Regulatory T Cell-related Prognostic Signatures, Immune Landscapes, and Related Drugs in Breast Cancer

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Abstract

Background: Tregs play a significant role in cancer development and the tumor immune microenvironment. We aimed to identify novel biomarkers associated with Treg cells in breast cancer through a comprehensive analysis to construct potential novel prognostic signatures. *Method:* Treg marker genes identified from scRNA-seq data were superimposed with Treg cell module genes identified by weighted gene co-expression network analysis to obtain Treg-like associated genes. Univariate Cox regression and LASSO regression analyses were used to screen prognostic genes from Treg-associated groups, followed by constructing prognostic markers, delineating risk groups, and the external validation of prognostic markers. To further elucidate the immune status of breast cancer patients, tumor mutation burden, immune cells, and immune checkpoint inhibitors were analyzed in high- and low-risk populations. *Result:* Using integrated analysis of RNA-seq and bulk-seq data, 54 Treg-related genes were discovered. Using univariate Cox regression and LASSO regression analysis, CLOCK, FUT7, and LTB were screened as prognostic genes for breast cancer. Then, prognostic tags predicting the survival of breast cancer patients were constructed and validated based on these genes. *Conclusion:* Treg cell-associated prognostic signatures may be a promising tool for predicting the prognosis of breast cancer patients. Treg cells should be emphasized as potential immunosuppressive cells in tumor immunotherapy.

Keywords

Breast Cancer, Treg, Bioinformatics, Prognosis