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Molecular genetics of autism spectrum disorders

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Abstract Autistic disorder belongs to a broad spectrum of pervasive developmental disorders. Autism is a clinically and genetically heterogeneous condition. It is characterized by impairment in a broad range of social interactions, communication, and repetitive patterns of behavior and interest. Although the exact etiology of the condition is not known, family and twin studies strongly support genetic factors in autism. Genome-wide scans suggest several susceptibility loci that may contain one or more predisposing genes. However, no such genes have been identified so far that predispose patients to autism. The condition is over 90% heritable, but the mode of inheritance is not clear. Moreover, it does not seem to be a single gene disorder. There is no cure for autism. Individualized structured education, family support services, and antipsychotic drugs are recommended. These may alleviate some behavioral problems. The identification of autism genes, an understanding of the neurobiology of the condition, and additional clinical studies may help to develop pharmacological interventions in the future.

Keywords Linkage · Gene · Cytogenetic · Chromosome

Introduction

Autism is a neurodevelopmental disorder with variable clinical presentations and usually occurs before 3 years of age (Bailey et al. 1996). It is a poorly understood condition and belongs to a group of several closely related pervasive developmental disorders (PDD) such as Asperger syndrome and childhood disintegrative disor-

ders. The more popular term for the condition is autism spectrum of pervasive developmental disorders. It is a life-long disorder and is clinically characterized by impairment in social interactions, communication, imagination, and language. Additionally, repetitive patterns of behavior such as movement of hands and fingers have been documented (Prater and Zylstra 2002; American Psychiatric Association 2000; Lewis and Thompson 1992; Bishop et al. 1995; Tomblin and Buckwalter 1998; Wing and Gould 1979; Wing 1997). The disorder can also be associated with a wide range of conditions. Autistic-spectrum disorders are a tremendous burden on the lives of affected individuals, their families, and society.

Pathology, epidemiology, and etiology

Magnetic resonance imaging studies and postmortem examination of the brain revealed changes in the limbic system and a larger volume of white matter (Casanova et al. 2002; Piven et al. 1996). Microscopic neuroanatomical abnormalities such as reduced neuronal cell size and increased cell packing found in the hippocampal and amygdala region support the notion that normal brain development is impaired (Critchley et al. 2000; Bauman 1996; Kemper and Bauman 1998). This is consistent with experiments involving primates in which early hippocampal damage produced stereotypies and loss of social affiliation, suggesting again that the hippocampal region may be involved in normal social interactions (Beauregard et al. 1995).

Additionally, neuropsychological findings suggest structural and functional abnormalities in the temporal lobe (Dawson 1996; Lainhart 1997; Fombonne 1999), which has been supported by experiments in newborn monkeys (Bachevalier 1994). In these experiments, a major behavioral disturbance was found in monkeys that have lesions in the medial temporal lobe structures. This has been further supported by positron emission tomography that showed a highly significant hypoper-

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fusion in both temporal lobes in school-aged children with autism (Zilbovicius et al. 2000). In addition, hypometabolism of both temporal lobes was found to be associated with autism (Chugani et al. 1996). However, it is not clear whether the abnormality in one part of the brain is responsible for autism or other areas are also involved. There are several pathological and pathophysiological questions that need to be answered before one can understand the full spectrum of the disorder. Developmental disturbance of the neuronal network in the medial temporal lobe on the other hand, appears to be a contributing factor to the development of autism.

A recent epidemiological survey involving preschool children suggests its prevalence of 58–67 per 10,000 when all forms of autism spectrum disorders are combined (Chakrabarti and Fombonne 2001; Baird et al. 2000). But this needs to be confirmed by more studies. When taking into consideration this value, it appears that it is a more common childhood disorder than previously thought. It is also three to four times more common in males than in females, and there is an increased incidence of the disorder among relatives of individuals with the disorder. According to a recent twin study in the general population, the lower prevalence of the disorder in girls could be due to early environmental influences (Constantino and Todd 2003). The biochemical basis of the disorder is not known. It is believed that an early insult to the central nervous system by a wide variety of heritable and nonheritable factors may cause the disease (Newschaffer et al. 2002). Available evidence strongly suggests that genetic factors may play a major etiological role in the pathogenesis of autism.

Chromosomal loci suggestive of linkage

Autism is a life-long neurodevelopmental condition. Although the molecular basis of the disorder is not known, family and twin studies strongly support genetic factors in autism (Folstein and Rutter 1977; Steffenburg et al. 1989; Bolton et al. 1994; Bailey et al. 1995; Cook 1998a; Spiker et al. 1994). Monozygotic and dizygotic twin studies suggest a concordance rate of 90% and 30% respectively (Folstein and Rutter 1977; Ritvo et al. 1985; Trottier et al. 1999) and there is a 75-fold greater risk among siblings. However, the twinning process itself is not found to be a risk factor for autism (Hallmayer et al. 2002), which is in contrast to what was previously suggested by others (Greenberg et al. 2001; Betancur et al. 2002).

Although it has a high heritability rate, the mode of transmission of autism is not clear, and the genetics of the disorder appears to be complex, involving multiple loci and interaction of multiple genes (Risch et al. 1999). In accordance with this, several genome-wide scans and linkage studies have identified multiple chromosomal regions (Risch et al. 1999; Folstein and Rosen-Sheidley 2001; Auranen et al. 2000; 2002; Philippe et al. 1999; Shao et al. 2002a; Liu et al. 2001; Barrett et al. 1999) that

may contain one or more susceptible genes. However, no such genes have been identified so far. Although in some cases results are not replicated by other studies (Salmon et al. 1999), these studies have provided mostly suggestive evidence for linkage and must be interpreted with caution. The discrepancies among studies could be due to genetic heterogeneity or clinical presentation of the disorder, or differences in geographic and sample size used in the experiments. For instance, the frequency of variant alleles may differ among racial or ethnic groups, and some mutations may occur uniquely at a high frequency within a single racial group (e.g., Ashkenazi, Amish, and French Canadians). This is particularly important in complex genetic disorders such as neuropsychiatric conditions, diabetes, and asthma, in which multiple interacting genes and environmental factors contribute to the phenotype. In such cases, more studies using larger sample size may be needed to resolve the differences.

Among the loci identified, the most promising regions have been found on chromosome 7q (IMGSA 1998; 2001a; Fisher et al. 1998; Ashley-Koch et al. 1999) and 2q (IMGSA 2001b; Buxbaum et al. 2001; Shao et al. 2002b) in which several genome scans identified overlapping linkage. This multiloci genetic etiology is also consistent with phenotypic variability of the disorder within families. It should be mentioned here that these genetic studies have been conducted with infantile autism in which some patients are associated with other phenotypes. In order to apply genetic methods, it will be helpful to identify families having a single disease phenotype.

Cytogenetic abnormality

Numerous studies have revealed that several cases of autism have been associated with chromosomal abnormalities such as deletion, duplication, balanced, unbalanced and complex translocations (Yu et al. 2002; Smith et al. 2000; Thomas et al. 1999; Vostanis et al. 1994; Michaelis et al. 1997; Nurmi et al. 2001; Burd et al. 1998; Ghazziuddin and Burnmeister 1999; Smith et al. 2001; Gillberg et al. 1991; Yan et al. 2000; Vincent et al. 2001; Tentler et al. 2001; Wolpert et al. 2001). Although in some cases deletions ranged from 5 to 260 kb and patients exhibited a varying degree of intellectual impairments (Bolton et al. 2001a), there is no clustering of breakpoints involved and deletions are scattered throughout the genome. It is possible that the above chromosomal abnormalities would cause autism in combination with other unidentified loci. Alternatively, chromosomal rearrangements and deletions could be due to autism susceptibility loci located in some other regions in the genome that may increase errors in meiosis. This notion is supported by the finding that in some autism patients, meiosis is altered relative to control families (Ashley-Koch et al. 1999; Bass et al. 1999). Since there is no such increased recombination rate or gene

defect so far reported in any other inherited diseases, further studies are needed to confirm the above hypothesis.

Candidate gene analysis

Since several genome-wide scans have identified many susceptibility loci, it is logical to extend these observations to identify candidate genes that predispose patients to autism spectrum disorders. However, when specific candidate genes such as *HOXA1*, *HOXB1* (Ingram et al. 2000), *EN-2*—a human homeogene (Petit et al. 1995), *FOXP2*—a forkhead transcription factor gene (Newbury et al. 2002; Wassink et al. 2002), serotonin transporter *SLC6A4* (Cook et al. 1997a; Yirmiya et al. 2001; Kim et al. 2002a), *reelin*—a large extracellular matrix protein gene involved in neuronal migration (Persico et al. 2001), vasoactive intestinal peptide receptor type 2 (Asano et al. 2001), *RAY1* (Vincent et al. 2000), GABA receptor (Cook et al. 1998b), *DLX6* (Nabi et al. 2003), *DOPA* decarboxylase (Lauritsen et al. 2002), tyrosine hydroxylase, dopamine receptors D2 and D5, proenkephalin, prodynorphin, monoamine oxidases A and B, brain-derived neurotrophic factors (Philippe et al. 2002), sodium channels *SCN1A*, *SCN2A*, *SCN3A* (Weiss et al. 2003), methyl-CpG binding protein 2 (Lobo-Menendez et al. 2003), gamma-aminobutyric acid type A receptor β -3 subunit (Buxbaum et al. 2002), glutamate receptor 6 (Jamain et al. 2002), arginine vasopressin receptor 1A (Kim et al. 2002b), members of carboxypeptidase gene family—*PEG1/MEST*, *COPG2*, *CPA1* and *CPA5* (Bonora et al. 2002), and *WNT2* (Wassink et al. 2001) have been analyzed, conflicting results are obtained and no gene has been conclusively identified as a candidate gene. Since some of the above candidate gene analyses are not replicated by other studies (Krebs et al. 2002), the results should be interpreted with caution. Interestingly however, mice lacking the *WNT2* gene that is implicated in brain development exhibited less social interaction, which is one of the hallmarks of human autism.

Recently, mutations in the neuroligins *NLGN3* and *NLGN4* (X-linked genes) have been found in siblings with autism spectrum disorders (Jamain et al. 2003), but this needs to be replicated by other studies before any conclusion can be made. If it holds, then autism could be due to defects in synaptogenesis.

Environmental factors

Although inheritance contributes substantially to autism, that does not mean that there are no other environmental risk factors (Rodier and Hyman 1998). Autism spectrum disorders could be due to heritable and nonheritable risk factors (Newschaffer et al. 2002). For instance, thalidomide and anticonvulsants taken during pregnancy seem to elevate the risk of the disorder (Zwaigenbaum et al. 2002; DeLong 1999). Similarly,

intrauterine rubella (Chess 1997), cytomegalovirus (Iversson et al. 1990; Stubbs et al. 1984) infection, and premature birth with retinopathy of prematurity (Chase 1972) are implicated as risk factors. Among other factors, there was a considerable discussion about the occurrence of autism by immunization with the measles, mumps, and rubella vaccines. However, further careful examination of the data found no association with autism (Dales et al. 2001; Taylor et al. 2002). Therefore, they are no longer considered to be environmental risk factors.

Association with other disorders

Autism is occasionally associated with other disorders. These include tuberous sclerosis (Smalley et al. 1992; Bolton and Griffiths 1997), infantile macrocephaly (Bolton et al. 2001b), Angelman (Steffenburg et al. 1996), de Lang (Berney et al. 1999) syndrome, untreated phenylketonuria (Lowe 1980), Prader-Willi syndrome (Gillberg et al. 1991; Cook et al. 1997b; Baker et al. 1994), mental handicap and epilepsy (Monaco and Bailey 2001), and chromosomal abnormalities (Gillberg 1998). The association of tuberous sclerosis and autism suggests that an early developmental abnormality in a brain region may lead to autism and atypical autism. This is further supported by experiments in newborn monkeys and very young children (Bachevalier 1994; Zilbovicius et al. 1995).

Concluding remarks

Autism is a childhood, complex, and heterogeneous life-long condition. Impairment in social skills, language, and behavior are hallmarks of autism. Genetic and neurobiological abnormalities appear to be the etiological factors for autism. The biological basis of the disorder is unknown, and most of the studies to date have addressed genetic components of the disease. Genome-wide scans suggest multiple susceptibility loci, but no single gene has been identified as a predisposing factor. It does not seem to be a single gene disorder, and a complex etiology involving multiple loci has been proposed. It is possible that autism may be a series of syndromes or a syndrome caused by many different genes.

In order to explain the role of multigenes (15–20 genes) in which each gene plays a minor role in the etiology of the condition, a risk-factor model of epistatic interaction has been recently proposed (Jones and Szatmari 2002). This model predicts that addition of factors to the preexisting genetic insult increases the total risk. This accumulated effect need not be an additive type.

One major problem in identifying the autism gene is the clinical heterogeneity of the condition. For instance, it is not clear whether all hallmarks of autism (social and behavioral deficits) are due to a single gene defect or if it

is a mixture of several disorders and several gene defects. Additionally, in some patients it could be a full and severe syndrome but in others it could be a milder syndrome (Piven J 2001). Identification of clinically homogeneous families and a kind of quantitative measure of phenotypes may help to understand the disorder at the genetic level (Silverman et al. 2002; Lord et al. 2001).

There is no cure for autism. Individualized structured or specialized education and appropriate advice and support for families may help affected individuals develop potential skills to handle behavioral disturbance effectively (Rogers 1998). In addition, antipsychotic medications, especially trazodone and serotonin reuptake inhibitors may minimize some of the behavioral problems such as severe agitation and self-destructive behavior. In the future, identification of predisposing autism genes, understanding the neurobiology of the condition, and contribution of environmental factors may lead to better diagnosis and improved treatment (Rapin and Katzman 1998).

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