MicroRNA in Neurosurgery

- Identify Key Genes and Construct the lncRNA-miRNA-mRNA Regulatory Networks Associated with Glioblastoma by Bioinformatics Analysis
- Analysis of the Expression Patterns of Tumor Necrosis Factor Alpha Signaling Pathways and Regulatory MicroRNAs in Astrocytic Tumors
- Engineered exosomes for targeted microRNA delivery to reverse liver fibrosis
- Recent advances in molecular mechanisms of microRNAs in pathogenesis and resistance of treatment in glioblastoma
- MicroRNA- 103 as a novel potential biomarker of poor prognosis and durg resistance in solid tumours
- Hsa_circ_0059511 promote glioma cell proliferation and migration through hsa-miR-194-5p/HBEGF axis
- MicroRNA-29a-5p attenuates hemorrhagic transformation and improves outcomes after mechanical reperfusion for acute ischemic stroke
- Peripheral MicroRNA Signatures in Adolescent Depression

MicroRNAs (miRNAs) are gaining significant attention in the field of neurosurgery due to their roles in regulating gene expression and their potential implications in various neurological conditions.

1. Role in Neurological Disorders

MicroRNA in brain tumors

Neurodegenerative Diseases: miRNAs are involved in the pathogenesis of diseases like Alzheimer's, Parkinson's, and multiple sclerosis by influencing processes like inflammation, apoptosis, and neuronal survival.

2. Mechanisms of Action

miRNAs can regulate signaling pathways related to cell proliferation, differentiation, and apoptosis, which are critical in neurosurgical contexts, particularly in tumor biology and recovery post-surgery.

3. Biomarkers for Diagnosis and Prognosis

Specific miRNA expression profiles have been linked to the progression of various brain disorders. Identifying these profiles can assist in early diagnosis, determining treatment strategies, and predicting patient outcomes.

4. Therapeutic Targets

miRNAs are being explored as therapeutic targets. For example, modulating miRNA activity could potentially reverse pathological processes in neurodegenerative diseases or enhance the effectiveness of existing therapies for brain tumors.

5. Regenerative Medicine

In the context of brain injury or neurodegeneration, certain miRNAs are being investigated for their roles in promoting neurogenesis and recovery. They may help in designing strategies to enhance brain repair mechanisms.

6. Challenges and Future Directions

While the potential of miRNAs in neurosurgery is promising, challenges remain in terms of delivery methods, specificity, and understanding the full range of their biological effects. Research is ongoing to explore these aspects, with the aim of integrating miRNA-based strategies into clinical practice.

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microRNAs (MicroRNAs) regulate gene expression and significantly influence the essential cellular processes associated with CNS repair after trauma and neuropathological conditions including stroke and neurodegenerative disorders. A number of specific MicroRNAs are implicated in regulating the development and propagation of CNS injury, as well as its subsequent regeneration [1].

Alteration in microRNAs (MicroRNAs) expression is a frequent finding in human cancers. In particular, widespread MicroRNAs downregulation is a hallmark of malignant transformation.

Circulating MicroRNAs are emerging as an interesting research area, because of their potential role as a novel biomarkers and therapeutic targets.

They mediate transcriptional silencing of various metabolic enzymes that are involved in various life processes,

Remarkably, 98% of the RNA within a cell is not translated into proteins.

MicroRNAs bind to 3′untranslated regions (UTRs) of mRNAs and then affect the translation and/or stability of that mRNA, leading to a reduction in protein levels.

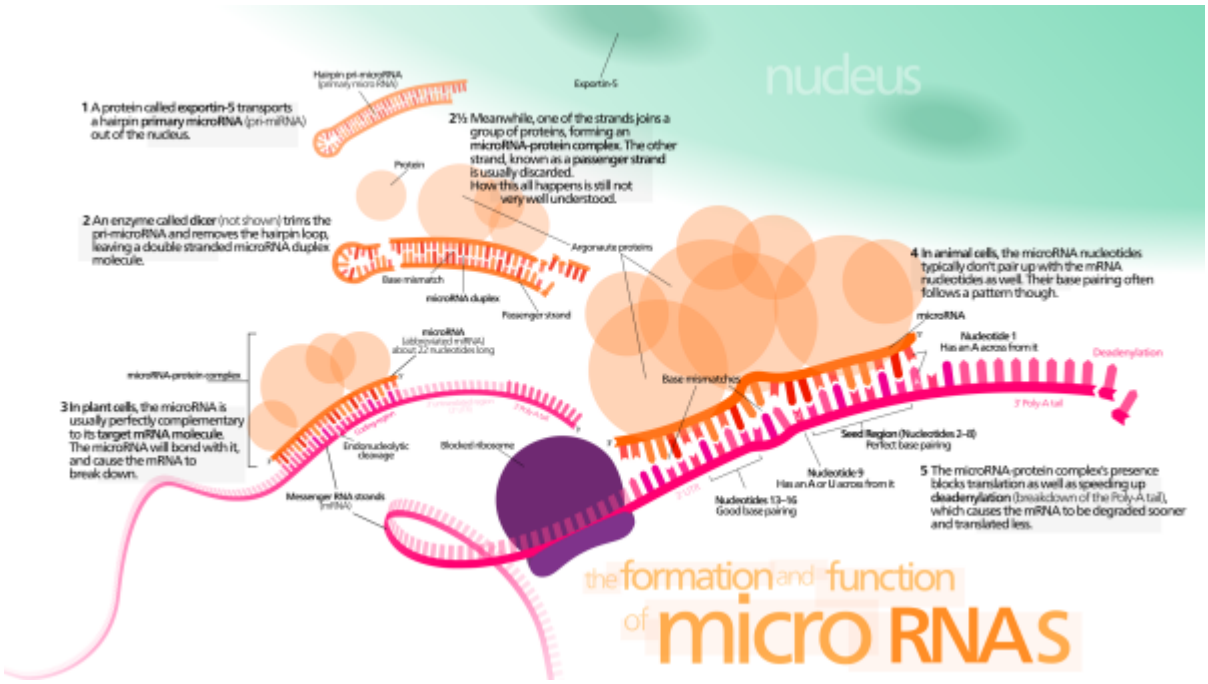
Tumors analyzed by MicroRNA profiling have exhibited significantly distinct MicroRNA signatures compared to normal cells from the same tissue [2] [3].

The abnormal levels of MicroRNAs in tumors have important pathogenetic consequences.

Some MicroRNAs are over-expressed in tumors and act as oncogenes, promoting tumor aggravation by down-regulating tumor suppressors.

Aberrant MicroRNA expression has been observed in human glioblastoma (Glioblastoma).

Circulating microRNAs (MicroRNAs) hold great promise as novel clinically blood-based biomarkers for cancer diagnosis and prognosis.



A growing number of studies suggest that dysregulation of MicroRNAs is a frequent event contributing to the pathogenesis of gliomas.

The RNAse III endonuclease DICER is a key regulator of microRNA (MicroRNA) biogenesis and is frequently decreased in a variety of malignancies.

Among noncoding RNAs, microRNAs (MicroRNAs) have been most extensively studied, and their biology has repeatedly been proven critical for central nervous system pathological conditions.

Circulating microRNAs (MicroRNAs) are a new class of highly promising cancer biomarkers.

Depending on the genes targeted, MicroRNAs can act as either oncogenes or tumor suppressors.

Deregulation of microRNAs (MicroRNAs) expression has been associated with cancer formation through alterations in gene targets.

MicroRNA (MicroRNA) contributes to the pathogenesis of various types of tumor, including glioblastoma (Glioblastoma). So far, MicroRNA has been shown to function in regulating protein-coding gene expression. This allows MicroRNAs to have direct function in regulation of various cellular events, including cell proliferation, apoptosis, and differentiation. Great progress has been made in identifying novel tumor-related MicroRNAs and their potential target genes [4)].

MicroRNA may play a critical role during progression from Low-grade gliomas to anaplastic gliomas or secondary glioblastomas and not contribute to the malignant progression from anaplastic gliomas to secondary glioblastomas [5)].

Wnt/beta-catenin signaling pathway is frequently dysregulated in human tumors and plays a critical

role in tumorigenesis; however, the roles of microRNAs in mediating Wnt/β-catenin pathway are not well understood.

As the involvement of MicroRNAs in the carcinogenesis is well known, Ivo D'Urso et al carried out a pilot study to identify, as potential biomarkers, differentially expressed microRNAs in blood samples of patients affected by glioma. We studied the MicroRNAs' expression, by means of microarray and Real-Time PCR, in 30 blood samples from glioma patients and in 82 blood samples of patients suffering from: (a) various neurological disorders (n=30), (b) primary B-lymphoma of the Central Nervous System (PCNSL, n=36) and © secondary brain metastases (n=16). By quantitative real-time reverse-transcriptase polymerase chain reaction (qRT-PCR), we identified significantly increased levels of two candidate biomarkers, miR-15b and miR 21, in blood of patients affected by gliomas. ROC analysis of miR-15b biomarker levels allowed to differentiate patients with tumour from patients without glioma. Furthermore, combined expression analyses of miR15b and miR-21 distinguished between patients with and without glioma (90% sensitivity and 100% specificity). In addition, a decrement in the expression levels of miR-16 characterized glioblastomas compared to low grade and anaplastic gliomas. In conclusion, this pilot study suggest that it's possible to identify the disease state by meaning miR-15b and miR-21 markers in blood, while miR-16 can be used to distinguish glioblastoma from other grade gliomas. They can potentially be used as biomarkers for non-invasive diagnosis of gliomas; further studies are mandatory to confirm our preliminary findings [6].

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