Although O(6)-methylguanine DNA methyltransferase (MGMT) promoter methylation status is an important marker for glioblastoma multiforme (Glioblastoma), there is considerable variability in the clinical outcome of patients with similar methylation profles. OBJECTIVE: We examined whether a MicroRNA (MicroRNA) signature can be identified for predicting clinical outcomes and helping in treatment decisions. METHODS: The differentially expressed MicroRNAs were evaluated in 6 pairs of short- (\leq 450 days) and long-term survivors (> 450 days) by using microarray. real-time quantitative PCR (gRT-PCR) was applied to further verify screened MicroRNAs with a greater number of samples (n= 48). Meanwhile, functional interpretation of MicroRNA profile was carried out based on MicroRNAtarget databases. In addition, MGMT promoter methylation status was tested by means of pyrosequencing (PSQ) testing. RESULTS: Six MicroRNAs were upregulated in the long-term survival group (fold change \ge 2.0, P< 0.05). The further verification by gRT-PCR indicated that the increase in let-7g-5p, miR-139-5p, miR-17-5p and miR-9-3p level in long-term survivors was statistically significant. Kaplan-Meier survival analysis showed that high expression of a prognostic 4-MicroRNA signature was significantly associated with good patient survival (p = 0.0012). The signature regulated signaling pathways including Calcium, MAPK, ErbB, mTOR and cell cycle involved in carcinogenesis from glial progenitor cell to primary Glioblastoma. CONCLUSIONS: The 4-MicroRNA signature was identified as an independent prognostic biomarker that identified patients who have a favorable outcome¹⁾.

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