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# PharmGKB summary: dopamine receptor D2

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#### Keywords

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#### Overview

Dopamine is a catecholamine neurotransmitter and controls a variety of functions including cognition, emotion, locomotor activity, food intake, and endocrine system regulation in the central nervous system [1]. In the periphery, dopamine modulates cardiovascular and renal functions, hormone secretion, and gastrointestinal motility [1]. Several pathological conditions, such as Parkinson's disease (PD), schizophrenia, restless leg syndrome, and endocrine tumors, for example, pituitary adenomas have been linked to dysregulation of dopaminergic signal transmission [1,2]. The dopamine D<sub>2</sub> receptor (DRD2) is one of the five different dopamine receptors that have been identified in humans, and shows high expression in both the pituitary gland and the central nervous system [3]. The dopamine receptors belong to the family of G protein coupled receptors. They are grouped into D<sub>1</sub>-like receptors, including DRD1 and DRD5, generally associated with stimulatory functions, and D<sub>2</sub>-like receptors, including DRD2, DRD3, and DRD4, generally associated with inhibitory functions [1]. The distinct subfamily of G protein coupled receptors, to which DRD2, DRD3, and DRD4 belong, was derived likely from gene duplication before the vertebrate expansion; these receptors are also known to share similar pharmacological profiles [4,5].

In 1989, Grandy *et al.* [6] cloned and mapped the *DRD2* gene to the 11q22–q23 junction by in-situ hybridization [7]. The gene is interrupted by six introns [6]. Alternative splicing of this gene results in short (D2S) and long (D2L) isoforms [8]. The short isoform is also known as D2(415), whereas the long isoform is known as D2(444). The difference between the long and short isoforms is the inclusion of an alternatively spliced exon that accounts for the 29 extra amino acids found in third cytoplasmic loop in the protein structure of the long isoform [9]. D2L is primarily located postsynaptically, whereas D2S functions as a presynaptic autoreceptor [10]. The two isoforms have similar pharmacological characteristics [1,11]. The length modification of the third cytoplasmatic loop suggests that there may be downstream signaling differences between the two isoforms. Differences in Gi protein subtype preferences and in regulation of receptor internalization were found for D2S and D2L [10,12–16]. A third longer isoform was reported in brains from patients who died

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with psychosis, but this isoform has not been fully characterized [17]. A study, which investigated regulatory polymorphisms in *DRD2* gene, showed that the T allele of two highly linked single nucleotide polymorphisms (SNPs) in intron 5, rs2283265 (G > T) and intron 6, rs1076560 (G > T) shift splicing from D2S to D2L [18].

Many dopamine receptor agonists that bind to the D<sub>2</sub>-like family of dopamine receptors are used as antiparkinsonian medications, such as apomorphine, bromocriptine, cabergoline, dihydroergocryptine, lisuride, pergolide, piribedil, pramipexole, ropinirole, and rotigotine [19,20]. Most antipsychotics antagonize the DRD2 as part of their pharmacological profile but also act at a number of other neurotransmitter receptors including other dopamine receptor subtypes, serotonin and histamine receptors [21–23]. First generation or typical antipsychotic drugs such as chlorpromazine and haloperidol cause both antipsychotic actions and many side effects, which are contributed to their high affinity DRD2 antagonism [24]. Side effects of antipsychotics include risk of tardive dyskinesia (TD), extrapyramidal side effects, and hyper-prolactinemia [24]. Olanzapine, quetiapine, and ziprasi-done are second generation or atypical antipsychotics that have a more pronounced serotonin antagonism than dopamine antagonism but still antagonize DRD2 [24]. Risperidone, another second generation antipsychotic, has a more balanced serotonin-dopamine antagonism profile [25]. Aripiprazole [26] and bifeprunox [27] are the newest atypical antipsychotic drugs [28]. Unlike other antipsychotics, aripiprazole and bifeprunox act as partial DRD2 agonists. Aplindore, another partial DRD2 agonist, was originally developed as an antipsychotic and is currently being studied as a potential treatment for PD [28,29]. Kapur and Seeman [30] also postulated a fast dissociation hypothesis based on a study of clozapine and quetiapine toward D2 receptor, and suggested that it is the possible explanation for the low extrapyramidal side effects induced by these two drugs as compared with other atypical and typical antipsychotics.

More than 200 polymorphisms have been identified in the DNA encompassing the genomic sequence of this gene; most are in the introns and the downstream flanking region [7,15,31–36], but some are in the coding [37] and the upstream promoter regions [38]. Allele frequencies of a number of these polymorphisms have been determined in different populations

(http://alfred.med.yale.edu/alfred/recordinfo.asp?condition=loci.locus\_uid=`LO000168P). Variants of the *DRD2* gene have been associated with alcoholism and other addictive disorders such as cocaine, nicotine and opioid dependence, mood disorders, schizophrenia, and movement disorders, reviewed in [39]. *DRD2* variants are not only relevant to disease susceptibility but also have been associated with the pharmacogenetics of several antipsychotics [40]. In addition, *DRD2* is among the several candidate genes that have been reported to be associated with the efficacy of bupropion and nicotine replacement therapy (NRT) for smoking cessation [41]. The four SNPs, discussed in more detail in the important variant section below, are the most commonly investigated SNPs in the *DRD2* gene.

Online content for the DRD2 gene (PA27478) and very important pharmacogene summary information is available at *http://www.pharmgkb.org/search/annotatedGene/drd2*.

Important variants:

DRD2: -141C Insertion/Deletion (Ins/Del); rs1799732 DRD2: Taq1A; rs1800497 DRD2: 957C > T; rs6277 DRD2: Ser311Cys; rs1801028

# Rs1799732; -141C Ins/Del

The -141C Ins/Del polymorphism of *DRD2* has been reported to influence the outcome of both antipsychotic [40] and addiction treatments [42,43]. The -141C Ins/ Del polymorphism is located in the promoter region of the DRD2 gene

(http://www.ncbi.nlm.nih.gov/SNP/snp\_ref.cgi?rs=rs1799732) and is found at an allele frequency of approximately 22% of the Japanese population. This allele is less common among Chinese and Caucasian populations (9%) [44]. Allele frequencies are known for a number of different populations, and of these, the deletion polymorphism is the most common allele in only the Yoruban sample set (see Alfred;

http://alfred.med.yale.edu/alfred/mvograph.asp?siteuid=SI000135J). A number of studies have shown that the -141C Ins/Del polymorphism of *DRD2* seems to have a role in determining the response to antipsychotic drugs in schizophrenic patients, in which the Ins allele is associated with favorable treatment outcome (see Table 1). But there are contrary results also which report no association (Table 1). A recent meta-analysis examined the relationship of *DRD2* genetic variation and clinical response to antipsychotic treatment (risperidone, olanzapine, chlorpromazine, clozapine, and aripiprazole) [40]. This analysis included six studies, which met the inclusion criteria for reported results on the -141C Ins/ Del polymorphism, with a total sample size of 687 patients [40]. The investigators showed that the group of Del allele carrier was significantly associated with poorer antipsychotic drug response relative to the Ins/Ins genotype [40].

The -141C Ins/Del variant has also been investigated in the context of substance addiction and treatments. Li *et al.* [42] found a positive association between nasal inhaled but not injected heroin use and the -141C Ins/Del *DRD2* polymorphism in Chinese patients. Lerman *et al.* [43] suggested that the -141C Ins/Del polymorphism may influence whether bupropion or NRT would be more effective for tobacco dependence treatment. The investigators found that bupropion was more effective for patients who were homozygous for the Ins allele, whereas NRT seemed to be more helpful for patients who were homozygous for the Del allele [43].

# Rs1800497, Taq1A (32806C > T) (now associated with ANKK1)

The Taq1A polymorphism is the most studied polymorphism in association with the DRD2 gene. It is not clear whether it is associated with effects of antipsychotic drugs, although some reports support such a conclusion. It is, however, quite clear that it is associated with nicotine dependency and treatment. The frequency of the minor T allele differs among ethnic populations. It occurs in approximately 22% of the European Caucasian population but is more frequent in Asian and African populations (42%) (HapMap data set, dbSNP http://www.ncbi.nlm.nih.gov/SNP/snp\_ref.cgi?rs=1800497). The Taq1A site is a SNP in a Taql restriction site located 10 kb downstream of the DRD2 gene [7]. Neville et al. [54] showed that the variation is an amino acid changing polymorphism (Glu713Lys) within the 11th ankyrin repeat of ANKK1 gene. Neville et al. [54] showed low level expression of ANKK1 in placenta and whole spinal cord RNA, whereas Hoenicka et al. [55] showed that ANKK1 mRNA and protein were expressed in the adult central nervous system in human and rodents, exclusively in astrocytes. In contrast, this variation is also associated with the DRD2 gene. Zhang et al. [18] found that the Taq1A A1 allele was in linkage disequilibrium with the minor allele of the intronic SNPs rs2283265 (G > T) and rs1076560 (G > T). Both the intronic SNPs were involved in splicing modification of the DRD2 gene and affected working memory [18]. Taq1A was also part of DRD2 haplotypes associated with vulnerability to heroin dependence [56], risk of opiate addiction [57], alcohol dependence [58], and clozapine treatment response [50]. In addition, this variation was associated with reduced DRD2 gene expression and lower glucose metabolic rate in dopaminergic regions in

the human brain [59–61]. In this overview we refer to the *DRD2* gene for consistency with the majority of the existing literature.

Taq1A variation was associated with clinical response to antipsychotic drug treatment and adverse effects. Individual studies have shown that after short-term treatment, the effects of antipsychotic drugs (haloperidol [62], nemonapride [63], ripiprazole [53], risperidone [64]) on positive psychotic symptoms are better in patients with the A1 allele than in patients homozygous for A2/A2. In contrast, a meta-analysis focusing on the relationship of *DRD2* variants and antipsychotic drug response was not able to detect an association between clinical response and the Taq1A variant [40]. The analysis included eight studies, which assessed the Taq1A polymorphism and antipsychotic response (risperidone, haloperidol, chlorpromazine, clozapine, nemonapride, bromperidol, and aripiprazole), with a total sample size of 748 patients [40].

Antipsychotic agents have been associated with hyperprolactinemia, or elevated prolactin levels. This effect is particularly frequent with first generation antipsychotics and with the second generation antipsychotic risperidone and paliperidone [65]. A study of 25 Japanese schizophrenic inpatients suggested that female patients with the A1 allele showed a greater prolactin response to nemonapride. These patients may be at high risk for adverse effects associated with neuroleptic-induced hyperprolactinemia [66]. Another study including several antipsychotics also showed that patients carrying the A1 allele had higher prolactin levels and were overrepresented among those with hyperprolactinaemia [67]. Calarge et al. [68] also concluded that the Taq1A and -241A > G (rs1799978) variants of the DRD2 gene could be useful in predicting the emergence of hyperprolactinemia. The study determined that the Taq1A A1 and the -241G alleles were associated with higher prolactin concentration in children and adolescents in long-term treatment with risperidone [68]. Alenius et al. [69] found that patients with one or two A1 alleles had a greater risk of significant side effects. (This study did not report the specific side effects observed.) TD is a movement disorder often caused by a history of neuroleptic use. Thelma et al. [70] reviewed the possible pharmacogenetic influences on TD in association with antipsychotics. A metaanalysis indicated an association of the A2 with TD by showing that TD-positive patients have a higher A2 allele frequency [71]. Another meta-analysis suggests multiple genetic influences on TD, including the DRD2 Taq1A SNP with A2 as the risk-increasing allele [72].

Different DRD2 variants have been reported to be associated with nicotine dependence and the efficacy of bupropion and NRT. Several studies found no evidence for an association of Taq1A with smoking behavior [73] or nicotine dependence [74,75]. The DRD2 Taq1A was implicated in association with response to bupropin and NRT. Johnstone et al. [76] found that in the first week of use, smokers with the T variant allele (A1) showed the greatest benefit from the nicotine transdermal patch. Results of a NRT randomized trial did not support the association of the T allele with improved response to NRT [77]. However, Swan et al. [78] reported that the DRD2 gene Taq1A polymorphism was associated with 12-month smoking cessation outcomes after treatment with a combination of bupropion SR and behavioral counseling in women. In this study women carrying at least one A1 allele were more likely to report that they stopped taking bupropion because of the side effects of the medication [78]. An analysis of pooled data from two clinical trials also found that smokers carrying the A2/A2 genotype using bupropion were more than three times as likely, relative to placebo, to be abstinent at the end of the treatment [79]. David and Munafo [41] reviewed the association of variation in the dopamine pathway with smoking cessation and concluded that there is some degree of replication regarding the association of the rs1800497 CC genotype with improved response to bupropion.

An association of Taq1A with alcoholism was first identified by Blum *et al.* [80] with an even more robust association of the A1 allele in case of severe alcoholism [81]. A recent meta-analysis by Smith *et al.* [82] which included 44 studies with 9382 participants, found only a small but significant association of the Taq1A polymorphism with alcohol dependency. The investigators point out that the relatively small effect for this association indicates a multigene causality [82]. Another meta-analysis regarding the association of Taq1A with alcoholism is part of a recent review by Le Foll *et al.* [83], which concludes a significant association. The investigators also summarize studies related to *DRD2* variants and nicotine, opiates, and psychostimulants [83]. Doehring *et al.* [57] showed that opiate addicts had a higher frequency of the T allele, and a number of other minor alleles of *DRD2* (e.g. rs1076560G > T SNP or the ATCT haplotype of DRD2 rs1799978A > G, rs1076560G > T, rs6277C > T, and ANKK1 rs1800497C > T) relative to controls.

Dopamine agonists are part of the pharmacotherapeutic management of patients with PD. Paus *et al.* [84] concluded that TaqIA polymorphism alone had no effect on interindividual variability of dopaminergic requirement in PD. A study exploring the effect of several *DRD2* variants for the discontinuation of nonergoline dopamine agonists ropinirole and pramipexole found no association with Taq1A or -141C Ins/Del polymorphism [85]. The study identified the  $15 \times DRD2$  CA repeat allele as genetic determinants for the discontinuation [85]. Liu *et al.* [86] found no impact of the TaqIA SNP on the efficacy of pramipexole in treating patients with PD.

## Rs6277, 957C > T

It has been reported that the 957C > T polymorphism of DRD2 is associated with both schizophrenia susceptibility substance addiction and treatment. This variant is a synonymous coding SNP located in exon 7. The minor allele (T) frequency varies among geographic groups ranging from 3 to 8% in African and Asian populations to over 50% in Caucasian populations (see dbSNP http://www.ncbi.nlm.nih.gov/SNP/snp\_ref.cgi?rs=6277). Lawford *et al.* [87] conducted a study that examined the effect of the 957C > T polymorphism on mRNA levels of DRD2. The investigators found that the T allele led to a decrease in mRNA levels and stability whereas the C allele was not found to be associated with any mRNA changes, which led to a relative increase in the expression of DRD2 in carriers of the C allele [87]. Results of an invivo study with [<sup>11</sup>C] raclopride indicated that the variant increased binding potential by decreasing DRD2  $K_D$  (C/C > C/T > T/T), whereas  $B_{max}$  was not significantly altered [88].

The 957C > T polymorphism is implicated in schizophrenia susceptibility. Several studies have postulated a protective role against schizophrenia for the minor T allele [89–92]. Shen *et al.* [53] studied the effect of *DRD2* variation (–141C Ins/Del, Ser311Cys, 957C > T, and Taq1A) on aripiprazole response in schizophrenic patients with the use of the positive and negative syndrome scale for assessment of drug efficacy. The effect of 957C > T polymorphism on positive and negative syndrome scale performance was an association of poor aripiprazole response with C/C genotype compared with T/T genotype for excitement symptoms [53]. The 957C > T SNP was also investigated in association with substance addiction and treatment. Lerman *et al.* [43] reported that smokers homozygous for the 957C > T T allele exhibited a better response to NRT. Carriers of the wild-type C allele had a higher likelihood of not responding to methadone substitution therapy [93]. Recent studies also found that the 957C > T polymorphism in *DRD2* was related to learning differences associated with the risk of developing psychiatric disorders in individuals that are carriers of the homozygous CC genotype [94].

## Rs1801028, Ser311Cys

It is not clear whether the Ser311Cys polymorphism is associated with schizophrenia. There have been reports supporting and refuting such results. This variant is a C > G SNP in exon 7 that alters the codon 311 from the more common Ser to the less common Cys. The Cys311 variant has decreased affinity for dopamine [95]. The minor allele frequency (G allele) is 0.02 based on the 102 individuals of self-described heritage (African/African-American, n =24; Caucasian, n = 31; Hispanic, n = 23; and Pacific Rim, n = 24) (see dbSNP http://www.ncbi.nlm.nih.gov/SNP/snp\_ref.cgi?rs=1801028). From the same data set, the frequency of the G allele is higher in a self-described Pacific Rim population (0.043) than that in a Caucasian population (0.016). There is published evidence both supporting [96– 101] and refuting [102] the association between Ser311Cys polymorphism of the DRD2 gene and schizophrenia. A possible link between the Cys allele of 311 Ser > Cys in DRD2 and schizophrenia was first reported in the mid 1990s [96-98], although Goldman et al. [102] found no correlation between carriers of Cys 311 and schizophrenia in a Native American population. Jonsson et al. [100] examined the possible association of Ser311Cys and schizophrenia in control and schizophrenic populations, both of Swedish origin. The schizophrenic patient population (n = 173) showed a higher allele frequency of Cys 311 than the control population (n = 236) [100]. Interestingly, this association was detected only in male patients [100]. In a more recent study by Glatt and Jonsson [101], an analysis was conducted of several different studies, which contained a total of 3707 schizophrenia patients and 5363 control individuals. The investigators found that the Cys 311 allele had a significant effect [101]. In the same study, the investigators reported that Cys/Ser heterozygotes were at increased risk for schizophrenia as compared with the Ser/Ser homozygotes, but there was no increased risk detected for Cys/Cys homozygotes [101].

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Patients (population)	Antipsychotic drug	Treatment duration (weeks)	Response measurement	Genotyped DRD2 polymorphisms	-141C Ins/Del effect	References
151 schizophrenics; 95 controls (Caucasian)	Clozapine	I	GAS	-141C Ins/Del	No association	[45]
170 schizophrenics; 121 controls (Japanese)	Antipsychotic drugs not specified	I	PANSS	-141C Ins/Del	No association	[46]
49 schizophrenic inpatients (Japanese)	Bromperidol or nemonapride	ε	BPRS	-141C Ins/Del	Ins allele associated with greater improvement (only for anxiety-depression symptoms)	[47]
73 schizophrenic patients (Japanese)	Risperidone	×	PANSS	-141C Ins/Del, Taq1A	Ins-A2/Del-A1 diplotype associated with better response	[48]
135 schizophrenic inpatients (Chinese)	Chlorpromazine	×	BPRS		Del (–) genotype associated with higher degree of improvement	[49]
DSM-III-R or DSM-IV schizophrenics (183 Caucasian; 49 African- American)	Clozapine	Q	BPRS	–141C Ins/Del, Taq1A, Taq1B, and rs1125394	No association	[50]
61 first-episode schizophrenia patients (41% African- American: 28% Caucasian: 18% Hispanic; 5% Asian; 8% other)	Olanzapine or risperidone	16	CGIIS	-141C Ins/Del, -241A>G	-141C Del allele showed significantly longer time to respond relative to Ins/Ins homozygotes	[51]
125 schizophrenia patients (Chinese)	Risperidone	×	BPRS	-141C Ins/Del, Taq1B, rs1076562, Taq1A	No association	[52]
128 schizophrenic inpatients (Han Chinese)	Aripiprazole	4	PANSS	–141C Ins/Del, Taq1A, C957T, Ser311Cys	No significant effect	[53]

BPRS, brief psychiatric rating scale; CGIIS, clinical global impression improvement scale; DRD2, dopamine receptor D2; DSM-IV; Diagnostic and Statistical Manual of Mental Disorders, fourth edition; DSM-III-R, revision of DSM-III: GAS, global assessment scale; PANSS, positive and negative symptom scale.

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