

Genetics in Psychiatry – Up-to-date Review 2011

Radek PTACEK¹, Hana KUZELOVA^{1,2}, George B. STEFANO³

¹ Clinic of Psychiatry, 1st Faculty of Medicine, Charles University in Prague, Czech Republic

² Department of Biology and Medical Genetics, 2nd Faculty of Medicine, Charles University in Prague, Czech Republic

³ Neuroscience Research Institute, State University of New York, College at Old Westbury, Old Westbury, NY, U.S.A.

Correspondence to: Radek Ptacek, PhD.
Clinic of Psychiatry, 1st Faculty of Medicine
Ke Karlovu 11, 128 01 Praha 2, Czech Republic.
E-MAIL: ptacek@neuro.cz

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Abstract

Psychiatric genetics is a popular and much-discussed topic. Many candidate genes have been investigated in relation to psychiatric disorders and many connections have been found. The utilization of these investigations is currently at a theoretical level. Nevertheless, these findings of candidate genes will be important for further research and subsequent clinical use, for example in pharmacogenetics). Due to the rapidly growing number of empirical studies that provide profound analysis of different genes and their variants in different psychiatric symptomatology, the field is highly divided, and providing a succinct overview is challenging. This article attempts to provide an up-to-date review of the most important and most discussed genes (mainly transporter and receptor genes) contributing to the etiology of psychiatric disorders.

INTRODUCTION

Knowledge and understanding of the biological and genetic foundations of mental disorders is rapidly growing (Arai 2011; Stefano *et al.* 2010; Croonenberghs *et al.* 2010; Formisano *et al.* 2010; Atmanene *et al.* 2009; Pastucha *et al.* 2009a; Pastucha *et al.* 2009b), but the field still remains on a more or less theoretical level (Vithoulkas & Carlino 2010; Prasko *et al.* 2009; Raszka *et al.* 2009). Rapid progress in biological (Sokolowska *et al.* 2010; Hernando 2010; Galinska *et al.* 2009) and genetic (Dogan *et al.* 2009; Smolarek *et al.* 2010; Pietras *et al.* 2010; Sokolowska 2010; Pietras *et al.* 2010) research, especially in psychiatry and in prenatal diagnostics (Vlkova *et al.* 2010) has significantly aided assessment of a few developmental disorders; but this progress has only been in monogenic disorders. In reality, the majority of psychiatric disorders are complex; therefore application of these recent research find-

ings is limited. Many disorders are multifactorial (with interaction of environment and genetics) and polygenic, where multiple genes play roles, or oligogenic, with epistasis. These genes are usually responsible for vulnerability to a specific disorder. This fact complicates genetic tests because these genes currently represent only a risk factor for development of disorders, as is the case with psychiatric genetics.

Results from recent studies indicate that genetics plays a substantial role in most major mental illnesses, including schizophrenia, affective disorders, autism, neurotism, anxiety disorders, ADHD (attention deficit hyperactivity disorder), learning disabilities, OCD (obsessive compulsive disorder), alcoholism and drug dependence. Family studies

confirm the genetic basis of many disorders; bipolar disorder, major depression and other common psychiatric conditions are more frequent among close relatives.

Genome-wide association studies cannot test every gene in the genome for each gene's relationship to illness. Genetic analysis investigates whether there is a significant difference in the frequency of a given genetic variant (alleles of a polymorphism) between case and control groups. The polygenicity of a disorder means that very large samples are needed to detect relationships.

The genetic background is usually examined through three primary types of investigation: family studies, twin studies, and candidate gene association studies. Association studies help to find candidate genes for specific psychiatric disorders (Kovacs-Nagy 2009). The identification of candidate genes should be performed by specialized collaborative groups such as the International Molecular Genetic Study of Autism Consortium (IMGSAC), the Autism Genome Project Consortium, and the Autism Genetic Resource Exchange (AGRE).

CANDIDATE GENES

Gene-gene and gene-environment interactions make searching for candidate genes in psychiatric conditions very complicated. In psychiatric genetics, candidate genes are tested for associations with neurobiological and clinical signs of a disorder (Lobo *et al.* 2009). Genes active in the dopaminergic, serotonergic and noradrenergic systems are thought to participate in development of psychiatric disorders via their central role in neurotransmitter pathways. These systems are also important in self-regulation and management of stress (Esch & Stefano 2010), and genes determine how certain neurotransmitters are produced, transmitted and metabolized. The most-used markers are single nucleotide polymorphisms (SNP) and copy number variations (CNV), important in receptor and transporter genes.

Many specific candidate genes have been associated with bipolar disorder: dopamine transporter SLC6A3, brain-derived neurotrophic factor (BDNF), the NMDA glutamate receptor, subunit 2B GRIN2B, D-amino-acid oxidase activator (DAOA), peroxisome proliferator-activated receptor delta (PPARD), neuregulin1 (NRG1), the 5-HT transporter SLC6A4, tryptophan hydroxylase-2 (TPH2) and catechol-o-methyl transferase (COMT) (McQueen *et al.* 2005a). The situation is much more complicated in disorders with clinical and etiological heterogeneity, such as OCD (Samuels 2009). Heritability of alcoholism is thought to range from 50% to 60%, indicating the importance of both genetic and environmental factors in its etiology (Stacey *et al.* 2009). Genetic factors explain between 35% and 54% of the risk of developing any particular symptom of pathological gambling, with each gene accounting for less than 2%, and about 54% of environmental factors (Lobo *et al.* 2009). No specific genes have been found to determine development of

nicotine addiction, but several have been found to cause susceptibility to it (Davies *et al.* 2009).

This paper presents a review of only the most studied genetic variants, primarily those that are associated with more than one psychiatric disorder.

DOPAMINERGIC SYSTEM

DRD1

Dopamine D1 receptor, 5q35.1

The DRD1 gene encodes the D1 subtype of the dopamine receptor, the most abundant dopamine receptor in the central nervous system, which regulates neuronal growth and development and mediates behavioral responses.

Single-nucleotide polymorphisms (SNPs) in DRD1 have been investigated in connection with psychiatric disorders such as A-48G *DdeI*. SNPs in the promoter region may play a role in the neurobiology of addictions and may affect vulnerability to addictions (Novak *et al.* 2010) and disorder-associated decreased impulse control such as attention deficit hyperactivity disorder (ADHD) (Oades *et al.* 2008; Bobb *et al.* 2005), nicotine and alcohol dependence (Novak *et al.* 2010; Batel *et al.* 2008; Huang *et al.* 2008) and pathological gambling (da Silva Lobo *et al.* 2007). According to Hoenicka *et al.* (2010), the SNPs *rs11746641* and *rs11749676* are associated with schizophrenia.

DRD2

Dopamine D2 receptor, 11q23

DRD2 encodes the D2 subtype of the dopamine receptor – G-protein coupled receptor inhibits adenylyl cyclase activity.

Variants in this gene (*TaqIA*, *ANKK1*) have been published in association with dependences (Kasiakogias-Worley *et al.* 2011) or ADHD (Paclt *et al.* 2010) and some symptoms of schizophrenia (Zahari *et al.* 2011).

Initial studies reported associations of pathological gambling with allele T of the dopamine 2DRD2 *TaqIA* polymorphism (Comings *et al.* 2001; Lobo *et al.* 2010). Some studies have found associations with neighboring polymorphisms on *ANKK1* (Dick *et al.* 2007; Huang *et al.* 2009). According to Zhang *et al.* (2010), DRD2 genetic variation is associated with clinical response to anti-psychotic drug treatment and can explain variation in the timing of clinical response to antipsychotics in patients with first-episode schizophrenia (Lencz *et al.* 2009; Zahari *et al.* 2011). A highly positive correlation was described between the combined type of ADHD without co-morbidity and *ANKK1* polymorphism (Paclt *et al.* 2010). An association of the DRD2 genetic variants with impulsive self-injurious behaviors was also demonstrated (Namoda *et al.* 2010).

DRD3

Dopamine D3 receptor, 3q13.3

The DRD3 gene encodes the D3 subtype of the dopamine receptor – G-protein coupled receptor, which inhibits adenylyl cyclase.

Few variants in this gene have been shown to be involved in psychiatric disorders. However, DRD3 variant (Ser9Gly) has been studied together with other DRD genes, mainly in pharmacogenetics (Leggiou *et al.* 2011; deKrom *et al.* 2009), genetics of ADHD (Kopeckova *et al.* 2008; Davis *et al.* 2009), and bipolar disorder (Lee *et al.* 2010), and associations with schizophrenia have been recently published (Pawel *et al.* 2010; Zai *et al.* 2010; Aguilar-Pulido *et al.* 2010).

DRD4

Dopamine D4 receptor, 11p15.5

DRD4 gene encodes the D4 subtype of the dopamine receptor – G-protein coupled receptor, which inhibits adenylyl cyclase.

A length polymorphism in *exon III* (7-repeat allele) has been reported to encode a receptor with lower affinity for dopamine (Jovanovic *et al.* 1999) and associated with various psychiatric disorders (Nemoda *et al.* 2010) including ADHD (Becker *et al.* 2010; Smith 2010), dependences, pathological gambling (Comings *et al.* 1999), alcoholism (Du *et al.* 2010) and drug dependence (Chien *et al.* 2010). Levitan *et al.* (2010) found an association between DRD4 variants and bulimia nervosa, and Emanuele *et al.* (2010) described associations with autism, where the understanding of biological mechanisms becomes more and more important (Boso *et al.* 2010; Emanuele *et al.* 2010a; b; Martirosian *et al.* 2009; Hrdlicka 2008a; b). DRD4 length polymorphism has been described in connection with specific behavioral phenotypes including externalizing behavior problems (Hohman *et al.* 2009), the personality trait of novelty seeking, impulsive personality traits (Misterska *et al.* 2010; Strobel *et al.* 1999), anger (Kang *et al.* 2008), short temper and thrill seeking in males (Dmitrieva *et al.* 2010), and aggressive and delinquent behavior, as compared to other genotypes (Hohmann *et al.* 2009). Khang *et al.* (2008) found that the short allele had significantly lower anger in tendency to anger and higher forgiveness traits. DRD4 variants also play an important role in pharmacogenetics (Kranzler *et al.* 2010).

DRD5

Dopamine D5 receptor, 4p16.1

The DRD5 gene encodes the D5 subtype of the dopamine receptor – G-protein coupled receptor, which stimulates adenylyl cyclase. This receptor is expressed in neurons in the limbic regions of the brain.

DRD5 gene variants were described in association with ADHD (Husarova *et al.* 2010; Ptacek *et al.* 2009), dependences and schizophrenia. Several studies have investigated the association between a dinucleotide (CA)(n) repeat polymorphism and ADHD (Banschewski *et al.* 2010; Coghill *et al.* 2009; Gizer *et al.* 2009; Kebir *et al.* 2009). Despite the fact that several studies have suggested that DRD5 repeat polymorphism confers significant risk for ADHD (Squassina *et al.* 2008; Langley *et al.* 2009), results are inconsistent and insignificant (Manor *et al.* 2004). An association of schizophrenia with DRD5 SNP variant was found (Pal *et al.* 2009; Golimbet *et al.* 2008), and associations with drug addiction (Le Foll *et al.* 2009) and alcohol dependence (Hack *et al.* 2011) have been published.

DAT

Dopamine transporter (DAT, DAT1), SLC6A3

DAT gene encodes dopamine transporter, a membrane-spanning protein, which pumps the neurotransmitter dopamine out of the synapse back into cytosol.

Length variants in the DAT gene (40-bp VNTR) have been investigated in association with several disorders (Guo *et al.* 2007); variants with 10 repetitions (10R) are associated with depression (Felicio *et al.* 2010), ADHD (Sharp *et al.* 2009) and delinquency (Guo *et al.* 2007; 2010). According to Reese *et al.* (2010), DAT polymorphism is also associated with antisocial personality disorder in alcoholics. Variants with 9 repetitions (9R) exert a general protective effect against a spectrum of risky behaviors (Guo *et al.* 2010).

The 10-repeat variant is also thought to be associated with left-sided inattention in ADHD (Bellgrove *et al.* 2005) and has been linked to an enhanced response to methylphenidate (Bellgrove *et al.* 2005); however, results from these studies are very contradictory (Contini *et al.* 2010).

DBH

Dopamine-beta-hydroxylase, 9q34

DBH gene provides instructions for producing the enzyme dopamine beta (β)-hydroxylase, which converts dopamine to norepinephrine.

The DBH gene and its variants (SNP) are one of the candidate genes studied for anxiety disorders (Itoi *et al.* 2010). *DBH-1021C/T* gene polymorphism and lower DBH activity was studied in correspondence to post-traumatic stress disorder (Mustapic *et al.* 2007) and in ADHD (Paclt *et al.* 2009). According to Hessel *et al.* (2009), *DBH-1021T/T* genotype is significantly associated with increased neuroticism scores and impulsive and aggressive behavior in ADHD. DBH variants were also examined in association with addictions (Fernández-Castillo *et al.* 2010). *SNP rs3025343G* is significantly associated with smoking cessation (Tobacco and Genetics Consortium 2010); however, other results contradict this (Breitling *et al.* 2010).

SEROTONERGIC SYSTEM

5HTT

Serotonin transporter (SLC6A4), 17q11.1–q12

The 5HTT gene encodes serotonin transporter, which transports the neurotransmitter serotonin from synaptic spaces into presynaptic neurons and plays a major role in serotonin transmission.

The most extensively studied variant in genetic studies is a length polymorphism (variable number of repeats) in the promoter region of the serotonin transporter gene (*5HTTLPR*). The short (S) allele is associated with lower transporter activity and mental illness, high trait anxiety, mood and anxiety disorders (Blom *et al.* 2011), predispositions to fear-related behaviors, negative emotionality, both unipolar and bipolar forms of depression and neuroticism (Ohaeri *et al.* 2010; Hariri & Holmes 2003), pathological gambling (Perez de Castro *et al.* 1999), sui-

cidal behavior, alcohol dependence and treatment of alcohol dependence (Kenna 2010), eating disorders, post-traumatic stress disorders and other disorders (Kuzelova *et al.* 2010; Anguelova *et al.* 2003a; 2003b). It may have a role in human aggression (Craig *et al.* 2009). Long allele (L) is associated with ADHD and binge eating (Kuzelova *et al.* 2010).

HT1A

Serotonin receptor 5-HT1A

The 5-HT1A receptor is a subtype of the 5-HT receptor, which binds the endogenous serotonin.

The receptors associated with serotonergic neurons, together with the serotonin transporter, appear to be key players in the control of aggression (Olivier & van Oorschoot 2005). Altered transcription of the 5-HT1A receptor caused by genetic variants (C(-1019)G polymorphism) can lead to increased predisposition to depression (Benedetti *et al.* 2011; Albert *et al.* 2004; Gleason *et al.* 2010; Liu *et al.* 2011; Idova *et al.* 2010), psychosis (Kishi *et al.* 2010), panic, phobic and anxiety disorders (Lanzenberger *et al.* 2007; Gleason *et al.* 2010) and eating disorders (Lim *et al.* 2010).

HTR2A

Serotonin receptor 5-HT2A

The 5-HT2A receptor is a subtype of the 5-HT2 receptor, which is the main excitatory receptor subtype.

Several polymorphisms have been identified for HTR2A (A-1438G [rs6311], C102T [rs6313] and His452Tyr [rs6314]). HTR2A is thought to play a role in impulsiveness (Salo *et al.* 2010). Several studies have seen links between the -1438G/A polymorphism and mood disorders such as bipolar disorder and major depressive disorder (Chee *et al.* 2001). An association with schizophrenia has also been suggested (Tsunoka *et al.* 2010; Kim *et al.* 2011). Mutation in intron 2 is connected with changes in treatment response and therapeutic effect of several clinically effective and potential atypical antipsychotics, as well as several antidepressants (Kishi *et al.* 2010; Hruby *et al.* 2010).

HTR2C

Serotonin receptor 5-HT2C

The 5-HT2C receptor is a subtype of the 5-HT receptor, which binds the endogenous neurotransmitter serotonin. It modulates serotonergic neurotransmission in the central nervous system.

Studies in humans have reported abnormalities in patterns of HTR2C (functional polymorphism 68G>C [Cys23Ser] and in promoter polymorphism-995G>A) editing in depressed suicide victims (Videtic *et al.* 2009; Serreti *et al.* 2009). Several studies suggest associations with specific symptoms in schizophrenia (Bai *et al.* 2011). Yasseen *et al.* (2010) found possible association with alcohol use disorder comorbidity. Polymorphisms in HTR2C (rs498207, C-759T, G-697C and Ser23Cys) can be associated with weight gain after using psychiatric medication (Sicard *et al.* 2010).

ENZYME GENES

MAO-A

Monoamine oxidase A, Xp11.3

MAO-A and MAO-B are two related enzymes that play an important role in the metabolism of biogenic amines in the central nervous system and in the periphery.

The most investigated is of these is MAO-A. The MAO-A gene is located on the X chromosome, thus sex differences in its expression may occur. Most research in this area has centered on detecting behavioral associations with SNPs, microsatellites and/or promoter VNTR variants in MAO-A (Craig *et al.* 2009). A functional promoter-region polymorphism of this gene has been described in connection to mental illnesses. MAO-A promoter-region polymorphism is also thought to influence risk for ADHD development (Coccini *et al.* 2009; Nedic *et al.* 2010; Gizer *et al.* 2009) and plays an important role in effectiveness of pharmacotherapy (Fisar *et al.* 2010; Dell'osso *et al.* 2010). Subsequent investigations revealed an association of the more severe forms of pathological gambling and polymorphisms in MAO-A (3 repeat in promoter region) (Perez de Castro *et al.* 2002).

COMT

Catechol-O-methyl transferase, 22q11.2

COMT is the enzyme that degrades catecholamines such as dopamine, epinephrine and norepinephrine.

COMT variants (Val158Met, rs737865 and rs165599) were studied for association with personality traits. COMT (Val158Met) plays a role in determining interindividual variability in the proclivity for violent behavior in subjects without major mental disorder (Vevea *et al.* 2009). This variant also is connected with schizophrenia (Hoenicka *et al.* 2010; Costas *et al.* 2010; Kong *et al.* 2011), novelty seeking (Hosak *et al.* 2006) and some symptoms of ADHD (Kebir *et al.* 2011) including bulimia nervosa in ADHD patients (Yilmaz *et al.* 2011). COMT variants are also important for pharmacogenetics (Kereszturi *et al.* 2008; Hamidovic *et al.* 2010).

TPH

Tryptophan hydroxylases 1 and 2 (TPH1 and TPH2)

Tryptophan hydroxylase enzyme (TPH1) catalyses the rate-limiting step in the synthesis of serotonin.

TPH1 has two well-characterized SNPs (A218C and A779C) in intron 7. An association between the A218C polymorphism with the disorders on the schizophrenia spectrum was demonstrated (Efimov *et al.* 2009; Watanabe *et al.* 2007). Connection of TPH expression with anxiety (Charoenphandhu *et al.* 2011) and endogenous psychoses (Efimov *et al.* 2009) was described, and Kim *et al.* (2010) found an association with drinking behavior.

OTHER TRANSPORTER GENES

NET

Noradrenaline transporter, monoamine transporter, SLC6A2, 16q12.2

This gene encodes a member of the sodium: neurotransmitter symporter family.

Several studies revealed a positive association of the *NET-T182C* polymorphism with susceptibility to and severity of depression (Min *et al.* 2009) and response to antidepressants with homologous monoamine transporter targets (Kim *et al.* 2006). The variant *NET G1287A* GG genotype (56% of the population) was associated with better response to the NRI than to SSRI. Inconclusive results were published on an association with ADHD (Cho *et al.* 2008; Kollins *et al.* 2008).

VMAT1

Vesicular monoamine transporter, member 1, SLC18A1, 8p21

VMAT2

Vesicular monoamine transporter, member 2, SLC18A2, 10q25

VMATs act to accumulate cytosolic monoamines into synaptic vesicles. Their function is essential to the correct functioning of the monoaminergic systems, which has been implicated in several human neuropsychiatric disorders.

VMATs are an important target for biological research in neuropsychiatric disorders. Linkage studies

found associations with schizophrenia, bipolar disorder and anxiety-related phenotypes (Lohoff 2010).

VMAT2 was investigated mainly in connection to schizophrenia (Talkowski *et al.* 2008; Iritani *et al.* 2010).

OTHER CANDIDATE GENES

Many other gene variants have been investigated in relation to psychiatric disorders (Galecki *et al.* 2010), mainly in connection to autism and schizophrenia (Melkersson 2011; Kałuzna-Czaplińska *et al.* 2010a; b). For example, **GABA** (gamma-amino butyric acid) receptor genes are associated with autism (e.g. Fasemi *et al.* 2010), **Sry** locus (Sex-determining region Y) on **Y** chromosome has been investigated in connection with aggressive behavior (Miczek *et al.* 2007; Gatewood *et al.* 2006), and a missense polymorphism in **GPR55** (G protein-coupled receptor 55) receptor gene is associated with anorexia nervosa (Ishiguro *et al.* 2010). Rajender *et al.* (2008) found a highly significant association between violent criminal activity and the shorter CAG repeats in the gene for androgen receptor **AR**.

Table 1 summarizes findings on association of genes and psychiatric disorders.

MORPHINERGIC PROCESSES

After many years of investigation by various groups' it has now been demonstrated that morphine can be synthesized in human and other animal tissues (Mantione *et al.* 2010d; Kream & Stefano 2006a, b; Stefano *et al.* 2008; Zhu *et al.* 2005a, b). This complements other studies demonstrating novel

Tab. 1. The main candidate genes in psychiatric genetics.

	Attention-deficit and disruptive behavior disorders	Substance-related disorders	Schizophrenia	Mood disorders	Anxiety disorders	Eating disorders	Treatment response
DRD1	x	x	x				
DRD2	x	x	x				
DRD3	x		x				
DRD4	x	x					x
DRD5	x						
DBH					x		
DAT	x			x			x
5HTT	x	x		x	x	x	x
5-HT1A				x		x	
5-HTR2A							
5-HTR2C		x		x			
MAO A	x	x					
COMT			x				x
TPH			x	x			
NET					x		x
VMAT1,2			x		x		

opiate receptors that are opiate alkaloid selective and opioid peptide insensitive in human and other animal tissues, including neural (see Fricchione *et al.* 2005; Kream & Stefano 2005a). Both the mu3 (mu3 opiate receptor subtype) and 4 receptors have been cloned (see Kream & Stefano 2005a) and found to be 6 transmembrane in nature (Kream & Stefano 2005a). Furthermore, these opiate receptors are coupled to constitutive nitric oxide release (Kream & Stefano 2009; Mantione *et al.* 2008; Stefano *et al.* 2008a, b; Stefano & Kream 2007; 2010). In addition, the enzymes associated with endogenous morphine biosynthesis have been determined and shown to be regulated by end product inhibition and/or nitric oxide generated via mu3-4 occupancy (Kream & Stefano 2006a; Mantione *et al.* 2008, 2010a, b, c; Stefano 2007; Zhu 2005a, b). The enzymes/genes include among others CYP2D6 (Cytochrome P450 2D6), COMT (Catechol-O-methyltransferase), TH (tyrosine hydroxylase), PNMT (phenylethanolamine N-methyltransferase), DDC (DOPA decarboxylase 5) (Kream & Stefano 2006a; Mantione 2008, 2010a, b, c; Stefano 2007; Zhu 2005a, b). Not surprisingly some are linked to dopamine synthesis, which is an important feature of this pathway since dopamine serves as a morphine precursor (see Kream & Stefano 2006a). Thus, in previous reports it has been surmised that morphine has functions that transcend analgesia (Esch & Stefano 2011; Kream & Stefano 2008; Mantione *et al.* 2010c; Salamon *et al.* 2005; Stefano *et al.* 2005, 2007, 2008b). Given the anatomical localization of endogenous morphine, the presence of its novel receptors and its coupling to nitric oxide release and linkages to the catecholamine pathway authors have also speculated on its role in psychiatry (Kream *et al.* 2010). Here too, as documented by these reports polymorphisms and splice variations will play a critical role in mental health.

DISCUSSION AND CONCLUSION

Many psychiatric disorders are highly heritable; however, psychiatric disorders are not monogenic and many interactions participate in the development of a disorder. The utility of a candidate gene is limited because most disorders are determined by a combination of genetic and environmental factors (Norrholm *et al.* 2009; Latalova *et al.* 2010). Moreover, the situation could be complicated by the presence of many other comorbid disorders (Ohaeri *et al.* 2010). The mechanism of heritability has not yet been adequately elucidated, and limitations also exist in the validation of the interactions (Bill *et al.* 2009).

Candidate genes have been intensively studied through modern methods, but the methods of these studies are very heterogeneous and in many cases incorrect. Many studies investigated only one gene polymorphism in connection to psychiatric disorders, and on the basis of their results formed questionable conclusions. In reality, psychiatric disorders are mainly polygenic, and multiple genes and interactions take part in their development. For example, Hohmann *et al.* (2009) suggested that there could be an epistasis between DRD4 and 5-HTTLPR.

Many polymorphisms have been so widely studied that they have been associated with an implausibly large number of psychiatric and non-psychiatric phenotypes, many of which are likely to be false positives. In this regard, the study of gene pattern expression, i.e., microarray (Casares *et al.* 2009), promises to be a valuable technique since it relies on observing many expressions at once. Clearly this approach is more realistic since so many chemical messengers are involved in both normal and abnormal activity.

As more studies are conducted it is possible to understand more clearly the biological mechanisms of psychiatric disorders. The aim of psychiatric genetics is to better understand the etiology of psychiatric disorders and improve treatment methods. The basic assumption of studies investigating genetic relations of psychiatric disorders is that correct diagnostic methods were used.

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