Identification of molecular markers related to human alveolar bone cells and pathway analysis in diabetic patients

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ABSTRACT. Alveolar bone osteoblasts are widely used in dental and related research. They are easily affected by systemic diseases such as diabetes. However, the mechanism of diabetes-induced alveolar bone absorption remains unclear. This study systematically explored the changes in human alveolar bone cell-related gene expression and biological pathways, which may facilitate the investigation of its mechanism. Alveolar bone osteoblasts isolated from 5 male diabetics and 5 male healthy adults were cultured. Total RNA was extracted from these cells and subjected to gene microarray analysis. Differentially expressed genes were screened, and a gene interaction network was constructed. An enrichment pathway analysis was simultaneously performed on differentially expressed genes to identify the biological pathways associated with changes in the alveolar bone cells of diabetic humans. In total, we identified 147 mRNAs that were differentially expressed in diabetic alveolar bone cells (than in the normal cells; 91 upregulated and 36 downregulated mRNAs). The constructed

co-expression network showed 3 pairs of significantly-expressed genes. High-enrichment pathway analysis identified 8 pathways that were affected by changes in gene expression; three of the significant pathways were related to metabolism (inositol phosphate metabolism, propanoate metabolism, and pyruvate metabolism). Here, we identified a few potential genes and biological pathways for the diagnosis and treatment of alveolar bone cells in diabetic patients.

Key words: Diabetes; Alveolar bone cell; Biological pathway; Bioinformatics

