Low-grade glioma tumor immune microenvironment

The methylation levels of 6 autophagy-related genes (ARGs) (ARSB, CFLAR, WIPI2, RB1, ERN1, RAB24) have a strong predictive potential for low-grade glioma, and the methylation regulation of ARGs has an important impact on the tumor immune microenvironment of LGGs¹⁾.

Aging tumor microenvironment (aging TME) is emerging as a hot spot in cancer research for its significant role in the regulation of tumor progression and tumor immune response. The immune and stromal scores of low-grade gliomas (LGGs) from TCGA and CGGA databases were determined by using ESTIMATE algorithm. Differentially expressed genes (DEGs) between high and low immune/stromal score groups were identified. Subsequently, weighted gene co-expression network analysis (WGCNA) was conducted to screen out aging TME related signature (ATMERS). Based on the expression patterns of ATMERS, LGGs were classified into two clusters with distinct prognosis via consensus clustering method. Afterwards, the aging TME score for each sample was calculated via gene set variation analysis (GSVA). Furthermore, TME components were quantified by MCP counter and CIBERSORT algorithm. The potential response to immunotherapy was evaluated by Tumor Immune Dysfunction and Exclusion analysis. We found that LGG patients with high aging TME scores showed poor prognosis, exhibited an immunosuppressive phenotype and were less likely to respond to immunotherapy compared to those with low scores. The predictive performance of aging TME score was verified in three external datasets. Finally, the expression of ATMERS in LGGs was confirmed at protein level through the Human Protein Atlas website and western blot analysis. This novel aging TME-based scoring system provided a robust biomarker for predicting the prognosis and immunotherapy response in LGGs²⁾.

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