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Short Review on Epithelial-Mesenchymal Transition in Relation to Bone Metastasis

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Abstract

The GSE20685 dataset served as the training set, and genes related to prognosis were selected using univariable Cox regression and a p-value of 0.01 as the filtering condition. The correlation coefficients of prognosis-related DEGs between primary and metastatic samples were then identified with the help of the LASSO–Cox regression model. On the basis of these genes and coefficients, a risk prognosis model was developed. Each patient's risk score was estimated using the model, the median score was used as the cut-off value, and the sample was divided into two groups: the high-risk group (HRG) and the low-risk group (LRG). The HRG and LRG survival curves were analyzed, and the 3-, 5-, and 10-year survival rates were predicted using a time-dependent ROC curve. The prognostic risk model was validated with the help of the GSE45255 dataset. The independent predictive ability of the prognostic model was evaluated by comparing the correlations between risk scores and other clinical prognostic factors using both univariable and multivariable Cox regression analyses.

Keywords: Bone metastases; Prognostic model; Immune infiltration pattern

Introduction

Weighted co-expression network analysis (WGCNA) is a method that builds scale-free networks from gene expression data. Using the expression profile data for the obtained candidate gene set, we constructed a weighted co-expression network using the R WGCNA package [1]. The modules related to BC metastasis were then screened, the genes were extracted, and the top 50 were chosen as hub genes based on their degree of inter-gene connectivity.

The CIBERSORT software, which can be found at http://CIBERSORT.stanford.edu/, was used to predict the percentage of 22 immune cells in each dataset's sample. The CIBERSORT package in R was used to measure the number of the 22 immune cells in HRG and LRG. We arranged the extents of certain cell types for all examples to investigate the clinical meaning of various examples with various extents of invulnerable cells. For the purpose of the survival analysis, the samples were divided into high-ratio and low-ratio groups using the median as a dividing line [2]. After that, Kaplan-Meier analysis was only performed on cases with a CIBERSORT p value of less than 0.05.

Results

Results Evaluation of DEGs We downloaded three sets of BC chip data from GEO—GSE20685, GSE12276, and GSE16446—which contained 244 primary cancer samples versus 83, 19 versus 185, and 83 versus 24 metastasis samples, respectively. For differential analysis, the Wilcox rank-sum test was utilized. We found 2950 DEGs in GSE20685 [3], including 1429 upregulated genes and 1521 downregulate genes, using a P-value of 0.05 as the cutoff. In GSE12276, there are 1209 DEGs, with 719 upregulated and 490 downregulate genes; and 830 DEGs in GSE16446, including 544 genes that are upregulated and 286 genes that are downregulate.

EMT-related DEG set The DEGs and EMT-related genes from the EMT database were examined together, and 304 genes were analyzed at intersections between the differential genes from the three sets of GEO data and the EMT database [4]. For the WGCNA, we utilized the 304 genes' expression data from GSE20685.

Discussion

Functional enrichment analysis of EMT-related DEGs (KEGG pathway and GO analysis) Using R's cluster Profiler software, the EMT-related DEGs was subjected to KEGG pathway and GO functional enrichment analyses (Fig. 2). The majority of these genes were found to be associated with cancer proteoglycans, the PI3K/Akt and TGF-signaling pathways, mesenchyme development, focal adhesion, and cytokine binding, respectively.

Development of a differential gene protein interaction network The DEGs from three datasets—GSE20685, GSE12276, and GSE16446—were uploaded to the string protein database (https://string- db.org/) for analysis of protein interactions. Homo sapiens was selected as the species, the minimum interaction threshold was set at 0.4 (the medium confidence level), and the other parameters remained unchanged [5]. There are 3121 edges and 288 nodes and 288 genes that interact with one another among them. GAPDH, VEGFA, FN1, CDH1, STAT3, Notch1, CD44, ERBB2, ESR1, and ITGB1 were the top ten genes. For more information, see Supplementary files 1 and 2 [6].

Conclusion

Up-and-comer quality set weighted co-articulation network development and center point quality screening. We planned a weighted co-articulation network for the up-and-comer quality set utilizing the WGCNA programming bundle of R. Research has shown that the co-articulation network follows a without scale organization, i.e., the log\ (k) of a hub with an association (k) is conversely connected with the log of the likelihood of the hub (P [k]), and the relationship coefficient > 0.85. We selected the optimal = 6 to guarantee that the

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network was scale-free [7]. 3A, "$\boldsymbol{\beta}$": power, or "point": a bunch of delicate thresholding power). The expression matrix was transformed into an adjacency matrix in the subsequent step; after that, a topological matrix was created from the adjacency matrix. We clustered genes according to a hybrid dynamic shear tree standard using the average-linkage hierarchical clustering method and set the minimum number of genes for each gene network module at 30 on the basis of topological overlap measure (TOM) [8]. After determining the gene modules using dynamic shearing, we performed cluster analysis on the modules to merge those that were closer to the new module and had a set height of 0.25. Next, we calculated the eigen- genes of each module once. Two modules were obtained in total. The ME (module eigengene) of each module and the sample characteristics (primary vs. metastatic) were used to calculate the Pearson's correlation coefficient (the higher the module, the more significant it was) [9].

Each module's feature vector gene is shown in a row, and the sample classification data is shown in a column. The correlation coefficients decrease from high to low from red to blue. The correlation coefficients of the gene modules and the corresponding features (BC metastasis and primary BC) are indicated by the numbers in each small box, and the P-value is indicated by the numbers in parentheses. In addition, the cluster dendrogram reveals a single turquoise-colored module containing 72 genes most relevant to the metastasis. Based on the degree of connection, the top 50 genes were chosen as hub genes [10].

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