#216 Alexandra Seidenstein Advisor(s): Bradley Aouizerat

Gene expression changes in response to PTSD: a multi-cohort approach to discovering the biological correlates of PTSD and exploration of its relationship to HIV pathogenesis

The impact of Post Traumatic Stress Disorder (PTSD) on a molecular and physiological level, is thought to influence a number biological processes involved in the health of affected persons. The physiological consequences of PTSD include inflammation, immune disfunction, impaired wound healing, and abnormalities in stress response. Our objective is to perform gene expression profiling of blood samples from individuals with and without PTSD to identify genes, pathways, and biomarkers of PTSD to provide targets for intervention. In addition, we will perform an exploratory analysis designed to evaluate for enrichment of PTSD-linked genes in a disease model associated with worse outcomes in the setting of PTSD: infection with HIV.

In order to investigate the impact of PTSD and HIV on gene expression we leveraged existing cohort studies and gene expression data, in order to rigorously identify and validate gene expression differences associated with PTSD, and genes, pathways and networks that are perturbed in the setting of HIV infection.

Leveraging data from PTSD studies and using cutting-edge approaches to gene expression analyses we aim to: Discover and validate differentially expressed genes associated with PTSD in blood samples. 2. Define the subset of genes associated with PTSD that are perturbed in peripheral blood mononuclear cells (PBMC) of HIV-infected individuals.

Preliminary results based on dataset, GSE83601 consisting of 10 war veterans, 5 with and 5 without PTSD post-deployment. This preliminary analysis was performed in order to test our QC pipeline. As expected, genes associated with antigen, and chemokine activity a a crucial component of the innate and adaptive immunity, were up-regulated. In addition, endoplasmic reticulum, and genes associated with protein packaging are also significant, as theyThese changes can be related to numerous up-regulated proteins associated with metabolic rate, immune cell production, neuronal activity, and inflammation.