miR 182

Previous studies showed the aberrant expression of miR 182 in glioma tissue. However, the exact role of circulating miR-182 in glioma remains unclear.

Xiao et al confirmed the expression of plasma circulating miR-182 in glioma patients, and further explored its potential diagnostic and prognostic value.

real-time polymerase chain reaction(RT-PCR) was used to measure circulating cell-free miR-182 from 112 glioma patients and 54 healthy controls.

The findings showed that the level of circulating miR-182 in glioma patients was higher than that in healthy controls (P<0.001), which was significantly associated with KPS score (P=0.025) and WHO grade (P<0.001). The area under the receiver operating characteristic (ROC) curve (AUC) was 0.778. The optimal cut-off value was 1.56, and the sensitivity and specificity were 58.5% and 85.2%, respectively. Interestingly, a high predictive value of circulating miR-182 was observed in high grade glioma (AUC=0.815). However, the AUC was lower in low-grade glioma (AUC=0.621). Kaplan Meier analysis demonstrated that the cumulative 5-year overall survival rate in the high miR-182 group was significantly lower than that in the low miR-182 group in both overall survival (OS) (P=0.003) and disease-free survival (DFS) (P=0.006). Moreover, multivariate Cox analysis revealed that circulating miR-182 was an independent prognostic indicator for OS (P=0.034) and DFS (P=0.013).

These results suggest that circulating miR-182 may be a potential noninvasive biomarker for the diagnosis and prognosis of human glioma [1].

Circadian rhythm disorder is a common neurological deficit caused by neonatal hypoxic-ischemic brain damage (HIBD). However, little is known about its underlying mechanisms.

Previous studies revealed a significant elevation of clock genes at the protein, but not mRNA, levels in the pineal gland after neonatal HIBD. To investigate the mechanisms of post-transcriptional regulation on clock genes, we screened changes of MicroRNA levels in the pineal gland after neonatal HIBD using high-throughput arrays. Within the MicroRNAs whose expression was significantly down-regulated, we identified one MicroRNA (miR182) that targeted the 3'-untranslated region (3'-UTR) of Clock, a key component of clock genes, and played a crucial role in regulating CLOCK expression after oxygen-glucose deprivation in primarily cultured pinealocytes. This findings therefore provide new insight on studies of therapeutic targets for circadian rhythm disturbance after neonatal HIBD [2].

1)
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2)
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