

Submitter: Robert Hitzemann
Submitter email: hitzeman@ohsu.edu

Transcriptional Features Associated with Delay Discounting in HS Rats

Robert Hitzemann, Denesa Oberbeck, Priscila Darakjian, Deborah Sevigny-Resetco, Jordan Bromley, Katherine Garland, Suzanne Mitchell.

Department of Behavioral Neuroscience, Oregon Health & Science University, Portland OR 97239.

385 heterogeneous stock (HS) rats were phenotyped for delay discounting (DD) using an adjusting amount procedure. The hyperbolic $\ln k$ was normally distributed with no obvious sex differences. RNA-Seq (25 million paired-end reads) was performed on samples obtained from the first 86 of these animals (43 each males and females); brain regions examined were the prelimbic cortex (PL), the nucleus accumbens core (NAcc) and the basolateral amygdala (BLA). We focus here on the correlations between gene expression and $\ln k$. The analyses revealed significant (FDR < 0.05) gene ontology differences between the male and female data. In the BLA and for females, significant annotations detected included intrinsic component of synaptic membrane (FDR < 10^{-14}), glutamate receptor signaling (FDR < 2×10^{-3}) and translation (FDR 2×10^{-11}). The glutamate genes include *Grm 1, 5 and 6*; *Gria 2a, 2b and 3a*; *Gria 1 and 2*. For males the only significant association was for cell adhesion genes (FDR < 2×10^{-2}); this annotation was highly enriched in cadherins and protocadherins. In the PL significant female annotations included transporter complex (FDR < 2×10^{-7}) and voltage-gated cation channel activity (FDR < 3×10^{-4}) whereas for males the most significant annotation was for mitochondrial protein complex (FDR < 10^{-6}). For the NAcc there were no significant female annotations whereas for the males there were several annotations associated with the regulation of gene expression (FDR < 10^{-4}). To our knowledge this is the first genome-wide DD transcriptome analysis. Supported by DA 046077.