Conservation and Functional Enrichment of Neurotransmitter Receptors in Addiction

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Addiction is a disease in which the structures and function of the brain’s dopamine pathways are altered, resulting in compulsive indulgence in a substance or activity. Although much progress has been made in recent years in understanding addictive behavior, its underlying mechanisms are still largely unknown. To investigate the underlying transcriptional mechanisms of addiction, we conducted a bioinformatic study analyzing data from several online databases, including GEO2R, and the Therapeutic Target Database. Through the NCBI GEO database, we identified two datasets that compared gene expression changes in control individuals and those affected by cocaine dependence. Our analysis revealed 30 genes changed within the context of both a rat and human study of cocaine addiction. Moreover, the Reactome Knowledgebase as well as the DAVID Functional Annotation database revealed the neuronal systems pathway is enriched in these inter-species datasets. When comparing our list of 30 altered genes to those involved in the neurophysiological process, we found 12 gene expression changes conserved in both rat and human studies important for neurophysiological processes. Overall, we were able to find highly conserved gene expression changes that occur in humans and rats, with 4 of these differentially expressed associated with nervous system processes.

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