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Identification of a nomogram predicting overall survival based on ADAP2-related apoptosis genes in gliomas

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Abstract

Background: Apoptosis continues to be a pivotal area of investigation in glioma research. ADAP2 mediates the malignant progression of gliomas through the inhibition of apoptosis and predicts the overall survival(OS) of glioma patients based on prognostic modeling of the apoptotic gene set.

Methods: The study encompassed 686 glioma patients, with 413 allocated to the training group and 273 to the validation group. Differential expression of ADAP2 across various glioma subtypes was assessed through bioinformatics analysis and Western blotting. The correlation between ADAP2 and apoptosis was examined using Gene Set Enrichment Analysis (GSEA). Multivariate Cox regression analysis and LASSO dimension reduction analysis were employed to identify apoptosis-related genes with prognostic significance in glioma patients and to construct a nomogram. Biological functions and mechanisms associated with risk scores were explored via Gene Ontology (GO), Kyoto Encyclopedia of Genes and Genomes (KEGG), and GSEA analyses, with validation through Western blotting, flow cytometry, and AM/PI staining.

Results: ADAP2 was found to be enriched in more aggressive glioma subtypes and was closely linked to glioma cell apoptosis, modulating this process via the NF-κB and P53 signaling pathway. A nomogram for OS in glioma patients was constructed using thirteen apoptosis-related genes. Additionally, ROC curves, calibration curves, and C-indices confirmed the robust applicability of the nomogram.

Conclusion: ADAP2 functions as a prognostic biomarker for glioma patients, regulating glioma cell apoptosis through the NF-κB and P53 signaling pathway. Moreover, prognostic models based on apoptosis-related genes can accurately predict OS for glioma patients at 1, 2, 3, 5, and 10 years.

Keywords: ADAP2; Apoptosis; Glioma; NF-κB; Nomogram.