IADS Presentation on the Genetics of Anxiety Disorders

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Abstract:

Anxiety disorders are illnesses that present in the context of environmental and genetic vulnerability and protective factors. These disorders have complex genetic etiology, as demonstrated by family, twin, linkage, segregation and association studies. The current session will review available evidence regarding genetic contributions to these diseases as well as to the related trait known as Behavioral Inhibition (BI). Given the richness of available study data, obsessive-compulsive disorder (OCD) will be a focus of this anxiety disorder presentation. OCD family studies report four-fold elevation of risk among relatives, and twin studies provide OCD heritability estimates of 45-65% in children and 27-47% in adults. Linkage scans identified regions of interest on chromosomes 9p and 10p for OCD, and on 3q and 14 for compulsive hoarding. More than 80 OCD positional and functional candidate gene studies have been reported over the last decade. Specifically, genes within serotonin, dopamine and glutamate pathways and those involved in white matter formation have been the center of focus. The glutamate transporter gene *SLCL1A1* is the only of these consistently associated across OCD samples, although not at genome-wide significance levels. Most recently, a collaborative group of over 20 international research sites has undertaken a genome-wide association study (GWAS) of OCD, in search of common single nucleotide polymorphism (SNP) markers, copy number variants (CNVs) and other rare genetic events that may contribute to its etiology. The relatively small sample sizes and broad heterogeneity of samples have been limitations of genetic studies for anxiety disorders such as OCD to date. Areas for future progress in the genetic study of anxiety disorders will also be discussed, including a search for rare variants, combining analyses with neuroimaging and other potential OCD endophenotypes, and development of clinical risk models.