Computational screening

Considering the high invasiveness and mortality of glioma as well as the unclear key genes and signaling pathways involved in the development of gliomas, there is a strong need to find potential gene biomarkers and available drugs.

Eight glioma samples and twelve control samples were analyzed on the GSE31095 datasets, and differentially expressed genes (DEGs) were obtained via the R software. The related glioma genes were further acquired from the text mining. Additionally, Venny program was used to screen out the common genes of the two gene sets and DAVID analysis was used to conduct the corresponding gene ontology analysis and cell signal pathway enrichment. We also constructed the protein interaction network of common genes through STRING, and selected the important modules for further drug-gene analysis. The existing antitumor drugs that targeted these module genes were screened to explore their efficacy in glioma treatment.

The gene set obtained from text mining was intersected with the previously obtained DEGs, and 128 common genes were obtained. Through the functional enrichment analysis of the identified 128 DEGs, a hub gene module containing 25 genes was obtained. Combined with the functional terms in GSE109857 dataset, some overlap of the enriched function terms is both in GSE31095 and GSE109857. Finally, 4 antitumor drugs were identified through drug-gene interaction analysis.

In this study, we identified that two potential genes and their corresponding four antitumor agents could be used as targets and drugs for glioma exploration [1)].

1)
Jiang Z, Shi Y, Tan G, Wang Z. Computational screening of potential glioma-related genes and drugs based on analysis of GEO dataset and text mining. PLoS One. 2021 Feb 26;16(2):e0247612. doi: 10.1371/journal.pone.0247612. PMID: 33635875.