Bioinformatic analysis of the effect of type II diabetes on skin wound healing

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ABSTRACT. We examined the relationship between type 2 diabetes and skin wound healing. GSE38396 was downloaded from the Gene Expression Omnibus database and preprocessed using the RMA function of the Affy package. Differentially expressed genes (DEGs) were identified using the limma package, then DAVID was applied to perform Gene Ontology functional annotation and Kyoto Encyclopedia of Genes and Genomes pathway enrichment analysis. MicroRNAs and their target genes were screened from the miRecords database and subjected to functional analysis. Finally, the STRING online database was applied to identify the protein-protein interaction relationships, and a combined score > 0.5 was considered to indicate an interaction. A total of 421 DEGs (208 upregulated and 213 downregulated genes) were identified in the skin lymphatic endothelial cells of patients with type II diabetes. Twenty-four microRNAs and 34 target genes were screened, including those involved in cell migration, regulation of cell proliferation, cell death, and cell adhesion regulation, among others. Protein-
protein interaction network clustering analysis identified a module composed of 25 genes, and INTERPRO protein domain enrichment analysis showed that the protein domain of the clustering module mainly contained the insulin-like growth factor binding proteins IGFBP3 and CYR61. IGFBP3 and CYR61 may play important roles in skin wound healing in diabetes patients. This information may be useful for developing methods to treat skin refractory wounds in type II diabetes.

**Key words:** Cysteine-rich angiogenic inducer 61; Wound healing; Insulin-like growth factor-binding protein 3; Type II diabetes