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Abstract
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Machine Learning-Based Integration Develops a Robust Mitophagy-Related Multigene Model to Predict Patient Prognosis and Immune Microenvironment in Head and Neck Squamous Cell Carcinoma

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Abstract

Objectives:

Head and neck squamous cell carcinoma (HNSCC) is a clinical challenge. Mitophagy in cancer cells is related to the tumor's high energetic metabolism. The tumor immune microenvironment (TME) has a profound impact on clinical outcomes and treatment effectiveness. However, the correlation of mitophagy and TME remains unknown in HNSCC.

Methods:

Based on machine learning, a prognostic multigene signature was built with mitophagy-related differentially expressed genes (MPGs) in TCGA cohort. Moreover, we systematically correlated risk signature with immunological characteristics in TME, which included immune checkpoints, tumor-infiltrating immune cells (TIICs), immunomodulators. To further invalidate CSNK2A2, we employed immunohistochemistry to examine its expression.

Results:

MPGs-related prognostic model showed good prediction performance. Patients who had high-risk scores had significantly shorter progression-free survival (PFS) and overall survival (OS) than those with low-risk scores, according to the results of the survival analysis ($p < 0.0001$). The CD8+ T cells infiltrated less in samples with higher risk scores. The immunological characteristic markers were expressed at higher levels in the low-risk group. Furthermore, immune therapy might be effective for the low-risk subtype of HNSCC patients ($p < 0.001$). Samples with higher risk scores were more sensitive to chemotherapy. CSNK2A2 was validated to be higher expressed in HNSCC tissues, according to immunohistochemistry.

Conclusion(s):

We have constructed a prognostic signature and provided innovative insights that may improve HNSCC management, which might give a more precise prognostic prediction. CSNK2A2 might be a novel biomarker to predict immune efficacy.