Modeling Genetic and Neurological Changes With Alcohol Use Disorder

Khan, Zoya (School: Cheyenne Central High School)

Alcoholism is a leading cause of premature death and disability globally. Alcohol use has profound mental and physical impacts including impaired decision-making skills and diseases related to the brain, liver, and pancreas. Alcohol dependence can rely on several factors, but 50-70% of susceptibility to alcohol is due to genetics. Genetic influence impacts not only susceptibility to alcohol dependence and abuse but continued reliance on the substance. Through running differential gene expression analysis (DESeq2), genes that were over-regulated were discovered in moderate and heavy drinkers. Gene set enrichment analysis (GSEA) was done to discover the significantly overexpressed genes between the two different groups as well as discover enrichment pathways using a p-value of 0.001. The genes were then filtered to 32 based on the highest blood gene expression levels, a random forest model predicted whether an individual was a moderate or heavy drinker based on their gene expression accurately 85% of the time. A logistic regression model was then used to analyze these 32 genes individually, and 5 genes with a direct connection to alcohol use disorder were identified. This shows that alcohol use disorder may be linked to more diseases and conditions than previous studies have shown. Additionally, the development of a machine learning model to determine a moderate or heavy drinker based on gene expression has profound clinical applications including better treatment options and pathways to rehabilitation.

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