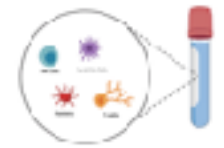


Investigation of Differentially Regulated Genes in the PBMC of Obese Adolescents



Project ID: 1902, Category: Translational Medical Science, Division: Senior, Science Type Project

Background Information: There is still much to be explored about the biological effects of obesity on adolescents. I found that the roles of microRNAs in adolescent obesity are currently very underrepresented in literature and was interested in exploring this further.

Research Question/Focus: This study hopes to determine novel biomarkers and explore significantly dysregulated pathways in male obese adolescents compared to male control samples for use in future clinical trials regarding adolescent obesity.

Methods:

- The R package *LIGER* was utilized to integrate and compare two datasets of peripheral blood mononuclear cells(PBMC): male obese and male control.
- The *dplyr*, and *ArrayTools* R packages were used to create labeled, cluster-specific data frames and matching phenotype data frames.
- Gene set enrichment analysis(GSEA) was run on each set of cluster files to determine significantly enriched gene sets between male obese and male control samples(miR and Gene Ontology gene sets used).

Data Analysis/Results

- The following microRNAs were found to be significantly unregulated in male obese samples(FWER p-value<0.05): **miR-3194-5p, miR-6791-5p, miR-302A-5p, miR-3184-5p**
- In-depth research into the functions and processes targeted by these microRNAs revealed connections to several types of cancer and Type 2 diabetes.

Interpretation and Conclusions:

- The microRNAs above and their target genes can be used as novel biomarkers in future clinical studies in order to provide novel insight into the sharing of mechanisms involved in various chronic diseases and adolescent obesity.
- The early screening of a dysregulated circulating miRNA profile may be a promising strategy to identify obese children who may suffer from metabolic abnormalities.
- Further clinical research into these identified microRNAs and their target genes is proposed.