miRNA Profile Differentiates Keloid and Normal Skin

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Running Title
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Word Count
1,287; Abstract: 197 words

Keloid disease (KD) is characterized by benign fibroproliferative tumors of the skin which result from injury in genetically predisposed individuals. Since its description, there has been little progress in treating KD, mainly due to an incomplete understanding of its pathogenesis. miRNA have emerged as important influencers of disease because of their tissue specificity and ability to modulate gene expression. Growing evidence supports their role in KD. However, significant gaps remain. In this study, we identified 17 significant differentially expressed miRNA (DEM) in a cohort of 15 primary untreated keloid and matched normal tissue samples from the head and neck area (n=30, $p<0.5$), using the TaqMan Advanced Human miRNA assay. Using Random Forest and Support Vector Machine, the DEM profile was able to differentiate keloid from normal (AUC > 0.969). The results were validated in an independent cohort (n=7), using single rtPCR (AUC 1.00). The DEM target genes were found to lie in pathways important for tumorigenesis, wound healing and fibrosis, supporting their likely involvement in KD. Seven of the DEMs are novel while 10 have been previously linked to KD. The results of this study support the KD diagnostic capability and biomarker potential of the 17-miRNA profile.