

# Recent developments in the genetics of ADHD.

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## Abstract

Attention deficit hyperactivity disorder (ADHD) is a developmental psychiatric disorder which affects children and adults. ADHD is one of the psychiatric disorders with the strongest genetic basis according to familial, twin and SNP-based epidemiological studies. In this review, we provide an update of recent insights in the genetic basis of ADHD. We discuss recent progress from genome-wide association studies (GWAS) looking at common variants as well as rare copy number variations (CNVs). New analysis of gene groups, so-called functional ontologies, provide some insight into the gene networks afflicted, pointing to the role of neurodevelopmentally expressed gene-networks. Bioinformatic methods such as functional enrichment analysis and protein-protein network analysis are used to highlight biological processes of likely relevance to the aetiology of ADHD. Additionally, CNVs seem to map on important pathways implicated in synaptic signalling and neurodevelopment. While some candidate gene associations of e.g. neurotransmitter receptors and signalling have been replicated, they do not seem to explain significant variance in recent GWAS. We discuss insights from recent case-control SNP-GWAS which gave whole-genome significant SNPs in ADHD.