





Comparative genomics of alcohol and substance use disorders: Translational insights from the Drosophila model

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Alcohol and substance use disorders are significant public health problems in many countries. Whereas the metabolic effects of alcohol consumption and the neurological basis of alcohol and drug addiction have been well documented, relatively little is known about the genetic underpinnings predisposing to their adverse effects. Prenatal exposure to ethanol can cause fetal alcohol spectrum disorder (FASD), a prevalent, preventable pediatric disorder. Identifying genetic risk alleles for FASD is challenging since the time, dose, and frequency of exposure are often unknown, and manifestations of FASD are diverse and evident long after exposure. Similarly, the identification of genetic risk factors for cocaine addiction is hampered in human populations due to limited sample and histories sizes. heterogeneity in genetic backgrounds of environmental exposure, and difficulty in subject recruitment due to criminalization. Drosophila melanogaster presents an excellent model to study the genetic basis of the effects of developmental alcohol exposure and cocaine consumption since many individuals of the same genotype can be reared under controlled environmental conditions. Drosophila also provides an advantageous system to assess the effects of acute cocaine consumption and developmental alcohol exposure on differential gene expression in the brain, since gene expression across the entire brain can be surveyed at once using singlecell RNA sequencing technology. I will describe the effects of alcohol exposure and cocaine consumption on organismal phenotypes and illustrate how transcriptional analyses in Drosophila can provide a blueprint for translational studies on cocaine or alcohol-induced effects on gene expression in the brain in human populations.



Host: Dr. Howard Lipshitz

Date: Tuesday, January 31st, 2023 **Time:** 4:00 PM **Place:** Red Room, Donnelly Centre