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Differential Expressed Genes Identified Between African American and European American Keloid Fibroblasts

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Keloids are benign fibroproliferative tumors due to dysregulation of collagen remodeling and abnormal wound healing. Although worldwide, there is a higher incidence of keloid disease (KD) in skin of color, little is known about this predisposition. In this study, we used one tissue micro array slide comprised of six AA and 6 EA punch biopsies of primary untreated keloid tissue from the head and neck area was created, following the NanoString® DSP Technology Access Program protocol. The GeoMx Human Whole Transcriptome Atlas Assay was performed, using morphology marker FAP. Polygonal region of interests selection strategy for Fibroblast Activation Protein (FAP) positive cells was conducted. Univariate analysis was performed, using linear regression models to identify differentially expressed genes (DEG) at a false discovery rate (FDR) of 0.05. Ingenuity pathway analysis (IPA) software was used to determine DEG pathway enrichment. 1,450 DEG were identified (p-val <0.05) between AAs and EAs. The top 5 conical pathways identified by IPA were Breast Cancer regulation by Stathmin1, Chondroitin Sulfate Biosynthesis, Dermatan Sulfate Biosynthesis, G- Protein Coupled Receptor signaling, and sirtuin signaling pathway. The purpose of this study is to gain insight into ethnic differences in KD by comparing KF gene expression between AAs and EAs. Our data shows that KF gene expression differs by ethnicity. Moreover, IPA identified conical pathways that may underly ethnic differences in KD. Additionally, further studies are needed to better understand racial differences in KD.