Name: Elissa Chesler Email: elissa.chesler@jax.org

Using Mouse Behavioral Phenomics to Interpret and Model Genetic Variation in Substance Use Disorders

Robyn L. Ball1, Molly A. Bogue,, Vivek M. Philip, and Elissa J. Chesler1,4

1The Jackson Laboratory

A major challenge in human genetic studies of addiction is to understand precisely when the variant acts in the addiction trajectory information that can inform the therapeutic potential of specific biological or behavioral interventions. Historically, mouse population studies of addiction related traits including drivers of exploration, initial exposure response, initiation, maintenance, withdrawal, extinction, reinstatement and overdose, among many other predisposing characteristics. Increasingly sophisticated assays are being applied to these mouse populations, many of which have been thoroughly genetically characterized, with extensive genetic and genomic resources. The aggregation and integration of these data, associated to human orthologs provide a means of interpretation of the effects of specific targeting variants, and to find existing models that best reflect particular genetic vulnerabilities to specific aspects of SUD. All analyses are performed through the application of suite of data and analytic services applied to summary statistics from human GWAS, including the Mouse Phenome Database, GeneWeaver, GenomeMuster, mouse eQTL data services and other resources that are accessed programmatically, with many of the same services also accessible via web interafaces. We use mouse phenomic studies in genetic mapping and reference populations to characterize GWAS variants, identify strains with specific benefits as preclinical models of addiction based on the resemblance of phenotypic, genetic and genomic states to human disease.

https://pubmed.ncbi.nlm.nih.gov/38290977/