Quantitative multi-organ transcriptome in the Hybrid Rat Diversity Panel: A resource for systems genetics studies of substance use disorders

Laura Saba¹, Spencer Mahaffey¹, Jennifer Mahaffey¹, Cheyret Wood², Jack Pattee², Samuel Rosean¹, Harry Smith¹, Keenan Manpearl², Angela Yoder², Paula Hoffman^{1,3}, and Boris Tabakoff¹

¹Department of Pharmaceutical Sciences, University of Colorado Anschutz Medical Campus; ²Department of Biostatistics and Informatics, University of Colorado Anschutz Medical Campus; ³Department of Pharmacology, University of Colorado Anschutz Medical Campus

Although genetics play a significant role in predisposition to substance use orders (SUDs), the exact mechanisms often remain elusive. While studies in humans can be logistically and ethically challenging, rat models can provide insight. The Hybrid Rat Diversity Panel (HRDP) is made up of 99 inbred and recombinant inbred strains and combines the benefits of genetic diversity across strains and genetic stability within strains to become a valuable resource for interrogating genetic influences on behaviors and physiology related to substance use and for exploring the role of genetic interactions with environment and drug exposure on phenotypes. As a genetically renewable resource, behavioral, physiological, and molecular phenotypes can be accumulated across generations and laboratories. The PhenoGen project is developing a transcriptome database for the HRDP that currently includes extensive transcriptome information from 56 HRDP strains with more RNA being processed regularly. This includes long RNA transcripts (>200 nt; polyadenylated and non-polyadenylated) and short RNA transcripts from brain and liver with additional data on kidney and heart. Data are available for download and visualization (http:/phenogen.org) in a processed format that includes a transcriptome reconstruction to identified unannotated transcripts and information on co-expression networks and expression QTL related to individual transcripts and networks. Raw sequencing data (over 75 billion reads) are also available via GEO. These transcriptome data can be combined with public information on DNA sequence, other omics, and behavioral/physiological phenotypes in a truly integrative systems genetics approach to studying mechanisms of SUD. Supported by NIDA (P30DA044223) and NIAAA (R24 AA013162).