Submitter Name: Vivek Philip
Submitted email: Vivek.Philip@jax.org
PI Name (if different): Elissa Chesler
PI email (if different): Elissa.Chesler@jax.org

Genetic correlations and quantitative trait locus mapping reveals shared and unique mechanisms underlying addiction predisposing novelty response traits

Hao He[1], Vivek Philip[1], Center for Systems Neurogenetics of Addiction[1,2,3,4], Elissa J. Chesler[1]

[1]The Jackson Laboratory; [2]Department of Genetics, UNC Chapel Hill; [3]Psychology, SUNY Binghamton; [4]Department of Psychiatry, Pittsburgh University

Behavioral traits related to novelty response such as novelty seeking, reactivity and preference predispose individuals to either initiate or escalate psychostimulant use. This predictive and predisposing relationship suggests that there exist common underlying genetic mechanisms. Limitations in past investigation towards understanding the relation between novelty and addiction related traits in mouse and rat populations include low genetic diversity and limited behavioral variation along with a comprehensive experimental design that enhances the ability in elucidating these common genetic underpinning. The Center of System Neurogenetics of Addiction (CSNA) utilizes an experimental design strategy that enables the assessment of novelty related behaviors through open field, light dark, hole board and novelty place preference tests followed by assessment of in-depth addiction related phenotypes encompassing impulsivity, cocaine sensitization, circadian rhythms and cocaine self-administration. These phenotypes are collected on high-diversity advanced mouse populations such as the Collaborative Cross (CC), Diversity Outbred (J:DO) and their founders. These populations possess increased behavioral and genetic variation, which enables the identification of genetic mechanisms. Here, leveraging the CCs we show the presence and extent of genetic correlations across novelty-related behaviors analyzed by the CSNA using a panel CC RI lines. In addition to these genetic correlations, we provide a insight in to the common underlying genetic architecture of addiction predisposing novelty related traits by presenting results from the quantitative trait locus mapping within a large population of 2400 J:DO animals.