

عنوان مقاله:

Diagnosis and Treatment B non-Hodgkin Lymphoma with System Biology Approaches

محل انتشار:

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خلاصه مقاله:

Lymphomas are solid tumors of immune system and Non-Hodgkin Lymphomas (NHL) is the most prevalent lymphomas; with wide ranges of histological and clinical features, it is so difficult to identify them. Herein, various bioinformatics tools (such as gene differential expressions, epigenetics and protein analysis) employed to find new treatment approach for NHL based on gene expression variation between classic Hodgkin and B NHL. Microarray libraries GSE20011 downloaded from NCBI database and analyzed with GEO2R software, then differential expression genes analyzed by four databases (DAVID, Wikipathways, BioCarta and KEGG databases). Kinase, transcription factor, microRNA analysis and protein-protein interaction network performed by XTK, ChEA, microRNA TargetScan and Genes2Networks software respectively. Finally, drug target identified and carried out by Drug Pair Seeker and Connectivity MAP databases. The results showed GATA2 Transcription Factor (TF) up-regulates genes while Sox2 down-regulates them. Functional analysis of up-regulated genes showed highly activation in B cell receptor signaling pathway while programmed cell death and apoptosis program noted in down-regulated genes. Drug discovery facilities revealed that Verteporfin drug induces down-regulated genes while Prochlorperazine represses up-regulated genes. Three microRNAmiR-34a, miR-34c and miR-449 repressed up-regulated gene networks. The finding paves the roads toward B-NHL therapy with miR-34a/b and miR-449 microRNAs and Prochlorperazine / Verteporfin drugs.

کلمات کلیدی:

B non-Hodgkin lymphoma, Enrichment analysis, System Biology

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