Submitter Name: Lisa Tarantino
Submitter Email: lisat@med.unc.edu
PI Name: Lisa Tarantino
PI Email: lisat@med.unc.edu

Acute locomotor activation and behavioral sensitization to cocaine in the Collaborative Cross and Diversity Outbred mouse populations

Lisa M Tarantino[1,2,4], Sarah A Schoenrock[1,4], Ashley Olson[3,4], Leona Gagnon[3,4], Vivek Philip[3,4], and Elissa J Chesler[3,4]

[1]Department of Genetics, School of Medicine, University of North Carolina; [2]Division of Pharmacotherapy and Experimental Therapeutics, Eshelman School of Pharmacy, University of North Carolina; [3]The Jackson Laboratory; [4]Center for Systems Neurogenetics of Addiction

The Center for Systems Neurogenetics of Addiction (CSNA) was formed with the goal of identifying and characterizing the shared genetic, molecular and neurobiological mechanisms underlying susceptibility to stimulant abuse. The CSNA is focused on performing multi-dimensional genetic characterization of biobehavioral risk factors for the self-administration of cocaine. The Tarantino laboratory is characterizing the Collaborative Cross (CC) and Diversity Outbred (DO) populations for acute locomotor sensitivity and behavioral sensitization to cocaine. We have previously published data describing two CC strains, CC004 and CC041, with divergent locomotor responses to cocaine as well as differences in drug self-administration and circadian behavior (Schoenrock et al., Psychopharmacology, 2020). Here we present behavioral sensitization data for 45 additional CC strains. Our data highlight the wide phenotypic distribution observed in this genetically diverse inbred population and allow us to identify additional extreme-responding CC strains that can be used to explore the genetic and neurobiological mechanisms underlying drug response and reward. We have also completed a preliminary mapping study of almost 400 DO mice. We have leveraged exploratory and novelty seeking data from 2800 DO mice to conduct reference trait analysis and increase our power to detect significant loci. These mapping efforts have identified several QTL regions that are currently being explored to identify candidate genes for follow up studies.