عنوان مقاله:

Identification of genes with significant differential expression in breast cancer patients using transcriptome data analysis

محل انتشار:

اولین همایش بین المللی و دهمین همایش ملی بیوانفورماتیک ایران (سال: 1400)

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خلاصه مقاله:

Background: Breast cancer is a common cancer that starts in the breast tissue. This disease is the mostcommon cancer in women worldwide with a poor prognosis due to its aggressive biological behaviour andlack of therapeutic targets. Therefore, identifying the key genes involved in potential initiation andprogression mechanisms of breast cancer can be useful in the diagnosis, prognosis and treatment of thisdisease. Accordingly, the aim of the present study was to identify some novel genes with significantdifferential expression affecting breast cancer patients through bioinformatics analysis.Materials and Methods: Illumina-sequenced transcript data from three samples with breast cancer and fourhealthy individuals as control were collected from the NCBI database, and after controlling the quality of thereadings with FastQC program, the reads alignment were performed with reference genomes by STARsoftware. Then, data features were evaluated using featureCounts program. DESeq۲ software was used toidentify the genes with differential expression between breast cancer samples and healthy individuals ascontrol. Finally, Volcano graph, bar plot and point diagrams were traced to determine genes with significantdifferential expression.Results: RNA sequencing data analysis between patients with breast cancer and healthy individuals showedvaluable results. The results of these study were identified ۱۱ downregulated differentially expressed genes(DEGs) and ۲۰ upregulated DEGs. Among the key genes of this study can be noticed RNF۲۲۳, ETV۳L,CACNA۱S, UPS۳۴, NEURL۳, CRYBG۳ and FABP۴ and other important genes such as CCL۲۰, CXCL۵,CEP۲۹۵ and FLG۲ that significantly associated with breast cancer pathogenesis.Conclusion: In this study, we found some key genes with important roles in the pathways and molecularmechanisms involved in the pathogenesis of breast cancer that can be candidate targets for diagnostic,therapeutic and preventive purposes.

کلمات کلیدی:

Keywords: Breast cancer; Differential gene expression; Transcriptome; Bioinformatics; NCBI

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