Whole-Exome Sequencing Reveals Increased Burden of Rare Functional and Disruptive Variants in Candidate Risk Genes in Individuals With Persistent Attention-Deficit/Hyperactivity Disorder

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Abstract

Attention-deficit/hyperactivity disorder (ADHD) is a common neurodevelopmental disorder affecting 3% to 6% of school-age children. In follow-up studies, approximately 77% of children with ADHD display full or subsyndromal persistent ADHD. ADHD has a high genetic risk component, and heritability has been estimated to be approximately 0.80. Many studies have attempted to identify genetic risk loci for the disorder, including numerous candidate gene studies and several moderately sized genome-wide association studies, the largest by the Psychiatric Genomics Consortium, but so far no single markers have passed the threshold for genome-wide significance.