GENETICS AND GENODERMATOSES

INTEGRATED TRANSCRIPTOME ANALYSIS OF MICRORNA AND MRNA IN MOUSE SKIN DERIVED PRECURSORS (SKPS) AND SKP DERIVED FIBROBLAST (SFBS) BY RNASEQ

Li Li [1] - Rongying Zhou [2] - Anqi Li [1]

West China Hospital,sichuan University, Dermatology, Chengdu, China [1] - Sichuan University, Dermatology, Chengdu, China [2]

Background: Skin-derived precursors (SKPs) display the characteristics of self-renewal and multilineage differentiation.

Objective: In order to explore the molecular mechanisms of mouse SKPs differentiation into SKP-derived fibroblasts (SFBs).

Method: We compared the microRNA (miRNA) profile in mouse SKPs and SFBs by RNA sequencing. Real-time quantitative reverse transcription PCR (qRT-PCR) was performed to validate the miRNA expression. The integrated analysis of miRNA and mRNA expression data was performed to explore the potential crosstalk of miRNA-mRNA in SKP differentiation. Results: 207 differentially expressed miRNAs and 835 miRNA target genes in the gene list of integrated mRNA expression profiling were identified. Gene Ontology (GO) enrichment analysis revealed that cell differentiation and cell proliferation process were significantly enriched. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis revealed the target genes were significantly most enriched in the cytokine-cytokine receptor interaction, cancer pathways and axon guidance signaling pathway. The most upregulated and downregulated target genes were involved in the Wnt, Notch, cytokine-cytokine receptor interaction, TGF-β, p53 and apoptotic signaling pathway. The miRNA-mRNA regulatory networks and 507 miRNA-mRNA pairs were constructed. Seven miRNAs (miR-486-3p, miR-504-5p, miR-149-3p, miR-31-5p, miR-484, miR-328-5p and miR-22-5p) and their target genes Wnt4, Dlx2, Sema4f, Kit, Kitl, Inpp5d, Igfbp3, Prdm16, Sfn, Irf6 and Clu were identified as miRNA-mRNA crosstalk pairs.

Conclusion: These genes and signaling pathways might control SKPs proliferation and SKPs differentiation into SFBs during the process of SKPs differentiation, which might promote the application of SKPs in the clinical treatment of skin-related diseases by regulating SKPs proliferation and SKPs differentiation.

Keywords: Skin derived precursors, Fibroblasts, Stem cell, RNA sequencing,

Transcriptome analysis, microRNA.