Data Analysis of the Epigenetics of Drug and Alcohol Dependence

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Substance use disorder is characterized by the chronic use of addictive substances, to the point where substance use is beyond the user’s control. Both genetic and environmental factors determine an individual’s predisposition to drug addiction; suggesting that epigenetic mechanisms trigger changes within the transcriptome of an individual. GeneWeaver allows for efficient analysis of cross-species data using functional genomics. Curated literature was uploaded to GeneWeaver and grouped into projects for further analysis. In the first analysis, data sets containing genes directly affected by alcohol exposure were compared to sets containing epigenetic modifying genes that were affected by alcohol exposure. In the second analysis, a true positive set of H3K4me3 promoter sites was compared to H3K4me3 promoter sites after exposure to alcohol or cocaine. Two plausible genes and a protein family were found after comparison of the created gene sets: Rac3, TCF7L2, and kallikreins. Previous evidence shows that all of these genes may play a role in behavioral response. The analysis tools used were helpful in refining the large and noisy data sets from epigenetic and genomic studies of alcoholism, now GeneWeaver contains a more extensive collection of epigenomic data sets that are free for other investigators to use.

Awards Won:
National Institute on Drug Abuse, National Institutes of Health &amp the Friends of NIDA: Second Award of $1,500