Precision Medicine in Head and Neck Squamous Cell Carcinoma

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Background: Head and neck squamous cell carcinoma (HNSCC) is diagnosed in approximately 890,000 new cases per year, with survival rates improving only modestly over the past four decades[1]. Current multimodal treatment strategies rely on staging criteria that fail to account for molecular differences between tumors, limiting the ability of physicians to predict which patients will respond to treatment. Recent landmark trials have demonstrated the benefits of perioperative immunotherapy[2], but the lack of predictive biomarkers prevents tailoring treatment to a patient's tumor. This narrative review examines the current state of proteomics in HNSCC, focusing on its potential to predict treatment response, guide the aggressiveness of treatment, and personalize therapy for patients with unique biomarkers.

Methods: A narrative review of literature within the past 10 years was conducted through PubMed and Google Scholar using search terms "single cell RNAseq for HNSCC," "proteomics HNSCC," "scRNA seq HNSCC," "tumor microenvironment HNSCC," "spatial transcriptomics HNSCC," "artificial intelligence head and neck cancer", and "biomarkers HNSCC immunotherapy."

Results: Proteomic approaches show significant promise across multiple clinical applications in HNSCC treatment. Serum proteomics can identify patients likely to respond to treatment before initiation. Single-cell RNA sequencing has revealed the immune environment differs between HPV-positive and HPV-negative tumors and identified molecular subtypes with treatment implications. Spatial proteomics have identified structures such as tertiary lymphoid structure, dendritic cell networks, and neutrophil-associated protein signatures which have demonstrated stronger predictive insight of immunotherapy success than traditional bulk biomarkers. Similarly, panels that evaluate multiple biomarkers perform better than relying on a single marker such as the PD-L1 combined positive score. Despite strong evidence, some obstacles to proteomic use in clinical practice include a lack of standardized protocols for biomarker treatment, limited prospective validation studies, small sample size studies, high costs, and limited elucidation of regulatory pathways in protein synthesis.

Conclusion: Proteomics in HNSCC is a powerful tool that can reshape how we approach treatment of patients with HNSCC with biomarker-driven care. However, clinical implementation requires prospective validation studies, standardized protocols, and multi-omics integration to fully develop individualized treatments for HNSCC patients.

References:

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