Discovery of Significant Tissue Specific DNA Methylation Patterns and Motif Analysis in NPAS3 Gene in Schizophrenia-Diseased Individuals

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This project focuses on identifying and characterizing DNA methylation patterns and motif reoccurrences in the Neuronal PAS Domain Protein 3 gene in schizophrenia. Schizophrenia was in the past thought to be based on solely environmental factors. However, emerging research is increasingly supporting a genetic aspect to schizophrenia. Current treatments involve the use of anti psychotics, which blanket the disease's symptoms but fail to combat the physiological problems. This research sought to answer the question of how epigenetic mechanisms, such as DNA methylation, alter DNA in schizophrenia, as well as how these alterations differ in parts of the brain. The ultimate goal is to identify abnormal methylation in diseased subjects and/or in specific parts of the brain to contribute to the possibility of the creation of a demethylating agent as a treatment. NPAS3 was analyzed in the auditory cortex and dorsal lateral prefrontal cortex brain tissues. Utilizing Python 3.3 and algorithmic models, along with other computational programs (such as MEME) and data from the database MethylomeDB, the methylation patterns and locations of significant motifs were measured among the different tissues through a combination of visual and statistical analysis. In the diseased AC, methylation was more varied while non-diseased showed a more uniform pattern, with a greater number of regions that either had full or no methylation. The DLPFC, however, showed great variation between the diseased and non-diseased tissues. Methylation patterns were almost opposite in magnitude, even in areas such as the promoter that normally exhibit high methylation. Further extension of this research would include testing and comparing more brain tissues and expanding to include different age groups.

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