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# Microbes, Novelty-Related Behavior, and Cocaine Addiction

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Our objective is to understand the interaction of the microbiome and host genetics in substance use disorders (SUD). A number of genes have been identified as associated with addiction, however genes identified so far only account for a small proportion of the genetic variation. Accumulating evidence suggests the gut microbiome plays a significant role in behavioral responses to cocaine, as well as anxiety- and depression-like behaviors, many of which are comorbid with addiction. Host genetics can influence the composition of the gut microbiome and our hypothesis is that some host genes that affect addiction do so through their effect on abundance of bacteria. We are leveraging an ongoing project (P50DA039841) for samples and phenotype data from Diversity Outbred (DO) mice to test our hypothesis. Our preliminary data demonstrates that higher/lower abundance of specific bacterial species in the gut correlates with results of novelty response, novelty seeking and preference behavior tests. We have used these samples to identify several QTL affecting the abundance of microbes in the cecum. We will also identify correlations between the microbiome and addiction related behaviors using a cocaine intravenous drug self-administration (IVSA) system. The congruence of microbial abundance with novelty and IVSA behaviors will also be determined. Ultimately the causal role of the microbiota in addiction will be demonstrated by analyzing Collaborative Cross mice, microbial transplants, overlap between QTLs affecting microbes and addiction, and editing of QTL variants.

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