MiR-362-3p

MiR-362-3p is important in regulating the genesis of different cancers; however, the mechanism of miR-362-3p in the progression of glioma remains largely unknown.

A study aimed to elucidate pathobiological functions of miR-362-3p by targeting PAX3 in glioma.

qRT-PCR and western blotting were used to examine miR-362-3p and PAX3 expression in glioma tissues and cells. CCK-8 assay and transwell assays were used to examine the functions of miR-362-3p on human glioma. Two bioinformatics analysis software and luciferase reporter assay were performed to analyze the relationship between miR-362-3p and PAX3.

MiR-362-3p was downregulated, and PAX3 was upregulated in glioma tissues and cells. Functional assays revealed that ectopic expression of miR-362-3p inhibited glioma cell proliferation and migration. Further, PAX3 was confirmed as direct target gene of miR-362-3p, and downregulation of PAX3 reversed the suppressive effects of miR-362-3p in glioma. In addition, miR-362-3p also exhibited suppressive effect on epithelial-mesenchymal transition and Wnt/β-catenin pathway.

CONCLUSIONS: MiR-362-3p downregulation or PAX3 overexpression predicted poor prognosis in glioma. MiR-362-3p played a role in the suppressive effect on glioma by targeting PAX3 through suppressing Wnt/ β -catenin pathway ¹⁾.

A prospective controlled observational cohort study assessed the performance of a novel panel of serum microRNA (MicroRNA) biomarkers on indicators of concussion, subconcussive impacts, and neurocognitive function in collegiate football players over the playing season. Male collegiate student football athletes participating in a Division I Football Bowl Subdivision of the National Collegiate Athletic Association (NCAA) were enrolled. There were a total of 53 participants included in the study, 30 non-athlete control subjects and 23 male collegiate student football athletes. Neurocognitive assessments and blood samples were taken within the week before the athletic season began and within the week after the last game of the season and measured for a panel of pre-selected MicroRNA biomarkers. All the athletes had elevated levels of circulating MicroRNAs at the beginning of the season compared with control subjects (p < 0.001). Athletes with the lowest standard assessment of concussion (SAC) scores at the beginning of the season had the highest levels of MicroRNAs. The area under the curve (AUC) for predicting pre-season SAC scores were miR-195 (0.90), miR-20a (0.89), miR-151-5p (0.86), miR-505* (0.85), miR-9-3p (0.77), and miR-362-3p (0.76). In athletes with declining neurocognitive function over the season, concentrations of MicroRNAs increased over same period. There were significant negative correlations with miR-505* (p = 0.011), miR-30d (p = 0.007), miR-92 (p = 0.033), and (p = 0.008). The MicroRNAs correlating with balance problems were miR-505* (p = 0.007), miR-30d (p = 0.028), and miR-151-5p (p = 0.023). Those correlating with poor reaction times were miR-20a (0.043), miR-505* (p = 0.049), miR-30d (p = 0.031), miR-92 (p = 0.015), and miR-151-5p (p = 0.044). Select MicroRNAs were associated with baseline concussion assessments at the beginning of the season and with neurocognitive changes from pre to post-season in collegiate football players. Should these findings be replicated in a larger cohort of athletes, these markers could potentially serve as measures of neurocognitive status in athletes at risk for concussion and subconcussive injuries²⁾.

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