Identification of Differentially Expressed Genes in Pancreatic Regulatory T Cell Survival

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Diabetes affects 347 million individuals worldwide and is the seventh leading cause of death in the US. While current treatments cause broad-based immunodeficiency, future organ-specific therapies may be developed by exploiting genotypic differences found in regulatory T cell (Treg) subpopulations. This study goaled to determine genes preferentially expressed in pancreatic Tregs relative to other Treg subpopulations, tissues, & immune cells to serve as targets in Diabetes therapy. Through multi-step microarray analysis, genes specific to pancreatic Tregs have been identified, with the top three genes (Clps, Pnliprp1, & Pla2g1b) expressed at values 23x, 12x, & 7x higher in pancreatic Tregs than in other Treg subpopulations ($p<0.05$). Microarray datasets (n=2236) curated from the NCBI GEO database were processed (via RMA normalization, outlier-array exclusion, & global median transformation) to confirm the specificity of these genes to the pancreas, with the pancreatic gene expression almost triple that of other tissues (n=29). Comparisons among other immune-cell types indicated that these genes were expressed 32x, 12.8x, & 7.5x higher, respectively, in pancreatic Tregs than in other immune cell-types, eliminating the possibility of augmenting the autoimmune response in future treatments. Further microarray comparisons (in R programming language via Mas-5 normalization, log2 transformation, & “trimmed mean” algorithm) between diabetics & non-diabetics confirmed the link of these genes in diabetes. Future Diabetes therapies should target these genes to solely regulate pancreatic Treg levels, avoiding the broad-based immunosuppression caused by current therapies. However, gene knockout studies should be performed to further validate the functionality of the identified genes.