



COMPREHENSIVE MODEL FOR PREDICTING BREAST CANCER THERAPY OUTCOMES BASED ON IMMUNOLOGICAL BIOMARKERS

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ABSTRACT

This study presents a comprehensive model for predicting breast cancer therapy outcomes based on immunological biomarkers. Levels of cytokines (IL-2, IL-6, IL-10, TNF- α , IFN- γ), lymphocyte subpopulations, and immune checkpoint expression (PD-1/PD-L1) were analyzed in 290 patients. Key parameters influencing treatment efficacy and recurrence risk were identified. The developed model enables accurate prediction of therapeutic outcomes and supports personalized treatment strategies. The findings provide a scientific basis for implementing immune-oriented technologies in clinical oncology, improving therapeutic effectiveness, and enhancing the quality of life in patients with breast cancer..

Relevance

Breast cancer remains the leading cause of cancer-related morbidity and mortality among women worldwide. Despite advances in targeted and hormonal therapies, recurrence and therapy resistance remain significant challenges. Understanding immune mechanisms underlying tumor progression and treatment response is critical for improving therapeutic outcomes. Cytokine profiles, lymphocyte subpopulations, and immune checkpoint molecules such as PD-1 and PD-L1 reflect the state of antitumor immunity and serve as objective prognostic indicators. Developing a comprehensive predictive model based on these biomarkers allows assessment of recurrence risk and individualized therapy outcomes. Such an approach facilitates personalized, immune-oriented strategies that improve survival rates and optimize treatment for breast cancer patients.

Aim

To develop a comprehensive model for predicting breast cancer therapy outcomes based on immunological biomarkers to improve the accuracy of prognosis and optimize therapeutic strategies.

Materials and Methods

A total of 290 women aged 28–75 years with histologically confirmed breast cancer were examined. Serum cytokine levels (IL-2, IL-6, IL-10, TNF- α , IFN- γ) were determined using ELISA, and PD-1/PD-L1 expression was measured by flow cytometry. Lymphocyte subpopulations (T-helper, T-suppressor, and NK cells) were analyzed to assess immune activity. Statistical analysis included correlation and regression models using IBM SPSS 26.0,

with significance set at $p < 0.05$. Clinical, immunological, and molecular data were integrated to develop a predictive model for therapy outcomes.

Results

Elevated IL-6 and TNF- α levels and increased PD-L1 expression were significantly associated with disease progression ($r=0.61$; $p < 0.01$) and poor therapy response. Reduced NK and T-helper cell activity correlated with higher recurrence risk. The developed comprehensive model, integrating immune, clinical, and molecular parameters, achieved 87% accuracy in predicting treatment outcomes. The model allows for individualized assessment of therapeutic effectiveness and risk of recurrence, providing a foundation for adaptive treatment optimization in breast cancer management.

Conclusion

The developed comprehensive model for predicting breast cancer therapy outcomes demonstrated high accuracy and clinical applicability. Immunological biomarkers such as IL-6, TNF- α , PD-1, and PD-L1 possess strong prognostic value, reflecting the state of antitumor immune activity. The model enables precise evaluation of treatment response and recurrence risk, supporting the implementation of personalized, immune-oriented therapeutic strategies. These findings emphasize the importance of integrating immunological parameters into clinical decision-making, enhancing therapeutic precision, reducing relapse rates, and improving long-term outcomes in breast cancer patients.

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