MicroRNA

MicroRNAs (miRNAs) are small, non-coding RNA molecules, typically about 20-25 nucleotides long, that play a crucial role in regulating gene expression. They function by binding to complementary sequences in messenger RNA (mRNA) molecules, leading to the degradation of the mRNA or the inhibition of its translation into proteins.

They play essential roles in post-transcriptional gene regulation. They are involved in various biological processes, including cell development, differentiation, proliferation, apoptosis, and response to environmental cues.

More and more evidence shows that microRNAs (MicroRNAs) play an important role in the diagnosis and prognosis of human diseases.

MicroRNAs (miRs) act as oncogenes or tumor-suppressor genes and regulate the proliferation, apoptosis, invasion, differentiation, angiogenesis, and behavior of glioma stem cells, which are important in glioma recurrence and development.

Key Features of MicroRNAs

Biogenesis

miRNAs are transcribed from DNA and initially exist as longer primary transcripts (pri-miRNAs). They undergo several processing steps involving enzymes like Drosha and Dicer to become mature miRNAs. Mechanism of Action:

Once processed, miRNAs are incorporated into the RNA-induced silencing complex (RISC). The RISC then uses the miRNA as a guide to bind to target mRNAs based on sequence complementarity.

Regulation of Gene Expression

miRNAs can regulate multiple target genes, influencing various biological processes such as development, cell differentiation, proliferation, and apoptosis. They can act as tumor suppressors or oncogenes depending on the context.

Role in Diseases

Dysregulation of miRNAs has been implicated in various diseases, including cancer, cardiovascular diseases, and neurological disorders. They are being explored as potential biomarkers for disease diagnosis and as therapeutic targets. Research and Therapeutics:

miRNA-based therapies are being developed, including miRNA mimics and inhibitors (antagomiRs) to restore normal function in diseased states.

MicroRNA in Neurosurgery

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Types

miR 9

miR 16

miR 19a

miR 21

miR 22

miR 24

miR 25-5p

miR 26a

miR 26b

miR 29a

miR 34

miR 105

miR 126

miR 128

miR 130b

miR 132

miR 144

miR 145

miR 148

miR 151

miR 152

miR 155

miR 181c

miR 181d

miR 182

miR 199

miR 200

miR 203

miR 205

miR 206

miR 210

miR 215

miR 218

miR 221

miR 302a

miR 328

miR 351

miR 361-5p

miR 375

miR 378

miR 431

miR 433

miR 448

miR 489

miR 494

miR 497

miR 588

miR 613

miR 720

miR 942

miR 944

miR 1118

miR 1297 .....

Jiang et al., found a positive correlation between the levels of miR-127-3p and the cell migration and invasion abilities in several human Glioblastoma cell lines. Theyshowed that miR-127-3p promoted cell migration and invasion of Glioblastoma cells using in vitro cell lines and in vivo mouse models. They identified SEPT7, a known tumor-suppressor gene that has been reported to suppress Glioblastoma cell migration and invasion, as a direct target of miR-127-3p. SEPT7 was able to partially abrogate the effect of miR-127-3p on cell migration and invasion. In addition, microarray analysis revealed that miR-127-3p regulated a number of migration and invasion-related genes. Finally, they verified that miR-127-3p affected the remodeling of the actin cytoskeleton mediated by SEPT7 in Glioblastoma cells [1].

MiR-132, miR-15a and miR-16 have been implicated in the pathogenesis of many types of cancer, including pituitary tumors. However, the molecular mechanism of these MicroRNAs in pituitary tumor growth and metastases is still unclear. Here, we showed that miR-132 and miR-15a/16 were less expressed in pituitary tumor cell lines, as well as in invasive pituitary tumor tissues, compared to non-invasive tumor tissues. We described that overexpression of miR-132 and miR-15a/16 resulted in the suppression of pituitary tumor cell proliferation, migration and invasion, respectively, and also inhibits the expression of proteins involved in Epithelial to Mesenchymal Transition (EMT). Then, we show that these MicroRNAs synergistically target Sox5 in pituitary tumor. Moreover, we found that Sox5 overexpression partially rescued miR-132, miR-15a and miR-16-mediated inhibition of cell migration, invasion and cell growth. Finally, we confirmed that Sox5 was upregulated in invasive pituitary tumor tissues, compared to non-invasion tissues. In conclusion, our data indicate that miR-132 and miR-15a/16 act as tumor suppressor genes in pituitary tumor by directly targetting Sox5, and imply that these MicroRNAs have potential as therapeutic targets for invasive pituitary tumor [2].

MicroRNA and aneurysm

Results support that dysregulated microRNAs may have a pathogenic role in intracranial aneurysms. Disruption of the protein translation process may have a pathogenic role in the development of intracranial aneurysms [3].

The molecular mechanisms behind intracranial aneurysm formation and rupture remain poorly understood.

The MicroRNA and mRNA interactions and expression levels in cerebral aneurysm tissue from human subjects were profiled.

A prospective case-control study was performed on human subjects to characterize the differential expression of mRNA and MicroRNA in unruptured cerebral aneurysms in comparison with control tissue (healthy superficial temporal arteries [STA]). Ion Torrent was used for deep RNA sequencing. Affymetrix MicroRNA microarrays were used to analyze MicroRNA expression, whereas NanoString nCounter technology was used for validation of the identified targets.

Overall, 7 unruptured intracranial aneurysm and 10 STA specimens were collected. Several

differentially expressed genes were identified in aneurysm tissue, with MMP-13 (fold change 7.21) and various collagen genes (COL1A1, COL5A1, COL5A2) being among the most upregulated. In addition, multiple MicroRNAs were significantly differentially expressed, with miR-21 (fold change 16.97) being the most upregulated, and miR-143-5p (fold change -11.14) being the most downregulated. From these, miR-21, miR-143, and miR-145 had several significantly anticorrelated target genes in the cohort that are associated with smooth muscle cell function, extracellular matrix remodeling, inflammation signaling, and lipid accumulation. All these processes are crucial to the pathophysiology of cerebral aneurysms.

This analysis identified differentially expressed genes and MicroRNAs in unruptured human cerebral aneurysms, suggesting the possibility of a role for MicroRNAs in aneurysm formation. Further investigation for their importance as therapeutic targets is needed [4].

MicroRNA and mesial temporal lobe epilepsy

A total of 50 microRNAs were found to be differentially expressed in mesial temporal lobe epilepsy with hippocampal sclerosis (mTLE-HS) compared with healthy controls. Among them, 2 were increased and 48 were decreased. The 6 significant differentially expressed candidate microRNAs (miR-3613-5p, miR-4668-5p, miR-8071, miR-197-5p, miR-4322, and miR-6781-5p) in exosome were validated. The bioinformatics analysis showed that the potential target genes of these microRNAs were involved in biological processes, molecular functions, and cellular components. Similarly, these microRNAs also affected axon guidance, pathways in cancer, regulation of the actin cytoskeleton, focal adhesion, the calcium signaling pathway, the MAPK signaling pathway, and the PI3K-Akt signaling pathway. Among 6 candidate microRNAs, miR-8071 had the best diagnostic value for mTLE-HS with 83.33% sensitivity and 96.67% specificity, and was associated with seizure severity. This study indicated that exosomal microRNAs, may be regulators for the seizure development in mTLE-HS, and can be used as potential therapeutic targets and biomarker for diagnosis in mTLE-HS [5].

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