Transcriptional Features Associated with Delay Discounting in HS Rats

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385 heterogeneous stock (HS) rats were phenotyped for delay discounting (DD) using an adjusting amount procedure. The hyperbolic Ink 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 Ink. 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 \times 10^{-3}) and translation (FDR 2 \times 10^{-11}). The glutamate genes include \textit{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 \times 10^{-2}); this annotation was highly enriched in cadherins and protocadherins. In the PL significant female annotations included transporter complex (FDR < 2 \times 10^{-7}) and voltage-gated cation channel activity (FDR < 3 \times 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.