Cell Type-Specific Expression of the Molecular Players in Mouse Prefrontal Cortex During Cocaine Addiction

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Cocaine addiction is an issue that affects more than 5 million people in America per year. Despite past progress in cocaine addiction research, there are many specific questions left unanswered, namely what molecules and types of cells are involved, which my experiment tackles. Attempting to further previous research into certain molecular players, I followed up with their use of single-cell RNA sequencing on the prefrontal cortex cells of mice undergoing intravenous cocaine self-administration. Data from 12 samples from saline and cocaine-treated mice found on the Gene Expression Omnibus public database were retrieved. Using the Seurat function of RStudio, the data was merged into objects, normalized, clustered, and labeled into one of eight cell types. What resulted was a detailed UMAP plot displaying the clusters, their gene expression level, expression frequency, and their cell type. With this plot, I was able to determine the specific cell types that express the genes encoding the pre-established molecular players (ΔFosB, MeCP2, and BDNF). When the analysis was expanded to a cell-type specific level, it was discovered some of these genes were selectively expressed in excitatory neurons and non-neuronal cells. Going further into the analysis, I determined the 6 genes with the most varied gene expression over the 3 stages of cocaine addiction for each of the 8 cell types. Overall, my computational analysis of publicly available transcriptome datasets from mouse addiction model provides new insights into the molecular basis of cocaine addiction.