Genetic Insights Into ADHD Biology

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Abstract

ADHD is a neurobiological disorder with a large worldwide prevalence causing significant impairment in children, adolescents, and adults. While there is general agreement about genetic contributions toward the disorder, progress in leveraging genetics to learn more about the biology and risk factors for ADHD has been limited. In this perspective, we identified 105 genes from the literature showing at least nominal statistical significance in association with ADHD. We analyzed these genes for enrichment in biological pathways and in known interacting biological networks. We also analyzed the expression patterns of candidate genes across brain regions and across periods of human development. From our analysis, we identify 14 genes that cluster within an interactive gene network, with enrichment in nitric oxide synthase and alpha-1 adrenergic pathways. Furthermore, these genes show enrichment for expression in the cerebellum during childhood through young adulthood, and in the cortex in adolescence and young adulthood. Gene discovery holds great potential for elucidating the unknown biological underpinnings of ADHD. Genome-wide sequencing efforts are underway and are likely to provide important insights that can be leveraged for new treatments and interventions.