Hsa-miR-192-5p, and Hsa-miR-129-5p Prominent Biomarkers in Regulation Glioblastoma Cancer Stem Cells Genes Microenvironment

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Abstract : Glioblastoma is one of the most frequent brain malignancies, having a high mortality rate and limited survival in individuals with this malignancy. Despite different treatments and surgery, recurrence of glioblastoma cancer stem cells may arise as a subsequent tumor. For this reason, it is crucial to research the markers associated with glioblastoma stem cells and specifically their microenvironment. In this study, using bioinformatics analysis, we analyzed and nominated genes in the microenvironment pathways of glioblastoma stem cells. In this study, an appropriate database was selected for analysis by referring to the GEO database. This dataset comprised gene expression patterns in stem cells derived from glioblastoma patients. Gene clusters were divided as high and low expression. Enrichment databases such as Enrichr, STRING, and GEPIA were utilized to analyze the data appropriately. Finally, we extracted the potential genes 2700 high-expression and 1100 low-expression genes are implicated in the metabolic pathways of glioblastoma cancer progression. Cellular senescence, MAPK, TNF, hypoxia, zimosterol biosynthesis, and phosphatidylinositol metabolism pathways were substantially expressed and the metabolic pathways were downregulated. After assessing the association between protein networks, MSMP, SOX2, FGD4 ,and CNTNAP3 genes with high expression and DMKN and SBSN genes with low were selected. All of these genes were observed in the survival curve, with a survival of fewer than 10 percent over around 15 months. hsa-mir-192-5p, hsa-mir-129-5p, hsa-mir-215-5p, hsa-mir-335-5p, and hsa-mir-340-5p played key function in glioblastoma cancer stem cells microenviroments. We introduced critical genes through integrated and regular bioinformatics studies by assessing the amount of gene expression profile data that can play an important role in targeting genes involved in the energy and microenvironment of glioblastoma cancer stem cells. Have. This study indicated that hsa-mir-192-5p, and hsa-mir-129-5p are appropriate candidates for this.
Keywords : Glioblastoma,Cancer Stem Cells,Biomarker Discovery,Gene Expression Profiles,Bioinformatics Analysis,Tumor Microenvironment