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Decoding Glioblastoma: The Role of *CENPA* and *BIRC5* as Key Biomarkers in Diagnosis and Prognosis

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ABSTRACT

Introduction: Glioblastoma (GBM) is a leading cause of cancer-related deaths in adults globally, accounting for approximately 15% of all primary brain tumors. GBM remains one of the most aggressive and challenging forms of cancer to treat. The aggressive nature and poor prognosis of GBM highlight the urgent need for improved diagnostic and therapeutic strategies. Conventional diagnostic techniques, such as imaging and biopsy, are often invasive, expensive, and time-consuming, limiting their effectiveness and accessibility. Hence, there is a critical need for more effective approaches for early detection and management of GBM. This study aimed to identify potential diagnostic and prognostic biomarkers for GBM.

Methods and Materials: RNA-sequence (RNA-Seq) data for GBM and standard tissue samples were obtained from TCGA using the TCGAbiolinks package in R. Genes that were differentially expressed (DEGs) were selected based on a p < than 0.05 and a log fold change greater ≥1. The prognostic value of DEGs was investigated. Survival curves were generated for these groups using Kaplan-Meier analysis, and the statistical significance of differences in survival was assessed using the Log-rank test. The functional importance of the DEGs was explored using gene ontology (GO) and KEGG pathway analyses. Protein-protein interaction (PPI) networks were constructed using the STRING database and visualized with Cytoscape. The miRNA-target interactions were examined using TargetScan, while transcription factor (TF)-target interactions were analyzed using JASPAR databases.

Results: The initial analysis identified 847 DEGs in GBM compared to normal brain tissue. Kaplan-Meier survival analysis was conducted to evaluate the prognostic significance of *CENPA* and *BIRC5* in GBM. The results showed that the survival analysis did not demonstrate a significant difference in overall survival between patients with high and low expression levels of CENPA. The Log-rank p value was 0.85, indicating no statistically significant association between *CENPA* expression and survival outcomes. The analysis also showed that high expression of *BIRC5* was associated with a trend towards reduced overall survival compared to low expression, although this was not statistically significant (Log-rank p = 0.4). The hazard ratio for high *BIRC5* expression was 0.86, suggesting a possible, albeit non-significant, trend towards poorer survival outcomes. GO analysis revealed that the DEGs involved critical biological processes such as cell cycle regulation. PPI network analysis identified hub genes, highlighting the central roles of *CENPA* and *BIRC5* in the GBM regulatory network. The miRNA-target interactions identified several miRNAs, including hsa-mir-503-5p, hsa-mir-23b-3p, and hsa-mir-34a-5p, which suggest their regulatory influence on the expression of these hub genes. Additionally, TF-target interactions revealed PRDM1 as a key TF, indicating its significant role in the regulatory mechanisms of these DEGs.

Conclusion and Discussion: The study identified *CENPA* and *BIRC5* as potential diagnostic and prognostic biomarkers for GBM. These findings underscore the importance of further.

Keywords: Biomarkers, Genetic transcription, Glioblastoma, RNA-Seq

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