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The Relationship Between Pyroptosis-related Gene Cytochrome C, Somatic, and Invasive Breast Cancer

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Abstract

Background: As one of the most prevalent malignancies affecting women, breast cancer stands as a formidable challenge to female health. Specifically, invasive breast carcinoma (BRCA), a subtype of breast cancer, exhibits comparatively unfavorable prognostic outcomes, imposing significant survival pressures on those affected. However, the current cause for concern lies in the absence of adequately effective biomarkers, creating a challenge in accurately guiding clinical decisions for breast cancer treatment. There is an imperative need for thorough research to discover potential biological markers. *Method:* We developed a prediction signature related to pyroptosis-related genes (PRGs), and further screened and analyzed the prognostic genes in the signature, and confirmed one gene, cytochrome C, somatic (CYCS), as the biomarker of BRCA. The expression of CYCS in normal breast tissues and BRCA tissues was analyzed, and its correlation with tumor immune infiltration and methylation was evaluated. In the end, candidate drugs were screened according to it. *Result:* Based on GSE21422 and GSE45827, we identified 14 differentially expressed PRGs. Functional enrichment analysis indicated that they were involved in the role of the immune system. TF-miRNA networks showed the highest correlation between CYCS and TP63, and they may interact by hsa-miR-590-3p or JUN. According to the results of LASSO analysis, the prognostic signature of PRGs was established, including IL18, CASP3, BAX, CYCS, TP63 and IL6R. It was verified that the signature can predict the overall survival of BRCA patients with high accuracy. Then, through univariate and multivariate Cox regression analysis, it is confirmed that CYCS has the highest accuracy of prediction among the six PRGs. We further revealed that CYCS in BRCA tissues was significantly higher than that in normal breast tissues. Also, CYCS participated in the regulation of immune microenvironment (IME), and the prognosis of CYCS with high methylation level in BRCA was worse. The last drugs screened were minocycline and artenimol. *Conclusions:* In conclusion, we developed a prognostic signature of PRGs, further screened and comprehensively analyzed a biomarker CYCS, related to BRCA. We also determined the correlation between the immune microenvironment, the methylation level of CYCS and the prognosis of BRCA patients, and the screening of targeted drugs was completed.

Keywords

Breast Invasive Carcinoma, Infiltrating Ductal Carcinoma, Biomarkers, Apoptosis-Related Gene, CYCS, Prognostic Features, Immune Microenvironment