Despite extensive research, the prognosis of high-grade glioblastoma multiforme (GBM) has improved only slightly because of the limited response to standard treatments. Recent advances (discoveries of molecular biomarkers) provide new opportunities for the treatment of GBM. The aim of the present study was to identify diagnostic biomarkers of high-grade GBM. First, we combined 3 microarray expression datasets to screen them for genes differentially expressed in patients with high-grade GBM relative to healthy subjects. Next, the target network was constructed via the empirical Bayesian coexpression approach, and centrality analysis and a molecular complex detection (MCODE) algorithm were performed to explore hub genes and functional modules. Finally, a validation test was conducted to verify the bioinformatic results. A total of 277 differentially expressed genes were identified according to the criteria $P < 0.05$ and $|log2(fold change)| \geq 1.5$. These genes were most significantly enriched in the cell cycle pathway. Centrality analysis uncovered 9 hub genes; among them, TFDP1 showed the highest degree of connectivity (43) and is a known participant in the cell cycle pathway; this finding pointed to the important role of TFDP1 in the progression of high-grade GBM. Experimental validation mostly supported the bioinformatic results. According to our study results, the gene TFDP1 and the cell cycle pathway are strongly associated with high-grade GBM; this result may provide new insights into the pathogenesis of GBM [1].

[1]

Lu X, Lv XD, Ren YH, Yang WD, Li ZB, Zhang L, Bai XF. Dysregulation of TFDP1 and of the cell cycle pathway in high-grade glioblastoma multiforme: a bioinformatic analysis. Genet Mol Res. 2016 Jun 10;15(2). doi: 10.4238/gmr.15027646. PubMed PMID: 27323154.