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DNA Methylation Correlates with Network Surface Area in Discordant ADHD Twins

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Keywords

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Abstract

Globally, attention-deficit/hyperactivity disorder (ADHD), affects children, adolescents and adults, and can cause reduced academic achievement, occupational struggles, and social disability. Past research has attempted to explain the contributions of genetic and environmental factors in the functional connectivity of the human brain using twin's studies. The variation in genetic risk factors for ADHD explain a minimal proportion of observed cases, which suggests how genes are expressed and appear to affect the likelihood of diagnosis. While differences in neural functional connectivity have been observed on ADHD and typically developing children, the extent which these epigenetic factors contribute to differential neural behavior has not been investigated. To investigate epigenetic factors, one needs a cohort of twins that has discordant ADHD diagnoses, high quality resting-state functional magnetic resonance imaging (MRI) data, and epigenetic markers. We found that methylation at specific DNA sites was significantly correlated with surface area of the visual, dorsal attention, and salience networks in the cortex. This suggest that these three networks are expressing certain genes deferentially due to environmental factors, which affects the topology of the brain and may account for diagnosis outcome.

