Glycogen metabolism in glioma progression

- PSMC2 upregulation enhances epithelial-to-mesenchymal transition in glioblastoma via activating AKT/GSK3β/β-catenin axis
- Targeting legumain-mediated cell-cell interaction sensitizes glioblastoma to immunotherapy in preclinical models
- PDE4 inhibitor rolipram represses hedgehog signaling via ubiquitin-mediated proteolysis of GLI transcription factors to regress breast cancer
- Nanoparticle-enhanced delivery of resveratrol for targeted therapy of glioblastoma: Modulating the Akt/GSK-3beta/NF-kB pathway in C6 glioma cells
- PYGL regulation of glycolysis and apoptosis in glioma cells under hypoxic conditions via HIF1alpha-dependent mechanisms
- Pharmacological Modulation of the Cytosolic Oscillator Affects Glioblastoma Cell Biology
- A molecular signature for the G6PC3/SLC37A2/SLC37A4 interactors in glioblastoma disease progression and in the acquisition of a brain cancer stem cell phenotype
- Chrysomycin A Regulates Proliferation and Apoptosis of Neuroglioma Cells via the Akt/GSK-3β Signaling Pathway In Vivo and In Vitro

Glycogen metabolism plays a significant role in glioma progression, with several key genes implicated in this process:

1. Glycogen Branching Enzyme 1 (GBE1): GBE1 is crucial for glycogen synthesis. In gliomas, elevated GBE1 expression has been linked to enhanced tumor growth. GBE1 reduces the expression of fructose-1,6-bisphosphatase (FBP1) via the NF-κB pathway, promoting a shift towards glycolysis and intensifying the Warburg effect, thereby facilitating glioma progression.

2. Pyruvate Kinase M2 (PKM2): PKM2 is a glycolytic enzyme that catalyzes the final step of glycolysis. In glioma cells, PKM2 predominantly exists in a less active dimeric form, leading to the accumulation of glycolytic intermediates that are diverted into biosynthetic pathways, supporting rapid tumor cell proliferation. This metabolic reprogramming is a hallmark of cancer cells, including gliomas.

3. Isocitrate Dehydrogenase 1 (IDH1): Mutations in IDH1 are common in gliomas and result in the production of the oncometabolite 2-hydroxyglutarate (2-HG). This accumulation leads to widespread changes in histone and DNA methylation, contributing to tumorigenesis. Additionally, IDH1 mutations can alter cellular metabolism, including pathways related to glycogen metabolism.

4. Glycogen Synthase Kinase-3 (GSK-3): GSK-3 is involved in various cellular processes, including glycogen metabolism. In gliomas, GSK-3 has been implicated in promoting tumor cell proliferation and survival. Inhibition of GSK-3 has been shown to induce apoptosis in glioma cells, suggesting its role in tumor progression.

These genes contribute to the metabolic reprogramming observed in gliomas, facilitating tumor growth and survival. Understanding their roles offers potential therapeutic targets for glioma treatment.

Recent studies have investigated the roles of glycogen metabolism-related genes in glioma, focusing on their impact on prognosis and the tumor immune microenvironment. While specific clustering of

glycogen metabolism-related genes has not been extensively detailed, research on related metabolic pathways provides valuable insights:

1. Glycosylation-Related Gene Signatures: A study established a glycosylation gene model to predict glioma patient survival and the tumor immune microenvironment. This model revealed a significant correlation between glycosylation gene expression patterns and clinical outcomes, highlighting the clinical significance of metabolic gene clusters in glioma.

2. Serine and Glycine Metabolism-Related Genes: Research has stratified glioma patients into clusters based on the expression of serine and glycine metabolism-related genes (SGMGs). These clusters exhibited distinct clinicopathological features, prognoses, and immune cell infiltration profiles. A serine and glycine metabolism-related gene signature (SGMRS) was developed, with higher SGMRS correlating with poorer prognosis and a 'hotter' immunological phenotype, indicating increased immune cell infiltration.

3. Immune and Cell Cycle Gene Modules: Another study identified gene modules associated with immune response and cell cycle regulation in glioma. Lower expression levels of genes in these modules were linked to more favorable prognoses, while higher expression levels corresponded to poorer outcomes. This suggests that the activity of specific gene clusters can influence both prognosis and the immune landscape in glioma.

These findings underscore the importance of metabolic gene expression patterns in glioma prognosis and immunity. While direct studies on glycogen metabolism-related gene clusters are limited, the observed associations in related metabolic pathways suggest that glycogen metabolism may similarly impact glioma progression and the tumor immune environment [1)]

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Li W, Yuan Y, Chen S, Liu Y. Prognosis and immunity of different cluster groups of glycogen metabolism-related genes in glioma. Asian J Surg. 2024 Nov 26:S1015-9584(24)02574-0. doi: 10.1016/j.asjsur.2024.10.240. Epub ahead of print. PMID: 39603936.