# Association of ADHD with genetic variants in the 5'-region of the dopamine transporter gene: evidence for allelic heterogeneity



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Multiple studies have reported an association between attention deficit hyperactivity disorder (ADHD) and the 10-repeat allele of a variable number tandem repeat (VNTR) polymorphism in the 3'-untranslated region (3'UTR) of the dopamine transporter gene (DAT1). Yet, recent meta-analyses of available data find little or no evidence for this association; although there is strong evidence for heterogeneity between datasets. This pattern of findings could arise for several reasons including the presence of relatively rare risk alleles on common haplotype backgrounds or the functional interaction of two or more loci within the gene. We previously described the importance of a specific haplotype at the 3' end of DAT1, as well as the identification of associated single nucleotide polymorphisms (SNPs) within or close to 5' regulatory sequences. In this study we replicate the association of SNPs at the 5' end of the gene and identify a specific risk haplotype spanning the 5' and 3' markers. These findings indicate the presence of at least two loci associated with ADHD within the DAT1 gene and suggest that either additive or interaction effects of these two loci on the risk for ADHD. Overall these data provide further evidence that genetic variants of the dopamine transporter gene confer an increased risk for ADHD.
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