

MULTIMODAL STRATIFICATION OF PREDICTIVE BIOMARKERS IN HEAD AND NECK CANCERS: A FOCUS ON CYTOKINE-BASED IMMUNOTHERAPY

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Background Immunotherapy, particularly cytokine-based therapy, has been gaining traction in the treatment of head and neck cancers. Cytokines are small proteins that play a crucial role in the immune response to cancer. However, not all patients respond to cytokine-based immunotherapies, and some may experience severe side effects. The ability to predict which patients are most likely to benefit from these therapies could greatly improve the efficacy and tolerability of treatment.¹ In this context, the study of predictive biomarkers, such as the expression of immune checkpoint molecules like PD-L1 and TIGIT, and the profiling of cytokines within the tumor microenvironment, has become crucial. These biomarkers could provide valuable information about the patient's immune response to the tumor and their likelihood of responding to cytokine-based immunotherapies.^{2 3}

Methods A multimodal approach to stratify predictive biomarkers in head and neck cancers was used. The methodology was founded on combining metabolic, transcriptomic, and proteomic data to offer a comprehensive understanding of potential biomarkers. The data from different modalities were integrated using bioinformatics and machine learning algorithms. This comprehensive dataset was analyzed to identify multimodal biomarker signatures that could predict patient responses to cytokine-based therapies.

Results Preliminary finding showed significant heterogeneity in the expression of PD-L1, TIGIT, and cytokines across the tumor microenvironment. This underscored the complexity of head and neck cancers. Certain multimodal biomarker signatures, which included specific patterns of immune checkpoint molecule expression, cytokine profiles, and immune cell infiltration, correlated robustly with patient responses to cytokine-based therapies.

Conclusions Our study demonstrates the considerable potential of a multimodal stratification approach in deciphering the complexity of head and neck cancers and predicting responses to cytokine-based immunotherapies. By integrating metabolomic, transcriptomic, and proteomic data, we identified unique biomarker signatures that strongly correlated with therapy responses. This work underscores the role of integrated predictive biomarker profiles in enhancing the precision of immunotherapy.

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