

Abstract

Integrated Analysis of Glioblastoma: Unravelling Molecular Signatures across Diverse Datasets for Enhanced Diagnosis [†]

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1. Background

Glioblastoma Multiforme (GBM) presents significant diagnostic and therapeutic challenges due to its complex molecular pathogenesis. Current diagnostic methods often fail to detect early molecular signatures critical for timely intervention. This study integrates microarray and RNA-Seq datasets from both serum and tissue samples to explore differentially expressed genes (DEGs) and protein–protein interaction networks with the aim of identifying robust biomarkers and understanding the molecular underpinnings of GBM.

2. Methods

Utilizing microarray datasets (GSE116520 and GSE90604) and RNA-Seq datasets (GSE165595 and GSE228512) from both brain tissue and serum samples, this study conducted integrative differential gene expression analysis using limma and DESeq2 packages. Functional annotation and gene ontology analyses were performed using DAVID and ShinyGO tools. Protein–protein interaction (PPI) networks were constructed using the STRING database and analysed via Cytoscape to identify central hub genes.

3. Results

The analysis and cross-technology validation highlighted 1051 common DEGs across tissue datasets where 87 were upregulated and 255 were downregulated. Notably, three genes, *MAST3*, *ADAM11*, and *PTPRK*, were consistent across tissue and serum datasets, suggesting their utility as non-invasive biomarkers. Functional annotation identified critical biological processes and pathways disrupted in GBM, such as cell division, angiogenesis, and cell adhesion. The PPI network analysis identified central hub genes, offering insights into the molecular interactions contributing to the pathophysiology of GBM.

4. Conclusions

This study underscores a complex network of molecular interactions pivotal to the pathophysiology of GBM. The identified DEGs and pathways provide a foundation for developing diagnostic panels and therapeutic targets, emphasizing the need for further research to translate these biomarkers from bench to bedside.

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Data Availability Statement: All data used in this study can be found in Gene Expression Omnibus (GEO) database.

Conflicts of Interest: The authors declare no conflict of interest.

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