

عنوان مقاله:

Analysis of the Gene Expression Profile of Bone Marrow Mesenchymal Cells from Follicular Lymphoma Patients

محل انتشار:

بیست و یکمین کنگره ملی و نهمین کنگره بین المللی زیست شناسی ایران (سال: 1399)

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خلاصه مقاله:

Mesenchymal stem cells (MSCs) are multipotent cells with the ability to self-renew and differentiate into a variety of cell types, tissue-repair and immuno regulatory. Follicular lymphoma (FL) is a systemic neoplasm of the lymphoid tissue arises from a germinal center B cell proliferation which is affected by a tumor microenvironment, mesenchymal stromal cells. regulating molecular mechanism related follicular lymphoma, seem to be useful for developing a new strategy to control its progression. Here, the microarray dataset GSE85229 from the Gene Expression Omnibus (GEO) that have the expression data for normal human bone marrow mesenchymal cells and bone marrow mesenchymal cells from follicular lymphoma patient. Differential expressed genes (DEGs) were investigated with GEO2R (p values < 0.05 and $|\log FC| \geq 1.5$). the Enrichr database was used to find significantly gene ontology terms (GO), namely biological process, cellular component and molecular function. To find the signaling pathways associated with upregulated DEGs, the KEGG database was used. To find top ten transcription factors (TFs) that presumably control DEGs, ChEA database was used. MiRTarBase database used to finding microRNA related to upregulated genes. GO analysis revealed that DEGs contain 240 upregulated and 208 downregulated genes. They were extensively involved in various biological process such as DNA replication, mitotic sister chromatid segregation, DNA metabolic process. KEEG pathway analysis showed that Cell cycle, p53 signaling pathway, Human T-cell leukemia virus 1 infection are the most significant pathways associated with upregulated genes. FOXM1, E2F4, AR and E2F5 were the top TFs controlling the upregulated genes. microRNAs analysis revealed that the top microRNAs associated with up DEGs were hsa-miR-193b-3p, hsa-miR-215-5p, hsa-miR-192-5p. Controlling molecular mechanisms of Mesenchymal stem cells might be useful to control Follicular lymphoma.

کلمات کلیدی:

Bioinformatics, Microarray, Transcription factors, MicroRNA

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