

microRNA-106a induces the proliferation and apoptosis of glioma cells through regulating JNK/MAPK pathway

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Abstract. – **OBJECTIVE:** To investigate the expression of microRNA-106a (miRNA-106a) in the brain tissue and the plasma of glioma patients, and explore the mechanism underlying the effect of miRNA-106a on the proliferation and apoptosis of glioma cells.

PATIENTS AND METHODS: Brain tissues from 42 glioma patients admitted in our institution were included in study group, whereas normal brain tissues collected from 10 patients undergoing brain tissue resection due to decompression or exposure during cerebral surgery. Quantitative fluorescent RT-PCR (QF RT-PCR) was performed to measure miRNA-106a mRNA in the brain tissue and peripheral blood of patients in two groups. Human M059K glioma cells were transfected with miRNA-106a mimic and inhibitor, and the proliferation and apoptosis of glioma cells were analyzed. In addition, JNK/MAPK in glioma cells was measured at mRNA and protein levels.

RESULTS: Compared with the normal population, miRNA-106a expression was significantly increased in the brain tissue of glioma patients ($p < 0.05$). Besides, miRNA-106a expression level was significantly elevated in the plasma of peripheral blood of glioma patients ($p < 0.05$). After the interference of miRNA-106a in M059K glioma cells, the proliferation of glioma cells was significantly reduced. However, apoptotic regulatory factor Bcl-2, was significantly increased, and JNK/MAPK protein level was significantly decreased. Overexpression of miRNA-106a in glioma cells resulted in significant increase in the proliferation of glioma cells and JNK/MAPK protein level, but obvious suppression in Bcl-2 protein level.

CONCLUSION: Elevated expression of miRNA-106a plays a crucial role in the development and progression of glioma, probably by promoting proliferation and suppressing the apoptosis of glioma cells through the JNK/MAPK signaling pathway.

Key words:

Glioma, microRNA-106a, Proliferation, JNK, MAPK.

Glioma is the most common primary intracranial tumor that arises from neuroectoderm, and thereby is also known as neuroectodermal tumors or neuroepithelial tumors, which accounts for 70% of primary intracranial tumors^{1,2}. However, the key signaling networks regulating glioma cell proliferation remain poorly defined³. To date, the etiology of glioma remains elusive and is likely to be closely associated with multiple factors, including tumor growth, infection, genetic factors, environmental factors and N-nitroso compounds³. Gliomas can infiltrate adjacent normal tissues and even form satellite lesions, which become the origin of tumor recurrence. Conventional treatment for gliomas includes surgery, chemotherapy and radiotherapy, which result in poor outcomes. Along with the advance in the research on the cellular immunology as well as the molecular etiology and pathology of gliomas, novel therapeutic strategies such as immunological therapy and genetic therapy has emerged⁴. MicroRNAs (miRNAs) are a class of 22 nucleotide (nt)-long, non-coding, single-stranded RNAs. A large body of evidence has shown that aberrant miRNA expression is critical for the development and progression of a variety of tumors⁵⁻⁷. miRNA-106a is a newly discovered miRNA that has been shown to be upregulated in patients with gastric cancer and the inhibition of its expression can suppress the proliferation, migration and invasiveness of gastric cancer cells⁸. In addition, miRNA-106a has been reported to be highly expressed in colorectal cancer cells⁹, indicating that miRNA-106a, as an important tumor-promoting factor, involves in the migration of colorectal cancer cells. However, to date, few studies have been reported on miRNA-106a expression in glioma patients and its potential function and underlying mechanism in gliomas. In the present work, miRNA-106a ex-

pression in the brain tissues and serum of glioma patients were compared and further study was conducted on whether it regulates the proliferation and apoptosis of glioma cells through JNK/MAPK signaling pathway.

Patients and Methods

Patients

During May 2011 to May 2014, surgically resected specimens were harvested from 52 patients treated at the Department of Neurosurgery of our institution. Among these patients, 42 glioma patients were included in study group, which consisted of 22 males and 20 females with the age ranging from 27 to 68 years. According to WHO classification criteria, these gliomas were classified as 25 astrocytomas (12 fiber type, 8 protoplasmic, 5 anaplastic) and 17 glioblastomas. Control group comprised of pathologically confirmed normal brain tissues, which were collected from 10 patients undergoing brain tissue resection due to decompression or exposure during cerebral surgery. Among these patients, 4 were males and 6 were females with the age ranging from 31 to 65 years.

Reagents

TRIzol RNA isolation kit was purchased from Life Technologies (Carlsbad, CA, USA). Takara reverse transcription kit was purchased from Yunnan Guangzhou-Dimensional Biotech Instruments (Guangzhou, Guangdong, P.R. China). PCR kit and DNA Marker were purchased from Sangon Biotechnology (Nanjing, Jiangsu, P.R. China). miRNA-106a mimic and inhibitor as well as the primers for internal reference U6 were designed and synthesized by Guangzhou RioBio Co. Ltd. (Guangzhou, Guangdong, P.R. China).

RNA Isolation and Quantitative Fluorescent RT-PCR (qf RT-PCR)

A total of 5 mL of fasting peripheral venous blood samples was collected from each glioma patient or normal subject in the morning. Blood samples were anticoagulated with EDTA followed by centrifugation at 4000 g for 5 min at 4°C. The plasma at upper layer was collected and stored at -80°C.

A specimen of 150 mg brain tissue or 200 μ L plasma was homogenized in 1 mL Trizol reagent on ice. Total RNA isolated from these samples was dissolved in 20 μ L DEPC treated water, and reverse transcription was conducted using Femantes

reverse transcription kit (MA, USA). The resulting cDNA products were stored at -20°C. PCR reaction conditions were as follows: denaturation at 95°C for 20s, followed by 40 cycles of 95°C for 20s and 70°C for 1s. The primers for miR-106a were as follows: F: 5'-CGCACTGAGTGCTTACAGTGCA-3' and R: 5'-GTGGGGTCCGAGGT-3'. The primers for internal reference U6 were F: 5'-CTCGCTTCGCCAGCAC-3' and R: 5'-AACGCTTCACGATGCGT-3'. PCR was performed on ABI 7900 Real-Time PCR system and relative quantitative analysis was performed using $2^{-\Delta\Delta C_t}$ method.

Cell Transfection

Transfection of human glioma cell line M059K was performed using Lipofectamine 2000 purchased from Invitrogen (Carlsbad, CA, USA) to interfere the expression of miRNA-106a, and the interference efficiency was examined after 48h.

Cell Counting Kit-8 (CCK-8) Assay

Transfected human glioma M059K cells were seeded into 96-well plate and incubated with CCK-8 solution purchased from Wuhan Boster Bioengineering Inc. (Wuhan, Hubei, P.R. China) at a ratio of 1:10 (V/V) in serum-free Dulbecco's Modified Eagle Medium (DMEM). Optical absorbance at 450nm was determined at 24, 48 and 72h after incubation, respectively; and cell growth curve was generated.

Western Blot Assay

Transfected human glioma cells were lysed in 1 \times SDS. Cell proteins were collected, separated by SDS-PAGE and transferred to PVDF membrane at 120V for 100 mins. The membrane was blocked with 5% non-fat milk at 37°C for 80 mins followed by incubation with rabbit anti-human-JNK, -MAPK and -Bcl-2 antibodies (1:1000, Dakewe Biotech Company, Shanghai, P.R.China) at 4°C overnight and incubation with HRP-conjugated mouse anti-rabbit secondary antibodies (1:1000 dilution, Sunshine Biotechnology, Nanjing, Jiangsu, P.R. China) at 37°C for 30 min. The result was examined using ECL luminescence detection. Anti-human β -actin (1:3000 dilution, Cell Signaling Technology, Danvers, MA, USA) was used as internal reference.

Statistical Analysis

Statistical analysis was performed using SPSS software version 17.0 (SPSS Inc., Chicago, IL,

Table I. Expression of microRNA-106a mRNA in brain tissues.

Group	Number of cases (n)	microRNA-106a mRNA	t/p
Normal brain tissues	42	1.12 ± 0.41	
Glioma brain tissues	10	3.48 ± 0.63*	14.66/0.000

*vs. normal brain tissues, $t = 14.66$, $p < 0.05$.

USA). Differences between two groups were analyzed using Student's t -test, and $p < 0.05$ was considered as statistically significant.

Results

Expression of miRNA-106a mRNA in Two Groups

Compared to normal brain tissue, miRNA-106a mRNA expression was significantly increased in brain tissues of glioma patients ($t = 14.66$, $p < 0.05$), indicating that elevated miRNA-106a expression in glioma patients was closely associated with the development and progression of glioma (Table I).

miRNA-106a mRNA Expression in the Plasma

Further analysis of miRNA-106a mRNA expression in the plasma of glioma patients revealed that miRNA-106a expression was significantly higher in the plasma of glioma patients

than in that of normal population ($t = 11.81$, $p < 0.05$). This result further proved that miRNA-106a might be closely associated with the development of glioma.

Effect of Low Expression of miRNA-106a on the Proliferation and Apoptosis of Glioma Cells

The expression of miRNA-106a mRNA was significantly decreased in M059K glioma cells transfected with miRNA-106a inhibitor (Figure 1A), indicating that interference of miRNA-106a expression was achieved. In addition, the proliferation of the interfered glioma cells was significantly reduced ($p < 0.05$) (Figure 1B). However, the apoptotic regulatory factor, Bcl-2, was significantly increased (Figure 1C) and JNK/MAPK protein level was significantly decreased (Figure 1D).

Effect of Elevated miRNA-106a Expression on the Proliferation and Apoptosis of Glioma Cells

miRNA-106a mRNA level was significantly increased in M059K cells transfected with miR-

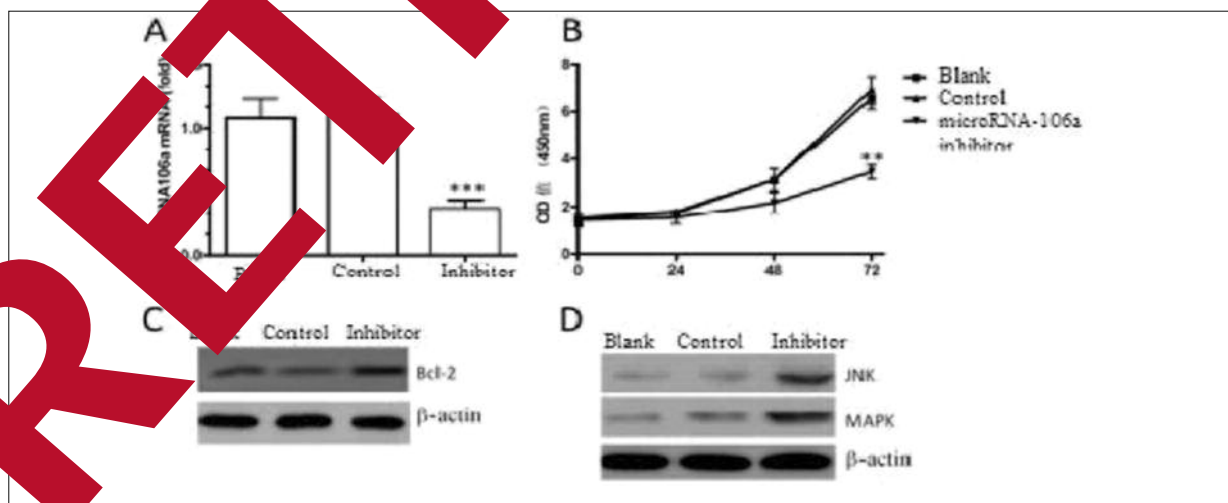


Figure 1. Effect of low expression of miRNA-106a on the proliferation and apoptosis of glioma cells as well as on JNK/MAPK pathway (**vs. control group, $p < 0.01$; ***vs. normal group, $p < 0.001$).

Table II. Expression of microRNA-106a mRNA in the plasma.

Group	Number of cases (n)	microRNA-106a mRNA	t/p
Normal brain tissue	42	1.31 ± 0.39	
Glioma brain tissues	10	3.14 ± 0.62*	11.81/0.000

*vs. normal brain tissues, $t = 11.81$, $p < 0.05$.

miRNA-106a mimic (Figure 2A), and miRNA-106a overexpression resulted in significantly increased proliferation of glioma cells (Figure 2B). However, Bcl-2 protein level was significantly decreased (Figure 2C) and JNK/MAPK protein level were significantly decreased ($p < 0.05$) (Figure 2D). These results suggested that miRNA-106a promoted the proliferation but suppressed the apoptosis of glioma cells, which might be closely associated with JNK/MAPK signaling pathway.

Discussion

Glioma is a common malignant tumor originating from neuroectoderm. The diagnosis and treatment of the disease remains a big challenge in clinical practice. Gliomas comprise of several subtypes, including astrocytoma (including glioblastoma multiforme), oligodendroglioma, medulloblastoma and colloid cyst, accounting for 35-45% of total incidence of intracranial tumors¹¹. The onset of most gliomas is insidious, which

usually lasts for several weeks to months, and even for several years in some cases. The clinical manifestation of glioma is divided into two major categories. One category of symptoms resulted from increased intracranial pressure, which includes headache, vomiting and psychiatric symptoms. The other one is focal symptoms caused by tumor suppression, infiltration and brain tissue damage. Glioma is difficult to be completely removed surgically due to its invasive nature. To this end, increasing attention has been drawn to the research on the cellular and molecular mechanisms underlying pathogenesis of glioma, in an effort to discover a more rational and effective treatment at cellular or molecular level.

microRNAs, as a group of small RNAs regulating gene expression at transcriptional level, are widely distributed in the tissue, the plasma and the serum of human body. microRNAs have multiple functions. Besides, aberrant expression of microRNAs in many cancer patients have been reported in recent years and these molecules are believed to play a crucial role in the initiation

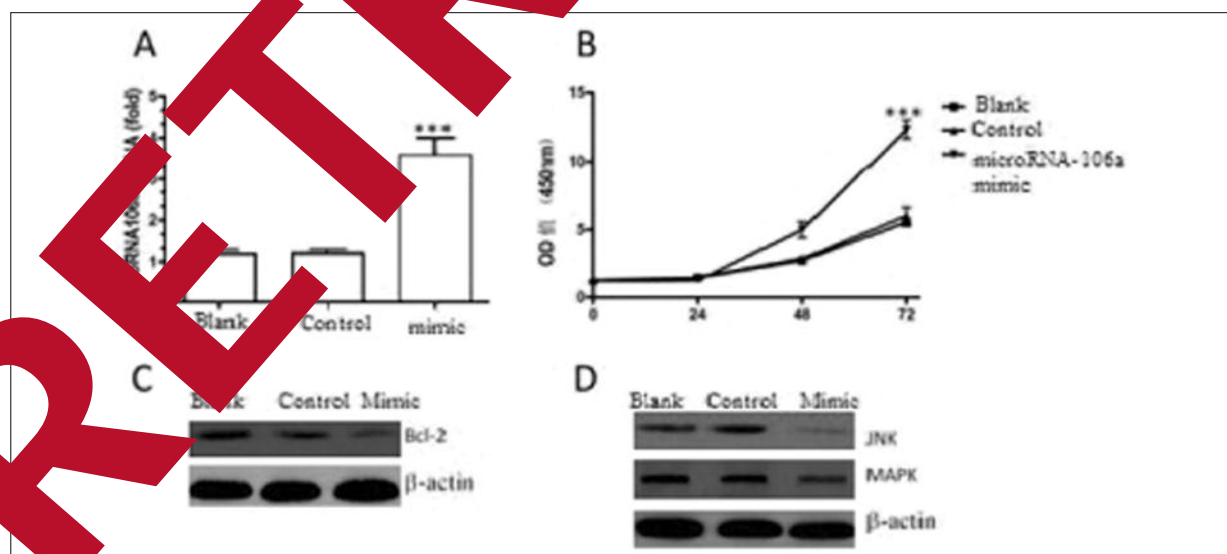


Figure 2. Effect of high expression of microRNA-106a on the proliferation and apoptosis of glioma cells as well as on JNK/MAPK pathway (**vs. normal group, $p < 0.001$).

and development of tumors. Currently, miRNA has been shown to have both carcinogenic and tumor suppressive function¹²⁻¹⁶. Numerous studies have focused on the relationship between miRNA-106a and tumors, and aberrant expression of miRNA-106a has been mainly reported in patients with gastric cancer and colorectal cancer^{8,9}. However, few studies are done on miRNA-106a expression in glioma patients.

In the present work, miRNA-106a expression in the brain tissues and the plasma of glioma patients was investigated with an effort to explore the function and the implication of miRNA-106a in glioma patients. The results showed that miRNA-106a expression was significantly increased in the brain tissues and the plasmas of glioma patients than in those of normal population, indicating that aberrant expression of miRNA-106a in glioma patients might be closely associated with the initiation and development of glioma. Zhu et al¹⁷ have reported that miRNA-106a expression is up-regulated in gastric cancer tissue compared to normal tissue, suggesting that miRNA-106a as a potential target for the diagnosis of gastric cancer, which supports the results of the present study.

In addition, miRNA-106a expression in glioma cells was interfered with an effort to investigate the effect of miRNA-106a on the proliferation and apoptosis of glioma cells. The results demonstrated that miRNA-106a promoted the proliferation of glioma cells. Besides, miRNA-106a was involved in the regulation of tumor cell apoptosis by suppressing Bcl-2 expression.

Previous studies have suggested that JNK/MAPK signaling pathway influences biological activities of cells (as proliferation, differentiation, conversion, and apoptosis) by affecting gene transcription and regulation in animal cells. Therefore, further analysis was performed to observe the relevant mechanisms by which miRNA-106a affects the proliferation and apoptosis of glioma cells. To this end, JNK/MAPK expression was examined in glioma cells transfected with miRNA-106a mimics/inhibitors. The results showed that JNK/MAPK expression was decreased in glioma cells with low expression of miRNA-106a but increased in the cells with high expression of miRNA-106a. These results suggested that miRNA-106a promoted the proliferation of glioma cells through stimulating JNK/MAPK pathway and suppressed the apoptosis of cancer cells via Bcl-2.

Conclusions

The up-regulation of miRNA-106a in glioma patients may play an important role in the development and progression of glioma, and miRNA-106a is involved in the proliferation and apoptosis of glioma cells mainly through JNK/MAPK pathway. Hence, detection of miRNA-106a in glioma patients may have potential value in the diagnosis of glioma.

Conflict of Interest

The Authors declare that there are no conflicts of interest.

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