Publication Digest

MICROFLUIDICS

Biomarker Discovery and Target Validation

Novak, M. et al. “The Slovenian translational platform GlioBank for brain tumor research: Identification of molecular signatures of glioblastoma progression.” *Neuro-Oncology Advances* 7 (2025): vdaf015.

Researchers at the National Institute of Biology in Ljubljana, Slovenia, have established GlioBank, a Slovenian glioblastoma biobank consisting of patient tissue samples and their corresponding cellular models and clinical data. Real-time quantitative PCR (RT-qPCR) was performed using the Standard BioTools™ Biomark™ platform to determine the expression of genes associated with tumor subtype, overall patient survival and cancer cell invasiveness. This study demonstrates that gene expression analysis can uncover molecular signatures for patient stratification, prognosis, and drug target discovery and validation.

Key takeaways

- GlioBank, a centralized biobank of glioblastoma patient tissue samples, was established to facilitate the discovery of new biomarkers and treatment approaches to improve outcomes for glioblastoma patients
- Targeted analysis using the Standard BioTools Biomark platform revealed gene expression signatures significantly associated with survival and identified an independent prognostic marker for poor overall survival in glioblastoma patients
- Further comparative gene expression profiling between the tumor core and tumor rim regions identified distinct molecular signatures associated with glioblastoma invasiveness
- High-throughput qPCR with the Biomark platform enabled rapid and efficient profiling of 56 genes in over 100 samples

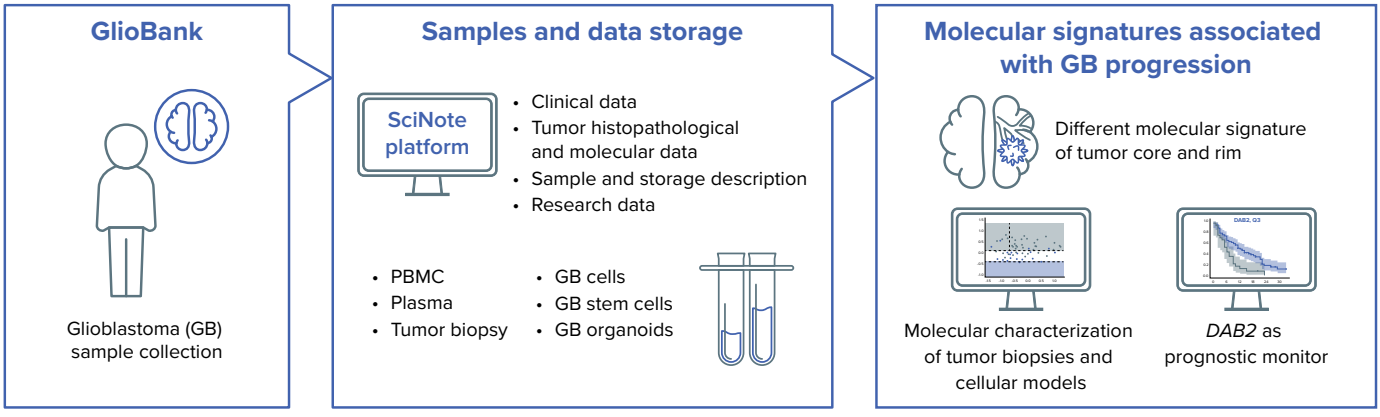

Figure 1. Graphical abstract of study overview

Background

Glioblastoma is one of the most lethal and aggressive cancer types in humans due to its cellular and molecular heterogeneity, highly invasive nature and resistance to treatment. This study aimed to establish GlioBank as a centralized resource of glioblastoma-related biological materials and associated data in Slovenia to accelerate translational research efforts. Gene expression analysis was used to demonstrate the utility of the biobank through discovery and validation of molecular signatures associated with glioblastoma progression, invasiveness and patient survival, thereby identifying potential biomarkers and therapeutic targets.

Study design

Tumor tissue and blood samples were collected from patients at the Department of Neurosurgery at the University Medical Center Ljubljana, Slovenia, and further processed to obtain peripheral blood mononuclear cells, plasma, glioblastoma cells, glioblastoma stem cells and organoids. Corresponding neuroclinical, histopathological and oncological data was collected.

A subset of 101 patients with complete samples and corresponding data was used for analysis. Total RNA was extracted from snap-frozen GB tissue samples. Complementary DNA (cDNA) was synthesized and analyzed using RT-qPCR with 56 TaqMan Gene Expression Assays (Thermo Fisher Scientific) on the **Standard BioTools Biomark HD system and 48.48 Dynamic Array™ integrated fluidic circuit (IFC)**. Genes related to tumor subtype, tumor microenvironment, immune response and signaling pathways were included in the panel. Relative mRNA copy numbers were normalized to the housekeeping genes HPRT1 and GAPDH. Correlations between gene expression and variables including tumor subtype, survival, glioblastoma stem cells, epithelial-to-mesenchymal transition and immune response were calculated.

Results

- GlioBank was established, consisting of over 200 tissue and blood samples from glioblastoma patients
- Gene expression analysis found that high expression of *DAB2*, *S100A4* and *STAT3* were significantly associated with poor survival, suggesting these genes may serve as indicators of disease aggressiveness and biomarkers for patient stratification. *DAB2* was identified for the first time as an independent prognostic marker for poor overall survival in glioblastoma patients.
- Comparative gene expression analysis of patient-matched tumor core and tumor rim samples revealed distinct molecular signatures between these regions. *STMN4*, *ERBB3* and *ACSBG1* were found to be upregulated in the invasive tumor rim, suggesting a strong association with the aggressive spread of glioblastoma and positioning these genes as potential targets for therapies aimed at limiting tumor invasion.

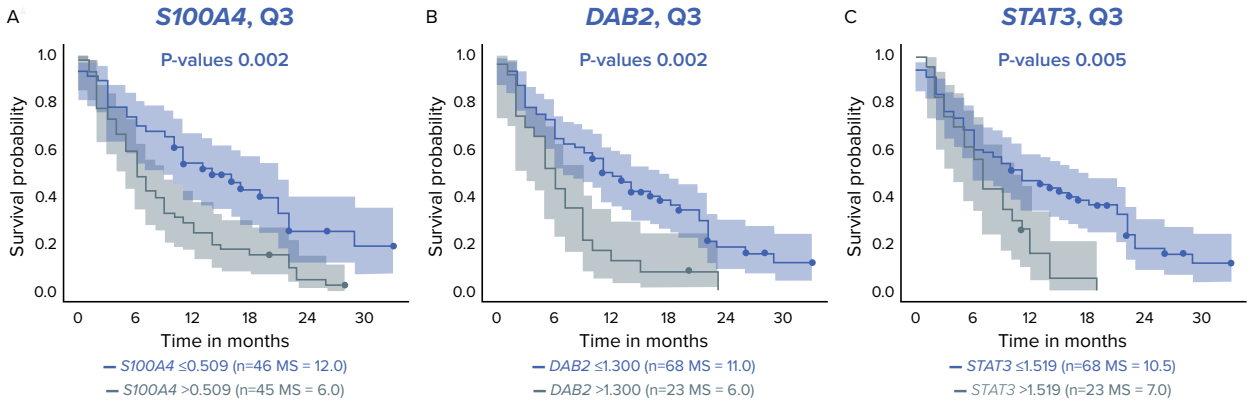

Figure 2. High *S100A4*, *STAT3* and *DAB2* gene expression are associated with poor prognosis of glioblastoma patients. Kaplan-Meier overall survival curves for *DAB2*, *S100A4* and *STAT3* are shown.

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