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Using RNA expression from immune-related cell types in blood to better understand potential influences of THC and CBD on human health

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Research on the effects of THC and CBD in products now widely available to the public has been lacking. We explored the influence of THC and CBD on immune cells by measuring RNA expression levels in T cells and monocytes from 10 subjects along with levels of THC, CBD, and their metabolites in blood. We identified genes that were differentially expressed between subjects with any vs. no THC (or its metabolites) detected and between subjects with any vs. no CBD (or its metabolites) detected. We also identified genes with expression levels associated with THC-COOH levels detected in these cell types. We identified 34, 11, and 2 differentially expressed (FDR<0.05) genes (any THC, any CBD, quantitative THC-COOH, respectively) in monocytes and 35, 23, and 11 differentially expressed genes in T cells. There was very little overlap between cell types and between CBD and THC. Of particular interest among the differentially expressed genes are the transcription factors FOS and FOSB (differentially expressed with THC in T cells) and MKI67 (differentially expressed with CBD in T cells), a common marker for T cell proliferation. In a hypothesis-driven fashion, we also examined differential expression in 5 core endocannabinoid system genes (CNR1, CNR2, FAAH, MGLL, and DAGL). MGLL was under-expressed in the presence of THC in monocytes. In conclusion, these preliminary data indicate that substantial cell type-specific changes to molecular phenotypes in immune cells are observed with exposure to THC and CBD and that further studies are warranted. Supported by DA032555.