a PKA inhibitor, whereas forskolin reverses it [109], suggesting that normally the  $\text{D}_1$  receptor exerts a negative influence on CaMKII autophosphorylation.

The elevated CaMKII autophosphorylation enhances kinase association with the NMDA receptor subunits NR<sub>2A</sub> and NR<sub>2B</sub> [109]. The NMDA receptor is a heteromeric complex, most often comprising two NR<sub>1</sub> and two NR<sub>2</sub> subunits (identical or different), and the subunit composition is an important determinant of the receptor's functional properties [110] as is phosphorylation of the receptor subunits [111]. Many studies report alterations in the NMDA receptor subunit abundance, composition, and phosphorylation in the DA-depleted striatum. The results are, unfortunately, inconsistent. Different studies demonstrated either a decrease in the abundance of NR<sub>1</sub> and/or NR<sub>2B</sub> subunits in the DA-depleted striatum in rats and monkeys [109, 112–114] or no change [115]. This discrepancy likely depends, at least partially, on the purity of the synaptic membrane fraction used in different studies, since no changes are usually seen in the total homogenate fraction but the availability of NMDA subunits is selectively reduced in synaptic membranes. The basal serine and tyrosine phosphorylation of NR<sub>1</sub> and NR<sub>2B</sub> subunits was found to be decreased [112, 116] or increased [109, 115, 117] following dopaminergic denervation. It appears that when the reduction in the abundance of subunits is accounted for, most studies find a modest net increase in phosphorylation. Inhibitors of CaMKII reduce serine phosphorylation of NR<sub>2</sub> subunits [109, 115]. Additionally, the synaptic concentration of PSD95 in the DA-depleted striatum is reduced [116, 118, 119], and the interaction of NMDA receptor subunits with protein components of the postsynaptic density is suppressed, leading to altered subcellular localization of NMDA receptors [116]. Although the details remain obscure, there is little doubt that dopaminergic denervation causes multiple modifications in the functions of glutamate receptors brought about by changes in the subunit composition, their phosphorylation, and/or abundance or function of other components of the postsynaptic density. These modifications result in profound deficits in synaptic plasticity in striatal neurons [109, 120, 121] that might play an important role in parkinsonian symptoms.

It is important to remember that in most cases there is no evidence that these changes occur exclusively or even predominantly in the D<sub>1</sub> receptor-bearing neurons. The CaMKII hyper-phosphorylation and changes in the CaMKII-NMDA receptor interaction are likely due to D<sub>1</sub> receptor dysfunction, suggesting that the disturbances in the NMDA receptor function are also D<sub>1</sub> receptor dependent. The GABAergic transmission may also be modified in striatonigral neurons, although the extent of these modifications is uncertain. The down-regulation of the vesicular GABA transporter has been reported [122], but the level of the GABA biosynthetic enzyme glutamic acid decarboxylase 67kD (GAD67) was found to be unchanged [123] or increased [124].

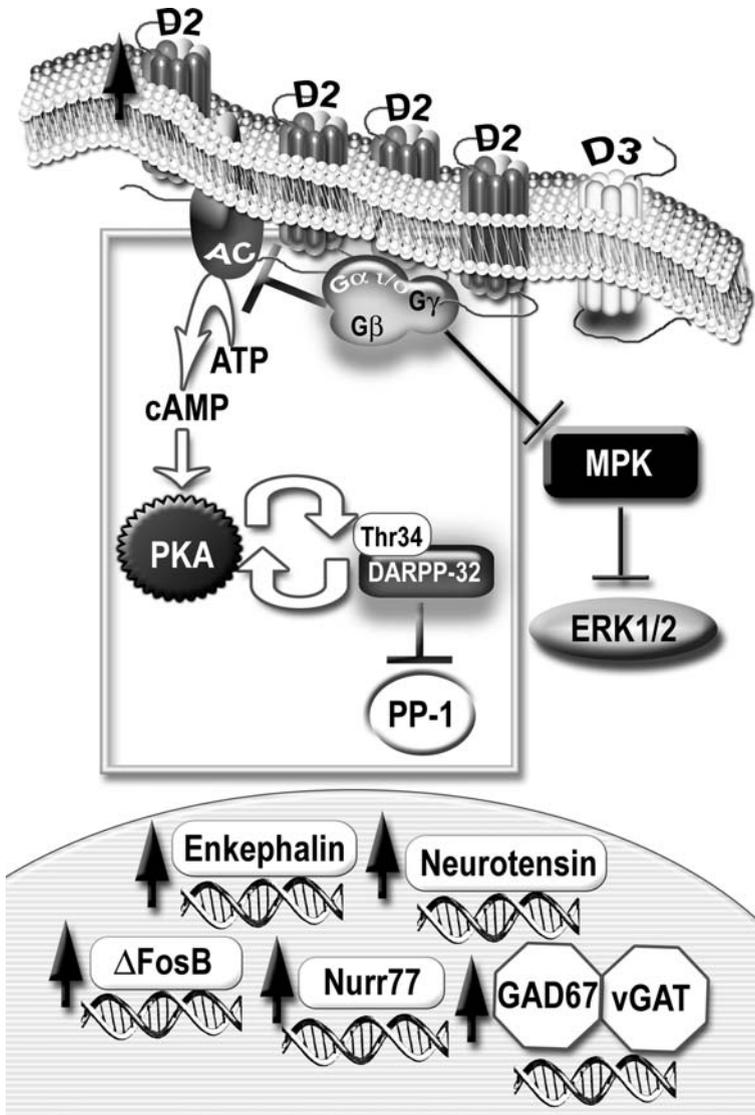
#### **18.1.3.4 Changes in D<sub>2</sub> Receptor-Mediated Signaling**

The data discussed above demonstrate the supersensitivity of the D<sub>1</sub> receptor-dependent signaling pathways brought about by DA depletion (Fig. 18.2). The fact that rotational behavior in hemiparkinsonian rodents can be induced by both D<sub>1</sub> and D<sub>2</sub> selective agonists [60, 118, 125–129] suggests supersensitivity of both receptor

subtypes. Similarly, the behavioral supersensitivity in DA null mice reflects the supersensitivity of both D<sub>1</sub> and D<sub>2</sub> receptors, since both D<sub>1</sub> and D<sub>2</sub> agonists induce hyperactivity, and antagonists of either receptor partially block L-DOPA-induced hyperlocomotion [76]. A comparison of the relative efficacies of D<sub>1</sub> and D<sub>2</sub> selective agonists in eliciting behavioral (or molecular) responses, although frequently made, is quite problematic, since it is difficult to match doses of the drugs, which have different pharmacokinetic and pharmacodynamic properties.

The molecular evidence for D<sub>2</sub> receptor supersensitivity is less impressive than that for the D<sub>1</sub> receptor (Fig. 18.3). In addition to the up-regulation of D<sub>2</sub> receptor number, the coupling of D<sub>2</sub> receptors to G $\alpha$ <sub>i</sub> may be enhanced by dopaminergic denervation [77, 130], although it was found to be unchanged in another study [82]. Early studies demonstrated that selective D<sub>2</sub> agonists, similarly to D<sub>1</sub> agonists, induce a supersensitive Fos response in the DA-depleted basal ganglia but in different regions: D<sub>1</sub> receptor stimulation induced Fos expression in striatal neurons, whereas D<sub>2</sub> stimulation caused Fos expression in the globus pallidus [128, 131, 132]. The latter effect may be due to excessive disinhibition of pallidal neurons by dopaminergic stimulation via supersensitive striatal D<sub>2</sub> receptors. Interestingly, the supersensitive ERK1/2 response in the DA-depleted striatum can be elicited by selective activation of D<sub>2</sub> receptors [129, 133]. Moreover, Cai and co-workers found that the D<sub>1</sub> agonist SKF38393 failed to induce ERK1/2 phosphorylation [129], which is directly contradictory to the findings of other teams [18, 85, 93]. The discrepancy cannot be readily attributed to any obvious difference in methods and, thus, remains a mystery. Importantly, inhibition of ERK1/2 activation or depletion of ERK1/2 by antisense oligonucleotide reduced the frequency of quinpirole-induced rotations [129] suggesting that ERK1/2 activation is part of the mechanism of D<sub>2</sub> receptor supersensitivity. The molecular mechanism by which D<sub>2</sub> receptor stimulation activates ERK1/2 involves inhibition of mitogen-activated protein kinase phosphatase (MKP), the enzyme responsible for ERK1/2 dephosphorylation [133]. Apparently, this coupling of the D<sub>2</sub> receptor with MPK activity is strongly enhanced by DA depletion, since no changes were seen in the intact striatum.

The presynaptic D<sub>2</sub> receptors localized to corticostriatal terminals, which inhibit the release of glutamate, were shown to do so more effectively in the DA-depleted striatum [134, 135], indicating that dopaminergic denervation does induce the supersensitivity of D<sub>2</sub> receptors. Loss of DA results in the loss of D<sub>2</sub> receptor-mediated inhibitory control over corticostriatal transmission and enhanced glutamatergic activity, and the same effect is produced by the loss of D<sub>2</sub> receptors [16]. The loss of DA profoundly alters GABAergic transmission in the striatopallidal neurons, which suggests the involvement of D<sub>2</sub> receptor-mediated signaling in the control of GABAergic activity. DA depletion induces the overexpression of GAD67 and vesicular GABA transporter in striatopallidal neurons, enhanced GAD enzymatic activity, and elevated GABA release [122, 123, 136] indicative of the overactivity of the indirect striatopallidal pathway. The dopaminergic lesion up-regulates the expression of enkephalin, which is co-expressed with D<sub>2</sub> receptors in striatal



**Fig. 18.3** Changes in the signaling pathways attributable to D<sub>2</sub> receptor activity. The loss of DA stimulation of D<sub>2</sub> receptors (the pathway in the box is inactive in the DA-depleted striatum) leads to constitutive upregulation of the expression of multiple genes (*short black arrows*). DA depletion enhances the coupling of the D<sub>2</sub> receptor to G<sub>i</sub>. Acute stimulation of D<sub>2</sub> receptors with selective agonists induces supersensitive ERK1/2 activation in the DA-depleted striatum, presumably due to the D<sub>2</sub> receptor-mediated inhibition of the mitogen activated protein kinase phosphatase (MKP) (129)

medium spiny neurons [60, 118, 137–143]. These effects could be interpreted as a result of the removal of the inhibitory influence of the D<sub>2</sub> receptors.

DA depletion also increases the expression of Nurr77, an orphan member of the nuclear receptor family of transcription factors, as well as that of neurotensin in enkephalin-positive neurons [144, 145]. These effects are replicated by chronic treatment with the D<sub>2</sub> receptor antagonist haloperidol [146]. The data suggest that tonic stimulation of D<sub>2</sub> receptors in the intact striatum inhibits Nurr77 and neuropeptide expression, which is disinhibited when that stimulation is removed. The up-regulation of Nurr77 in D<sub>2</sub> receptor-bearing neurons after the lesion may serve as a compensatory mechanism aimed at reducing the consequences of DA loss, since Nurr77 null mice demonstrate exaggerated rotational behavior following DA depletion, accompanied by blunted enkephalin and neurotensin up-regulation [143].

It appears that D<sub>1</sub> receptors mediate acute responses to DA causing “positive” signals in multiple downstream signaling pathways. Consequently, the D<sub>1</sub> receptor supersensitivity resulting from the lack of D<sub>1</sub> receptor stimulation following the DA depletion manifests itself in exaggerated responses to acute dopaminergic challenge in numerous signaling pathways. At the same time, loss of D<sub>1</sub>-mediated signaling leads to only a few changes in the basal levels of expression. The notable examples of D<sub>1</sub> receptor-dependent tonic regulation are the expression of dynorphin, substance P, and the D<sub>3</sub> DA receptor, all of which require periodic D<sub>1</sub> stimulation for maintenance. Conversely, D<sub>2</sub> receptors are more adapted for tonic inhibition of molecular pathways, and the removal of this influence results in basal up-regulation of a number of genes as well as of the corticostriatal glutamatergic and striatonigral GABAergic transmission (Fig. 18.3). The ERK1/2 activation appears to be the only example of D<sub>2</sub> receptor-dependent signaling supersensitivity in the DA-depleted striatum.

#### **18.1.3.5 Possible Role of the Synergism Between D<sub>1</sub> and D<sub>2</sub> Receptors in Parkinson's Disease**

One curious phenomenon, the synergism of D<sub>1</sub> and D<sub>2</sub> receptors, deserves mention here, since it may bear on the signaling mechanisms of PD. In many cases, concomitant administration of a D<sub>1</sub> and D<sub>2</sub> agonist produces much stronger behavioral or molecular effects than either drug alone. Thus, the addition of a low dose of the D<sub>1</sub> agonist SKF38393 potentiates rotations induced by the D<sub>2</sub> agonist quinpirole in hemiparkinsonian rats [128]. Similarly, quinpirole by itself induces minimal expression of Fos-like proteins in the DA-depleted caudate-putamen of 6-OHDA-lesioned rats, whereas the combined administration of quinpirole and SKF38393 induces much stronger Fos expression in striatonigral neurons than SKF38393 alone [17, 128].

The term “priming,” or “reverse tolerance,” is often used to describe an enhancement of a response to subsequent as compared to previous administrations of a drug. The behavioral sensitization to L-DOPA discussed above is one example of priming, and LID is another, since the probability of LID increases with each drug exposure. Usually, the term priming is applied to repeated treatment with the same drug such

as L-DOPA with administrations far enough apart to ensure washout of the previous dose. Thus, the priming is based on cumulative plastic adaptations in the brain caused by each drug dose, with the first dose applied to drug-naïve brain sensitized by loss of DA having a devastating effect [147]. Interestingly, D<sub>1</sub> and D<sub>2</sub> selective drugs can prime for each other. For example, a dose of quinpirole ineffective in a drug-naïve animal can induce robust rotations and Fos expression in striatonigral neurons if preceded by injections of the D<sub>1</sub>/D<sub>2</sub> agonist apomorphine or the D<sub>1</sub> agonist SKF38393 [148, 149]. Interestingly, if priming is done with SKF38393 in combination with the ineffective dose of quinpirole, the result is equivalent to priming with a 10-fold higher dose of SKF38393 alone [148] illustrating the role of D<sub>1</sub>-D<sub>2</sub> synergism in this “cross-priming” phenomenon. Similarly, SKF38393 alone does not induce Fos expression in the globus pallidus, but priming with quinpirole, which does, allows SKF38393 to induce Fos expression in this brain region [128]. Moreover, priming with apomorphine enhances the quinpirole-induced Fos stimulation in the globus pallidus [149], indicating that responses mediated by both D<sub>1</sub> and D<sub>2</sub> receptors are primed. The D<sub>1</sub>-D<sub>2</sub> synergism and priming are likely to be mechanistically related. The synergism seen with concomitant administration of D<sub>1</sub> and D<sub>2</sub> drugs can be considered as “simultaneous” priming, since priming occurs even after a single administration of the priming agent. The D<sub>1</sub>-D<sub>2</sub> synergism is inherent in the priming with L-DOPA, since DA produced from L-DOPA interacts with all DA receptors. The mechanisms of either phenomenon are unknown. The inhibition of NMDA receptors has been shown to counteract both synergism and priming, supporting an indirect mechanism dependent on glutamate release [128, 150, 151]. It is possible that D<sub>1</sub>/D<sub>5</sub> and D<sub>2</sub>/D<sub>3</sub> receptors co-expressed on the same neurons play a role. Alternatively, the effects could involve striatal interneurons, which are known to exert a powerful regulatory influence over striatal output neurons [26, 152].

It is important to remember that, although the striatum is the major recipient of dopaminergic projections and the site of massive alterations following DA depletion, extrastriatal areas also show changes. Thus, supersensitive activation of *c-jun* expression in the cortex of rats and monkeys unilaterally lesioned with 6-OHDA [92] suggests that the DA receptor supersensitivity is not restricted to the striatum. Similarly, the activation of the Akt pathway in the prefrontal cortex is supersensitive on the lesioned side in hemiparkinsonian rats, although the degree of supersensitivity is smaller than in the striatum [60]. The supersensitive D<sub>1</sub> receptor-mediated stimulation of adenylyl cyclase activity has been reported in the frontal cortex of PD patients at postmortem [84]. The functional significance of these phenomena in the clinical picture or progression of PD remains to be determined.

#### ***18.1.4 Molecular Mechanisms of the Dopamine Receptor Supersensitivity Induced by Dopaminergic Denervation***

The data concerning G protein coupling and cAMP production seem to indicate that the DA receptor supersensitivity, particularly that of the D<sub>1</sub> receptor, involves

signaling events immediately downstream of receptor stimulation, specifically, the activation of G proteins. Thus, it is likely that many signaling pathways further downstream of the D<sub>1</sub> receptor-induced signaling would be supersensitive. There also might be a cumulative effect on behavior. The magnitude of supersensitivity reported for many signaling events is modest, whereas the behavioral supersensitivity is quite substantial. It is possible that minor changes amplified in multiple signaling pathways converge on behavior, producing severe changes in behavioral responsiveness to dopaminergic drugs. The supersensitivity of DA receptors caused by the loss of dopaminergic stimulation due to degeneration of dopaminergic neurons appears to be a logical and useful adaptation aimed at counteracting the declining availability of endogenous DA. However, the molecular mechanisms of this adaptation remain elusive.

Two types of mechanisms can conceivably enhance the signaling via any G protein-coupled receptor (GPCR), including all five DA receptors. Signal transduction can be facilitated by an increased number of receptors, their cognate G proteins, and/or effectors. Signaling can also be prolonged by suppressing the processes that turn it off at the receptor and/or G protein level. The mechanism that attracted much attention at first was an increase in the receptor concentration. Although the lesion-induced up-regulation of DA D<sub>2</sub> receptors is consistently detected in animal models and human patients [58, 60, 73, 95], the magnitude of the effect is clearly insufficient to account for the strong increase in responsiveness to dopaminergic stimulation normally observed. Moreover, D<sub>1</sub> receptors, the major striatal DA receptor subtype, are not increased [95], and D<sub>3</sub> receptors are consistently down-regulated in animals and humans [30, 58, 66, 67, 73]. Yet, the supersensitivity of D<sub>1</sub> receptors is consistently observed in DA-depleted animals. Besides, it is unclear how receptor number translates into the level of signaling. In most systems, the receptor itself is not rate limiting, and activation of a small proportion of the available receptor molecules is sufficient for a full functional response. In DA null mice, dopaminergic responses are strongly supersensitive but the concentrations of DA receptors in the striatum are unaltered [76], suggesting that the signaling can be effectively regulated without modifying the receptor number. Therefore, it seems unlikely that the DA receptor supersensitivity is due to changes in the receptor availability, although some contribution from the elevated number of D<sub>2</sub> receptors cannot be completely ruled out.

Another possible mechanism that attracted considerable attention is an increase in the availability of signaling molecules downstream of the receptors, particularly G proteins. A substantial increase in the availability of G proteins should enhance G protein-mediated signaling. An increase in the concentration of G $\alpha_{olf}$  and G $\gamma_7$  was detected in the putamen of human PD patients [78] and hemiparkinsonian rats [78, 153]. The D<sub>1</sub> receptor-mediated production of cAMP is absent in G $\alpha_{olf}$  knockout mice [154], indicating that the G $\alpha_{olf}$  isoform is required for D<sub>1</sub> receptor signaling in the neostriatum. G $\alpha_{olf}$  levels are modulated by DA via D<sub>1</sub> receptors; the G $\alpha_{olf}$  concentration is elevated in D<sub>1</sub> receptor knockout mice and decreased in DA transporter knockout mice, which have elevated extracellular DA [155]. Thus, loss of DA in the parkinsonian brain should be expected to elevate the level of G $\alpha_{olf}$ . In rats and

humans, the magnitude of the increase is 50–60% [153]. Is this sufficient to produce the 4- to 5-fold greater behavioral response seen in DA null mice [76]? Hemizygous  $G\alpha_{olf}$  mice that have approximately half of the normal level of  $G\alpha_{olf}$  show a 2- to 3-fold lower locomotor response to amphetamine than wild-type mice [155], which suggests that a 50% reduction at the G protein level is translated into behavioral effects of similar magnitude. The elevation of the  $G\alpha_{olf}$  concentration seems attractive as the mechanism of the  $D_1$  receptor supersensitivity, since it is regulated by the receptor usage in the correct manner, and changes in the  $G\alpha_{olf}$  availability have been shown to have signaling and behavioral consequences. However, another study found increased DA receptor coupling to their cognate G proteins in the denervated striatum without changes in the G protein levels [77]. No changes in the expression of other signaling molecules such as PKA, protein kinase C (PKC), CaMKII, or DARPP-32 in the denervated striatum have been reported [91, 156], which leave  $G\alpha_{olf}$  as the only candidate.

Enhanced signaling via GPCRs such as DA receptors can also be achieved by suppressing the desensitization process. Upon activation by a ligand, GPCRs are phosphorylated by members of the G protein-coupled receptor kinase (GRK) family, and active phosphorylated receptors serve as preferred substrates for the binding of the uncoupling proteins arrestins (reviewed in [157]). Arrestin binding shields the cytoplasmic surface of the receptor and precludes further G protein activation. The receptors then need to be resensitized, which occurs in the endosomes upon receptor internalization. In the endosomes, the ligand dissociates, apparently causing conformational changes in the receptor protein resulting in the dissociation of arrestin. The receptor is then dephosphorylated and recycled back to the plasma membrane. If the desensitization process is suppressed or delayed, it would prolong the existence of the receptor state competent to activate G proteins and effectively enhance signaling.

A simple way to inhibit desensitization would be a reduction of the availability of arrestins and especially GRKs, since the phosphorylation step is rate limiting in the process [158, 159]. It has been demonstrated in many systems that a reduction in the availability of arrestins and GRKs inhibits receptor desensitization and facilitates GPCR signaling in cultured cells and live animals [160–167]. Specifically, the loss of the GRK6 isoform confers dopaminergic supersensitivity [163]. Analysis of the expression levels of GRK and arrestin isoforms in the hemiparkinsonian rat model demonstrated down-regulation of GRKs, but not arrestins, in the caudal striatum [118]. However, the GRK concentrations were unchanged or increased in the rostral subdivisions of the striatum. At the same time, the DA receptor supersensitivity, as measured by the responsiveness of downstream signaling pathways such as ERK and Akt, was just as strong in the rostral as in the caudal striatum [60]. Thus, the anatomical pattern of the GRK down-regulation does not match that of the DA receptor super-responsiveness, making it unlikely that the former is the sole cause of the latter. Moreover, GRK6 and arrestin2 were increased, rather than decreased, in the striatum of MPTP-lesioned monkeys [96]. No significant decrease in the concentrations of arrestins or GRKs was found in the striatum of patients with PD at postmortem [72], but it is important to remember that all patients had been treated

antemortem with dopaminergic drugs. Taken together, these data suggest that down-regulation of the components of the GPCR desensitization machinery is unlikely to be solely responsible for the DA receptor supersensitivity brought about by the loss of DA.

The arrestin- and GRK-mediated desensitization mechanism operates on many GPCRs regardless of the G proteins they couple to [157]. The  $G\alpha_i$ - or  $G\alpha_q$ -coupled GPCRs have alternative negative regulatory mechanisms responsible for the termination of signaling at the level of the G protein. Active GTP-liganded G protein  $\alpha$ -subunits self-inactivate due to their intrinsic GTPase activity. The regulators of G protein signaling (RGS) proteins are GTPase-accelerating proteins (GAPs) that negatively modulate GPCR signaling by accelerating GTP hydrolysis by  $G\alpha$  subunits [168, 169]. Most RGS proteins act as GAPs toward the  $G\alpha_{i/o}$  and some toward the  $G\alpha_{q/11}$  subfamilies of G proteins, whereas no RGS for  $G\alpha_s$  or  $G\alpha_{12}$  has been described [168]. Thus, in the striatum RGS proteins could directly regulate signaling via  $D_2$  or  $D_3$  receptors. Similarly to the arrestin- and GRK-mediated desensitization discussed above, attenuation of the RGS-mediated signal termination should lead to receptor supersensitivity. Up-regulation of RGS proteins would increase RGS availability and promote RGS-mediated attenuation of signaling, whereas a reduced concentration of RGS proteins should be expected to suppress RGS-dependent turnoff and prolong signaling.

Multiple RGS isoforms have been identified with several subtypes (RGS4, 7, 8, and 9) highly expressed in the brain [170]. The splice variant of RGS9, RGS9-2, is enriched in striatal medium spiny neurons [171, 172]. Overexpression of RGS9-2 reduces  $D_2$  receptor-mediated signaling in vitro [171, 173]. RGS9-2 expression is regulated by DA since chronic exposure to cocaine increases the level of the protein in the striatum [174]. The administration of L-DOPA or  $D_2$  antagonists, or DA depletion, alters the expression level of multiple RGS isoforms in the striatum in an isoform- and cell-specific manner [26, 175, 176]. In particular, RGS9 mRNA is decreased following DA depletion by 6-OHDA lesion or reserpine treatment [176]. Mice lacking RGS9-2 are more sensitive to dopaminergic stimulation [173, 174]. Conversely, viral overexpression of RGS9-2 reduces locomotor responses to  $D_2$ , but not to  $D_1$ , agonists [174]. Thus, the modulation of RGS9-2 availability by DA depletion appears to be a good candidate mechanism for the supersensitivity of  $D_2$  receptors. However, no changes in the expression of RGS9-2 were found in the MPTP monkey model of PD [177]. RGS9 was up-regulated in the striatum of PD patients at postmortem [178], but this could be the result of long-term dopaminergic treatment. Thus, we must conclude that if the RGS-mediated modulation of the  $D_2$  receptor signaling is involved in the supersensitivity of  $D_2$  receptors caused by DA depletion, it does not require changes in the RGS9-2 expression level.

To summarize, multiple alterations in striatal signaling mechanisms caused by the loss of DA have been described (Fig. 18.2 and 18.3). However, so far no coherent model of the molecular mechanisms responsible for the lesion-induced supersensitivity of DA receptors has been developed. The up-regulation of G proteins, leading to enhanced cAMP production, seems the most promising mechanism

for the D<sub>1</sub> receptor supersensitivity. This augmentation of the signal transduction at the G protein level can then be propagated to other cAMP-dependent mechanisms and, via various feedback loops, to cAMP-independent mechanisms, finally resulting in strong enhancement of behavioral responses to dopaminergic drugs. However, no analogous mechanism has been proposed for the D<sub>2</sub> receptor. It is equally unclear what molecular mechanism mediates the changes in the transcription of proteins caused by dopaminergic denervation. Changes in the mechanism of transcriptional control have been observed in the DA-depleted striatum. The up-regulation of specific  $\Delta$ FosB proteins (43 and 45 kD) is induced by DA depletion in striatopallidal neurons, resulting in a corresponding increase in AP-1-binding activity [179], suggesting that these transcription factors may mediate some of the changes in gene expression observed in striatopallidal neurons following the loss of DA. Since the same Fos proteins are selectively elevated by chronic administration of the selective D<sub>2</sub> antagonist haloperidol [180], this up-regulation appears to be mediated by the reduced activity of D<sub>2</sub> receptors. Paradoxically, no change in transcriptional activity has so far been found in nigrostriatal D<sub>2</sub> receptor-bearing neurons.

The success of studies aimed at identifying the molecular mechanisms of signaling alterations caused by DA depletion will be largely determined by the sensitivity and spatial resolution of experimental methods. A global measurement of the expression of any signaling protein in the whole striatum could easily miss a dramatic change in a small subpopulation of striatal neurons. However, the detection of changes restricted to specific neuronal populations is challenging. Neurons are highly compartmentalized cells with elaborate geometry, where a significant change in the local concentration of a particular protein could be achieved without an overall change of expression. It is evident that subcellular localization of the proteins, their intracellular trafficking, and dynamic recruitment to specific cellular compartments have high functional significance, and yet all these events are difficult to observe experimentally. Finally, simultaneous modest increases of the receptor, G protein, and effector expression (each being below the level of reliable detection) in conjunction with a moderate decrease in the rates of signal termination at the receptor and G protein level could yield a dramatic manifold increase in signaling.

## **18.2 DA Receptors and Treatment of the Motor Symptoms of Parkinson's Disease**

### ***18.2.1 Dopamine Replacement Therapy and the Pathophysiology of L-DOPA-Induced Dyskinesia***

Patients with PD are treated with the dopamine precursor L-DOPA with the goal of restoring lost DA. L-DOPA is normally produced from the amino acid tyrosine via hydroxylation by the enzyme tyrosine hydroxylase in dopaminergic and noradrenergic neurons. Exogenous L-DOPA bypasses this step and is converted to DA

by L-aromatic acid decarboxylase. L-DOPA was first introduced as a treatment for PD in the early 1960s [181], but remains the best available drug even today. L-DOPA is normally administered in combination with peripheral inhibitors of DOPA decarboxylase such as carbidopa or benzerazide to prevent peripheral conversion of L-DOPA to DA. In the brain, L-DOPA is converted into DA, and the newly produced DA acts at DA receptors, thereby restoring the balance within the striatal circuitry upset by the loss of endogenous DA. Acutely administered L-DOPA quickly restores movement in human PD patients and experimental animals. L-DOPA is a short-lived drug (half-life ~90 min). Therefore, repeated administration of L-DOPA results in surges of newly synthesized DA, stimulating DA receptors in a non-physiological pulsatile manner. In PD patients at early stages of the disease, the antiparkinsonian effect of acute L-DOPA lasts substantially longer than the L-DOPA life in the body, probably due to accumulation of DA in the synaptic vesicles of the surviving dopaminergic neurons. This storage process likely smoothes out the DA surges, producing a more physiological pattern of dopaminergic stimulation. L-DOPA therapy is remarkably efficacious at early stages of PD, but becomes less and less so as the disease progresses, necessitating higher L-DOPA doses to achieve adequate antiparkinsonian effect [182]. This is probably due to the continuing degeneration of dopaminergic neurons in PD patients, which increases the demand for DA and reduces the storage capacity for DA produced from exogenous L-DOPA. Moreover, multiple motor complications emerge within 5–7 years of L-DOPA treatment, such as motor fluctuations (on-off fluctuations, wearing off, delayed or no “on” response) and dyskinesia [182]. Since DA acts at all DA receptors, L-DOPA behaves as a non-selective agonist acting primarily through the most abundant D<sub>1</sub>, D<sub>2</sub>, and D<sub>3</sub> striatal receptors. It is important to bear in mind that an antiparkinsonian effect is produced by selective D<sub>1</sub> as well as D<sub>2</sub>/D<sub>3</sub> agonists in humans and animals [183–188], although L-DOPA remains the most effective antiparkinsonian therapy [189].

L-DOPA-induced dyskinesia (LID) is a debilitating condition characterized by involuntary purposeless movements involving the limbs, trunk, or face. The most common forms of LID are peak-dose dyskinesia, diphasic dyskinesia, and off-period dystonia. Peak-dose dyskinesia occurs at the peak plasma level of L-DOPA, diphasic dyskinesia correlates with the rise and fall of the L-DOPA plasma level, and off-period dystonia correlates with the akinesia that precedes the L-DOPA effect [190]. These forms are not mutually exclusive and can occur in the same patient. Since peak-dose dyskinesia is the easiest to reproduce in animal models, most of the mechanistic data available apply to this form of LID. LID poses a significant clinical challenge, since, as the disease progresses, it becomes increasingly difficult or impossible to produce adequate antiparkinsonian effects without triggering dyskinesia [191].

The neural mechanisms of LID remain obscure. The pathophysiological model of PD posits that akinesia is the result of excessive inhibition of the cortico-thalamic loop by the striatum. DA depletion shifts the balance within the striatal circuitry in favor of the indirect pathway, which is a negative feedback mechanism, causing hyperactivity of the striatal output nuclei and enhanced net inhibitory striatal output

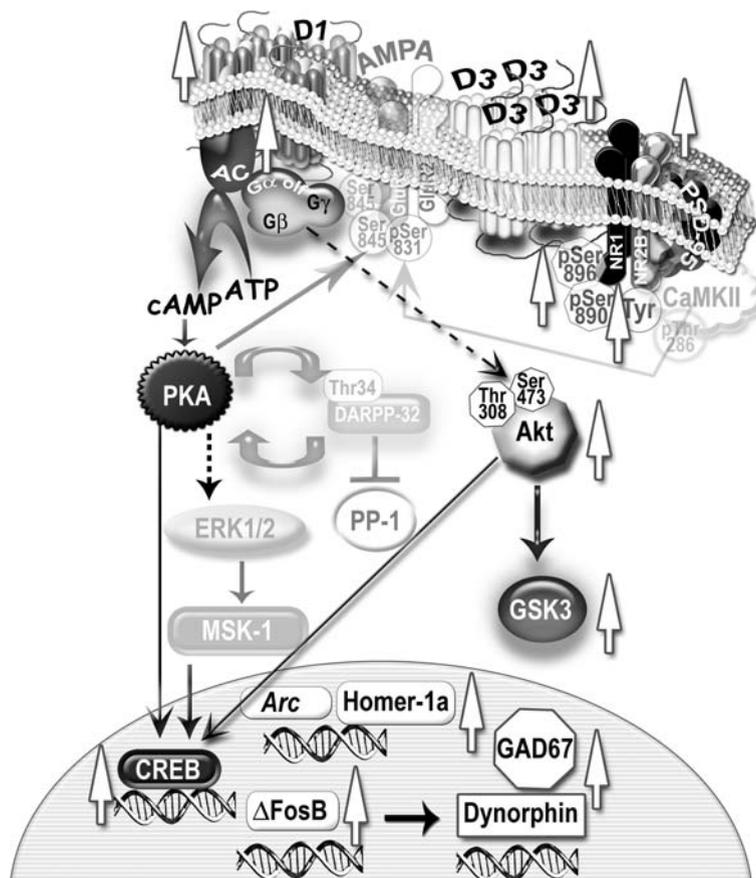
to the thalamus [1]. L-DOPA produces its antiparkinsonian effect via restoration of normal dopaminergic control over the striatal circuitry, which reduces the overall inhibitory striatal output and relieves the inhibition of the motor cortical activity, making movement possible. At first, based on studies of hyperkinetic disorders such as Huntington's disease and ballism, LID was considered a simple reversal of the parkinsonian condition; strong stimulation of DA receptors by DA produced from L-DOPA reduces the striatal output too much by facilitating transmission via the direct pathway at the expense of the indirect pathway [192, 193]. The lack of proper striatal inhibitory control disinhibits the motor cortex, causing hyperactivation and dyskinetic movements. Whereas the model of PD is well supported by the experimental data and is remarkably successful as a heuristic tool, the model of LID is much less satisfactory in this regard. The experimental support for the key prediction of the model, hypoactivity of the gateway structure of the striatal circuit, the globus pallidus internal, was never strong. The final blow to the model was dealt by the discovery that the ablation of the globus pallidus internal alleviates both parkinsonian symptoms (where it is hyperactive) and dyskinesia, where this nucleus, according to the model, is supposed to be hypoactive [190]. This result suggests that the difference between the parkinsonian and dyskinetic states is not a simple opposition between high (parkinsonian) and low (dyskinetic) output of the striatal circuit, but likely involves complex alterations of activity patterns throughout the striatal system.

### ***18.2.2 The Effects of L-DOPA Treatment on Dopaminergic Signaling***

The evidence seems to indicate that in the normal striatum DA serves to dampen signaling and behavioral responses to itself via some sort of desensitization mechanism. When this endogenous check is removed in PD, the responsiveness greatly increases. Can this supersensitivity be reversed by the application of dopaminergic stimulation to mimic the action of endogenous DA? Most importantly, does L-DOPA suppress supersensitive responses? The answer is yes and no.

#### **18.2.2.1 Signaling Consequences of Dopamine Depletion Normalized by L-DOPA**

L-DOPA certainly suppresses the supersensitivity of some signaling pathways (Fig. 18.4). In human PD patients and animal models of PD, L-DOPA reverses the denervation-induced up-regulation of D<sub>2</sub> receptors [47, 51, 52, 54, 60–62], supporting the explanation that this up-regulation is caused by the loss of DA. In DA null mice, chronic L-DOPA treatment eliminates exaggerated locomotor, *c-fos*, and ERK responses [76, 194]. L-DOPA also reverses the increase in the G<sub>α<sub>olf</sub></sub> concentration in hemiparkinsonian rats [78]. Similarly, the supersensitivity of the ERK pathway is reversed by L-DOPA in both 6-OHDA-lesioned rats and MPTP-lesioned monkeys [60, 96], as is the exaggerated basal phosphorylation of CaMKII [91, 109]



**Fig. 18.4 Signaling mechanisms of L-DOPA-induced dyskinesia.** Most proposed mechanisms of LID pertain to  $D_1$  receptor-mediated signaling. Chronic L-DOPA treatment reverses the denervation-induced supersensitivity of several signaling pathways (shown *dimmed*). *Short open arrows* facing up indicate the L-DOPA-induced augmentation of the expression or activity/phosphorylation of proteins beyond the pre-lesion level. The open arrow between adenylyl cyclase (AC) and  $G_{\alpha_{olf}}$  indicates increased coupling of  $D_1$  receptors to  $G_{\alpha_{olf}}$ . Note that increased Akt-mediated phosphorylation of GSK3 translates into decreased activity of the enzyme. *Solid arrows* denote known stimulatory connections in signaling pathways; *dashed arrows* indicate hypothetical connections

and DARPP-32 at Thr75 [91]. The lesion-induced super-responsiveness of many IEGs (*c-fos*, *junB*, *junD*, *c-Jun*) is reversed or at least significantly ameliorated by chronic L-DOPA administration [100, 101, 180]. L-DOPA also reverses the supersensitivity of presynaptic  $D_2$  receptors on corticostriatal terminals and the resulting glutamatergic hyperactivity in the striatum [135]. However, the exact functional role of the signaling changes observed in the DA-deprived striatum in the motor deficits caused by the loss of DA is unclear. Equally, it is not known whether the

reversal of these changes by L-DOPA plays a role in its therapeutic activity. The hyper-phosphorylation of CaMKII seems to be involved in the lesion-induced motor abnormalities, since intrastriatal administration of a selective CaMKII inhibitor rescues the motor performance in 6-OHDA-lesioned rats [109], thus mimicking the action of L-DOPA. It is possible that other effects are also part of the molecular mechanisms responsible for the therapeutic antiparkinsonian activity of L-DOPA, but their exact roles remain to be determined.

#### **18.2.2.2 Molecular Consequences of Dopamine Depletion Unchanged or Augmented by L-DOPA**

L-DOPA does not reverse the up-regulation of enkephalin induced by the dopaminergic lesion in hemiparkinsonian rats and MPTP-lesioned monkeys [60, 137, 139–141, 195, 196], and may even enhance enkephalin expression in the 6-OHDA-lesioned rat, MPTP-lesioned monkey, and human dyskinetic PD patients [138, 141, 197]. Neither the L-DOPA nor the long-lived DA agonist pergolide is successful in reversing the effect of DA depletion on the expression of arrestins and GRKs in the 6-OHDA-lesioned rat [118]. On the other hand, in MPTP-lesioned monkeys L-DOPA actually reverses the up-regulation of arrestin2 and GRK6 caused by the lesion [96]. Apparently, some alterations in signaling mechanisms induced by the loss of DA are permanent and, once developed, cannot be reversed by DA. It is also possible that the dose, duration of treatment, or administration mode used is inadequate to produce the reversal in some cases.

It stands to reason that the molecular aberrations caused by DA loss that are not reversed by the therapeutically active mode of L-DOPA administration likely underlie L-DOPA-induced motor fluctuations. Importantly, L-DOPA exaggerates some of the abnormalities in dopaminergic signaling in the striatum caused by DA depletion and/or induces *de novo* signaling perturbations beyond those already present due to DA depletion (Fig. 18.4). Acute L-DOPA administration induces contralateral rotations in hemiparkinsonian rats. Chronic L-DOPA treatment leads to a progressive increase in the frequency of the rotations [60, 66, 67, 118, 144], the phenomenon termed behavioral sensitization to L-DOPA.

At the molecular level, the down-regulation of D<sub>3</sub> receptors and dynorphin caused by DA depletion in hemiparkinsonian rats are reversible by L-DOPA, but in the course of chronic treatment both increase substantially beyond the pre-lesion level [60, 65–67, 137, 198]. Chronic L-DOPA also aggravates the lesion-induced hyper-phosphorylation of CREB in response to dopaminergic challenge [105]. Our data also demonstrate that the Akt-GSK3 pathway in the lesioned rat striatum is supersensitive to dopaminergic stimulation but shows little or no change in basal activity [60]. Chronic L-DOPA enhances the basal constitutive activity of the pathway to a level that is even higher than that induced by acute dopaminergic stimulation in drug-naïve hemiparkinsonian rats, and this level is no longer increased by dopaminergic stimulation. In the normal striatum, the Akt-GSK3 pathway is under the negative influence of DA acting via D<sub>2</sub> and D<sub>3</sub> receptors [199, 200]. It appears that the loss of DA brings forward a different, positive, mode of Akt regulation by

DA, which may be  $D_1$  receptor mediated.  $G\alpha_q$  and  $G\alpha_s$ -coupled receptors can activate Akt via  $Ca^{2+}$  or other second messengers [201]. The  $D_1$  receptor can couple to  $G\alpha_{q/11}$  [202]. DA can activate Akt via  $D_1$  receptors in a phosphoinositide-3-kinase-independent manner, possibly involving ERK1/2. Loss of Akt activation impairs phosphorylation of CREB [203]. Thus, in the lesioned and L-DOPA-treated striatum, persistent Akt activation may contribute to the persistent phosphorylation of CREB.

L-DOPA-induced perturbation of the glutamatergic and GABAergic transmission may play a role in LID. L-DOPA treatment increases the expression of GAD67 and vesicular GABA transporter in striatonigral neurons and the release of GABA in the substantia nigra reticulata [122, 124, 204, 205], indicative of hyperactivity of the direct striatonigral pathway. L-DOPA reverses the down-regulation of NMDA receptor subunits seen in parkinsonian monkeys and causes excessive expression of selected subunits in dyskinetic monkeys and PD patients [113, 206, 207]. L-DOPA also causes exaggerated tyrosine phosphorylation of  $NR_2$  [112, 115, 117] and serine phosphorylation of  $NR_1$  [112] subunits that correlate with L-DOPA-induced sensitization. The  $D_1$  receptor regulates the subcellular trafficking of the NMDA receptor, and its activation rapidly recruits the NMDA receptor, with the  $NR_{2A}$  and  $NR_{2B}$  subunits phosphorylated at tyrosines, to the synaptic membrane [208–210]. Loss of protein kinase Fyn abolishes tyrosine phosphorylation, the  $D_1$  receptor-mediated membrane recruitment of the NMDA receptor, and behavioral sensitization to L-DOPA (the interpretation of that result is equivocal because of less extensive DA depletion in Fyn null mice) [209]. Interestingly, the  $NR_2$  subunit tyrosine phosphorylation is DARPP-32 independent [209]. Thus, tyrosine phosphorylation of the NMDA receptor subunits and  $D_1$ -induced synaptic recruitment may play an important role in the development of LID.

### 18.2.2.3 Effects of L-DOPA in “Dyskinetic” Versus “Non-dyskinetic” Animal

The data cited above are based on effects detected in the entire population of animals treated chronically with L-DOPA. The importance of these signaling effects for LID is supported by their development over time in parallel with behavioral sensitization to L-DOPA. However, when people or animals are treated with L-DOPA, their response to the drug varies substantially. Between 40 and 80% of PD patients, according to different estimates, develop dyskinesia within 5 years of treatment, but some develop it earlier and some later [211]. Similarly, MPTP-lesioned monkeys treated with L-DOPA develop dyskinesia at individual rates [30, 96]. Hemiparkinsonian rats demonstrate different rotation frequencies following the first L-DOPA administration and the individual propensity for behavioral sensitization to L-DOPA varies widely [125, 212]. In addition to rotations, hemiparkinsonian rats show abnormal involuntary movements (AIMs) of the limbs, tongue, jaw, and trunk that have been proposed to model human LID with better fidelity than behavioral sensitization [213]. Rats show remarkably different propensities to develop AIMs in response to L-DOPA. Thus, parkinsonian animals, rodents and primates, can be classified into “dyskinetic” and “non-dyskinetic” categories based on the presence

of AIMS. It should be noted that, since the probability of dyskinesia is roughly proportional to the L-DOPA dose and duration of treatment (cumulative dose) [125], dyskinesia is inducible in “non-dyskinetic” animals by a higher dose or longer treatment. Therefore, this classification simply describes the situation at a given moment in the treatment schedule. Nonetheless, to elucidate the molecular mechanisms underlying dyskinesia, it is still important to explore signaling alterations that are present in overtly dyskinetic individuals, but absent in non-dyskinetic subjects (Fig. 18.4). Another possible approach would be to correlate the severity of dyskinesia (e.g., AIMS scores) with the level of expression or activation of signaling proteins and/or pathways.

Importantly, in some studies the distinction between “dyskinetic” and “non-dyskinetic” animals has no apparent correlation with the degree of DA depletion [214–216]. However, since experimental animals in those studies usually had extensive loss of DA, it is possible that above a certain level, individual differences in the degree of DA depletion no longer matter. It is a well-established fact that in human PD patients the risk of dyskinesia increases with the disease severity [217, 218]. When a wider range of DA depletion is considered in animal models, it is also found that the propensity to LID is proportionate to the degree of DA loss [216, 219].

Using this experimental approach, it has been determined that the level of D<sub>1</sub> receptor supersensitivity (measured by D<sub>1</sub> agonist-stimulated GTP $\gamma$ S binding to striatal sections) induced by loss of DA is further enhanced in dyskinetic MPTP-lesioned monkeys as compared to L-DOPA-naïve MPTP monkeys, whereas in non-dyskinetic animals L-DOPA reverses the supersensitivity [95]. The level of D<sub>1</sub> receptor supersensitivity in these animals correlates positively with the severity of LID and is accompanied by increased expression of DARPP-32 and cdk5 [95]. In dyskinetic monkeys, the expression of the D<sub>3</sub> DA receptor is dramatically increased, whereas the receptor was down-regulated by the MPTP lesion and restored to the normal level in non-dyskinetic animals [30]. Moreover, a partial D<sub>3</sub> agonist significantly ameliorates dyskinesia without reducing the antiparkinsonian effect of L-DOPA. These data suggest that in some individuals (eventually in all) the supersensitivity of DA receptors is not reversed or is even aggravated by L-DOPA and that leads to LID.

Supersensitive DA receptors convey signaling to downstream signaling pathways that are also selectively enhanced in “dyskinetic” animals (Fig. 18.4). The up-regulation of G $\alpha_{olf}$  is reversed by L-DOPA in hemiparkinsonian rats, but it is detectable in human PD patients in spite of decades of dopaminergic therapy, with the highest levels seen in patients with severe antemortem dyskinesia [78]. Although hyper-phosphorylation of DARPP-32 by PKA (at Thr34) is generally reduced by chronic L-DOPA treatment, it persists in 6-OHDA-lesioned mice and rats with a high frequency of AIMS [85, 120]. Moreover, the level of DARPP-32 phosphorylation positively correlates with the AIMS scores. Conversely, AIMS are attenuated in DARPP-32 knockout mice [85]. These data suggest that the failure of L-DOPA to suppress the DARPP-32 hyper-phosphorylation induced by DA loss contributes substantially to the induction of LID, possibly by virtue of maintaining the lesion-induced supersensitivity of D<sub>1</sub> receptors.

Hyper-phosphorylation of ERK1/2 proportional to the AIM frequency was observed in “dyskinetic” mice [85, 220] and rats [93]. The suppression of AIMs in DARPP-32 knockout mice was accompanied by reduced phosphorylation of ERK1/2 [85], suggesting that ERK1/2 activation is PKA mediated. Furthermore, direct blockade of ERK1/2 phosphorylation also reduced AIMs [85]. However, we found that the elevated level of ERK1/2 phosphorylation and expression was reversed by L-DOPA treatment in both “dyskinetic” and “non-dyskinetic” MPTP-lesioned monkeys [96]. We also found that both the L-DOPA and the D<sub>2</sub> agonist pergolide suppress the lesion-induced supersensitive ERK1/2 response equally well, in spite of their different ability to produce behavioral sensitization [60]. Lesion-induced supersensitive phosphorylation of the GluR<sub>1</sub> subunit of the AMPA receptor is also attenuated by chronic L-DOPA to a lesser degree in “dyskinetic” versus “non-dyskinetic” hemiparkinsonian rats [85]. These data implicate the enhanced responsiveness of the D<sub>1</sub> receptor-PKA pathway in LID (Fig. 18.4).

L-DOPA-induced abnormalities in NMDA receptor-mediated transmission develop (or, at least, appear to be more severe) in dyskinetic animals. Dyskinetic animals have higher synaptic availability of the NR<sub>2A</sub> [113, 116] and lower availability of the NR<sub>2B</sub> subunit than L-DOPA-treated non-dyskinetic animals [114, 116]. Since the D<sub>1</sub> receptor has been implicated in the control of NMDA receptor trafficking [209, 210], these changes are likely mediated by overactive D<sub>1</sub> signaling. The importance of mislocalization of the NR<sub>2B</sub> subunit for dyskinesia is highlighted by the fact that artificial disruption of the NR<sub>2B</sub> interaction with proteins in the postsynaptic density induces AIMs in non-dyskinetic rats [116]. The redistribution of NMDA receptors between the synaptic and the extrasynaptic compartments, in addition to changes in the subunit composition, may have important functional consequences. The signaling of synaptic and extrasynaptic NMDA receptors is different; calcium entry through synaptic NMDA receptors enhances CREB activation and CREB-dependent gene expression, whereas activation of extrasynaptic NMDA receptors suppresses CREB activity [221]. The exact nature and functional consequences of modifications in the expression, composition, trafficking, and signaling of NMDA receptors in LID are still poorly understood. NMDA antagonists generally ameliorate LID, and the noncompetitive NMDA antagonist amantadine is the only drug proven effective against LID in clinical practice [190]. This suggests that elevated activity of NMDA receptors, possibly the NR<sub>2B</sub>-containing receptors in the “wrong” non-synaptic compartments, induced by intermittent stimulation of D<sub>1</sub> receptors may be critical for LID development.

#### **18.2.2.4 Effects of L-DOPA on Immediate Early Genes and Transcription Factors**

The supersensitive activation in the DA-depleted striatum of some members of the Fos and Jun gene families such as c-Fos, JunB, c-Jun, and JunD is reduced by chronic treatment with L-DOPA [100–102, 183], although it takes a fairly prolonged treatment to substantially downregulate the response. For example, 5-day

treatment with 10 mg/kg/day of L-DOPA does not perceptibly reduce the supersensitive response in the DA-depleted striatum in unilaterally 6-OHDA-lesioned rats or common marmosets [97].

Some members of the Fos family are longer lived than immediate early gene types such as c-Fos. The 35 and 37 kDa isoforms of the  $\Delta$ FosB protein are not induced or are induced only slightly by acute stimulation but slowly accumulate in response to chronic stimuli and persist in the brain longer than other Fos proteins (weeks to months) [180]. These proteins are induced by an incredible variety of stimuli, including drugs of abuse, antipsychotics, some forms of antidepressant treatment, stress, etc. [180]. The expression of  $\Delta$ FosB isoforms is induced in the DA-depleted striatum by acute and is further promoted by chronic treatment with L-DOPA, with the 35 and 37 kDa isoforms being the most affected by chronic L-DOPA [93, 101, 102, 179, 212, 220]. Moreover,  $\Delta$ FosB proteins are found in the striatum of PD patients at postmortem and in MPTP-lesioned monkeys, and the levels of expression correlate with the degree of DA depletion and symptoms of dyskinesia [178, 179]. The severity of AIMs in the rodent model of PD correlates with the  $\Delta$ FosB expression [222]. The inhibition of  $\Delta$ FosB accumulation by the infusion of  $\Delta$ FosB antisense oligonucleotides into the striatum reduces the severity of dyskinesia in hemiparkinsonian rats [222, 223]. The accumulation of  $\Delta$ FosB occurs in dynorphin-expressing striatonigral neurons, and overexpression of dynorphin upon chronic L-DOPA treatment correlates well with dyskinesia scores [205, 222]. The DARPP-32-based amplification loop may be involved in the  $\Delta$ FosB accumulation, since removal of DARPP-32 attenuates the  $\Delta$ FosB buildup induced by dopaminergic stimulation [224, 225].

The accumulation of  $\Delta$ FosB during L-DOPA treatment may contribute to changes in the expression of proteins controlled by  $\Delta$ FosB-responsive promoters [180]. In particular,  $\Delta$ FosB regulates the expression of dynorphin [223], and dynorphin overexpression induced by L-DOPA in the lesioned striatum correlates well with indices of LID [60, 205, 212, 223]. However, the exact functional role of the  $\Delta$ FosB accumulation in LID remains unclear. From the data on LID, it seems that the  $\Delta$ FosB-mediated transcription acts as the positive feedback in the L-DOPA signaling. At the same time,  $\Delta$ FosB knockout mice have no cocaine-induced accumulation of the  $\Delta$ FosB 35 and 37 kDa isoforms, but demonstrate enhanced responsiveness to cocaine (place preference, locomotion), which suggests that  $\Delta$ FosB accumulation functions as a *negative*, rather than positive, feedback in the dopaminergic signaling [226]. However, virus-mediated overexpression of  $\Delta$ FosB in the nucleus accumbens sensitizes the animals to the locomotor and rewarding effects of cocaine [227]. To reconcile these data, it has been suggested that  $\Delta$ FosB, which is induced by chronic cocaine treatment, is responsible for the long-term increase in sensitivity [227], whereas loss of  $\Delta$ FosB results in a short-term increase in sensitivity but precludes sensitization to repeated treatment.

The L-DOPA-induced elevation of the expression of activity regulated cytoskeletal-associated (*Arc*) and *Homer-1a* genes shows a very similar pattern to that of dynorphin, being more prominent in dyskinetic than in non-dyskinetic rats [212]. The basal level of expression of these genes was not altered by the

DA depletion but increased with L-DOPA treatment, more substantially so in rats that developed AIMs. The up-regulation of *Arc* is largely restricted to dynorphin-expressing neurons, suggesting that this is a downstream effect of the D1 receptor activation. The exact function of the protein product of the *Arc* gene, Arc (also referred to as *activity regulated gene 3.1 protein homolog*, Arg3.1), is incompletely understood, but its enrichment in dendrites and recruitment to dendritic synaptic regions upon stimulation [228] suggests its involvement in synaptic plasticity. Recently, the Arc protein has been reported to regulate trafficking of the AMPA glutamate receptor by promoting its activity-dependent endocytosis [228, 229]. Overexpression of Arc reduces the AMPA receptor surface expression and AMPA-dependent synaptic transmission, whereas Arc knockout enhanced both [230, 231]. Thus, the up-regulation of Arc in dyskinetic animals may actually promote the reduction of AMPA activity, which is enhanced in LID, as evidenced by the antidyskinetic efficacy of AMPA antagonists [190, 232].

Homer proteins are part of postsynaptic densities and are involved in regulating the functions of metabotropic glutamate receptors [233]. The short Homer-1a isoform is rapidly induced by neuronal stimulation and acts as a negative regulator of the signaling via mGluR<sub>1/5</sub> metabotropic glutamate receptors [233, 234]. Transgenic mice expressing Homer-1a in striatal neurons are akinetic with impaired performance in motor tasks [235], which is similar to the parkinsonian phenotype. Interestingly, mice that express Homer-1a in the striosome striatal compartment (but not in the matrix) show behavioral and molecular supersensitivity to amphetamine [235], which is consistent with peak-dose dyskinesia. The striosome–matrix organization of the striatum has been identified based on differential staining with neurochemical markers and connectivity [236]. The striosomes (patches) have high density of  $\mu$ -opioid receptor but low calbindin immunoreactivity and receive dopaminergic projections mostly from the dorsal tier of the substantia nigra pars compacta. In contrast, matrix is innervated largely by the ventral tier [236, 237], although this innervation topography is less evident in primates than in rodents [238]. The functional role of the striosome–matrix dichotomy in PD and LID remains almost completely unexplored. Interestingly, apomorphine- or L-DOPA-induced expression of c-Fos and FosB in the DA-depleted striatum, which is uniform after acute injection, concentrates in the striosomes upon chronic administration [101, 239]. Thus, this limited evidence points to a special importance of the striosomal compartment in LID.

Such paradoxical effects of L-DOPA of the type that upset the balance in DA receptor signaling instead of restoring it may be responsible for the L-DOPA side effects, including LID. Interestingly, in DA null mice, even low concentrations of L-DOPA restore normal feeding behavior and suppress supersensitive behavioral and molecular responses without noticeable paradoxical effects. The difference between these mice and parkinsonian animals or humans is that the mice have intact dopaminergic neurons and terminals that are capable of packaging and releasing DA in the appropriately regulated manner. In contrast, in the parkinsonian brain, dopaminergic neurons are reduced in number or are no longer present, and complete, functionally appropriate restoration of the DA signaling is not possible.

## ***18.2.3 Dopamine Agonists in the Treatment of Parkinson's Disease***

### **18.2.3.1 Dyskinesia-Inducing Properties of DA Agonists**

It has been established that both D<sub>1</sub>- and D<sub>2</sub>/D<sub>3</sub>-selective agonists produce antiparkinsonian effects in experimental animals and human patients [184, 185, 240–242]. Similarly, both classes of drugs produce dyskinesia, although their propensity to do so is a complex function of the pharmacological profile and pharmacokinetic properties. One of the important features of L-DOPA is its short life (90 min half-life in the body), resulting in rapid changes in the DA concentration in the DA-depleted striatum following L-DOPA administration. Short-lived non-selective DA and selective D<sub>1</sub> or D<sub>2</sub>/D<sub>3</sub> agonists induce LID in humans and motor complications in animals [184, 186, 243]. Whether DA agonists have the same dyskinesic potential as L-DOPA is a matter of some controversy. Several studies reported that in therapeutically effective doses short-lived DA agonists induce the same level of dyskinesia as L-DOPA [184, 185, 244], whereas others found DA agonists less prone to induce dyskinesia than L-DOPA regardless of their properties [187, 245]. The data regarding the propensity of D<sub>1</sub>/D<sub>5</sub> or D<sub>2</sub>/D<sub>3</sub> selective agonists to induce dyskinesia is also highly controversial, with some studies favoring D<sub>1</sub>-targeting agonist [246, 247] and some D<sub>2</sub>-targeting agonists [183, 248]. The comparison is not easy to make due to differences in pharmacokinetic properties of the drugs and the higher propensity of D<sub>1</sub> agonists to induce tolerance [183, 249, 250]. It is often reported that in animal models D<sub>1</sub> antagonists block behavioral sensitization to L-DOPA [66, 67], although they may just reduce the absolute rotation frequency rather than block the sensitization process per se [145]. Agonists selective for the D<sub>2</sub> receptor are able to induce behavioral sensitization [60, 247].

A number of longer-lived DA agonists proved to possess antiparkinsonian properties combined with a lower propensity to induce dyskinesia. Many such drugs are now used in clinical practice, and their clinical and chemical properties have been extensively reviewed [240–242]. Their half-life ranges from 6 h (bromocriptine) to 76–100 h (cabergoline). All clinically used DA agonists are D<sub>2</sub>/D<sub>3</sub> selective. Importantly, DA agonists that have a lower propensity to induce dyskinesia also demonstrate lower antiparkinsonian efficacy than L-DOPA. Most are currently used for treatment of early PD with the aim of delaying the introduction of L-DOPA, but eventually all PD patients require L-DOPA to achieve adequate antiparkinsonian effects [241, 251, 252]. The importance of long half-life for reduced dyskinesic potential is best supported by the data that continuous infusion of the same drug (L-DOPA, apomorphine, etc.) causes less dyskinesia than intermittent administration [253, 254].

The long-lived DA agonists, in contrast to L-DOPA, cause minimal behavioral sensitization and a smaller increase in rotation frequency upon repeated administration [60, 118, 125], and they do not induce AIMs [125]. Short-lived agonists such as apomorphine induce behavioral sensitization and AIMs similarly to L-DOPA [137, 247]. Long-lived DA agonists do not induce some of the signaling effects characteristic of L-DOPA, such as up-regulation of dynorphin [60, 138, 142, 196, 255],

substance P [195, 196], or D<sub>3</sub> receptors [60] in the lesioned striatum. We showed that the clinically effective DA agonist pergolide (half-life ~21 h), in contrast to L-DOPA, does not induce constitutive activity of the Akt pathway [60]. The long-lived D<sub>2</sub> agonist cabergoline does not up-regulate  $\Delta$ FosB in MPTP-lesioned monkeys, but instead reverses the up-regulation of the basal level of  $\Delta$ FosB induced by the lesion [179]. The DA agonists also reverse the lesion-induced up-regulation of enkephalin [60, 138, 141, 195, 196], which is not reversed by L-DOPA. In our experiments, pergolide was more successful than L-DOPA in normalizing the expression of GRKs altered by the dopaminergic lesion [118]. The fact that these signaling changes correlate with the presence or absence of dyskinesia argues for their role in LID. The continuous administration of L-DOPA via pump also does not produce LID in PD patients [252, 254] or animal models of PD [67]. Thus, long-lived DA agonists do not, as a rule, exaggerate the signaling effects produced by DA depletion or induce them de novo. They are often capable of reversing those effects of the DA depletion that are not normalized by L-DOPA. These properties might be related to their lower propensity to induce dyskinesia in humans and experimental animals, but the exact signaling mechanisms remain to be elucidated.

### 18.2.3.2 Why Are Clinically Used DA Agonists Less Efficacious than L-DOPA?

One possibility is that they target only D<sub>2</sub>/D<sub>3</sub> receptors, whereas L-DOPA obviously targets all DA receptor subtypes. The dysfunctions of the D<sub>1</sub> receptor-mediated signaling in the DA-depleted striatum are well documented. Thus, the exclusion of D<sub>1</sub> receptors may reduce the efficacy of these drugs. The mixed D<sub>3</sub>/D<sub>2</sub>/D<sub>1</sub> agonist rotigotine has recently been shown to be effective in animal models and early [256] and advanced PD [257], although its signaling effects are yet to be explored. The synergism of the D<sub>1</sub>/D<sub>2</sub> activity in the striatum and the ability of D<sub>1</sub> and D<sub>2</sub> drugs to prime for each other (discussed in Section 18.1.3) suggest that the absence of D<sub>1</sub> action is likely to reduce the amplitude of the responses elicited by DA agonists, as well as limit the cells and brain regions involved.

Another possibility is that the same property of these drugs that ensures their lower propensity to cause dyskinesia, i.e., longer life, also contributes to their lower efficacy. Continuous receptor stimulation often reduces responses to subsequent stimuli, a phenomenon known as tolerance. Long-lived or short-lived continuously administered DA agonists induce behavioral tolerance in parkinsonian animals [59, 250, 258]. GPCRs desensitize upon continuous stimulation via GRK-mediated phosphorylation followed by arrestin binding, which uncouples the receptor from G proteins and precludes further signal transduction. The receptor is then internalized into the endosomes and needs to be relieved of arrestin and dephosphorylated before it can be recycled to the plasma membrane and reused [157]. If the stimulation persists, the receptor is sent to the lysosomes and degraded, which down-regulates the available cell surface receptors. DA agonists may differ from L-DOPA in the way they engage the receptor desensitization machinery.

The homologous desensitization system is aimed at rapid termination of the signaling to ensure high temporal resolution. It is specifically designed to allow the cell to ignore persistent background stimulation to ensure high sensitivity to changing stimuli. Thus, longer-lived DA agonists are likely to induce more pronounced receptor desensitization, internalization, and down-regulation than short-lived drugs such as L-DOPA.

There are reports that DA agonists down-regulate D<sub>2</sub> receptors in the striatum of PD patients more effectively than L-DOPA [259, 260]. In live animals, it is difficult to detect desensitization because it is a rapid process with minute kinetics, and internalization can only be seen at the resolution of electron microscopy. Down-regulation, however, can be easily detected by receptor-binding techniques, and overall inhibition of signaling can also be easily documented. Increased cytoplasmic localization of D<sub>1</sub> receptors has been found at postmortem in the putamen of PD patients chronically treated with L-DOPA [261], possibly indicative of increased internalization. It is impossible to establish whether this is indeed so from this type of experiment, but if it is, it means that L-DOPA promotes receptor desensitization, which makes sense. However, studies in MPTP-treated monkeys demonstrated increased recruitment of D<sub>1</sub> receptors to the plasma membrane both in drug-naïve MPTP-lesioned and in L-DOPA-treated dyskinetic animals [262], suggesting a *deficit* in receptor internalization in LID rather than excessive internalization. This result is in agreement with the evidence that L-DOPA down-regulates the expression of arrestins and GRKs in MPTP-lesioned monkeys and tends to do so slightly more in animals with overt dyskinesia [96]. In hemiparkinsonian rats, pergolide, but not L-DOPA, was able to reverse the lesion-induced down-regulation of GRK isoforms in the caudal striatum [72], which could promote the desensitization of DA receptors and a reduction of the signaling caused by the drug [60]. The limited available data confirm that long-lived DA agonists tend to suppress signaling and reduce the receptor number. We have demonstrated that pergolide reduced the concentration of D<sub>3</sub> receptors in the lesioned and even in the intact hemisphere of hemiparkinsonian rats, whereas L-DOPA significantly up-regulated them [60]. This effect of pergolide could be indicative of D<sub>3</sub> receptor desensitization by the drug. Interestingly, long-lived agonists selectively targeting D<sub>1</sub> receptors rapidly lose their antiparkinsonian effect due to the development of tolerance, and dose escalation usually fails to restore the response [183, 249, 250]. This is one of the reasons why no selective D<sub>1</sub> drug has reached the clinic in spite of demonstrated antiparkinsonian efficacy. Molecular studies found that D<sub>1</sub> receptors readily desensitize in an arrestin- and GRK-dependent manner [263], whereas D<sub>2</sub> and especially D<sub>3</sub> receptors are relatively resistant to the homologous desensitization [264–266]. These data agree well with preclinical and clinical evidence on the activity of D<sub>1</sub>- and D<sub>2</sub>-selective agonists in PD.

Another property of L-DOPA that DA agonists do not have is that L-DOPA is converted to DA, which is then packaged in synaptic vesicles and released by neurons upon stimulation in a phasic spike-dependent manner. Agonists are not packaged and provide task-independent continuous stimulation of DA receptors. Therefore, long-lived DA agonists mimic well the tonic mode of DA action but are unable

to act in the spike-dependent phasic mode. Thus, they should be less able to support goal-oriented behavior than DA. The potential importance of this feature in the treatment of PD is highlighted by studies of DA null mice. They are hypoactive and hypophagic and cannot survive without forced feeding. The mice can be rescued by administration of L-DOPA, which supports proper feeding behavior, but not by D<sub>1</sub>, D<sub>2</sub>, or mixed D<sub>1</sub>/D<sub>2</sub> agonists [267]. Apparently, the mode of DA release and receptor stimulation is critical in determining downstream signaling events, which are indispensable for the regulation of complex behaviors.

### 18.2.3.3 Continuous Versus Pulsatile Stimulation of DA Receptors

The lower propensity of DA agonists to induce dyskinesia is believed to be due to their longer life, which translates into more even stimulation of DA receptors. The successful use of long-lived DA agonists and infusion of L-DOPA and short-lived agonists gave rise to the concept that continuous stimulation of DA receptors should be the goal in the treatment of PD [252, 253, 268]. The idea that continuous stimulation of DA receptors is physiological is supported by the evidence that dopaminergic neurons fire constantly at a low rate, inducing tonic release of DA [269], which maintains a constant or nearly constant DA concentration in the striatum and an ongoing tonic modulatory influence of DA on striatal neurons [270, 271]. D<sub>2</sub> antagonists cause multiple signaling events in striatal neurons [180], which is easy to interpret as stemming from the removal of the constant inhibition of these pathways via D<sub>2</sub> receptors. Apparently, the numerous extrasynaptic DA receptors found on striatal neurons [15] are meant to mediate tonic spike-independent DA activity in the striatum. However, this continuous tonic mode is not the only type of DA release in the striatum, as evidenced by phasic massive DA release during task performance in animals and humans [271, 272].

Normally, efficient reuptake of DA by dopaminergic terminals rapidly reduces the DA concentration to basal. L-DOPA causes manifold higher elevation of DA in the lesioned than in the intact striatum [273–275], likely due to the reduced clearance capacity of the sparse dopaminergic terminals. Even by itself, without specific postsynaptic changes, such a huge short-term increase in the synaptic DA concentration might contribute to peak-dose dyskinesia. Therefore, for the prevention of LID it might be beneficial to smooth out such fluctuations in the DA availability. Partially this could be achieved via co-administration of catechol-*O*-methyl transferase (COMT) (entacapone, tolcapone) or monoamine oxidase (MAO) inhibitors (deprenyl) with L-DOPA to slow down the degradation of DA and prolong its effects. These drugs have been introduced into clinical practice and proved beneficial in patients at different stages of the disease [276].

When drug-naïve PD patients are treated with long-lived DA agonists, they experience a lower incidence of dyskinesia [240, 241]. A somewhat different question is whether continuous stimulation of DA receptors with continuously administered L-DOPA/short-lived DA agonists or with long-lived DA agonists can reverse already established LID. Clinical trials so far failed to unequivocally demonstrate an antidyskinetic effect of DA agonists on previously established LID [251], although

there is strong enthusiasm for continuous dopaminergic stimulation as the strategy to provide antiparkinsonian benefits while controlling LID [253, 268]. If the lower efficacy of clinically used DA agonists is due to the lack of D<sub>1</sub> activity, continuously administered L-DOPA should be just as efficacious as regular L-DOPA but without the motor fluctuations. It remains unclear whether this is the case, since no large, long-term, double-blind studies have been conducted so far. Tolerance might be less of a problem with L-DOPA, even continuously administered, than with long-lived DA agonists, since DA synthesized from L-DOPA can be packaged and released in a phasic manner. Very few studies have examined the signaling effects of continuous L-DOPA administration, and those that have show similar results to those with long-lived DA agonists [67], specifically, that continuous L-DOPA does not induce the effects typical for intermittent L-DOPA administration.

### ***18.2.4 Molecular Mechanisms of L-DOPA-Induced Dyskinesia***

Multiple biochemical changes discussed above are induced by prolonged L-DOPA treatment, and some of them appear to correlate with the severity of LID in humans and animals. However, the functional role of most of these effects in LID remains unknown. Unfortunately, even the most robust correlation does not mean cause-and-effect relationship. The correlation of a molecular process with LID by itself does not help to establish the place of the process in the chain of events that ultimately produces LID. Since L-DOPA has antiparkinsonian as well as dyskinetic activity, classifying molecular consequences of L-DOPA treatment as antiparkinsonian or dyskinetic is a formidable task. Moreover, to understand the molecular mechanisms of LID, it is critical to separate the core processes from downstream events. What we already know about the molecular mechanisms of GPCR regulation might be very helpful in achieving these goals. Here we attempt to reconstruct molecular events that might bring about modification of the DA receptor signaling underlying LID and point out the gaps in our knowledge.

#### **18.2.4.1 Critical Elements in the Development of L-DOPA-Induced Dyskinesia**

Three considerations are important for understanding the molecular mechanisms of LID. First, L-DOPA is taken by PD patients that have lost at least half of their dopaminergic neurons, which means that L-DOPA acts on the background of the DA depletion and the signaling changes already induced by it (Figs. 18.2 and 18.3). The requirement of dopaminergic degeneration for the induction of LID is well supported by clinical and experimental data [125, 218]. Normal people or animals do not respond to doses of L-DOPA that produce dyskinesia in PD patients or lesioned animals. The probability of LID increases with the severity of dopaminergic degeneration in PD patients and experimental animals. It is conceivable that the lesion-induced supersensitivity of DA receptors is a prerequisite for LID induction. This view is supported by the evidence that a single administration of L-DOPA

induces multiple persistent proteomic changes in the DA-depleted, but not the normal, monkey striatum [147]. These effects may underlie the priming phenomenon, which is believed to be critical for the development of LID.

The second point is that L-DOPA is taken for a long time, and its clinical effects change over time. LID emerges after a few years of L-DOPA therapy and progresses thereafter. One reason for the delay may simply be the continuing degeneration of dopaminergic neurons that eventually reaches the LID threshold. Another possibility is that chronic L-DOPA induces plastic changes in the striatal signaling pathways that require time and chronic drug administration to develop, irrespective of the progression of the degeneration. In human PD patients, both processes are likely at work. Using animal models of PD, which have stable and often quite extensive loss of dopaminergic neurons, we can distinguish between lesion-induced changes and plastic effects that require chronic L-DOPA administration.

The third point is that, because of its short life, L-DOPA causes rapid elevation of the DA concentration followed by rapid clearance, resulting in a pulsatile mode of DA receptor stimulation: strong stimulation followed by periods of little or no stimulation.

#### **18.2.4.2 DA Receptor Supersensitivity and L-DOPA-Induced Dyskinesia**

If the presence of a particular signaling process is necessary and sufficient for the induction of LID, it would prove that this process is part of the molecular mechanism underlying LID. Since LID undoubtedly involves multiple mechanisms, it will likely be possible to demonstrate only that the process significantly contributes to LID severity. The behavioral sensitization phenomenon in the 6-OHDA-lesioned hemiparkinsonian rat is the most frequently used animal model of LID, particularly in molecular studies. Although the L-DOPA-induced rotations in this model do not resemble LID in the least, the progressive increase in the rotation frequency upon chronic administration of L-DOPA mimics the progressive nature of LID quite well. The progressive behavioral sensitization to L-DOPA in animals with stable depletion of dopaminergic neurons argues for the role of plastic signaling changes produced by chronic L-DOPA in LID induction. Since rotations induced by dopaminergic stimulation are attributed to the supersensitivity of DA receptors in the striatum, the increased rotation frequency due to behavioral sensitization suggests that receptor responsiveness is further increased by chronic L-DOPA administration. However, different signaling pathways respond differentially to the L-DOPA treatment. As discussed in Section 18.2.2, the sensitivity of several pathways is actually reverted to normal levels by L-DOPA, suggesting that these pathways are probably not responsible for the behavioral sensitization to L-DOPA. The signaling abnormalities caused by DA loss that are aggravated by L-DOPA are more likely candidates (Fig. 18.4).

The pathway(s) leading to LID appear to start from the supersensitivity of DA receptors, apparently both D<sub>1</sub> and D<sub>2</sub> subtypes. The molecular mechanism of this supersensitivity may include increased availability of D<sub>1</sub> receptors at the plasma membrane [262] and increased D<sub>1</sub> receptor coupling to G proteins [95], although

the mechanisms that bring about these changes remain undefined. The up-regulation of  $G\alpha_{olf}$  that has been proposed to mediate the lesion-induced supersensitivity of  $D_1$  receptors is actually reversed by chronic L-DOPA [78]. A number of downstream members of various pathways have been shown to be hyper-activated in the dyskinetic striatum as compared to non-dyskinetic L-DOPA-treated animals. Enhanced cAMP-mediated signaling has been implicated in LID, including enhanced activity of the DARPP-32-based amplification loop and ERK1/2 [85]. The substrate of ERK1/2, mitogen- and stress-activated kinase 1 (MSK-1), is also hyperphosphorylated in the striatum of dyskinetic animals [85]. LID is accompanied by enhanced PKA-mediated phosphorylation of the GluR1 subunit of the AMPA receptor [85] indicative of elevated AMPA transmission. However, the supersensitivity of these pathways is attenuated by L-DOPA, although to a lesser extent in dyskinetic animals.

Conversely, the accumulation of  $\Delta$ FosB seems to have a causal connection with LID [223].  $\Delta$ FosB is known to regulate dynorphin expression [223], and strong up-regulation of dynorphin by L-DOPA closely parallels the time course of behavioral sensitization to L-DOPA [66, 144, 205, 223]. The  $D_3$  receptor is also strongly up-regulated by L-DOPA, with a time course parallel to that of behavioral sensitization, and abolition of the  $D_3$  receptor up-regulation by blockade of  $D_1$  receptors inhibits the behavioral response [60, 66, 67]. Moreover, treatment of dyskinetic monkeys with a partial  $D_3$  receptor agonist co-administered with L-DOPA reduces LID without affecting the antiparkinsonian benefits, presumably via a judicious reduction of the  $D_3$  receptor-mediated signaling [30]. Enhanced constitutive activity of the Akt-GSK3 pathway also parallels behavioral sensitization to L-DOPA [60]. These signaling pathways might provide some mechanistic foundation for the enhanced dopaminergic responsiveness of the dyskinetic brain. Thus, it appears that dopamine depletion-induced supersensitivity of some, but not all, DA receptor-dependent pathways is further exacerbated or fixed by L-DOPA, thereby leading to LID (Fig. 18.4). It remains unclear how differential sensitivity of several pathways initiated by the same receptor can be achieved mechanistically. It is equally unclear which exaggerated molecular responses are the cause and which are the consequence of the abnormal dopaminergic signaling.

#### **18.2.4.3 Molecular Mechanisms of the Dopaminergic Supersensitivity in L-DOPA-Induced Dyskinesia**

The key point in this model that remains completely unexplained is the origin of the L-DOPA-induced supersensitivity of DA receptor-mediated signaling pathways. Strictly speaking, we do not know how DA depletion produces supersensitivity, but we understand even less the L-DOPA-induced sensitization of dopaminergic responses. Additionally, there is no ready explanation of why L-DOPA normalizes some signaling pathways while further upsetting the others. The lesion-induced receptor supersensitivity can be understood as one of many compensatory responses designed to maintain dopaminergic signaling upon the loss of DA. Mechanistically,

it could be explained by up-regulation of G protein(s) that enhances the G protein-mediated signaling, which is then propagated and amplified along the signaling pathways.

Assuming that striatal DA controls the expression of signaling proteins, the removal of that control upon DA depletion might be responsible for the  $G_{\alpha_{olf}}$  up-regulation via activation of specific transcription factors. L-DOPA, by replenishing striatal DA, should be expected to reverse that effect, and it does just that. Thus, no mechanistic explanation for the further enhancement of the signaling via  $D_1$  receptors by chronic L-DOPA administration is currently available. It is possible that L-DOPA augments the signaling via suppression of receptor desensitization. We found that L-DOPA, in contrast to the long-lived DA agonist pergolide, was largely unsuccessful in reversing the down-regulation of GRK isoforms induced by DA depletion in the caudal striatum [72]. The reduction in the availability of GRKs in the motor regions of the striatum, which is not reversible by L-DOPA, could actually contribute to LID or provide a favorable background for the development of LID. Lower concentrations of all GRK isoforms would impede receptor desensitization, and any factor that enhances the signaling would do it more effectively when the normal desensitization process is partially disabled. If this is the case, an increased GRK concentration should suppress LID. We have found that overexpression of GRK isoforms in the lesioned striatum using lentivirus-mediated gene transfer suppresses behavioral sensitization to L-DOPA and L-DOPA-induced AIMs in hemiparkinsonian rats [277].

Enhanced RGS-mediated attenuation of  $D_2$  receptor signaling may also be beneficial in LID. Indeed, overexpression of RGS9-2 was found to ameliorate LID in the rodent and monkey models of PD, whereas the loss of RGS9-2 augmented it [177]. Therefore, desensitization of  $D_1$  and  $D_2$  receptors appears to be beneficial for controlling LID without compromising the antiparkinsonian effect of L-DOPA. This is understandable, because facilitated desensitization ensures rapid signal shutoff but does not prevent the signal from going through, thus preserving antiparkinsonian activity. The efficacy of techniques promoting the desensitization process as antidyskinetic measures supports the idea that abnormally enhanced signaling by DA receptors is responsible for LID. This evidence suggests that the mechanisms of DA receptor desensitization are intimately involved in the development of LID and should be targeted for therapeutic purposes.

To date, numerous questions concerning the mechanism of LID remain unanswered. Many studies of LID mechanisms rely on the distinction between "dyskinetic" and "non-dyskinetic" animals. It has been repeatedly reported that in non-dyskinetic animals, L-DOPA reverses various signaling effects produced by DA depletion, whereas these changes persist or are even augmented in dyskinetic animals [85, 95, 121]. At first glance, these data suggest that the effects of L-DOPA are different or even opposite in the two categories of subjects. However, it is only a matter of time and/or L-DOPA dose before non-dyskinetic subjects become dyskinetic. The AIMs frequency in hemiparkinsonian rodents depends directly on the L-DOPA dose and the duration of treatment [121, 125, 216], and all MPTP-lesioned monkeys can be rendered dyskinetic and achieve similar dyskinetic scores with

prolonged and/or higher dose L-DOPA treatment [177, 278]. Similarly, a very large proportion, if not all human PD patients eventually develop LID [218]. Thus, it is much more likely that L-DOPA (as well as other antiparkinsonian treatments) induces qualitatively similar changes in signaling in all subjects, and the difference lies in the extent and/or the time course of these changes. For example, if ERK1/2 hyper-phosphorylation induced by DA depletion is reversed in non-dyskinetic animals, it is likely reversed in *all* animals to different degrees. Indeed, the data show that there is a reversal of the lesion-induced super-responsiveness of ERK1/2, DARPP-32, and GluR<sub>1</sub> in both dyskinetic and non-dyskinetic groups [60, 154]. The difference between the drug-naïve and the L-DOPA-treated hemiparkinsonian animals is actually greater than the difference between dyskinetic and non-dyskinetic ones. It should be emphasized that these data do not mean that the residual supersensitivity does not contribute to LID. In particular, DARPP-32 acts as an amplifier of the PKA-mediated signaling, and its removal may suppress dyskinesia by blunting the signaling via multiple pathways [88]. However, the pathways that respond to chronic L-DOPA in this manner are unlikely to be at the core of the LID pathology. A few “master” modifications propagated along the signaling network, eventually fixing the overactive state of DA receptors are likely to be responsible for LID. The candidate pathways should be progressively distorted by L-DOPA to a varying degree in all individuals. A few signaling effects described so far meet this criterion: accumulation of  $\Delta$ FosB, *Arc*, *Homer-1a*, GAD67, dynorphin, and D<sub>3</sub> receptors, as well as sensitization of CREB phosphorylation and the Akt pathway (Fig. 18.4). Technically, the dynorphin and D<sub>3</sub> receptor effects could be considered a reversal of the lesion-induced down-regulation, but the L-DOPA-induced expression of both proteins overshoots the pre-lesion levels very rapidly in all animals. The molecular processes that elicit these disparate effects and the specific roles of each in the generation of LID need to be determined.

It is obvious that L-DOPA exerts multiple effects on signaling mechanisms in all individuals. Some of these actions may be beneficial and the others detrimental from the clinical standpoint. The beneficial action mimics the normal effects of DA, thus reversing the signaling deficits induced by DA depletion. The detrimental action likely represents a further distortion of the signaling already damaged by DA depletion, rather than a simple reversion of the depletion effects. It is likely that even a single dose of L-DOPA has damaging potential, which is reflected in the well-known “priming” phenomenon. Upon prolonged treatment or administration of higher doses, these detrimental signaling effects of L-DOPA might grow strong enough to block and/or overshadow its beneficial effects, which restore normal signaling. These effects also seem to become permanent or semi-permanent, maintaining sensitized signaling even after a prolonged “drug holiday.” Due to individual differences, the detrimental activities of L-DOPA might be stronger in some individuals and weaker in others, which is reflected in the different L-DOPA doses and treatment times required to induce overt LID in different individuals. The goal should be to identify the alterations induced by L-DOPA that persist or increase with time and/or dose and have the potential to establish a positive feedback mechanism,

further elevating the DA receptor signaling. Unfortunately, most studies have been performed with a single dose of L-DOPA administered for a fixed time. If we are to identify the mechanisms of LID, it is crucial to quantitatively evaluate the dose and time dependence of L-DOPA-induced signaling changes in animals with both low and high propensities for LID.

### ***18.2.5 Mechanisms of L-DOPA-Induced Motor Fluctuations***

Treatment with L-DOPA, in addition to dyskinesia, gives rise to a number of effects collectively referred to as motor fluctuations. Different types of motor fluctuations are known but all describe a short, uncertain, or unstable therapeutic effect of a dose of the drug, which can appear or disappear without connection to the actual presence of the drug in the body. The therapeutic action of L-DOPA becomes shorter (wearing off) as the disease progresses. Occasionally, the therapeutic relief is delayed or does not appear at all (delayed or no “on” effect), and sometimes a person alternates between the “off” and the “on” stages (on-off fluctuations), even though the concentration of the drug in the body remains stable. In the worst case, the person may alternatively experience the “off” state and dyskinesia without any positive “on” effect at all [182].

If LID represents an unwanted response to L-DOPA that emerges with time due to some sort of sensitization, motor fluctuations reflect a loss of the therapeutic effect of the drug present in the system and may be due to tolerance [251]. The shortened response to L-DOPA is likely to be partially due to progressive loss of dopaminergic terminals and the capacity for storage of DA. Since the response to DA agonists, which are not stored in the brain, is also shortened with repeated administration [185, 279–282], additional explanation involving modifications of postsynaptic striatal machinery is necessary. It is important to bear in mind that therapeutic, appropriate motor responses to L-DOPA become larger with shorter latency to peak [279, 281–284] at the same time as they become shorter in duration. The increased amplitude of the responses is analogous to the sensitization mechanism involved in LID, which also becomes more severe with time [284], whereas the reduced duration seems to reflect the opposite process of tolerance.

What are the possible molecular mechanisms of L-DOPA-induced motor fluctuations, and how do they relate to those of dyskinesia? The common feature of dyskinesia and motor fluctuations is that they seem to be based largely on postsynaptic modifications of the responsiveness of striatal neurons. These modifications are probably initiated by alterations in the DA receptor signaling caused by DA depletion and L-DOPA treatment and then spread to other signaling systems. The development of LID and motor fluctuations go hand in hand, and many patients have both [211, 217], although phenotypically LID and motor fluctuations, or insufficient “on” response, appear to be the opposite ends of the spectrum. In the clinic, it has been a challenge to control LID while maintaining adequate antiparkinsonian response, which suggests that the mechanisms of LID and the antiparkinsonian

action are intertwined. Only a handful of drugs have been found to ameliorate LID without reducing the antiparkinsonian effect [251]. Thus, the clinical practice indicates that LID and motor complications cannot be entirely suppressed at the same time, and only a trade-off between LID and motor complications can be achieved. The mechanistic implication of this conclusion is that, although both LID and motor complications develop as a result of the signaling changes induced by chronic L-DOPA treatment on the background of dopamine denervation, these phenomena rely on molecular mechanisms opposite in nature and yet co-existing and interconnected. The current challenge is to identify these mechanisms.

A possibility has been suggested that continuous stimulation of DA receptors by mixed DA agonists or L-DOPA delivered constantly (via transdermal patches or intraintrastrially) may provide antiparkinsonian benefits without inducing dyskinesia, thus avoiding the Scylla and Charybdis of LID and motor fluctuations [251, 253, 268]. This idea is based on the tonic mode of DA release in the striatum, the low dyskinetic potential of long-lived DA agonists, and the experimental evidence that dyskinesia is more easily avoided with continuous than with intermittent delivery of the same drugs [243, 244]. However, round the clock delivery of L-DOPA or short-lived DA agonists is frequently associated with psychiatric problems such as hallucinations [251]. Similarly, long-lived DA agonists cause psychiatric problems, such as hallucinations, pathological gambling, hypersexuality, compulsive behaviors, and addiction to dopaminergic medication [285–287]. This necessitates the delivery to be confined to daytime hours, which usually alleviates the problems [191]. If the dopaminergic stimulation is not continuous, troughs of the stimulation seem to be particularly detrimental [254]. So far, no large, randomized clinical studies have been conducted to prove the benefits of continuous stimulation. The presence of dyskinesia combined with modest antiparkinsonian effects in patients with fetal nigral transplants, which, supposedly, provide continuous release of DA, is at odds with the idea that continuous stimulation is the optimal therapy [288–290].

Very few mechanistic studies of motor fluctuations have been performed due to the paucity of animal models of this phenomenon. In hemiparkinsonian rats, chronic treatment with L-DOPA induced a progressively shorter rotational response [105, 291], the behavioral process closely resembling wearing off in PD patients. The effect may require specific conditions to emerge, since it was not noted in other labs [125]. Longer treatment with L-DOPA is needed to induce the response shortening (approximately 3 weeks) than behavioral sensitization (a few days), which mimics the time course of these complications in PD patients [292]. This effect is associated with sensitized CREB phosphorylation in response to acute challenge with L-DOPA [105]. D<sub>1</sub>, but not D<sub>2</sub>, agonists mimic the elevation. The increase in CREB responsiveness parallels the time course of the shortening of the rotational response, which remains decreased for several weeks after L-DOPA withdrawal and returns to normal by the sixth week. Moreover, intrastriatal administration of a PKA inhibitor or CREB antisense oligonucleotide restored the normal duration of the rotational response. Up-regulation of PKC activity by viral gene transfer of the PKC catalytic subunit accelerates the shortening of the response in the course of chronic L-DOPA treatment, a process apparently mediated by enhanced phosphorylation of the GluR<sub>1</sub>

subunit of the AMPA receptor at the PKC site Ser831. Inhibition of PKC in animals overexpressing PKC attenuates both GluR<sub>1</sub> phosphorylation and response shortening. Interestingly, the reversal of the response shortening during chronic L-DOPA treatment by an adenosine<sub>A2A</sub> receptor antagonist was concomitant with a further increase in the expression of dynorphin as compared to L-DOPA alone [293], supporting opposing mechanisms for LID and motor fluctuations and providing a certain mechanistic basis for the increase in LID by suppressing motor fluctuations. However, the relationship between the shortening of the response and the severity of LID was not addressed in these studies. In some cases, the same drugs that relieved LID also restored the normal response duration [232, 294–296], implicating similar mechanisms in both types of L-DOPA-induced motor complications. In spite of superficial similarity, it remains unclear whether the shortening of the motor response to L-DOPA in hemiparkinsonian rats is mechanistically analogous to L-DOPA-induced motor fluctuations in human patients. The amount of available data is grossly insufficient to identify the overlapping or contrasting molecular processes underlying LID and motor fluctuations.

### 18.3 Dopamine Receptors and Neuroprotection in Parkinson's Disease

Dopaminergic drugs used in the symptomatic treatment of PD, such as L-DOPA and DA agonists, exert their therapeutic effects via interaction with DA receptors in the striatum. However, the dopaminergic neurons of the substantia nigra pars compacta that provide DA to the striatum express DA receptors, suggesting that DA and dopaminergic drugs can exert direct regulatory influence on these neurons. The expression of D<sub>2</sub> and D<sub>3</sub> receptors in the substantia nigra pars compacta and, specifically, in dopaminergic neurons of the rodent and primate brain is well documented [7, 11, 13, 28, 297, 298]. D<sub>4</sub> receptors are abundant in the neuropil and are detected in GABAergic cells of the substantia nigra pars reticulata [40, 299]. D<sub>4</sub> receptors are present in the small proportion of tyrosine hydroxylase (TH)-positive terminals in the nucleus accumbens [300] suggesting that a fraction of dopaminergic neurons may express these receptors. Most studies failed to detect D<sub>1</sub> receptor protein or mRNA in neurons of the substantia nigra compacta [6, 7, 301]. In contrast, immunohistochemical and in situ hybridization experiments demonstrated the presence of D<sub>5</sub> receptors in dopaminergic neurons [42, 44, 302]. D<sub>1</sub> receptors are abundant in the neuropil in the substantia nigra reticulata, presumably localizing on striatonigral terminals of the direct pathway [6, 24] including terminals forming synapses on TH-positive dendrites [301]. In the monkey brain, occasional D<sub>1</sub> receptor-positive perikarya are detected in the substantia nigra [24].

Since dopaminergic neurons, which progressively die in PD, possess DA receptors, it is possible that dopaminergic drugs affect viability of these neurons. By the time PD is diagnosed, approximately 50–70% of the dopaminergic cells of the substantia nigra have been lost. The remaining cells are believed to slowly degenerate as the disease progresses, contributing to the worsening of the symptoms and

of the side effects of L-DOPA therapy. Therefore, the welfare of the surviving dopaminergic neurons is of prime concern for the success of the PD treatment.

The effect of DA replacement therapy on the survival of these neurons is a highly controversial subject. In the course of its normal metabolism, DA produces a number of reactive oxygen species that can cause oxidative stress. L-DOPA, being a close relative of DA, can do the same, as can DA synthesized from L-DOPA. Since L-DOPA administration creates surges of L-DOPA and DA in the DA-depleted brain, this situation may be toxic for dopaminergic cells, which are vulnerable to oxidative stress [303], and promote cell death. Numerous *in vitro* studies have demonstrated L-DOPA toxicity in dopaminergic cell lines and cultured mesencephalon neurons [304–311]. The opposite view holds that L-DOPA can be neuroprotective under specific circumstances [304, 309, 312, 313]. L-DOPA induces oxidative stress and at the same time protects from it by engaging cellular antioxidative mechanisms, since inhibition of L-DOPA-induced oxidative stress also inhibits neuroprotection [304, 309]. These L-DOPA effects might be based solely on L-DOPA metabolism and independent of DA receptors [313]. The stimulation of DA receptors by DA may also be toxic to neurons [314, 315]. The most important question is, of course, whether L-DOPA is toxic *in vivo* in humans and animals in the situation when nigral neurons are under oxidative stress as occurs in PD. The answer to this question has immediate clinical implications for whether or not to delay L-DOPA introduction. Most *in vivo* studies in animals have found so far that L-DOPA is harmless [125, 316] or even neuroprotective [317, 318]. The large ELLDOPA clinical study aimed at resolving the issue failed to do so [319, 320]. The patients on L-DOPA showed a better clinical picture after the 2-week L-DOPA washout period than those on the placebo, but the concern was raised that long-term drug effects might have been responsible. The imaging studies included in the trial added insult to injury by demonstrating a greater decline in nigrostriatal biomarkers in the L-DOPA as compared to the placebo group. Thus, the problem of the potential toxicity of L-DOPA remains unresolved.

In contrast to L-DOPA, DA agonists are generally believed to be neuroprotective, although hard evidence remains scarce. Clinical studies have demonstrated better preservation of the nigrostriatal system in patients treated with DA agonists than in those treated with L-DOPA [321, 322]. Many DA agonists have been found to protect dopaminergic neurons against neurotoxins in animal models of PD [323–330]. The mechanism of the neuroprotection provided by DA agonists is puzzling. The neuroprotection by DA agonists may be independent of DA receptors, relying instead on the free radical scavenging properties of the drugs [327]. However, the action at DA receptors may also be involved. *In vitro*, DA agonists protect dopaminergic neurons from death induced by a variety of insults via stimulation of D2-like [327, 331–333] or D1-like [334] DA receptors. In particular, a case has been made for the prime role of the D<sub>3</sub> receptor in the neuroprotective activity of DA agonists [335]. Indeed, most clinically used DA agonists have a higher affinity for the D<sub>3</sub> than for the D<sub>2</sub> receptor [242]. Furthermore, the neuroprotective activity of the D<sub>3</sub>/D<sub>2</sub> agonist pramipexole against the MPTP toxicity is attenuated in mice lacking D<sub>3</sub> receptors and by co-administration of a selective D<sub>3</sub> antagonist, the

effect of which is abrogated in D<sub>3</sub> knockout mice [336]. The neuroprotective effect of pramipexole and another D<sub>3</sub>/D<sub>2</sub> agonist, S32504, against the MPTP toxicity in terminally differentiated neuroblastoma SH-SY5Y cells depends on the recruitment of brain-derived neurotrophic factor (BDNF) [333, 337], glial-derived neurotrophic factor (GDNF) [337], and the Akt pathway [333]. To summarize, a number of studies have demonstrated the neuroprotective activity of D<sub>2</sub>/D<sub>3</sub> DA agonists in vitro and in vivo. However, the signaling mechanisms mediating this effect remain largely unexplored, and no convincing mechanistic model has emerged so far. The inherent difficulties of these complex studies are further compounded by the obscure signaling pathways of the D<sub>3</sub> receptor, even if the D<sub>3</sub> receptor does play the starring role in neuroprotection in PD.

## 18.4 Conclusions

The available evidence strongly indicates that the hallmark feature of PD, DA depletion, results in profound changes in several signaling pathways. These alterations, including the supersensitivity of DA receptor signaling, apparently first emerge as adaptive responses to the reduced supply of endogenous DA. Administration of L-DOPA and DA agonists in parkinsonian patients and animal models of PD brings about additional changes in cell signaling. Certain therapy-induced modulations appear to represent the reversal of disease-induced changes and a rebalancing of signal transduction at or near normal levels, whereas others constitute further deviations that are likely involved in the pathogenesis of dyskinesia and other motor complications arising in the process of chronic treatment.

Our understanding of the cellular and molecular mechanisms underlying different aspects of Parkinson's pathology and motor complications is very uneven. For example, our current model of the circuit effects translating DA depletion into akinesia is fairly well developed, whereas the mechanisms producing another typical feature of Parkinson's pathology, tremor, remain obscure. At the molecular level, G protein-mediated signaling via D<sub>1</sub> receptors and its connection with PKA activity and modulation of its targets are much better documented than the signaling via the D<sub>2</sub> and D<sub>3</sub> receptors that are also affected in PD. To improve the effectiveness of existing therapies and, especially to devise novel treatments for PD, we urgently need to elucidate how the network of cellular signaling pathways is regulated by each of the DA receptors in the normal and diseased brain. The field needs to take full advantage of the available molecular approaches and the opportunities opened by the creation of knockout and transgenic mice to identify all the key players in DA signaling via each of the DA receptors. In each pathway, we need to establish which proteins are up- or downstream of each other and which players are rate limiting in the normal and diseased striatum. Manipulation of the most upstream and rate limiting elements usually changes the pathway output more effectively, which would make these signaling proteins the most promising therapeutic targets. Although this approach would require a lot of additional experimentation, it offers the best hope for selective enhancement of the antiparkinsonian effects of L-DOPA or DA agonists with simultaneous suppression of the signaling events responsible

for dyskinesia and other unwanted side effects of currently used treatments. Only a mechanism-based approach can lead to the “holy grail” of PD therapy, the preservation of dopaminergic neurons using molecular tools to enhance pro-survival and suppress pro-apoptotic signaling in the substantia nigra, which would make DA replacement strategies obsolete.

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# Chapter 19

## Dopamine Receptor Genetics in Neuropsychiatric Disorders

Frankie H.F. Lee and Albert H.C. Wong

**Abstract** The dopamine system modulates a diverse set of neural functions relevant to neuropsychiatric disorders and is modulated by some drugs used to treat these conditions. As a result, dopamine receptor genes have been a major focus for genetic studies that have analyzed putative associations between polymorphic variants and a wide range of clinical syndromes including alcoholism, substance abuse, schizophrenia, ADHD, anxiety disorders, bipolar and unipolar mood disorders, as well as related traits thought to contribute to these syndromes. In the following chapter, we review the basic genetic organization of the dopamine receptor genes and the evidence for association with these diagnoses. There is considerable inconsistency in the results from these genetic association studies, which is consistent with a complex genetic phenotype, and the neurobiological complexity of behaviors affected in neuropsychiatric illness. Overall, the strongest findings are the associations between variation in the DRD2 gene and alcoholism and the DRD4 gene and ADHD. While these associations do not suggest a major effect on risk in most patients, they do provide important insights into the pathophysiology of these disorders.

**Keywords** Dopamine · Receptor · Genes · Genetic association · SNP · Alcoholism · ADHD · Schizophrenia · Bipolar disorder · Substance abuse

### 19.1 Introduction

Over the past two decades, the genetics of dopamine receptors and their role in neuropsychiatric diseases have been studied extensively. The dopamine system is involved in neural functions including locomotion, movement, reward, cognition, and endocrine regulation [1]. Thus, genetic variation in dopamine receptors

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A.H.C. Wong (✉)  
Centre for Addiction and Mental Health, Department of Psychiatry,  
University of Toronto, Toronto, ON M5T 1R8, Canada  
e-mail: albert.wong@utoronto.ca

may influence symptoms in, or susceptibility to, various neuropsychiatric diseases. In addition, dopamine receptors are targets for antipsychotic medications that are used to treat delusions and hallucinations in schizophrenia and other psychotic disorders. Important side effects caused by antipsychotics include dopamine system-mediated extrapyramidal motor impairment and prolactin elevation [2]. Conversely, dopamine receptor agonists are psychostimulants that help to alleviate hypokinesia in Parkinson's disease and can cause psychotic symptoms in some cases [3]. Thus, alterations in dopamine receptor function, expression, and localization can have significant implications for both therapeutic efficacy and side effects of several classes of drugs.

There has been an accumulation of evidence to support the notion that variation in dopamine receptor genes can affect susceptibility to a number of neuropsychiatric diseases. In particular, schizophrenia, attention deficit hyperactivity disorder (ADHD), substance abuse, and bipolar disorder have the strongest association. However, even for these disorders, there are conflicting results and no clear evidence of variants exerting a strong effect on susceptibility in the majority of patients. As with other complex diseases and phenotypes, it is probably unrealistic to expect a single genetic variant to account for a large proportion of risk in all patients. With regard to behavioral disorders in particular, there are several additional complications. Symptoms and functional impairments in neuropsychiatric disease are not regulated by single molecular pathways or clearly defined anatomical structures, and neurotransmitter system components act in multiple brain circuits. Thus, the net impact of a given change in dopamine receptor function, expression, or localization cannot predict overall clinical presentation in a deterministic fashion.

A related issue is the heterogeneity of diagnostic groups based largely on clinical criteria like those in the DSM [4], in which patients with similar symptoms do not necessarily share the same genetic etiology. Finally, there are environmental and epigenetic factors that also affect behavior, creating even more variation that cannot be attributed to simple variation in DNA sequence [5]. Nevertheless, the identification of genetic variation that contributes to neuropsychiatric disease susceptibility or progression can generate important insights into pathophysiology, and in conjunction with other kinds of neurobiological studies can enhance our understanding of these complex and heterogeneous diseases. Ultimately, these genetic data will need to be supplemented by mechanistic understanding to determine the role of genetic variation that influences disease predisposition. In this chapter, we will review the polymorphisms present in dopamine receptor genes, survey their association with neuropsychiatric diseases, and discuss the conflicting results in the literature.

## 19.2 Characteristics of Dopamine Receptors

Five distinct dopamine receptor subtypes, D<sub>1</sub>–D<sub>5</sub>, have been cloned and characterized [6–9]. These are further subdivided into D<sub>1</sub>-like (D<sub>1</sub> and D<sub>5</sub>) and D<sub>2</sub>-like (D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub>) receptors based on their ability to stimulate adenylyl cyclase [10]

(Table 19.1). Dopamine receptors belong to the family of seven transmembrane domain G protein-coupled receptors (Fig. 19.1). D<sub>1</sub>-like receptors are able to stimulate adenylyl cyclase and promote the production of cyclic AMP (cAMP) whereas D<sub>2</sub>-like receptors inhibit this downstream signaling cascade. Subsequent structural and pharmacological studies confirm this broad functional grouping of dopamine receptor subtypes.

Both the D<sub>1</sub>-like and D<sub>2</sub>-like receptors show a high degree of DNA and amino acid sequence homology within their transmembrane domains (TMD) [11–15]. D<sub>1</sub> and D<sub>5</sub> receptors share an 80% homology in their TMDs while the D<sub>2</sub> receptor shares a 75% homology with the D<sub>3</sub> receptor and 53% with D<sub>4</sub>. The main difference in genomic organization between the two classes of dopamine receptors is

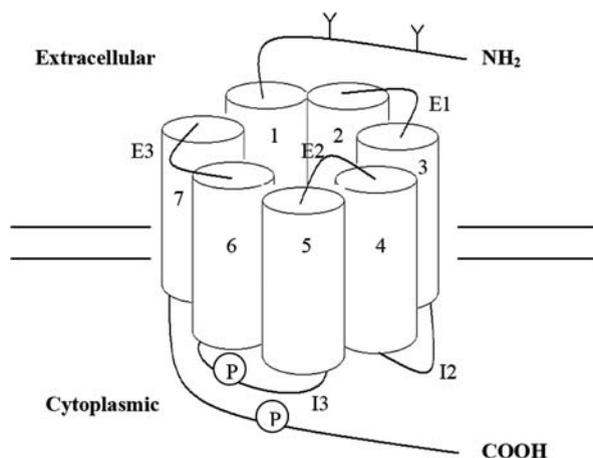
**Table 19.1** Molecular characteristics of dopamine receptors

|                      | D <sub>1</sub> -like |                | D <sub>2</sub> -like |                 |                |                      |
|----------------------|----------------------|----------------|----------------------|-----------------|----------------|----------------------|
|                      | D <sub>1</sub>       | D <sub>5</sub> | D <sub>2S</sub>      | D <sub>2L</sub> | D <sub>3</sub> | D <sub>4</sub>       |
| Chromosomal location | 5q35.1               | 4p16.1         | 11q22-23             |                 | 3q13.3         | 11p15.5              |
| Amino acids          | 446                  | 477            | 414                  | 443             | 400            | 387–515 <sup>a</sup> |
| Exons <sup>b</sup>   | 2                    | 1              | 8                    | 8               | 7              | 4                    |
| Introns <sup>c</sup> | 0                    | 0              | 5                    | 6               | 5              | 3                    |

<sup>a</sup> Depends on the number of repeats in exon 3.

<sup>b</sup> Includes coding region, 5'- and 3'-untranslated region.

<sup>c</sup> Within coding region



**Fig. 19.1** Dopamine receptor structure. D<sub>1</sub>-like and D<sub>2</sub>-like receptors differ in the number of potential glycosylation sites which are represented on the NH<sub>2</sub>-terminus. D<sub>1</sub>-like receptors are also characterized by a longer C-terminal tail and a shorter third intracellular loop. Several phosphorylation sites are illustrated on the COOH-terminal as well. E1–E3: extracellular loops; 1–7: transmembrane domains; I2 and I3: intracellular loops

the absence or presence of introns in their coding sequences. D<sub>1</sub>-like receptors are encoded by genes lacking introns whereas they are present in D<sub>2</sub>, D<sub>3</sub>, and D<sub>4</sub> receptor genes. Further analysis revealed that the D<sub>2</sub> receptor-coding region contains six introns, D<sub>3</sub> receptor five introns, and D<sub>4</sub> receptor three [16].

### ***19.2.1 Structural Characteristics of Dopamine Receptors***

In terms of structural characteristics of dopamine receptors, the NH<sub>2</sub>-terminal stretch of all receptor subtypes has a similar number of amino acid residues but differs in the number of N-glycosylation sites, with D<sub>1</sub> and D<sub>5</sub> having two sites, D<sub>2</sub> four, D<sub>3</sub> three, and D<sub>4</sub> only one. The carboxy-terminus length is about seven times longer for D<sub>1</sub>-like receptors than D<sub>2</sub>-like. Like other G protein-coupled receptors, the C-terminus is rich in serine and threonine residues which can be phosphorylated by kinases, and contains cysteine residues that are probably involved in the anchorage of the cytoplasmic tail to the membrane [16]. In addition, two cysteine residues are also present in the second and third extracellular loops, enabling the formation of a disulfide bridge for stabilization of the whole receptor structure. One major structural difference between the two groups is that the third intracellular loop is shorter in D<sub>1</sub>-like receptors than in the D<sub>2</sub>-like. As the third intracellular loop is mainly responsible for G protein coupling and signal transduction, this accounts for the differences in downstream signaling. The shorter third intracellular loop associated with D<sub>1</sub>-like receptors typically interacts with the G-stimulatory (G<sub>s</sub>) proteins to activate adenylyl cyclase and the production of cAMP. In contrast, the longer loop associated with D<sub>2</sub>-like receptors interacts with G-inhibitory (G<sub>i</sub>) proteins that inhibit adenylyl cyclase and reduce the production of cAMP [16].

As mentioned previously, D<sub>2</sub>-like receptors possess introns in their coding regions. This allows the generation of receptor variants via alternative splicing. Indeed, the D<sub>2</sub> receptor has two main variants, the short isoform D<sub>2S</sub> and the long isoform D<sub>2L</sub>, produced by alternative splicing of an 87 bp exon between intron 4 and 5 [12, 17–19]. The D<sub>2L</sub> isoform has a stretch of 29 amino acid residues in the third cytoplasmic loop that is absent D<sub>2S</sub> [20]. For D<sub>3</sub> receptors, splice variants appear to generate non-functional proteins [21–23]. No splice variants of the D<sub>4</sub> receptor have been found, but the D<sub>4</sub> receptor gene locus is highly polymorphic, producing great diversity of D<sub>4</sub> receptor isoforms (discussed in more detail below). Although the D<sub>5</sub> receptor gene contains no introns, two pseudogenes sharing 98% identity are found on human chromosomes 1 and 2. With respect to the D<sub>5</sub> receptor, these pseudogenes show 95% amino acid identity but interestingly, they code for a truncated, non-functional form of the receptor [24, 25].

### ***19.2.2 Pharmacological Characteristics of Dopamine Receptors***

In addition to structural differences, the D<sub>1</sub>-like and D<sub>2</sub>-like receptors have differing pharmacological profiles based on variable binding affinity of ligands for the receptor subtypes [16]. Table 19.2 lists several ligands that bind to dopamine receptor

**Table 19.2** Pharmacological profile of dopamine receptors on selected agonists and antagonists

|                    | D <sub>1</sub> -like |                | D <sub>2</sub> -like |                |                |
|--------------------|----------------------|----------------|----------------------|----------------|----------------|
|                    | D <sub>1</sub>       | D <sub>5</sub> | D <sub>2</sub>       | D <sub>3</sub> | D <sub>4</sub> |
| <b>Agonists</b>    |                      |                |                      |                |                |
| Apomorphine        | 1 μM                 | 100 nM         | 1 nM                 | 10 nM          | 1 nM           |
| Bromocriptine      | 100 nM               | 100 nM         | 1 nM                 | 1 nM           | 100 nM         |
| Dopamine           | 1 μM                 | 100 nM         | 100 nM               | 10 nM          | 10 nM          |
| <b>Antagonists</b> |                      |                |                      |                |                |
| (+)-Butaclamol     | 1 nM                 | 10 nM          | 1 nM                 | Undetermined   | 10 nM          |
| Chlorpromazine     | 100 nM               | 100 nM         | 1 nM                 | 10 nM          | 10 nM          |
| Clozapine          | 100 nM               | 100 nM         | 100 nM               | 100 nM         | 10 nM          |
| Haloperidol        | 100 nM               | 100 nM         | 0.1 nM               | 10 nM          | 1 nM           |
| Raclopride         | 10 μM                | Undetermined   | 1 nM                 | 1 nM           | 1 μM           |
| SCH-23390          | 0.1 nM               | 0.1 nM         | 1 μM                 | 1 μM           | 1 μM           |
| Spiiperone         | 100 nM               | 1 μM           | 0.1 nM               | 1 nM           | 0.1 nM         |
| Sulpiride          | 10 μM                | 10 μM          | 10 nM                | 10 nM          | 10 nM          |

All values are given as inhibition constants ( $K_i$ ). Estimated orders of magnitude for each value are reported. Modified from Missale et al. [16]

subtypes with different affinities. Not surprisingly, dopamine itself is able to bind to all five receptors but has a higher affinity for D<sub>5</sub> receptors than D<sub>1</sub>. Among the D<sub>2</sub>-like receptors, dopamine binds D<sub>2</sub> receptors with a lower affinity than D<sub>3</sub> and D<sub>4</sub>. Moreover, there are other agonists and antagonists that preferentially bind to D<sub>1</sub>-like or D<sub>2</sub>-like receptors, permitting distinctions between receptor subtypes to be assessed pharmacologically. For example, the dopamine antagonist sulpiride binds to D<sub>2</sub>-like receptors preferentially. However, a clear differentiation between D<sub>1</sub> and D<sub>5</sub> receptors cannot be easily established pharmacologically as they have similar affinity profiles for most dopaminergic drugs. Besides dopamine, (+)-butaclamol is another discriminating dopamine antagonist that has a slightly higher affinity for D<sub>1</sub> receptors than D<sub>5</sub> [9, 14]. On the other hand, the D<sub>2</sub>-like receptors are more readily distinguished using drugs with variable affinity for D<sub>2</sub>, D<sub>3</sub>, or D<sub>4</sub> receptors. As for D<sub>2</sub> receptor isoforms, there is still no compound that is able to clearly discriminate between D<sub>2S</sub> and D<sub>2L</sub>. Only a marginal difference in the binding affinities toward the two isoforms has been described with sulpiride and raclopride [26, 27].

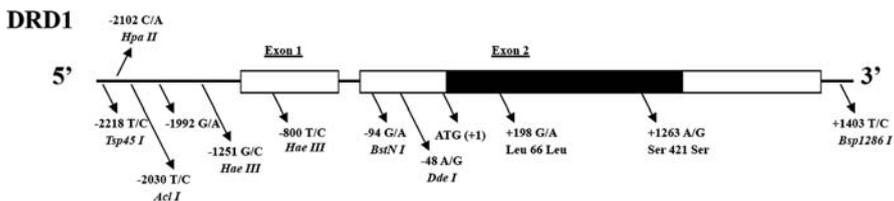
### 19.3 Dopamine Receptor Function and Neuropsychiatric Disease

Dopamine receptors are coupled to a variety of different downstream effectors and hence regulate different activities such as locomotor activity, positive reinforcement or reward, cognition, and endocrine control in the central nervous system. As mentioned before, the most important is the modulation of adenylyl cyclase activity that results in either stimulation or inhibition of cAMP production depending on

the receptor subtype. In most cases, cAMP further regulates the activity of protein kinase A, which is responsible for numerous downstream effects. In addition to cAMP production, dopamine receptors have been shown to modulate the activity of phospholipase C, the release of arachidonic acid, the regulation of calcium and potassium channels, as well as  $\text{Na}^+/\text{H}^+$  exchangers and  $\text{Na}^+/\text{K}^+$  ATPases [16]. Recent studies have also demonstrated that the activation of  $\text{D}_{25}$  isoform of the  $\text{D}_2$  receptors is able to stimulate phospholipase D via coupling with Rho family of G proteins [28]. Phospholipase D is an enzyme responsible for the hydrolysis of phosphatidylcholine to phosphatidic acid and choline, and the end result seems to be associated with an antiproliferative effect [29]. All of these downstream pathways have important implications for neuropsychiatric disease.

### 19.3.1 $\text{D}_1$ Receptors

The dopamine  $\text{D}_1$  receptor (DRD1) gene is mapped to chromosome 5q35.1 and contains two exons separated by a small intron in the 5' untranslated region (5' UTR) [30, 31] (Fig. 19.2). The coding region is located within exon 2 and encodes 446 amino acids. Several polymorphisms, most located in the 5' UTR, have been implicated in neuropsychiatric diseases. In most cases, they are recognized by different restriction enzymes such as Dde I, BstNI, and Hae III. Hence these restriction fragment length polymorphisms (RFLP) allow easy detection using polymerase chain reaction (PCR) methods together with the appropriate restriction enzyme. Screening of the 5' UTR polymorphisms showed that none of the mutations has an important influence on transcriptional activity [1]. Moreover, two silent mutations, +198 G/A (Leu<sup>66</sup>) and +1,263 A/G (Ser<sup>421</sup>), have been reported in the coding region of DRD1 that may play a role in disease susceptibility. Since these variants do not change amino acid sequence, they would not change protein structure, but possibly could affect mRNA abundance or stability.



**Fig. 19.2** Dopamine  $\text{D}_1$  receptor: Schematic representation of polymorphisms (not to scale). Coding regions of exons are marked by *black blocks*, and the 5' and 3'- UTR are represented by *white blocks*. The first base of the ATG start codon is denoted as +1 and the location of other polymorphisms are given relative to the start codon. Introns are represented as a *straight line* connecting the exons. Restriction enzymes, alteration of amino acids, and other distinct descriptions are given where applicable. (Modified from Kim et al. [42])

**Table 19.3** Dopamine D<sub>1</sub> receptor polymorphisms and neuropsychiatric diseases

| References                   | Polymorphisms   | Disease phenotype | Number of patients | Ethnicity             | Significance/notes   |
|------------------------------|---|-------------------|--------------------|-----------------------|--|
| Kojima et al. [34]           | -48 A/G   | SCZ               | 148                | Japanese              | Not significant  |
| Limosin et al. [41]          |   | ALC               | 72                 | -                     | Male-limited association with sensation seeking                      |
| Ryakowski et al. [39]        |   | SCZ               | 138                | -                     | G/G genotype associates with inferior results on WCST                |
| Severino et al. [38]         |   | BP                | 107                | Sardinian             | Significant  |
| Dmitrzak-Weglarz et al. [36] |   | SCZ               | 407                | Polish                | Not significant with SCZ but significant with BP                     |
| Kim et al. [42]              |   | ALC               | 535                | Korean                | Significant association with severity of alcohol-related problems    |
| Ni et al. [35]               | -48 A/G<br>-800 T/C<br>+1403 T/C  | BP                | 286                | -                     | Not significant for individual SNPs but significant with haplotype   |
| Del Zompo et al. [37]        |   | BP                | 170<br>229         | Sardinian<br>Canadian | Not significant for individual SNPs but significant with haplotype   |
| Misener et al. [40]          | -48 A/G<br>-800 T/C<br>-1251 G/C<br>+1403 T/C                             | ADHD              | 192                | -                     | Haplotype 3 (1.1.1.2) is associated with poor working memory in ADHD |
| Cichon et al. [33]           | -2218 T/C<br>-2102 C/A<br>-2030 T/C<br>-1992 G/A<br>-1251 G/C<br>-800 T/C | SCZ<br>BP         | 74                 | German                | Not significant with both SCZ and BP for all SNPs                    |

Table 19.3 (continued)

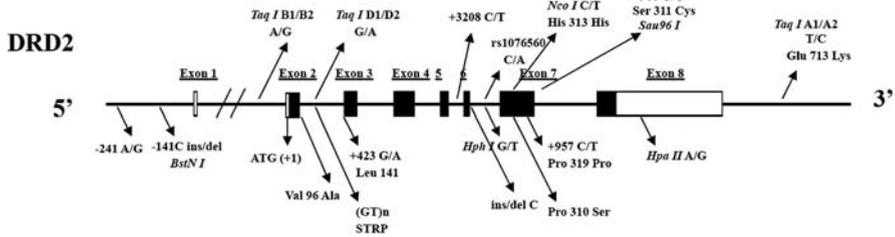
| References        | Polymorphisms                                   | Disease phenotype | Number of patients | Ethnicity                                     | Significance/notes |
|-------------------|---|-------------------|--------------------|---|--------------------|
| Liu et al. [32]   | -48 A/G<br>+198 G/A (L66L)<br>+1263 A/G (S421S) | SCZ               | 131                | Asian, African,<br>American, and<br>Caucasian | Not significant    |
| Maron et al. [43] | -94 G/A   | PD                | 127                | Caucasian                                     | Significant        |
| Koks et al. [44]  | -2102 C/A                                       | MDD               | 177                | Estonian                                      | Significant        |

Abbreviations: SCZ – schizophrenia; BP – bipolar disorder; ADHD – attention deficit hyperactivity disorder; ALC – alcoholism; PD – panic disorder; MDD – major depressive disorder; SNP – single nucleotide polymorphism; WCST – Wisconsin Card Sorting Test; – undetermined or not applicable

Overall, studies of individual polymorphisms in DRD1 have produced conflicting genetic linkage or association results in several different diseases (Table 19.3). Of all the single nucleotide polymorphisms (SNPs) reported, the  $-48$  A/G polymorphism has been the most extensively studied. Several case-control studies have reported negative findings in patients with schizophrenia and bipolar disorder [32–37]. In contrast, others have demonstrated significant association with bipolar disorder [36, 38]. Another interesting study conducted by Rybakowski's group found that the  $-48$  G/G genotype was associated with impairment on the Wisconsin Card Sorting Test (WCST) in schizophrenic patients when compared to controls [39]. This is consistent with executive dysfunction seen in schizophrenia, which is often assessed using the WCST. In addition, some haplotypes assessed with the transmission disequilibrium test (TDT) on the  $-48$  A/G,  $-800$  T/C, and  $+1,403$  T/C polymorphisms have been associated with bipolar disorder in two separate studies [35, 37]. Although there are no association studies of the two synonymous mutations (Leu<sup>66</sup> and Ser<sup>421</sup>) with schizophrenia, Liu et al. suggested that they are unlikely to contribute significantly to the schizophrenia [32]. Because of these inconsistent findings, no definitive association can be seen between DRD1 mutations and schizophrenia or bipolar disorder. As for ADHD and alcoholism, a smaller number of studies have investigated relationships with DRD1 polymorphisms. Misener et al. investigated four different polymorphisms ( $-48$  A/G,  $-800$  T/C,  $-1,251$  G/C, and  $+1,403$  T/C) and found a haplotype (haplotype 3 – 1.1.1.2) associated with poor working memory in ADHD [40], while others have found association between  $-48$  A/G and the severity of alcohol-related problems and sensation seeking in alcoholics [41, 42]. Studies have also reported significant association between  $-94$  G/A and  $-2,102$  C/A with panic disorder and major depressive disorder, respectively [43, 44]. Despite these significant association studies with ADHD and alcoholism, replication has been inconsistent, and so firm conclusions about the relationship of variation in the DRD1 gene to these disorders cannot yet be drawn.

### 19.3.2 D<sub>2</sub> Receptors

The dopamine D<sub>2</sub> receptor is located on chromosome 11q22-23 and consists of eight exons with the coding region spanning exons 2–8 [24, 45] (Fig. 19.3). The gene is over 65,000 bp long and encodes 414 amino acids in D<sub>2S</sub> and 443 in D<sub>2L</sub>. Several RFLPs distributed throughout the whole gene are recognized by Taq I, BstN I, Hph I, Nco I, and Hpa II. In particular, three polymorphisms of Taq I, termed Taq I A, B, and D, are the most extensively studied in relation to neuropsychiatric diseases (Table 19.4). Taq I A is located in the 3' UTR and has been shown to be associated with a reduction in the D<sub>2</sub> receptor density [46, 47]; Taq I B is near the end of intron 1 close to exon 2, and Taq I D is within intron 2. Allele frequencies of the various Taq I polymorphisms differ depending on ancestral background [48]. A number of polymorphisms are located within the coding region, with three of them resulting in a change of amino acid: Val<sup>96</sup>Ala, Pro<sup>310</sup>Ser, and Ser<sup>311</sup>Cys. Amino acid positions 310 and 311 are part of the third cytoplasmic loop where amino acid substitutions



**Fig. 19.3** Dopamine D<sub>2</sub> receptor: Schematic representation of polymorphisms (not to scale). Coding regions of exons are marked by *black blocks*, and the 5' and 3'- UTR are represented by *white blocks*. The first base of the ATG start codon is denoted as +1 and the location of other polymorphisms are given relative to the start codon. Introns are represented as a *straight line* connecting the exons. Restriction enzymes, alteration of amino acids, and other distinct descriptions are given where applicable. (Modified from Kim et al. [42])

can affect the magnitude of cAMP inhibition [1]. All three variants, however, are functionally active in Chinese hamster ovary cells [49]. Although the +957 C/T SNP is a synonymous variant resulting in the same amino acid (Pro<sup>319</sup>), the T allele has been shown to decrease translation of DRD2 mRNA, DRD2 mRNA stability, and dopamine-induced upregulation of D<sub>2</sub> receptors [50]. In the 5' promoter region, two mutations -241 A/G and -141C ins/del have been detected and are associated with D<sub>2</sub> receptor density [51].

A large number of studies have investigated the Taq I A polymorphism and its association with alcoholism, with inconsistent results. The first evidence of Taq I A association with alcoholism was reported by Blum et al. [52], and later replicated in several other studies [53–55]. In addition, greater severity of alcohol dependence [56] and early-onset alcoholism [57] have been associated with the Taq I A1 allele. In contrast, a lack of association has been reported in a number of case–control [51, 58–66] and family-based studies [67, 68]. Findings have been similarly inconsistent with the Taq I B polymorphism and alcoholism, with both positive [62, 69] and negative studies [66, 70] present in the literature. Other than the Taq I polymorphism, no association was observed between alcoholism and Ser<sup>311</sup>Cys, (GT)<sub>n</sub> short tandem repeat polymorphism (STRP), -141C ins/del, -241 A/G, and other mutations within the coding region [51, 60, 66–68, 71–74]. Linkage disequilibrium studies have not demonstrated associations with haplotypes including the Taq I A polymorphism [60], suggesting that the Taq I polymorphism may exert only a minor effect or interact with genes other than DRD2 to influence alcoholism. The Taq I A variant appears to alter an amino acid in the ankyrin repeat and kinase domain containing 1 (ANKK1) gene, near the DRD2 locus [75]. It remains unclear whether this significantly influences susceptibility to neuropsychiatric disease, but does represent a potential direction for future research. Pato et al. conducted a meta-analysis of eight studies and found an apparent increase in the relative risk associated with increased severity of alcoholism for the Taq I A1 allele [76]. More recently, a meta-analysis reviewing a total of 40 case–control studies on different ethnic groups indicates a small effect of the Taq I A polymorphism on risk for alcoholism [77] and was further supported by another recent meta-analysis [78].

**Table 19.4** Dopamine D<sub>2</sub> receptor polymorphisms and neuropsychiatric diseases

| References            | Polymorphisms      | Disease phenotype | Number of patients | Ethnicity            | Significance/notes  |
|-----------------------|--------------------|-------------------|--------------------|----------------------|---|
| Blum et al. [52]      | <i>Taq I</i> A1/A2 | ALC               | 70                 | –                    | Significant with A1 allele                                    |
| Amadeo et al. [53]    |                    | ALC               | 49                 | French               | Significant   |
| Arinami et al. [54]   |                    | ALC               | 78                 | Japanese             | Significant   |
| Goldman et al. [61]   |                    | ALC               | 119                | American-Indians     | Not significant   |
| Pato et al. [76]      |                    | ALC               | –                  | –                    | Significant with A1 allele (meta-analysis)                    |
| Noble et al. [236]    |                    | SMK               | 172                | Caucasian            | Significant with A1 allele                                    |
| Cruz et al. [63]      |                    | ALC               | 38                 | Mexican              | Not significant   |
| Chen et al. [64]      |                    | ALC               | –                  | Taiwanese            | Not significant   |
| Kono et al. [57]      |                    | ALC               | 100                | Japanese             | Significant with A1/A1 genotype                               |
| Gorwood et al. [105]  |                    | BP                | 122                | French               | Not significant with both BP and alcoholism                   |
| Gorwood et al. [58]   |                    | ALC               | 113                | French               | Not significant   |
| Lawford et al. [108]  |                    | HD                | 95                 | Caucasian            | Significant with A1 allele                                    |
| Conner et al. [56]    |                    | ALC               | 106                | Australian-Caucasian | Significant with A1 allele (greater severity)                 |
| Limosin et al. [237]  |                    | ALC               | 120                | French-Caucasian     | Significant with A1 allele only in males                      |
| Conner et al. [109]   |                    | SA                | 37                 | Caucasian            | Significant increase in children developing SA with A1 allele |
| Munafò et al. [77]    |                    | ALC               | 11                 | Hispanic             | Significant (meta-analysis)                                   |
| Smith et al. [78]     |                    | ALC               | 9382               | –                    | Significant association with A1 allele (meta-analysis)        |
| Laurent et al. [81]   | +960 C/G (S311C)   | SCZ               | 113                | Caucasian            | Not significant   |
| Craddock et al. [102] |                    | BP                | 82                 | –                    | Not significant   |
| Chen et al. [80]      |                    | SCZ               | 114                | Taiwanese            | Not significant   |
| Finckh et al. [72]    |                    | ALC               | 312                | German               | Not significant   |
| Kaneshima et al. [79] |                    | SCZ               | 78                 | Japanese (Okinawan)  | Not significant   |

Table 19.4 (continued)

| References            | Polymorphisms    | Disease phenotype | Number of patients | Ethnicity            | Significance/notes  |
|-----------------------|------------------|-------------------|--------------------|----------------------|---|
| Serretti et al. [107] |                  | BP<br>SCZ         | 1182               | Italian              | Not significant but may be involved in delusion and disorganization |
| Glatt et al. [84]     |                  | MDD<br>DD<br>SCZ  | -                  | -                    | symptomatology<br>Significant with C311 (meta-analysis)             |
| Jonsson et al. [87]   |                  | SCZ               | 173<br>9152        | Swedish              | Significant only in males (replicated in meta-analysis)             |
| Levinson et al. [86]  |                  | SCZ               | -                  | -                    | Significant (meta-analysis)   |
| Glatt et al. [85]     |                  | SCZ               | -                  | -                    | Significant with C311 (meta-analysis)                               |
| Lawford et al. [89]   | +957 C/T (P319P) | SCZ               | 153                | Caucasian            | Significant with C/C  |
| Hanninen et al. [88]  |                  | SCZ               | 188                | Finnish              | Significant   |
| Hoienicka et al. [90] |                  | SCZ               | 131                | Spanish              | Significant   |
| Furlong et al. [104]  | -141C ins/del    | BP                | 131                | East Anglian         | Not significant   |
| Li et al. [97]        |                  | SCZ               | 229 trios<br>151   | Chinese<br>Caucasian | Not significant   |
| Breen et al. [93]     |                  | SCZ               | 439                | British              | Significant   |
| Kirov et al. [103]    |                  | BP                | 122 trios          | British-Caucasian    | Not significant   |
| Glatt et al. [96]     |                  | SCZ               | -                  | -                    | Not significant (meta-analysis)                                     |
| Komishi et al. [238]  |                  | ALC               | 200                | Mexican-American     | Not significant   |
| Xu et al. [110]       | Taq I B1/B2      | HD                | 486<br>471         | Chinese<br>German    | Significant with B1 allele in Chinese and a low risk in Germans     |

Table 19.4 (continued)

| References            | Polymorphisms   | Disease phenotype | Number of patients  | Ethnicity                          | Significance/notes   |
|-----------------------|---|-------------------|---------------------|------------------------------------|--|
| Dubertret et al. [82] | <i>Taq I</i> A1/A2<br><i>Taq I</i> B1/B2<br><i>Taq I</i> D1/D2<br>-141C ins/del<br>+960 C/G (S311C)<br>(GT) <sub>n</sub> STRP | SCZ               | 103                 | French                             | Significant excess of A2 allele of <i>Taq I</i> A1/A2 and B2 allele of <i>Taq I</i> B1/B2<br>Not significant with <i>Taq I</i> D1/D2, -141C, S311C and (GT) <sub>n</sub> STRP<br>Significant haplotype with A2<br>Significant with B1 allele |
| Smith et al. [111]    | <i>Taq I</i> A1/A2<br><i>Taq I</i> B1/B2  | SA                | -                   | -                                  | Significant with A1 and B1 alleles   |
| Blum et al. [69]      | <i>Taq I</i> B1/B2  | ALC               | 115                 | White                              | Significant in White with A1 and B1 allele   |
| O'Hara et al. [239]   |   | SA                | 616 (with controls) | White and Black Americans          | Not significant in Black<br>Significant haplotype with A2/B2   |
| Dubertret et al. [95] |   | SCZ               | 100                 | French                             | Significant with <i>Taq I</i> B  |
| Foley et al. [62]     |   | ALC               | 161                 | Caucasian                          | Not significant with <i>Taq I</i> A  |
| Ambrosio et al. [98]  | <i>Taq I</i> A1/A2<br>+960 C/G (S311C)  | SCZ               | 90 trios            | Portuguese                         | Not significant  |
| Edenberg et al. [67]  | <i>Taq I</i> A1/A2<br>(GT) <sub>n</sub> STRP  | ALC               | 987 (with controls) | Non-Hispanic Caucasian<br>Japanese | Not significant  |
| Ishiguro et al. [55]  | <i>Taq I</i> A1/A2<br>-141C ins/del   | ALC               | 209                 |                                    | Significant with -141C ins   |
| Li et al. [106]       |   | BP                | 118<br>157          | Han Chinese<br>Caucasian           | Marginal significant with <i>Taq I</i><br>Significant in Chinese but not Caucasian with A1 allele and -141C del  |

Table 19.4 (continued)

| References              | Polymorphisms  | Disease phenotype | Number of patients | Ethnicity        | Significance/notes   |
|-------------------------|--|-------------------|--------------------|------------------|--|
| Sander et al. [60]      |  | ALC               | 310                | German           | Not significant with individual SNPs and A1/-141C ins haplotype  |
| Samochowicz et al. [68] |  | ALC               | 100 families       | Polish           | Significant with A2 allele<br>Not significant with -141C ins/del   |
| Parsons et al. [99]     |  | SCZ               | 119                | Spanish          | Significant with <i>Taq I</i> A1/A2 (less frequent in SCZ)<br>Not significant with -141C ins/del   |
| Konishi et al. [70]     | <i>Taq I</i> A1/A2<br><i>Taq I</i> B1/B2<br>-141C ins/del                                | ALC               | 130                | Mexican-American | Significant with -141C ins/del<br>Not significant with <i>Taq I</i> A and B  |
| Himei et al. [100]      | +960 C/G (S311C)<br>-141C ins/del  | SCZ               | 190                | Japanese         | Not significant but may be associated with symptoms (C311/-141C del)   |
| Sarkar et al. [101]     | +423 G/A (Leu141)<br>+3208 C/T<br><i>Nco I</i> C/T (H313H)                               | SCZ               | 14                 | Caucasian        | Not significant with no structural change in all SNPs  |
| Arinami et al. [94]     | -141C ins/del<br>-241 A/G  | SCZ               | 260                | Japanese         | Significant with -141C ins/del<br>Not significant -241 A/G   |
| Goldman et al. [65]     | +960 C/G (S311C)<br><i>Taq I</i> A1/A2<br>(GT) <sub>n</sub> STRP<br><i>Taq I</i> A1/A2   | SCZ<br>ALC<br>SA  | 459                | American-Indian  | Not significant  |
| Vijayan et al. [83]     | <i>Taq I</i> B1/B2<br><i>Taq I</i> D1/D2<br>+960 C/G (S311C)<br><i>Nco I</i> C/T (H313H) | SCZ               | 213                | South Indian     | Significant with <i>Nco I</i><br>Not significant with <i>Taq I</i> and S311C<br>Significant haplotype with <i>Taq I</i> A2 and <i>Nco I</i> T allele |

Table 19.4 (continued)

| References             | Polymorphisms  | Disease phenotype | Number of patients | Ethnicity                         | Significance/notes  |
|------------------------|--|-------------------|--------------------|-----------------------------------|---|
| Kukreti et al. [91]    | <i>Nco I</i> C/T (H313H)<br>+957 C/T (P319P)   | SCZ               | 101                | South Indian                      | Significant with <i>Nco I</i><br>Not significant with P319<br>Not significant   |
| Lu et al. [66]         | <i>Taq I</i> A1/A2<br><i>Taq I</i> B1/B2<br>(GT) <sub>n</sub> STRP   | ALC               | 128                | Taiwanese                         |   |
| Luo et al. [51]        | <i>Taq I</i> A1/A2<br><i>Taq I</i> B1/B2<br>-141C ins/del<br><i>Hph I</i> G/T<br><i>Nco I</i> C/T (H313H)<br><i>Hpa II</i> A/G | ALC               | 200                | Mexican-American                  | Significant with -141C del<br>Not significant with other<br>individual SNPs<br>Significant haplotype with H1,<br>H2, H4 and H8                  |
| Parsian et al. [73]    | -141C ins/del<br>-241 A/G<br>+960 C/G (S311C)  | ALC               | 173                | White and<br>African-American     | Not significant   |
| Gejman et al. [74]     | Val 96 Ala<br>Pro 310 Ser<br>+960 C/G (S311C)  | SCZ<br>ALC        | 219                | White                             | Not significant in both SCZ and<br>alcoholism   |
| Gelemtier et al. [112] | <i>Taq I</i> A1/A2<br><i>Taq I</i> B1/B2<br><i>Taq I</i> D1/D2   | CD                | 173                | European-<br>and African-American | Not significant   |
| Noble et al. [240]     | <i>Taq I</i> A1/A2<br><i>Taq I</i> B1/B2<br>-141C ins/del<br><i>Hph I</i> G/T<br>+957 C/T (P319P)                              | ALC               | 92                 | Caucasians                        | Not significant with + 957 C/T<br>and -141C ins/del<br>Significant haplotype with<br>minor alleles of <i>Taq I</i> A, B<br>and <i>Hph I</i> G/T |
| Finckh et al. [71]     | Intron 6 C ins/del   | ALC               | 270                | -                                 | Not significant   |
| Sasabe et al. [241]    | rs1076560 C/A  | ALC               | 248                | Japanese                          | Significant with A allele   |

Abbreviations: SCZ – schizophrenia; BP – bipolar disorder; ALC – alcoholism; SMK – smoking; SA – substance abuse; HD – heroin dependence; MDD – major depressive disorder; DD – delusional disorder; CD – cocaine dependence; SNP – single nucleotide polymorphism; STRP – short tandem repeat polymorphism

– undetermined or not applicable

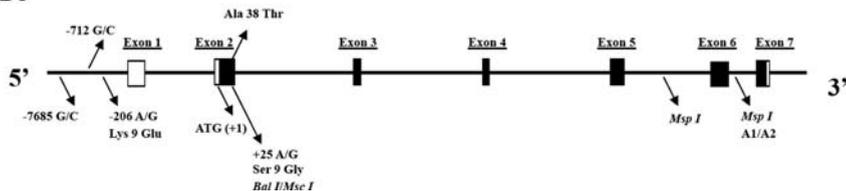
Neuroleptics that target the dopamine receptors are the mainstay of clinical pharmacological treatment for schizophrenia and bipolar disorder. The dopamine hypothesis of psychosis, in which excess dopamine or dopamine signaling is considered an important etiological factor, has been one of the most well-established theories in the field. Thus, much research has investigated whether mutations in the DRD2 gene confer susceptibility to disorders with prominent psychotic features like schizophrenia and bipolar disorder. Although some studies do not find an association between schizophrenia and the Ser<sup>311</sup>Cys missense mutation [65, 74, 79–83], several meta-analyses report a significant association with the Cys<sup>311</sup> allele [84–87]. The synonymous mutation Pro<sup>319</sup> (+957C/T) was found to be associated with schizophrenia in three European case–control studies [88–90], with a negative finding in a sample of 101 South Indians [91, 92]. This may be related to the ANKK1 protein kinase gene mentioned above, but further research is required to explain the relationship with schizophrenia.

Studies examining association between schizophrenia and other SNPs in the DRD2 gene have also generated inconsistent results (Table 19.4). Association was observed with –141C ins/del [93, 94], Taq I A and B [82, 95], and Nco I C/T [83, 91], whereas other studies have failed to find significant association for various DRD2 polymorphisms [65, 74, 82, 83, 94, 96–101]. Linkage and association studies with bipolar disorder have generally not found associations with the DRD2 gene [102–105]. In a study investigating the Taq I A and –141C ins/del polymorphisms, Li et al. found a significant association with bipolar disorder in a Chinese population but not Caucasian [106], suggesting ethnicity may account for conflicting results. Finally, Serretti et al. examined the missense mutation Ser<sup>311</sup>Cys and its association with four major psychiatric disorders (bipolar disorder, schizophrenia, major depressive disorder, and delusional disorder) [107], but did not find significant associations.

The association analysis of DRD2 polymorphisms with the abuse of substances other than alcohol has resulted in equivocal findings. The Taq I A1 allele has been shown to be associated with heroin dependence [108] and to increase risk for substance abuse in children of alcoholics [109]. The Taq I B1 allele was also found to predispose to heroin dependence [110] and other substance abuse [111]. In contrast, Goldman et al. examined Taq I A, Ser<sup>311</sup>Cys, and (GT)<sub>n</sub> STRP and found no association with substance abuse in a sample of 459 American-Indian subjects [65], while Gelernter et al. revealed a non-significant association between Taq I A, B, D polymorphism and cocaine dependence in an European- and African-American population [112].

### 19.3.3 D<sub>3</sub> Receptors

The dopamine D<sub>3</sub> receptor (DRD3) is located on chromosome 3q13.3 and contains seven exons separated by six introns (Fig. 19.4). The coding region spans six exons (exons 2–7) that are distributed over 40,000 bp and encodes for a 400-amino acid protein. The most common polymorphism studied in DRD3 is +25 A/G, which is

**DRD3**

**Fig. 19.4** Dopamine D<sub>3</sub> receptor: Schematic representation of polymorphisms (not to scale). Coding regions of exons are marked by *black blocks*, and the 5' and 3'- UTR are represented by *white blocks*. The first base of the ATG start codon is denoted as +1 and the location of other polymorphisms are given relative to the start codon. Introns are represented as a *straight line* connecting the exons. Restriction enzymes, alteration of amino acids, and other distinct descriptions are given where applicable. (Modified from Kim et al. [42])

a glycine–serine substitution at amino acid position 9, in the N-terminal extracellular domain of the receptor. This mutation creates a Bal I restriction enzyme site and alters the recognition site for Msc I [113]. The SNP –206 A/G located in the 5' region has also been studied in relation to neuropsychiatric disease. Moreover, polymorphic sites in introns 5 and 6 are identified by the restriction enzyme Msp I and a missense mutation Ala<sup>38</sup>Thr was also identified in the first transmembrane domain. The functional importance of these polymorphisms has not been examined in detail.

A large number of studies have examined the association between DRD3 Ser<sup>9</sup>Gly and schizophrenia (114), BP, ADHD, and substance abuse (Table 19.5). Contradictory results have been reported in studies with different ethnic populations and a variety of methods such as case–control, family based, and meta-analysis. The majority of studies report a lack of genetic association with disease [98, 115–128]. With respect to family-based association studies, the haplotype relative risk (HRR) and TDT strategy have been used. Weak association was reported in a case–control study conducted in a Japanese sample [129] while a positive association was found in a mixed sample of 117 North Americans and 97 Italians [130] and in 73 subjects in an East Anglian sample [131]. A meta-analysis of the relationship between Ser<sup>9</sup>Gly and schizophrenia conducted by the same group produced positive results. However, contradictory results were reported by the same group, who reviewed more than a total of 11,000 individuals and found no significant association between Ser<sup>9</sup>Gly homozygosity and schizophrenia [132]. Linkage disequilibrium approaches in two separate studies have revealed strong haplotype association with schizophrenia for haplotypes including Ser<sup>9</sup>Gly and –206 A/G [128, 129].

In bipolar disorder, a possible association with Ser<sup>9</sup>Gly polymorphism has been detected in a case–control study using a relative risk approach [133]. Although there was no difference in allele or genotype frequencies when compared to normal controls, a significant increase in the frequency of allele 1 was observed in bipolar disorder [133]. A lack of association was seen in a few case–control studies [103, 134, 135]. In ADHD, neither the Ser<sup>9</sup>Gly nor Msp I polymorphisms were associated

Table 19.5 Dopamine D<sub>3</sub> receptor polymorphisms and neuropsychiatric diseases

| References              | Polymorphisms      | Disease phenotype | Number of patients | Ethnicity          | Significance/notes                                |
|-------------------------|--------------------|-------------------|--------------------|--------------------|---|
| Nanko et al. [121]      | +25 A/G(Ser 9 Gly) | SCZ               | 91                 | Japanese           | Not significant                                   |
| Laurent et al. [124]    |                    | SCZ               | 76                 | French             | Not significant                                   |
| Gorwood et al. [140]    |                    | ALC               | 26                 | White and Black    | Not significant for all three samples             |
|                         |                    |                   | 35                 | Caucasian          |   |
|                         |                    |                   | 72                 | Scandinavian       |   |
| Kennedy et al. [130]    |                    | SCZ               | 117                | North American     | Significant                                       |
|                         |                    |                   | 97                 | Italian            |   |
| Parsian et al. [133]    |                    | BP                | 198                | Caucasian          | Significant increase in the frequency of allele 1 |
| Freimer et al. [242]    |                    | CD                | 124                | White and Black    | Not significant                                   |
| Higuchi et al. [137]    |                    | ALC               | -                  | Japanese           | Not significant                                   |
| Rietschel et al. [119]  |                    | SCZ               | 146                | German             | Not significant                                   |
| Rothschild et al. [120] |                    | SCZ               | 44 families        | -                  | Not significant                                   |
| Tanaka et al. [125]     |                    | SCZ               | 100                | Japanese           | Not significant                                   |
| Chen et al. [116]       |                    | SCZ               | 178                | Han Chinese        | Not significant                                   |
| Parsian et al. [138]    |                    | ALC               | 162                | White-Caucasian    | Not significant                                   |
| Duaux et al. [141]      |                    | OD                | 54                 | French             | Significant                                       |
| Krebs et al. [143]      |                    | SA                | 89                 | French-Caucasian   | Significant                                       |
| Comings et al. [142]    |                    | CD                | 47                 | Caucasian          | Marginal significant                              |
| Kirov et al. [103]      |                    | BP                | 122 trios          | British-Caucasian  | Not significant                                   |
| Joobar et al. [115]     |                    | SCZ               | 106                | Caucasian          | Not significant                                   |
| Kremer et al. [127]     |                    | SCZ               | 129                | Palestinian        | Not significant                                   |
| Elvidge et al. [134]    |                    | BP                | 454                | British-Caucasian  | Not significant                                   |
| Gorwood et al. [59]     |                    | ALC               | 131                | French             | Not significant                                   |
| Virgos et al. [118]     |                    | SCZ               | 540                | European-Caucasian | Not significant                                   |
| Lee et al. [139]        |                    | ALC               | 67                 | Korean             | Not significant                                   |

Table 19.5 (continued)

| References                     | Polymorphisms      | Disease phenotype | Number of patients | Ethnicity                                   | Significance/notes                         |
|--------------------------------|--------------------|-------------------|--------------------|---|--|
| Jonsson et al. [117]           |                    | SCZ               | 156                | Swedish                                     | Not significant with association study     |
| Ambrosio et al. [98]           |                    | SCZ               | 90                 | Portuguese                                  | Significant with meta-analysis             |
| Jonsson et al. [132]           |                    | SCZ               | 11066              | –   | Not significant                            |
| Szekeress et al. [243]         |                    | SCZ               | 75                 | Caucasian                                   | Not significant (meta-analysis)            |
| Rybakowski et al. [39]         |                    | SCZ               | 138                | –   | More perseverative errors in WCST with S/S |
| Van Den Bogaert et al. [135]   |                    | BP                | 182                | Swedish                                     | No association with WCST in SCZ            |
| Dominiquez et al. [123]        |                    | SCZ               | 260                | Galician                                    | Not significant                            |
| Lorenzo et al. [122]           |                    | SCZ               | 178                | Spanish                                     | Not significant                            |
| Fathalli et al. [126]          |                    | SCZ               | 408                | Caucasian from Canada, Tunisia, and Hungary | Not significant                            |
| Ishiguro et al. [129]          | +25 A/G(Ser 9 Gly) | SCZ               | 153                | Japanese                                    | Marginal significant with Ser 9 allele     |
|                                | –206 A/G           |                   |                    |   | Significant haplotype with +25, –206, –712 |
|                                | –712 G/C           |                   |                    |   |  |
|                                | Ala 38 Thr         |                   |                    |   | Not significant with A38T                  |
| Staddon et al. [128]           | +25 A/G(Ser 9 Gly) | SCZ               | 118                | Navarra of Basque origin                    | Not significant with S9G and –206 A/G      |
|                                | –206 A/G           |                   |                    |   | Significant excess of –7685C allele        |
|                                | –7685 G/C          |                   |                    |   | Significant haplotype with all three SNPs  |
| Sivagnanasundaram et al. [131] | +25 A/G(Ser 9 Gly) | SCZ               | 73                 | East Anglia, UK                             | Significant                                |
|                                | –206 A/G           |                   |                    |   |  |
|                                | –206 A/G           |                   |                    |   |  |
| Bariakci et al. [244]          |                    | SCZ               | 114                | Greece                                      | Not significant                            |

Table 19.5 (continued)

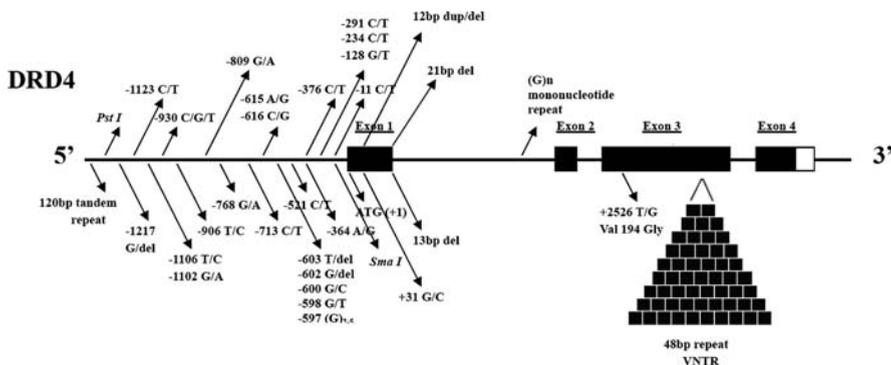
| References            | Polymorphisms      | Disease phenotype | Number of patients | Ethnicity | Significance/notes   |
|-----------------------|--------------------|-------------------|--------------------|-----------|--|
| Barr et al. [136]     | +25 A/G(Ser 9 Gly) | ADHD              | 100 families       | –         | Not significant  |
| Chiaroni et al. [245] | <i>Msp I</i>       | BP                | 60                 | –         | Homozygosity of S9G associates with manic monopolar form of BP |

Abbreviations: SCZ – schizophrenia; BP – bipolar disorder; ADHD – attention deficit hyperactivity disorder; ALC – alcoholism; CD – cocaine dependence; OD – opiate dependence; SNP – single nucleotide polymorphism; WCST – Wisconsin Card Sorting Test.  
 – undetermined or not applicable

with the disorder in a study of 100 small families [136]. Furthermore, no significant association with alcoholism was seen in several case–control studies involving various ethnic groups [59, 137–140]. In terms of substance abuse, there are reports of association between Ser<sup>9</sup>Gly and opiate dependence [141], cocaine dependence [142], and other substance dependence in schizophrenic patients [143]. As a whole, the present findings to date do not provide strong support for the role of DRD3 polymorphisms in neuropsychiatric diseases.

### 19.3.4 D<sub>4</sub> Receptors

The dopamine D<sub>4</sub> receptor (DRD4) gene is located on chromosome 11p15.5 and contains four exons comprising the coding region (Fig. 19.5). The gene is 3,399 bp in size, and encodes a variable number of amino acids depending on the number of repeats present in exon 3. The DRD4 locus is highly polymorphic with a remarkable number of polymorphisms, especially in the 5' UTR. The most extensively studied polymorphism is the 48 bp tandem repeat (VNTR) in exon 3. It is a hypervariable region located in the third intracellular cytoplasmic loop and consists of 2–11 repeats, typically written as D4.x, where x is the number of repeats. Allele frequencies vary considerably depending on ethnicity, with D4.2, D4.4, and D4.7 being the most common [144]. The number of repeats has been reported to influence some dimensions of personality such as novelty seeking [145–147] and has an impact on the pharmacological profile [148, 149]. Another 120 bp tandem repeat is found 1.2 kb upstream of the initiation codon and it has been shown to contain transcription factor binding sites [150]. Numerous SNPs are present in the 5' UTR as well [151]. The promoter for the DRD4 gene, located between position –591 and –123



**Fig. 19.5** Dopamine D<sub>4</sub> receptor: Schematic representation of polymorphisms (not to scale). Coding regions of exons are marked by *black blocks*, and the 5' and 3'- UTR are represented by *white blocks*. The first base of the ATG start codon is denoted as +1 and the location of other polymorphisms are given relative to the start codon. Introns are represented as a *straight line* connecting the exons. Restriction enzymes, alteration of amino acids, and other distinct descriptions are given where applicable. (Modified from Kim et al. [42])

relative to the start codon, is responsible for cell type-specific expression of the gene [152] and regulates transcriptional activity [153]. The T allele of the  $-521\text{C/T}$  polymorphism reduces transcriptional efficiency by 40% compared with the C allele [154]. In the coding region, other than the 48 bp VNTR, exon 1 contains a 12 bp duplication–deletion mutation, a 13 bp deletion that causes a frameshift mutation and a 21 bp deletion. The 12 bp mutation affects amino acids in the N-terminal, extracellular region [155]; the 13 bp frameshift mutation produces a truncated, non-functional form of the protein [1], and the 21 bp deletion removes codons 36–42 in the first transmembrane region [156]. A variable number of repeated G nucleotides are also present in intron 1 but it is not clear if this variant has significant functional impact.

The 48 bp VNTR has been investigated extensively for association with neuropsychiatric diseases, especially ADHD and schizophrenia, as well as variation in personality dimensions, particularly novelty seeking (Table 19.6). Again, conflicting results have been observed in various studies on different ethnic groups and using different methods. No difference in the D4.7 allele frequency or preferential transmission with ADHD was observed in several family-based studies that used the HRR and TDT approach [157–161] nor in case–control studies [158, 162]. Another study reported no association with ADHD in 123 subjects of mixed ethnic groups [163]. Moreover, Mill et al. detected a significant association but no linkage in a sample of British Caucasians using both case–control and family-based samples [164]. An interesting study investigated the relationship between the D4.7 variant and sustained attention in ADHD and found no impairment when compared with controls [165]. Despite the large number of negative findings, strong association between the D4.7 allele and ADHD has been well established in the literature [166–175]. Positive association with a refined phenotype, inattentive-type, and combined type of ADHD was also demonstrated [176, 177]. A recent analysis using neuropsychological tests revealed that the D4.7 allele is associated with significantly more incorrect and impulsive responses [178]. When considering the VNTR data in their entirety, it appears that more repeats ( $>\text{D}4.4$ ) are associated with a higher risk for ADHD, while a small number of repeats may even be protective [179–182]. Other DRD4 polymorphisms have not been investigated as thoroughly for association with ADHD. Nonetheless, several groups have found a lack of association for  $-521\text{ C/T}$ ,  $-615\text{ A/G}$ ,  $-616\text{ C/G}$ , the 120 bp tandem repeat, and the 12 bp dup/del variant [165, 175, 182, 183]. There are positive findings for  $-521\text{T}$  [184] and the 120 bp tandem repeat [183, 185] and ADHD. Some haplotypes with the D4.7 polymorphism and the 120 bp duplication have also been associated with ADHD [167, 175]. Moreover, two meta-analyses found a significant association between the D4.7 allele and ADHD [186, 187]. Despite the inconsistencies, the association between ADHD and the 48 bp VNTR in DRD4 is one of the strongest results in neuropsychiatric disease genetics.

The relationship between DRD4 polymorphisms and schizophrenia has also been inconsistent. For the 48 bp VNTR, positive results [188–192] involving most of the different repeats (D4.2–D4.8) are counterbalanced by reports of no association [193–199]. Interestingly, Lung et al. found a similar trend as in ADHD, with a

**Table 19.6** Dopamine D<sub>4</sub> receptor polymorphisms and neuropsychiatric diseases

| References  | Polymorphisms   | Disease phenotype                                    | Number of patients  | Ethnicity  | Significance/notes   |
|---|-----------------|--|---|--|--|
| Weiss et al. [188]<br>Rowe et al. [177]   | 48 bp VNTR (7R) | SCZ<br>ADHD  | 201<br>239  | German<br>Caucasian,<br>African-American,<br>Hispanic, Asian<br>Caucasian                                  | Significant<br>Significant with both<br>inattentive-type and<br>combined-type ADHD<br>Significant<br>Significant association with a<br>refined phenotype of<br>ADHD  |
| Smalley et al. [173]<br>Swanson et al. [176]  |                 | ADHD<br>ADHD   | 133<br>39   | –  | Significant<br>Significant association with a<br>refined phenotype of<br>ADHD  |
| Faraone et al. [169]<br>Eisenberg et al. [157]<br>Hawi et al. [158]<br>Kotler et al. [171]<br>Tahir et al. [172]<br>Faraone et al. [187]<br>Mill et al. [164] |                 | ADHD<br>ADHD<br>ADHD<br>ADHD<br>ADHD<br>ADHD<br>ADHD | 27 triads<br>48 triads<br>78<br>98 triads<br>104<br>–<br>132<br>85 trios<br>187 | –<br>Jews<br>Irish<br>Israeli<br>Turkish<br>–<br>British-Caucasian<br>–                                    | Significant<br>Not significant<br>Not significant<br>Significant<br>Significant<br>Significant (meta-analysis)<br>Significant association but no<br>linkage<br>Significant more symptoms<br>with fathers possessing 7R |
| Rowe et al. [174]<br>Grady et al. [167]   |                 | ADHD<br>ADHD   | 132<br>132  | European, Hispanic,<br>African-American,<br>Asian and<br>Native-American<br>Caucasian<br>British-Caucasian | Significant with 7R and<br>haplotype significant<br>associates with 7R<br>Significant with boys<br>Significant more incorrect<br>and impulsive responses<br>with<br>neuropsychological tests<br>Not significant        |
| El-Faddagh et al. [166]<br>Langley et al. [178]   |                 | ADHD<br>ADHD   | 265<br>133  | –  | Significant more symptoms<br>with fathers possessing 7R  |
| Barkley et al. [163]  |                 | ADHD   | 123   | White, Black, and<br>Hispanic  | Significant with 7R and<br>haplotype significant<br>associates with 7R<br>Significant with boys<br>Significant more incorrect<br>and impulsive responses<br>with<br>neuropsychological tests<br>Not significant        |

Table 19.6 (continued)

| References             | Polymorphisms              | Disease phenotype | Number of patients | Ethnicity  | Significance/notes   |
|------------------------|----------------------------|-------------------|--------------------|--|--|
| Brookes et al. [168]   |                            | ADHD              | 776                | European-American                                  | Significant  |
| Carrasco et al. [161]  |                            | ADHD              | 51                 | Chilean  | Not significant  |
| Gornick et al. [170]   |                            | ADHD              | 166                | Caucasian,<br>African-American,<br>Hispanic, Asian | Significant  |
| Zhang et al. [189]     | 48 bp VNTR (6R)            | SCZ               | 67                 | Han Chinese  | Significant  |
| Li et al. [106]        | 48 bp VNTR (1R)            | BP                | 275                | Caucasian and Han<br>Chinese                       | Not significant  |
| McCracken et al. [185] | 120 bp TR (5'-UTR)         | ADHD              | 371                | Caucasian  | Significant with 240 bp allele   |
| Cheuk et al. [160]     | 48 bp VNTR (4R, 7R)        | ADHD              | 64                 | Chinese  | Not significant  |
| Qian et al. [179]      | 48 bp VNTR (4-6R)          | ADHD              | 340                | Han Chinese  | Significant  |
|                        |                            |                   | 202 trios          |  |  |
| Qian et al. [180]      |                            | ADHD              | 542                | Han Chinese  | Marginal significant with<br>long repeats (4-6R)                             |
| Hong et al. [193]      | 48 bp VNTR (2R, 7R)        | SCZ               | 124                | Chinese and Caucasian                              | Not significant  |
| Leung et al. [162]     |                            | ADHD              | 32                 | Han Chinese  | Significant with 2R  |
| Kaiser et al. [194]    | 48 bp VNTR (2R, 3R)        | SCZ               | 638                | German-Caucasian                                   | Not significant with 7R  |
| George et al. [213]    | 48 bp VNTR (3R, 6R)        | ALC               | 72                 | Caucasian  | Not significant  |
| Glatt et al. [201]     | 48 bp VNTR (2R, 4R,<br>7R) | SCZ               | -                  | -  | Not significant but may have<br>sex-dependent association<br>(meta-analysis) |
| Bakker et al. [159]    |                            | ADHD              | 236                | Dutch  | Not significant  |
| Lim et al. [209]       | 48 bp VNTR (2-11R)         | BP                | 147                | English and Caucasian                              | Not significant  |
| Shaikh et al. [198]    |                            | SCZ               | 191                | English and Japanese                               | Not significant  |
| Kotler et al. [216]    |                            | OD                | 141                | Israeli Arabs and<br>Sephardic Jews                | Significant  |
| Li et al. [215]        |                            | OD                | 121                | Han Chinese  | Significant with long repeats<br>(5R-7R)                                     |

Table 19.6 (continued)

| References                | Polymorphisms                                     | Disease phenotype | Number of patients | Ethnicity           | Significance/notes  |
|---------------------------|---|-------------------|--------------------|---------------------|---|
| Parsian et al. [138]      |   | ALC               | 162                | White Caucasian     | Not significant   |
| Bocchetta et al. [208]    |   | BP                | 267                | Sardinian           | Not significant   |
| Franke et al. [214]       |   | OD                | 396                | German              | Not significant   |
| Tang et al. [190]         |   | SCZ               | 510                | Chinese             | Significant with lacking 2R, 3R and excess of 4R  |
| Lung et al. [200]         |   | SCZ               | 305                | Caucasian and Asian | Not significant with VNTR $\leq 5R$   |
| Maher et al. [186]        |   | ADHD              | 571                | –                   | Significant with VNTR $\geq 6R$   |
| Muglia et al. [210]       |   | BP                | 154                | Caucasian           | Significant (meta-analysis) Significant with 4R but 2R may have protective effect   |
| Tsai et al. [246]         |   | MA                | 116                | Taiwanese           | Not significant   |
| Li et al. [181]           |   | ADHD              | –                  | European and Asian  | Significant with 5R, 7R   |
| Hong et al. [247]         |   | SCZ               | 80                 | Chinese             | Not significant   |
| Arcos-Burgos et al. [175] | 12 bp dup/del<br>48 bp VNTR<br>120 bp TR (5'-UTR) | ADHD              | 79 families        | South American      | Significant with 7R<br>Not significant with 120 bp TR   |
| Aguirre et al. [191]      |   | SCZ               | 149                | Mexican             | Haplotype significant with 7R and 240 bp TR<br>Significant with 3R, 5R, 6R, 8R<br>Not significant with 120 bp TR<br>Haplotype significant with 3R, 5R, 6R, 8R |

Table 19.6 (continued)

| References             | Polymorphisms   | Disease phenotype | Number of patients | Ethnicity    | Significance/notes   |
|------------------------|---|-------------------|--------------------|--------------|--|
| Kohn et al. [196]      | 48 bp VNTR<br>12 bp dup/del                                     | SCZ               | 98                 | Israeli Jews | Not significant  |
| Serretti et al. [248]  |   | SCZ<br>BP<br>UP   | 651                | Italian      | Not significant  |
| Barr et al. [195]      | 48 bp VNTR (4R, 7R)<br>(G) <sub>n</sub> repeat (9R)<br>-521 C/T | SCZ               | Kindred            | Swedish      | Not significant  |
| Okuyama et al. [154]   |   | SCZ               | 252                | Japanese     | Marginal significant with<br>C-allele  |
| Jonsson et al. [205]   |   | SCZ               | 132                | Swedish      | Not significant  |
| Rybakowski et al. [39] |   | SCZ               | 138                | -            | Not significant with WCST<br>in SCZ  |
| Guan et al. [184]      |   | ADHD              | 401                | Han Chinese  | Significant with T-allele  |
| Ishiguro et al. [212]  | -521 C/T  | ALC               | 185                | Japanese     | Not significant  |
| Lung et al. [192]      | 48 bp VNTR  | SCZ               | 630                | Chinese      | Significant with long (>4R)<br>VNTR  |
| Munafò et al. [218]    |   | PT                | -                  | -            | Not significant with -521<br>Significant with -521<br>Not significant with 48 bp<br>VNTR (meta-analysis) |
| Szilagyi et al. [217]  | 120 bp TR (5'-UTR)<br>-521 C/T                                  | HD                | 73                 | Caucasian    | Significant with -521<br>Not significant with 120 bp<br>TR and 48 bp VNTR                                |
| Jonsson et al. [207]   | 48 bp VNTR<br>48 bp VNTR<br>-521 C/T<br>12 bp dup/del           | SCZ               | 5696               | -            | Significant with -521<br>Not significant with 48 bp<br>VNTR and 12 bp<br>duplication<br>(meta-analysis)  |

Table 19.6 (continued)

| References              | Polymorphisms   | Disease phenotype | Number of patients | Ethnicity             | Significance/notes   |
|-------------------------|---|-------------------|--------------------|-----------------------|--|
| Seeman et al. [249]     | +2526 T/G (V194G)   | SCZ               | 92                 | African and Caucasian | Not significant  |
| Bhaduri et al. [182]    | 120 bp TR (5'-UTR)<br>12 bp dup/del                             | ADHD              | 50                 | Indians               | Significant with 6R and 7R<br>Not significant with 120 bp TR and 12 bp duplication |
| Kereszturi et al. [183] | 48 bp VNTR (6R, 7R)<br>120 bp TR (5'-UTR)<br>-616 C/G           | ADHD              | 173                | Caucasian             | Significant with 120 bp TR (1 repeat)<br>Not significant with -616, -615 and -521  |
| Ambrosio et al. [197]   | -521 C/T<br>-616 C/G<br>-521 C/T                                | SCZ               | 90 trios           | Portuguese            | Not significant  |
| Bellgrove et al. [165]  | 48 bp VNTR<br>48 bp VNTR (7R)<br>-616 C/G                       | ADHD              | 54                 | European              | Not significant  |
| Petronis et al. [199]   | 48 bp VNTR (7R)<br>(G) <sub>n</sub> repeat<br><i>Sma</i> I RFLP | SCZ               | 50                 | European              | Not significant with all SNPs but a trend toward excess of 7R                      |
| Mitsuyasu et al. [202]  | 12 bp dup/del<br>-768 G/A<br>-616 C/G                           | SCZ               | 208                | Japanese              | Not significant  |
| Golimbet et al. [203]   | -521 C/T<br>48 bp VNTR<br>-809 G/A<br>-616 G/C<br>-521 C/T      | SCZ               | 240                | Russian               | Not significant  |

Table 19.6 (continued)

| References                                   | Polymorphisms   | Disease phenotype | Number of patients | Ethnicity           | Significance/notes  |
|--|---|-------------------|--------------------|---------------------|---|
| Xing et al. [204]                            | -616 G/C<br>-603 T/del<br>-602 G/del<br>-600 G/C<br>-521 C/T<br>-376 C/T  | SCZ               | 210                | Chinese             | Significant with 120 bp TR<br>Not significant with -616,<br>-603, -602, -600, -521,<br>-376                                       |
| Chang et al. [211]                           | 120 bp TR (5'-UTR)<br><i>Sma</i> I RFLP<br>12 bp dup/del<br>13 bp del<br>(G) <sub>n</sub> repeat<br>+ 2526 T/G (V194G)<br>48 bp VNTR<br><i>Pst</i> I<br>13 bp del | ALC               | 62                 | Taiwanese           | Haplotype significant with<br>120 bp TR, -616, -602,<br>-521, -376<br>Not significant with<br>individual SNPs or as<br>haplotypes |
| Paterson et al. [206]<br>Nothen et al. [250] | <i>Pst</i> I<br>13 bp del   | SCZ<br>SCZ<br>BP  | 41<br>236          | Caucasian<br>German | Not significant<br>Not significant  |
| Mitsuyasu et al. [151]                       | 120 bp TR (5'-UTR)<br>-1217 G/del<br>-1123 C/T<br>-1106 T/C<br>-1102 G/A<br>-930 C/G/T<br>-906 T/C<br>-809 G/A<br>-768 G/A<br>-713 C/T                            | SCZ               | 216                | Japanese            | Not significant with<br>individual SNPs and weak<br>association with<br>haplotypes  |

Table 19.6 (continued)

| References | Polymorphisms           | Disease phenotype | Number of patients | Ethnicity | Significance/notes |
|------------|-------------------------|-------------------|--------------------|-----------|--------------------|
|            | -616 C/G                |                   |                    |           |                    |
|            | -615 A/G                |                   |                    |           |                    |
|            | -603 T/del              |                   |                    |           |                    |
|            | -600 G/C                |                   |                    |           |                    |
|            | -598 G/T                |                   |                    |           |                    |
|            | -597 (G) <sub>2-5</sub> |                   |                    |           |                    |
|            | -521 C/T                |                   |                    |           |                    |
|            | -376 C/T                |                   |                    |           |                    |
|            | -364 A/G                |                   |                    |           |                    |
|            | -291 C/T                |                   |                    |           |                    |
|            | -234 C/A                |                   |                    |           |                    |
|            | -128 G/T                |                   |                    |           |                    |
|            | -11 C/T                 |                   |                    |           |                    |
|            | +31 G/C                 |                   |                    |           |                    |
|            | 12 bp dup/del           |                   |                    |           |                    |
|            | 21 bp del               |                   |                    |           |                    |
|            | 13 bp del               |                   |                    |           |                    |
|            | 48 bp VNTR              |                   |                    |           |                    |

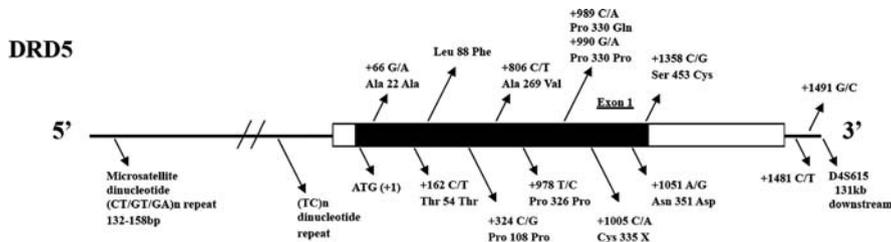
Abbreviations: SCZ – schizophrenia; BP – bipolar disorder; ADHD – attention deficit hyperactivity disorder; ALC – alcoholism; HD – heroin dependence; OD – opiate dependence; UP – unipolar disorder; PT – personality traits; SNP – single nucleotide polymorphism; VNTR – variable number of tandem repeats; TR – tandem repeats; MA – methamphetamine abuse.  
 – undetermined or not applicable

greater number of repeats in the VNTR (>5) associated with increased disease susceptibility [200]. A meta-analysis conducted by Glatt et al. concluded that there was no association for the 48 bp VNTR and schizophrenia, although sex-dependent association may be present [201]. The considerable ethnic variation in this polymorphism complicates the interpretation of inconsistencies between studies based on different ethnic groups. Other SNPs in the 5' UTR have been studied in several groups with their relation to schizophrenia, but the most comprehensive examined 28 polymorphisms tested for association with schizophrenia in a sample of 216 Japanese patients [151]. No significant association was observed with any individual SNP, but there was weak association for some particular haplotypes. This is consistent with the negative or weak findings of other studies that also investigated the same polymorphisms [154, 197, 202–206]. One meta-analysis reviewed several DRD4 polymorphisms and its relationship with schizophrenia in a total of 5,696 individuals [207]; a significant association was found with the –521 C/T allele but not for the 48 bp VNTR nor the 12 bp mutation in exon 1.

There are few studies investigating the association of DRD4 polymorphisms with bipolar disorder or substance abuse. Two groups found no association between the 48 bp VNTR variant and bipolar disorder [208, 209], whereas one study detected an association with D4.4 in 154 patients of Caucasian origin [210]. A rare D4.1 variant and the 13 bp deletion in exon 1 were tested as well; no association was found [106, 206]. For alcoholism, there are several studies reporting no association [138, 211, 212], and only one positive finding [213]. Case–control and family-based studies of opioid dependence include one case–control study of 396 German probands showing no association [214] and several studies reporting association between long repeats of the 48 bp VNTR and –521 C/T and opioid dependence [215–217]. The relationship between novelty seeking and the DRD4 gene has received considerable publicity, and there is an interesting meta-analysis of the association between 48 bp VNTR and –521 C/T polymorphisms with approach-related personality traits [218]. No overall effect was found for the 48 bp VNTR, but –521 C/T was shown to be significantly associated with traits such as novelty seeking and impulsivity.

### **19.3.5 D<sub>5</sub> Receptors**

The dopamine D<sub>5</sub> receptor (DRD5) has not been investigated as much as some of the other subtypes discussed above. The DRD5 gene is located on chromosome 4p16.1 and contains only one exon with the coding region embedded (Fig. 19.6). The gene is 2,031 bp long and encodes 477 amino acids. Not many polymorphisms have been discovered in the DRD5 gene, but a dinucleotide repeat microsatellite polymorphism (CT/GT/GA)<sub>n</sub>, located 18.5 kb from the 5' end of the gene is highly polymorphic with at least 12 possible alleles [219]. In particular, the 148 bp allele has been extensively studied in relation to neuropsychiatric disease (Table 19.7). Within the 5' UTR, a (TC)<sub>n</sub> dinucleotide repeat located within the promoter region has also been studied in schizophrenia and bipolar disorder [220]. However, there is no evidence that this repeat affects transcription activity or function. In addition,



**Fig. 19.6** Dopamine D<sub>5</sub> receptor: Schematic representation of polymorphisms (not to scale). Coding regions of exons are marked by *black blocks*, and the 5' and 3'-UTR are represented by *white blocks*. The first base of the ATG start codon is denoted as +1 and the location of other polymorphisms are given relative to the start codon. Introns are represented as a *straight line* connecting the exons. Restriction enzymes, alteration of amino acids, and other distinct descriptions are given where applicable. (Modified from Kim et al. [42])

Sobell et al. described nine different SNPs in the coding region, including five missense and four silent mutations [221]. Of the five missense mutations, Ala<sup>269</sup>Val in the third extracellular loop, Pro<sup>330</sup>Gln in the third cytoplasmic loop, Asn<sup>351</sup>Asp in the seventh transmembrane domain, and Ser<sup>453</sup>Cys in the C-terminus result in protein sequence changes and may have important functional consequences. A nonsense mutation Cys<sup>335</sup> results in a truncated protein. Moreover, two polymorphisms (+1,481 C/T and +1,491 G/C) present in the 3' end have been investigated [220]. Interestingly, one recently discovered novel SNP, D4S615, located far from the coding region, may be involved in schizophrenia [222].

As mentioned before, the most common allele of the microsatellite polymorphism is the 148 bp allele and a number of different studies have examined association with schizophrenia, bipolar disorder, ADHD, and substance abuse. As with other genetic association studies of dopamine receptor genes, contradictory results have been reported with both case-control and family-based studies. No association with ADHD was observed in some studies [159, 172, 223, 224], while others have demonstrated association [225–227]. A meta-analysis of European subjects revealed increased risk effect for ADHD with the 148 bp allele vs. a protective effect of the 136 bp allele [181]. This was further supported by another meta-analysis which also demonstrated a significant association between the 148 bp allele and ADHD [186].

No association with the 148 bp allele and schizophrenia was seen in two different pedigrees [228] and in a case-control Caucasian study [224], whereas a positive finding was reported in a larger Scottish sample ( $n = 428$ ) [222]. Sobell et al. also noted non-significant case-control results with schizophrenia for polymorphisms in the coding region [221], suggesting that the resulting changes in protein sequence do not affect susceptibility to schizophrenia. A lack of association and no difference in allele frequencies with both schizophrenia and bipolar disorder were found in a family linkage study [220]. To further support this notion, no association was seen in a family-based and a case-control study on the (CT/GT/GA)<sub>n</sub> dinucleotide repeat with bipolar disorder [103, 222]. In addition, the D4S615 microsatellite polymorphism has been shown to be associated with

**Table 19.7** Dopamine D<sub>5</sub> receptor polymorphisms and neuropsychiatric diseases

| References            | Polymorphisms  | Disease phenotype | Number of patients | Ethnicity                               | Significance/notes  |
|-----------------------|--|-------------------|--------------------|---|---|
| Vanyukov et al. [251] | (CT/GT/GA) <sub>n</sub> repeat<br>148 bp                       | SA                | 42                 | European-American                       | Significant with more robust differences in females                       |
| Daly et al. [225]     |  | ADHD              | 118                | Irish                                   | Significant   |
| Barr et al. [223]     |  | ADHD              | 116                | Caucasian                               | Not significant   |
| Maher et al. [186]    |  | ADHD              | 571                | –                                       | Significant (meta-analysis)   |
| Lowe et al. [227]     |  | ADHD              | –                  | Large combined homogenous international | Significant with inattentive and combined clinical subtypes               |
| Manor et al. [226]    |  | ADHD              | 164                | Israeli                                 | Marginal significant  |
| Bakker et al. [159]   |  | ADHD              | 236                | Dutch                                   | Not significant   |
| Li et al. [181]       | (CT/GT/GA) <sub>n</sub> repeat<br>136, 146 and 148 bp          | ADHD              | –                  | European                                | Significant effect of 148 bp from meta-analysis                           |
|                       |  |                   |                    |   | Not significant with 136 and 146 bp                                       |
| Muir et al. [222]     | (CT/GT/GA) <sub>n</sub> repeat<br>148 bp<br>D4S615             | SCZ<br>BP         | 428                | Scottish                                | Significant with SCZ for 148 bp and D4S615 but not with LD                |
| Asherson et al. [220] | (TC) <sub>n</sub> repeat<br>+978 T/C<br>+1481 C/T<br>+1491 G/C | SCZ<br>BP         | 227                | Caucasian from UK                       | Not significant with BP<br>Not significant                                |
| Kalsi et al. [228]    | (CT/GT/GA) <sub>n</sub> repeat<br>134–156 bp                   | SCZ               | 11                 | Icelandic                               | Not significant but maybe of etiological importance                       |
| Kirov et al. [103]    |  | BP                | 12 (pedigrees)     | English                                 | Not significant   |
| Tahir et al. [172]    |  | ADHD              | 122 trios          | British-Caucasian                       | Not significant   |
| Mill et al. [224]     | (CT/GT/GA) <sub>n</sub> repeat<br>148 bp<br>D4S615             | ADHD<br>SCZ       | 111<br>188         | Turkish<br>Caucasian                    | Not significant<br>Significant with D4S615<br>Not significant with 148 bp |

**Table 19.7** (continued)

| References          | Polymorphisms  | Disease phenotype | Number of patients | Ethnicity  | Significance/notes            |
|---------------------|--|-------------------|--------------------|--|-------------------------------|
| Sobell et al. [221] | Cys 335 X<br>Asn 351 Asp<br>Ala 269 Val<br>Ser 453 Cys<br>Pro 330 Gln<br>4 other silent SNPs | SCZ               | 78                 | Caucasian,<br>African-American,<br>Asian,<br>Native-American | Not significant with all SNPs |

Abbreviations: SCZ – schizophrenia; BP – bipolar disorder; ADHD – attention deficit hyperactivity disorder; SA – substance abuse; SNP – single nucleotide polymorphism; LD – linkage disequilibrium.  
– undetermined or not applicable

schizophrenia in two separate studies, suggesting that the downstream region of DRD5 may link to molecular mechanisms involved in schizophrenia [222, 224]. A possible interpretation of these results given by the group was that the D4S615 polymorphisms show independent linkage disequilibrium with an allele at 4p16 that increases susceptibility to schizophrenia [222]. Further evidence is required to confirm this hypothesis and the task of unraveling this putative mechanism remains a challenge.

## 19.4 Conclusion

The relationship between dopamine receptor polymorphisms and neuropsychiatric diseases has been studied extensively, but inconsistent results have emerged. Although there are some replicated associations between specific polymorphisms and some disorders, these examples are tempered by non-significant results from other studies. Overall, the associations between (1) alcoholism and the DRD2 Taq I A polymorphism, and (2) DRD4 variation, ADHD, and related traits of impulsivity and novelty seeking have the strongest support. A number of confounding factors may account for these inconsistencies. Case-control studies are susceptible to false associations due to population stratification, with some SNP frequencies varying considerably among different ethnic groups. Family-based association tests avoid this problem, but at the cost of smaller sample sizes due to the difficulty of recruiting multiple family members in addition to the proband [229]. In addition, neuropsychiatric diseases are both genetically and biologically complex. Polygenic disease models involve many susceptibility and protective genes that may interact, meaning that each candidate gene may exert only a small effect, may interact with other genetic variants, or may be operating only in some cases or families. As a result, single studies are often underpowered to detect these small signals amidst considerable noise. In this sense, haplotype analysis can be helpful, but the analysis of concurrent or combinatorial variation in many genes and SNPs remains a challenge, especially as whole-genome association data from large collaborative samples begin to emerge.

The genetic study of neuropsychiatric disease is complicated further by the lack of defining pathological signatures to establish diagnosis. This leads to problems of etiological heterogeneity, ascertainment bias, and phenocopies that no amount of analytical refinement can address. While genetic studies of complex diseases such as cancer, autoimmune disorders, cardiovascular, and metabolic disease are also affected by the complexity of polygenetic interactions, at least diagnosis can be established with objective biochemical or pathological markers. Perhaps the most difficult confounding factor is the multidetermined nature of behavior and the related issue of non-deterministic relationships between brain structure and function. With our current and limited understanding of the emergent properties of neuron, network, and circuit assemblies in the brain, it may not be possible to detect simple relationships between DNA variation and the higher level psychological functions involved in neuropsychiatric disease.

In conclusion, the source of inconsistency in individual genetic association and linkage studies cannot be easily explained, though variations in ethnic grouping, phenotype assignment, sampling bias, and etiological heterogeneity are certainly not helpful. Addressing these confounds will be a major challenge for the genetic analysis of any complex disease in the future [77]. Improved genetic analysis methods that incorporate information on gene–gene interactions will be useful, but gene–environment interactions and epigenetic mechanisms are also likely to be important, and a way of integrating data on all of these components is needed. In this review, we focused on genetic association studies of dopamine receptor polymorphisms and major neuropsychiatric disorders, but did not seek to cover all normal and disease phenotypes that have been investigated. These other disorders include Parkinson’s disease, Tourette syndrome, Huntington’s chorea, Alzheimer’s disease, and novelty seeking, for example. Furthermore, dopamine receptor gene variation has also been associated with differences in the efficacy and side effects of dopaminergic drugs [1]. Studies have demonstrated the association between DRD2 –241A/G polymorphism and risperidone response in schizophrenic patients [230], whereas the Taq I A allele has been reported to increase risk for hyperprolactinemia-related side effects with nemonapride [231]. In addition, one of the most important side effects in the long-term treatment of schizophrenia with typical antipsychotics is tardive dyskinesia (TD). Different dopamine receptor variants have been investigated, with DRD3 being the most extensively studied in relation to the risk of TD. A strong association was first reported with the Ser<sup>9</sup>Gly variant [232] and confirmed by a recent meta-analysis [233], although some studies do not support the original finding [234, 235]. However, the pharmacogenetics of dopamine receptor genes is itself a large area and beyond the scope of this review.

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