

# Genomic Structural Equation Modeling Offers Insight Into Expressive Differences Between Childhood and Late-Diagnosed ADHD: An Analysis of Genetic Overlap with External Trait



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*The following is an excerpt from a longer piece. For the full text, please visit [https://scholar.colorado.edu/concern/undergraduate\\_honors\\_theses/ng451j94g](https://scholar.colorado.edu/concern/undergraduate_honors_theses/ng451j94g) or scan the QR code.*

## **Abstract**

Recent literature on attention-deficit hyperactivity disorder (ADHD) has identified differences in the genetic influence of age at first diagnosis. In particular, genome-wide association studies (GWAS) have found that childhood, persistent, and late-diagnosed categories of ADHD exhibit divergent comorbidity patterns. Based on these findings, we hypothesized that there would be significant differences in genetic risk sharing across childhood and late-diagnosed ADHD with other external traits. The traits selected for analysis included 3 dimensions of risk-taking behavior, Automobile Speeding Propensity, Drinks Per Week, and Number of Sexual Partners, and 4 dimensions of diet-related behavior, Protein Intake, Fat Intake, Carb Intake, and Sugar Intake. Results from Genomic SEM applied to investigate differences in genetic risk sharing with these external traits and the two ADHD subgroups revealed significant differences for number of sexual partners ( $p = 0.003$ ) and automobile speeding propensity ( $p = 0.001$ ). Practical implications of these findings are discussed and offer reason to reevaluate the current treatment of ADHD.