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Long Noncoding RNA MEG3 Suppresses Glioma Cell Proliferation, Migration, and Invasion by Acting as a Competing Endogenous RNA of miR-19a

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Glioma, with varying malignancy grades and histological subtypes, is the most common primary brain tumor in adults. Long noncoding RNAs (lncRNAs) are non-protein-coding transcripts and have been proven to play an important role in tumorigenesis. Our study aims to elucidate the combined effect of lncRNA maternally expressed gene 3 (MEG3) and microRNA-19a (miR-19a) in human glioma U87 and U251 cell lines. Real-time PCR revealed that MEG3 was downregulated and miR-19a was upregulated in malignant glioma tissues and cell lines. Bioinformatics analyses (TargetScan, miRanda, and starBase V2.0) showed that phosphatase and tensin homolog (PTEN) is a target of miR-19a with complementary binding sites in the 3′-UTR. As expected, luciferase results verified the putative target site and also revealed the complementary binding between miR-19a and MEG3. miR-19a represses the expression of PTEN and promotes glioma cell proliferation, migration, and invasion. However, MEG3 could directly bind to miR-19a and effectively act as a competing endogenous RNA (ceRNA) for miR-19a to suppress tumorigenesis. Our study is the first to demonstrate that lncRNA MEG3 suppresses glioma cell proliferation, migration, and invasion by acting as a ceRNA of miR-19a, which provides a novel insight about the pathogenesis of glioma.

Key words: Maternally expressed gene 3 (MEG3); miR-19a; Glioma; Long noncoding RNAs (lncRNAs); Phosphatase and tensin homolog (PTEN); Competing endogenous RNA (ceRNA)

INTRODUCTION

Glioma is a malignant tumor with one of the highest mortality rates and accounts for more than 50% of all primary brain tumors[1]. Because of rapid proliferation, a high potential for invasion, and resistance to radiation and chemotherapy, the therapeutic effects of surgical resection and chemotherapy are unsatisfactory, and the prognosis of glioma patients remains poor[2]. The potential molecular mechanisms of glioma pathogenesis are still largely unknown, which causes much uncertainty in finding an effective treatment[3]. Therefore, it is essential to identify the critical mechanism in the glioma process and explore a truly valuable therapy pathway.

Long noncoding RNAs (lncRNAs) are transcripts with no protein-coding function, which are longer than 200 nucleotides. lncRNA maternally expressed gene 3 (MEG3), located at human chromosome 14q32.3, is an imprinted DLK1-MEG3 locus gene[4]. MEG3 has recently been shown to regulate tumorigenesis through its interaction with microRNA (miR). MEG3 has been verified to exist in various normal tissues, but it is often absent in tumor tissues because of gene deletion and promoter hypermethylation[5,6]. The loss or lowered expression of MEG3 has been proven to be a pathogenic factor tested in cultured tumor cell growth[7]. The in-depth mechanism of MEG3 on the pathogenesis of glioma is rarely reported.

miRs, small noncoding RNA molecules with 21 to 23 nucleotides, have been widely tested in the regulation of tumorigenesis, including cell proliferation, apoptosis, migration, and invasion[8]. Among these, miR-19a acts as a carcinogenic miR, attested in various types of cancer[9]. Phosphatase and tensin homolog (PTEN) gene, a well-known tumor suppressor, is mutated in a large number of cancers at a high frequency. Because PTEN is a common suppressor in tumor biology, the loss of PTEN function has been closely linked to glioma tumorigenesis. Bioinformatics analyses (TargetScan, miRanda, and miRGen) show that PTEN is a target of miR-19a.

In the present study, we have verified that MEG3 expression is downregulated, whereas miR-19a is upregulated in glioma tissues compared to adjacent normal tissues. Our research investigates the regulation of MEG3

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on migration, invasion, and the cell cycle of glioma cells by regulating miR-19a and its target PTEN.

MATERIALS AND METHODS

Human Tissue Samples and Ethical Statement

Glioma tissues and normal brain tissues were collected from patients undergoing surgery who had not had chemotherapy or radiotherapy at the Department of Neurosurgery, Huanhu Hospital, Tianjin. Written, informed consent was obtained from and signed by all enrolled patients. The study obtained the approval and supervision of the ethics committee of Huanhu Hospital. After resection of tissues, samples were immediately frozen in liquid nitrogen and stored at −80°C for future use. Glioma tissue samples were diagnosed by two experienced clinical pathologists according to the WHO classification, including two groups: low grade (grades I–II) and high grade (grades III–IV).

Cell Lines

Normal human astrocytes (NHAs) and human glioma cell lines (U87 and U251) were obtained from the Chinese Academy of Science Cell Bank (Shanghai, P.R. China). Cells were cultured in DMEM [containing 10% FBS, 2 mM glutamine, and 100 U/ml penicillin; Gibco, Carlsbad, CA, USA] at 37°C with 5% CO_2. Grades of glioma were evaluated according to WHO classification by neuropathologists.

Cell Transfection

Human glioma cell lines, U87 and U251, were plated into six-well culture plates and transfected after incubation for 24 h. miR-19a mimic and miR-19a inhibitor were purchased from GeneChem (Shanghai, P.R. China) and then transfected into glioma cell lines using Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA) according to the instruction manual. Primers of MEG3 were designed by Primer 5 software, and the synthesis and sequencing were completed by RiboBio Co., Ltd. (Guangzhou, P.R. China). Overexpression plasmid (pcDNA-MEG3) and negative control plasmid (pcDNA Mock) (Invitrogen) were structured and then respectively transfected into U87 and U251 using Lipofectamine 2000 (Invitrogen) according to the instruction manual.

Real-Time Quantitative PCR

Total RNA was extracted from cells using TRIzol reagent (Invitrogen). The concentration of RNA was measured at 260–280 nm, and the required value was 1.8–2.0 using a Nanodrop Spectrophotometer (ND-100). The extracted RNA (1 μg) was then used for cDNA synthesis with a Transcriptor First-Stand cDNA Synthesis Kit (Roche, Indianapolis, IN, USA). Real-time quantitative PCR (RT-qPCR) was performed using a SYBR Green PCR Kit (TaKaRa, Dalian, P.R. China). Expression levels of lncRNA and miRs were normalized to the housekeeping gene (GAPDH). Primers were provided by Sangon Biotech Co. Ltd. (Shanghai, P.R. China) and listed as follows: MEG3, 5′-GAATATGAGTTGTAAGTGGTAG AGTTT-3′ (forward) and 5′-TACAAACTTAACAAAA AAAAATCATACT-3′ (reverse); GAPDH, 5′-GCACCG TCAAGGCTGAGAAC-3′ (forward) and 5′-TGGTGAA GACGCCAGTGGA-3′ (reverse). The reaction conditions were as follows: at 95°C for 3 min (initial denaturation), followed by 30 cycles at 95°C for 20 s, 54°C for 30 s, 72°C for 2 min, and last at 72°C for 10 min (final elongation). Relative levels of gene expression were calculated with the $2^{-\Delta\Delta}$Ct method.

Luciferase Assays

The 3′-UTR sequences of miR-19a and PTEN were amplified using PCR and cloned into a pmirGlo Dual-Luciferase miRNA Target Expression Vector (Promega, Madison, WI, USA) to construct the 3′-UTR luciferase reporter vector. The sequences of putative binding sites were replaced as indicated to mutate the putative binding site of MEG3 or miR-19a in the 3′-UTR vector. Glioma cell lines (U87 and U251) were transfected with luciferase reporter plasmids (1 μg/well) using Lipofectamine 2000 according to the manufacturer's instructions. The luciferase activities were measured at 48 h after transfection by the dual-luciferase reporter assay kit (Promega) according to the manufacturer's instructions. The values of luciferase activity for each lysate were normalized to the *Renilla* luciferase activity. The relative transcriptional activity was converted into fold induction above the vehicle control value.

Migration and Invasion Assays

After glioma cell lines were harvested, the migration and invasion abilities were tested by the 24-well Transwell chambers with 8-μm pore size polycarbonate membrane (Corning, Corning, NY, USA) according to the manufacturer's instructions. Cells were resuspended in serum-free medium into the upper Transwell chamber (preapplied with 50 μl of Matrigel) with 1×10^5 cells/well, and 600 μl of medium containing 20% FBS (Gibco) was added into the lower chamber.

Cells were incubated at 37°C for 4 h before the assay was started. After 96 h, cells on the lower surface of the membrane were fixed with 4% paraformaldehyde for 30 min and stained with 0.1% crystal violet for 20 min. The upper surface of the membrane was wiped with a cotton swab and washed by PBS. Five areas of the membrane were randomly selected, photographed, and counted under an inverted microscope.

Apoptosis Assay

Cells were washed in cold PBS, and apoptotic cells were identified by Annexin-V/Dead Cell Apoptosis Kit (Invitrogen). Briefly, cells were resuspended in annexin-binding buffer, and 5 μl of FITC–annexin V and propidium iodide (Becton Dickinson, Heidelberg, Germany) were added. It was then incubated at room temperature for 15 min in the dark. FITC and propidium iodide fluorescence were analyzed by flow cytometry (Attune; Life Technologies, Darmstadt, Germany).

Cell Proliferation Assay

Cell proliferation assays were performed using the cell counting kit-8 (CCK-8; Beyotime, P.R. China) according to the manufacturer's instructions. Cells were seeded into 96-well cell culture plates. After 72 h of transfection, CCK-8 reagent was added into each well. At the indicated time, absorbance was measured at the wavelength of 450 nm.

Cell Cycle Analysis

Cell cycle analysis was performed by Cell Cycle Analysis Kit (Lianke, P.R. China). Cells (4×10^5 per well) were seeded into six-well plates for 24 h and starved in FBS-free medium for 12 h. Cells were then fixed with 70% cold ethanol for 2 h. DNA staining was carried with 10 mg of propidium iodide/ml PBS and 2.5 mg of Ag DNase-free RNase (Roche Diagnostics, Basel, Switzerland)/ml PBS for at least 30 min. Flow cytometry was performed by Coulter EPICS XL flow cytometer (Beckman Coulter, Inc., Fullerton, CA, USA).

Colony Formation Assay

Cells were seeded into a fresh six-well plate and maintained in 1640 medium (10% FBS). After 14 days, cells were fixed with 4% paraformaldehyde for 30 min and stained with 0.1% crystal violet (Beyotime). After being washed mildly with PBS and air dried, the visible colonies were manually counted.

Western Blot Assay

Total proteins were lysed by RIPA buffer (added with protease inhibitors) on ice and then were centrifuged at $12{,}000\times g$ at 4°C for 5 min. A mixture of equal protein and sample buffer was subjected to 15% SDS-PAGE. The separated protein was then transferred onto a PVDF membrane (Millipore Corporation, Billerica, MA, USA). The PVDF membrane was blocked in blocking buffer (containing TBST and 5% fat-free milk) for 1 h at room temperature. Primary antibody (rabbit anti-PTEN antibody, 1:1,000) was purchased from Cell Signaling Technology, Inc. (Danvers, MA, USA). GAPDH acted as the internal reference. PVDF membrane was incubated in the diluted primary antibodies at 4°C overnight. The PVDF membrane was then incubated with horseradish peroxidase (HRP)-conjugated goat anti-rabbit (1:500; Abcam, Cambridge, MA, USA) at 4°C overnight. Immunoblots were visualized by ECL kit (Santa Cruz Biotechnology, Santa Cruz, CA, USA) and scanned by ImageJ software. The band densities of each sample were normalized to the GAPDH band.

Statistical Analysis

Results were presented as means ± SEM for at least three independent experiments. All data were analyzed by Student's *t*-test or one-way ANOVA. Values of $p<0.05$ were considered to be statistically significant.

RESULTS

lncRNA MEG3 Expression Was Decreased and miR-19a Expression Was Increased in Human Glioma Tissues

Forty glioma patients were enrolled in our study. The expression levels of MEG3 and miR-19a were determined through RT-qPCR in glioma tissues and adjacent normal tissues. The average expression level of MEG3 in glioma tissues was significantly lower than those in normal control tissues (Fig. 1A). However, the average expression level of miR-19a was higher than in the normal control tissues (Fig. 1B). In summary, MEG3 expression was decreased, while miR-19a expression was increased, so these results show that MEG3 expression demonstrates a negative correlation to miR-19a in human glioma tissues.

lncRNA MEG3 and PTEN 3′-UTR Were the Target of miR-19a

In the previous results, we proved that MEG3 expression was decreased while miR-19a expression was increased in glioma tissues. Furthermore, MEG3 expression demonstrated negative correlation to miR-19a. Bioinformatics analyses (TargetScan, miRanda, and miRGen) showed that PTEN is a target of miR-19a with complementary binding sites in the 3′-UTR (Fig. 2A). Luciferase results showed that miR-19a had a high probability of binding with the 3′-UTR of PTEN mRNA in glioma cell lines (U87 and U251) (Fig. 2B and C). A putative target site between miR-19a and MEG3 3′-UTR is shown in Figure 2D. The dual-luciferase reporter assay manifested the alignment of complementary binding between miR-19a and MEG3 3′-UTR (Fig. 2E and F). Recombinant plasmid pcDNA-MEG3 and miR-19a mimics jointly regulated the expression of PTEN. RT-qPCR and Western blot analysis consistently indicated that miR-19a mimics suppressed PTEN expression; however, pcDNA-MEG3 recovered it

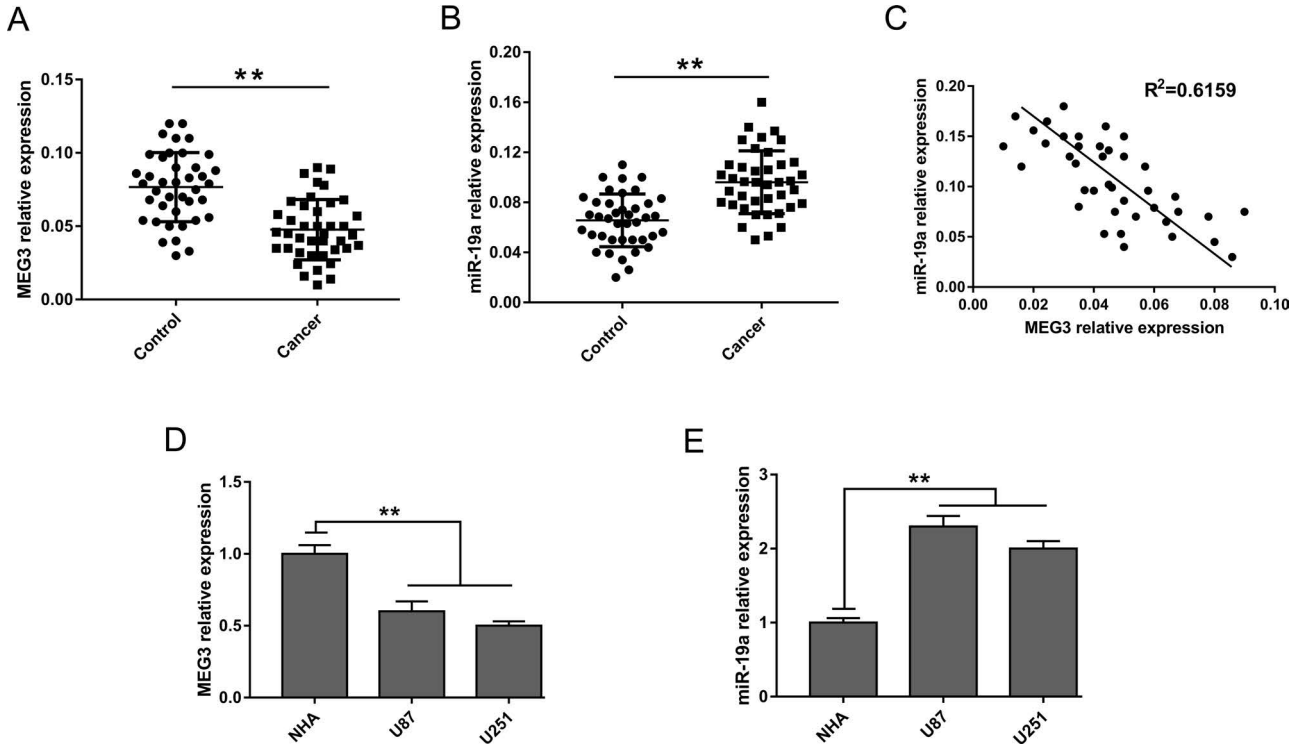

Figure 1. Expressions of long noncoding RNA (lncRNA) maternally expressed gene 3 (MEG3) and miR-19a in glioma tissues and cell lines were detected by real-time quantitative PCR (RT-qPCR). (A) MEG3 relative expression was analyzed by RT-qPCR in glioma tissues from 40 patients (Cancer) compared to normal tissues (Control). (B) miR-19a relative expression was similarly analyzed by RT-qPCR. (C) Pearson's correlation was performed to analyze the correlations between MEG3 and miR-19a expression in glioma tissues (R^2=0.6159). (D) MEG3 relative expression in normal human astrocytes (NHAs) and glioma cell lines U87 and U251. (E) miR-19a relative expression in NHA, U87, and U251. All assays were performed in triplicate. **$p<0.05$.

by specifically targeting miR-19a (Fig. 2G–I). The results showed that lncRNA MEG3 might function as a competing endogenous RNA (ceRNA) or a molecular sponge in modulating miR-19a.

lncRNA MEG3 and miR-19a Mediated Glioma Migration and Invasion

To determine the effect of MEG3 and miR-19a on the malignant progression of glioma cells, we detected the migration and invasion abilities of U87 and U251. Experimental results revealed that miR-19a significantly increased the migration and invasion abilities of glioma cells (Fig. 3A and B). Nevertheless, MEG3 overexpression recombinant plasmid could effectively repress the tumor-promoting effect. Meanwhile, addition of PTEN mimics similarly suppressed the migration and invasion abilities. In addition, the colony formation assay indicated that the number of cell line colonies was significantly increased by miR-19a and decreased following MEG3 and PTEN (Fig. 3C and D). These results indicate that MEG3 might act as a tumor suppressor by acting as an miR-19a inhibitor in glioma.

lncRNA MEG3 and miR-19a Mediated Glioma Proliferation, Apoptosis, and Cell Cycle

On the basis of the previous experiment, we detected the regulation of MEG3 and miR-19a on proliferation, apoptosis, and cell cycle. CCK-8 showed that cell proliferation was increased in the group treated with miR-19a and decreased in the group treated with MEG3 and PTEN mimics (Fig. 4A). Flow cytometry analysis revealed that miR-19a significantly decreased glioma cell apoptosis and MEG3 increased the apoptosis (Fig. 4B and C). Moreover, cell cycles were arrested at the G_1/S phase when treated with MEG3 and PTEN mimics. The above results indicate that MEG3 inhibits cell proliferation, promotes the apoptosis of glioma, and accelerates cell cycle arrest in the G_0/G_1 phase.

DISCUSSION

Emerging evidence has confirmed that lncRNAs might function as a ceRNA or a molecular sponge to modulate miR in the tumorigenesis of various cancers[10,11]. Moreover, lncRNAs are emerging as new modulators in epigenetics regulation and have been associated with the development of gliomas[12,13]. To investigate the in-depth

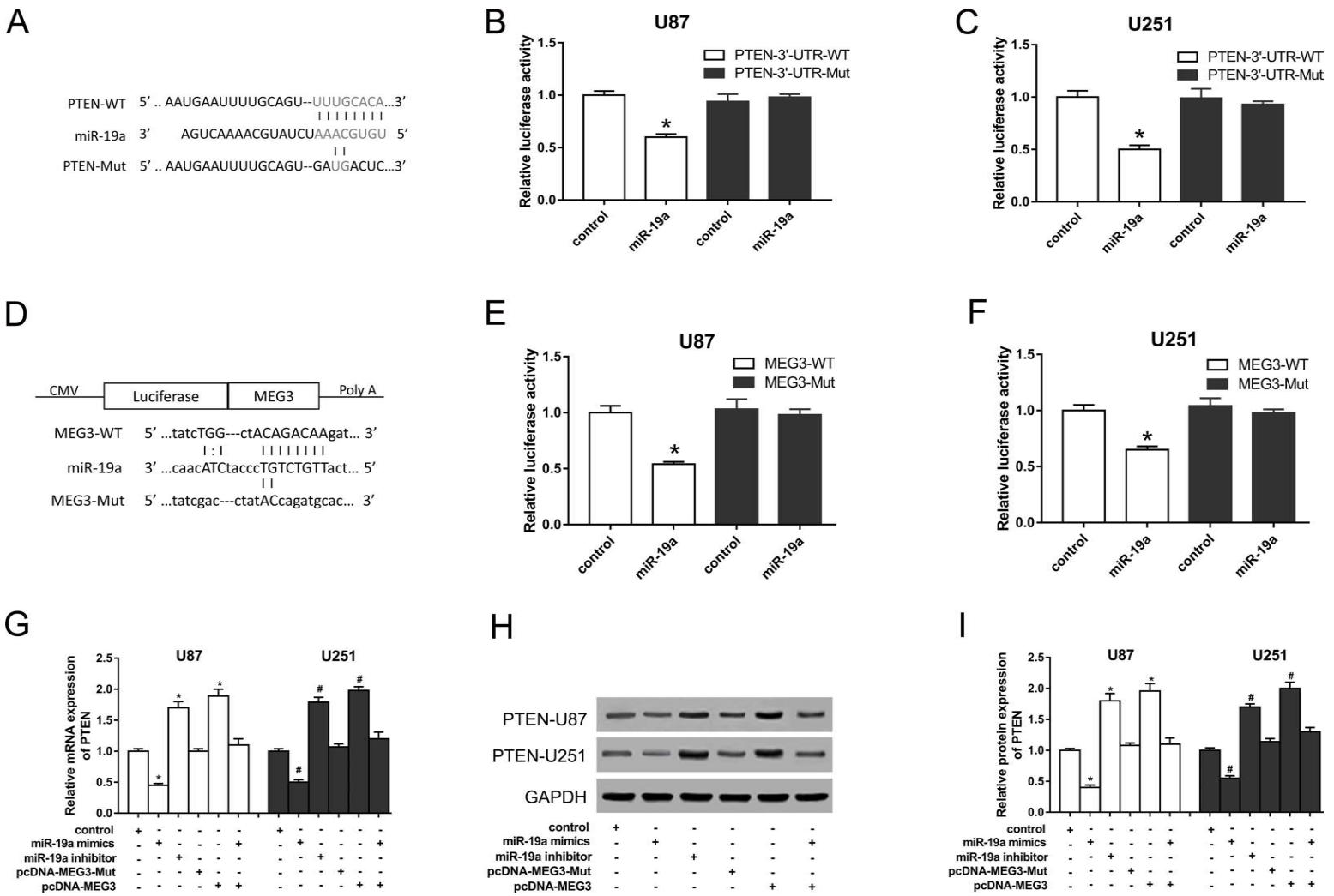

Figure 2. Alignment of complementary regions of lncRNA MEG3 and phosphatase and tensin homolog (PTEN) 3′-UTR between miR-19a. (A) A putative complementary binding target site between miR-19a and PTEN 3′-UTR was shown according to bioinformatics analyses (TargetScan, miRanda, and miRGen). (B, C) The luciferase results showed the probability of binding of miR-19a with the 3′-UTR of PTEN mRNA in the U87 and U251 cell lines. (D) A putative binding target site of miR-19a with MEG3 3′-UTR according to starBase V2.0. (E, F) The luciferase results of wild-type and mutant MEG3 3′-UTR with miR-19a. (G–I) RT-qPCR and Western blot analysis revealed the regulation of miR-19a and pcDNA-MEG3 on the expression of PTEN. Values represented the mean ± SD. Experiments were repeated three independent times. *$p < 0.05$ in U87, #$p < 0.05$ in U251 compared with control group.

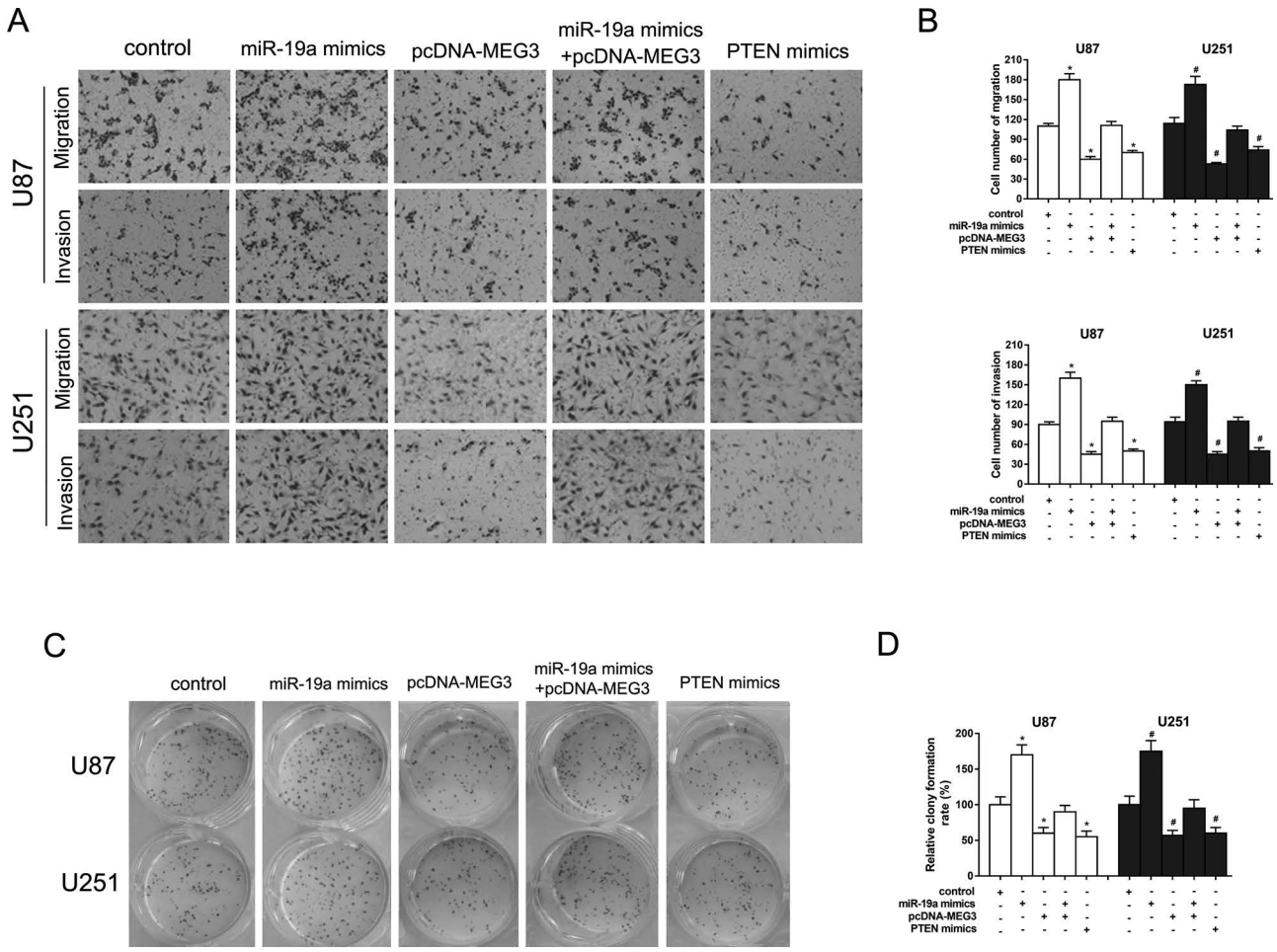

Figure 3. lncRNA MEG3 and miR-19a mediated glioma migration and invasion. (A) Representative images of migration and invasion assays in glioma cell lines U87 and U251 are presented. (B) Quantification of glioma cells accompanying migration and invasion assays. (C) Colony formation assay was performed to determine the proliferation, and colonies were counted and captured. (D) Quantification of relative colony formation. Experiments were repeated three independent times. *$p<0.05$ in U87, #$p<0.05$ in U251 compared with control group.

mechanism of lncRNA MEG3 and their corresponding miRs in the progression of glioma, we screened glioma tissues and their adjacent normal tissues and assessed the regulation through a series of experiments.

Our study detected the expression levels of MEG3 and miR-19a through RT-qPCR in glioma tissues and their adjacent normal tissues. Results revealed that the average expression level of MEG3 in glioma tissues was significantly lower than that of the control tissues. Conversely, the average expression level of miR-19a was higher than in normal control tissues. Therefore, MEG3 expression demonstrates a negative correlation to miR-19a in human glioma tissues. With the aid of bioinformatics analyses, we predicted the complementary binding sites of miR-19a corresponding with MEG3 and PTEN in the 3′-UTR. As expected, luciferase assay results verified the putative target site. PTEN is a well-known tumor suppressor and is mutated in a large number of cancers, which is closely linked to glioma tumorigenesis. RT-qPCR and Western blot analysis consistently indicated that miR-19a suppressed PTEN expression; however, MEG3 reversed that suppression. Apparently, lncRNA MEG3 may function as a ceRNA or a molecular sponge in modulating miR-19a.

So far, the mediation of MEG3 in glioma tumorigenesis has rarely been reported. In other types of tumor studies, MEG3 has been affirmed as a tumor suppressor molecule. For example, MEG3 inhibits cell proliferation and induces apoptosis via the activation of endoplasmic reticulum stress and the p53 pathway in HepG2 cell lines[14]. Our study assesses the interaction of MEG3 and miR-19a on tumorigenesis and its progression via a series of experiments, including migration, invasion, proliferation, apoptosis, and cell cycle assay. Results indicate that MEG3 suppresses the migration, invasion, and proliferation abilities; however, it promotes apoptosis of glioma as well as cell cycle arrest in the G_0/G_1 phase. These results

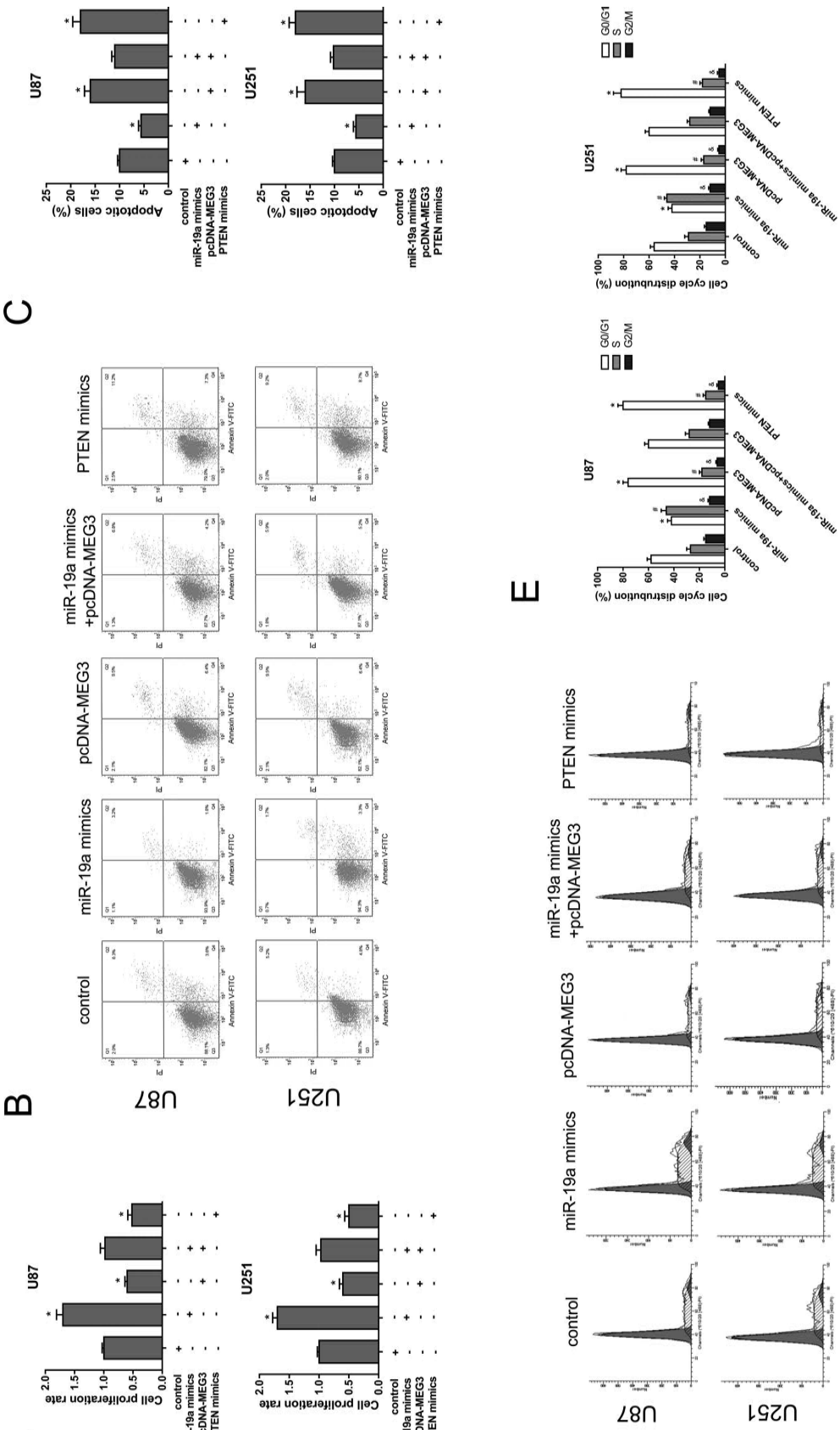

Figure 4. lncRNA MEG3 and miR-19a mediated glioma proliferation, apoptosis, and cell cycle. (A) Cell counting kit-8 (CCK-8) assays showed the proliferation of U87 and U251 cells in various groups. (B) The apoptosis of U87 and U251 cells was assessed by flow cytometry analysis. (C) The apoptotic cells in each group are shown. (D) Flow cytometry analysis was applied to evaluate the effect on cell cycle in U87 and U251 cells. (E) Cell cycle distribution of each group. Experiments were repeated three independent times. $^{*}p<0.05$, $\#p<0.05$, $\&p<0.05$ compared with control group.

indicated that MEG3 might act as a tumor suppressor by acting as an inhibitor of miR-19a in glioma, which is in accord with prior experimental results and speculation.

lncRNAs have been verified to regulate gene transcription and epigenetic regulations[15–17]. A large number of studies have shown that lncRNAs participate in physiological process regulation of tumors, and many lncRNAs have been confirmed as tumor suppressor genes and prognosis biomarkers. DNMT1-mediated MEG3 hypermethylation causes the loss of MEG3 expression and then inhibits the p53 pathways in glioma[18]. lncRNA BDNF-AS is associated with a shorter overall survival and may be used as a prognostic biomarker in human retinoblastoma[19]. Furthermore, some lncRNAs could act as miR sponges to bind with corresponding miRs and attenuate biological activity[20,21]. lncRNA SPRY4-IT1 positively regulates the expression of EZH2 and plays an oncogenic role in bladder cancer progression through sponging miR-101-3p[22]. With in-depth research, the potential mechanism of lncRNAs in malignant tumors, including glioma, will be further uncovered[23].

Our research results show that MEG3 suppresses migration, invasion, and cell cycle of glioma cells by negatively regulating miR-19a; however, it positively releases PTEN. Thus, MEG3 acts as a tumor suppressor by negative regulation of miR-19a, which may be a novel target for glioma therapy.

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REFERENCES

1. Taylor LP. Diagnosis, treatment, and prognosis of glioma: Five new things. Neurology 2010;75(18 Suppl 1):S28–32.
2. Zhou Y, Liu F, Xu Q, Wang X. Analysis of the expression profile of Dickkopf-1 gene in human glioma and the association with tumor malignancy. J Exp Clin Cancer Res. 2010;29:138.
3. Zhou C, Teng WJ, Zhuang J, Liu HL, Tang SF, Cao XJ, Qin BN, Wang CC, Sun CG. Analysis of the gene-protein interaction network in glioma. Genet Mol Res. 2015;14(4): 14196–206.
4. Mondal T, Subhash S, Vaid R, Enroth S, Uday S, Reinius B, Mitra S, Mohammed A, James AR, Hoberg E, Moustakas A, Gyllensten U, Jones SJ, Gustafsson CM, Sims AH, Westerlund F, Gorab E, Kanduri C. MEG3 long noncoding RNA regulates the TGF-beta pathway genes through formation of RNA-DNA triplex structures. Nat Commun. 2015;6:7743.
5. Yan J, Guo X, Xia J, Shan T, Gu C, Liang Z, Zhao W, Jin S. MiR-148a regulates MEG3 in gastric cancer by targeting DNA methyltransferase 1. Med Oncol. 2014;31(3):879.
6. Sun M, Xia R, Jin F, Xu T, Liu Z, De W, Liu X. Downregulated long noncoding RNA MEG3 is associated with poor prognosis and promotes cell proliferation in gastric cancer. Tumour Biol. 2014;35(2):1065–73.
7. Braconi C, Kogure T, Valeri N, Huang N, Nuovo G, Costinean S, Negrini M, Miotto E, Croce CM, Patel T. microRNA-29 can regulate expression of the long non-coding RNA gene MEG3 in hepatocellular cancer. Oncogene 2011; 30(47):4750–6.
8. Cheng AM, Byrom MW, Shelton J, Ford LP. Antisense inhibition of human miRNAs and indications for an involvement of miRNA in cell growth and apoptosis. Nucleic Acids Res. 2005;33(4):1290–7.
9. Lee S, Lee H, Bae H, Choi EH, Kim SJ. Epigenetic silencing of miR-19a-3p by cold atmospheric plasma contributes to proliferation inhibition of the MCF-7 breast cancer cell. Sci Rep. 2016;6:30005.
10. Liu D, Yu X, Wang S, Dai E, Jiang L, Wang J, Yang Q, Yang F, Zhou S, Jiang W. The gain and loss of long noncoding RNA associated-competing endogenous RNAs in prostate cancer. Oncotarget 2016;7(35):57228–38.
11. Lu MH, Tang B, Zeng S, Hu CJ, Xie R, Wu YY, Wang SM, He FT, Yang SM. Long noncoding RNA BC032469, a novel competing endogenous RNA, upregulates hTERT expression by sponging miR-1207-5p and promotes proliferation in gastric cancer. Oncogene 2016;35(27):3524–34.
12. Wang L, Yu Z, Sun S, Peng J, Xiao R, Chen S, Zuo X, Cheng Q, Xia Y. Long non-coding RNAs: Potential molecular biomarkers for gliomas diagnosis and prognosis. Rev Neurosci. 2017;28(4):375–80.
13. Balci T, Yilmaz Susluer S, Kayabasi C, Ozmen Yelken B, Biray Avci C, Gunduz C. Analysis of dysregulated long non-coding RNA expressions in glioblastoma cells. Tumour Biol. 2016;590(1):120–2.
14. Pan Y, Li C, Chen J, Zhang K, Chu X, Wang R, Chen L. The emerging roles of long noncoding RNA ROR (lincRNA-ROR) and its possible mechanisms in human cancers. Cell Physiol Biochem. 2016;40(1–2):219–29.
15. Gomez-Diaz E, Yerbanga RS, Lefevre T, Cohuet A, Rowley MJ, Ouedraogo JB, Corces VG. Epigenetic regulation of Plasmodium falciparum clonally variant gene expression during development in Anopheles gambiae. Sci Rep. 2017;7:40655.
16. Kita Y, Yonemori K, Osako Y, Baba K, Mori S, Maemura K, Natsugoe S. Noncoding RNA and colorectal cancer: Its epigenetic role. J Hum Genet. 2017;62(1):41–7.
17. Nainar S, Feng C, Spitale RC. Chemical tools for dissecting the role of lncRNAs in epigenetic regulation. ACS Chem Biol. 2016;11(8):2091–100.
18. Li J, Bian EB, He XJ, Ma CC, Zong G, Wang HL, Zhao B. Epigenetic repression of long non-coding RNA MEG3 mediated by DNMT1 represses the p53 pathway in gliomas. Int J Oncol. 2016;48(2):723–33.
19. Shang W, Yang Y, Zhang J, Wu Q. Long noncoding RNA BDNF-AS is a potential biomarker and regulates cancer development in human retinoblastoma. Biochem Biophys Res Commun. 2017. [E-pub ahead of print].
20. Tay Y, Rinn J, Pandolfi PP. The multilayered complexity of ceRNA crosstalk and competition. Nature 2014;505 (7483):344–52.
21. Thomson DW, Dinger ME. Endogenous microRNA sponges: Evidence and controversy. Nat Rev Genet. 2016; 17(5):272–83.
22. Liu D, Li Y, Luo G, Xiao X, Tao D, Wu X, Wang M, Huang C, Wang L, Zeng F, Jiang G. LncRNA SPRY4-IT1 sponges miR-101-3p to promote proliferation and metastasis of bladder cancer cells through up-regulating EZH2. Cancer Lett. 2016;388:281–91.
23. Boon RA, Jae N, Holdt L, Dimmeler S. Long noncoding RNAs: From clinical genetics to therapeutic targets? J Am Coll Cardiol. 2016;67(10):1214–26.