

Reduced microbiome alpha diversity in young patients with ADHD

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Abstract

ADHD is a psychiatric disorder which is characterized by hyperactivity, impulsivity and attention problems. Due to recent findings of microbial involvement in other psychiatric disorders like autism and depression, a role of the gut microbiota in ADHD pathogenesis is assumed but has not yet been investigated. In this study, the gut microbiota of 14 male ADHD patients (mean age: 11.9 yrs.) and 17 male controls (mean age: 13.1 yrs.) was examined via next generation sequencing of 16S rDNA and analyzed for diversity and biomarkers. We found that the microbial diversity (alpha diversity) was significantly decreased in ADHD patients compared to controls ($p_{\text{Shannon}} = 0.036$) and that the composition (beta diversity) differed significantly between patients and controls ($p_{\text{ANOSIM}} = 0.033$, $p_{\text{ADONIS}} = 0.006$, $p_{\text{betadisper}} = 0.002$). In detail, the bacterial family Prevotellaceae was associated with controls, while patients with ADHD showed elevated levels of Bacteroidaceae, and both Neisseriaceae and Neisseria spec. were found as possible biomarkers for juvenile ADHD. Our results point to a possible link of certain microbiota with ADHD, with Neisseria spec. being a very promising ADHD-associated candidate. This finding provides the basis for a systematic, longitudinal assessment of the role of the gut microbiome in ADHD, yielding promising potential for both prevention and therapeutic intervention.