Investigating Differential Gene Regulation in the PBMC of Obese Adolescents

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Obesity can weaken the immune system and increase the risk of contracting a plethora of life-threatening diseases. It currently affects 1 in 5 children in the U.S. This study investigated the genes and pathways involved in male adolescent obesity. Analysis was done on an RNAseq dataset of peripheral blood mononuclear cells and focused on identifying novel differentially regulated genes and pathways in male obese cells in comparison with male control cells. I used the R LIGER package to perform pre-processing and quantile normalization on the dataset in order to account for differences in sequencing and to create joint cluster assignments. I then determined the top differentially expressed genes for each cluster(adj p-value <0.05) and explored previous literature to assign cell type labels to each cluster. In order to find enriched pathways, I performed gene set enrichment analysis(GSEA) on each cluster grouping, with a focus on microRNA gene sets. I found several microRNA gene sets to be significantly upregulated in obese samples(FWER p-value <0.05): miR3194_5P, miR6791_5P, miR302A_5P, miR3184_5P. Several of these microRNAs have been represented in literature as potential drug targets for various cancers. This can provide novel insight into possible shared biological mechanisms between obesity and other diseases. Following clinical research, they can also be used in circulating microRNA screenings to identify the severity of certain metabolic abnormalities in adolescents. After further research into the functions of these gene sets, I concluded that these microRNAs and their target genes can serve as potential novel biomarkers for future clinical research into the metabolic characterization of adolescent obesity and its long-term biological effects.