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ASO AUTHOR REFLECTIONS

ASO Author Reflection: The TME-Related Gene AIF1 Signature Predicts Esophageal Carcinoma Prognosis

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PAST

For esophageal carcinoma (EC), chemoradiotherapy plus surgery has been the most effective therapy.[1] However, the 5-year overall survival (OS) rate for EC patients is only 15–25%.[2] Recently, immunotherapy has shown great efficacy in EC patients.[3,4] Hence, we need to further investigate the relationship between the tumor microenvironment (TME) and the pathology and prognosis of EC, which can help elucidate potential mechanisms and explore novel targets for EC immunotherapy.

PRESENT

Our study used the Cancer Genome Atlas (TCGA) database to investigate the correlations between TME and prognosis in EC and explore the prognosis-related genes of EC tissues based on transcriptional profiles. Fifteen TME-related genes, including AIF1, were identified as prognostic predictors. Furthermore, the Gene Expression Omnibus (GEO) database and tissue microarrays of 145 EC patients were used to perform validation analysis. Multiplex immunofluorescence staining was also performed to detect the relationship of AIF1 and TME-related makers in 90 EC patients. We further discovered that AIF1 might affect immune infiltration, including Th1 and NK cells, through T-cell immune receptors (TIGIT) with Ig and ITIM structural domains.[5]

FUTURE

These findings suggest that AIF1 is a promising prognostic factor and a potential target for immunotherapy in esophageal cancer. However, further mechanism studies are essential to explore the relationship between AIF1 and TIGIT-related pathways.

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