

MiR-16 inhibits pituitary adenoma cell proliferation via the suppression of ERK/MAPK signal pathway

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Abstract. – **OBJECTIVE:** Extracellular signal-regulated kinase (ERK)/mitogen activated protein kinase (MAPK) signal pathway participates in cell proliferation, cycle, and apoptosis. MiR-16 is down-regulated in the pituitary tumor. This study investigated the role and related mechanism of miR-16 on pituitary tumor proliferation, cycle, and apoptosis.

PATIENTS AND METHODS: Dual-luciferase reporter assay was conducted to demonstrate the targeted regulation between miR-16 and MEK1. MiR-16, MEK1, p-ERK1/2, Survivin and Cyclin D1 expression were compared between normal embryonic pituitary cells, HP75 tumor cells. Flow cytometry detection measured cell proliferation and cycle. Cultured HP75 cells were divided into four groups: miR-NC, miR-16 mimic, si-NC, and si-MEK1. Expressions of miR-16, MEK1, p-ERK1/2, Survivin, and Cyclin D1 were compared, and cell proliferation, cycle and apoptosis were tested by flow cytometry.

RESULTS: Bioinformatic analysis showed complementary binding between miR-16 and MEK1. Dual luciferase reporter assay indicated the direct regulation between miR-16 and MEK1. Comparison that of normal pituitary tissues, significantly lower miR-16 expression, but higher MEK1 level was found in adenoma tissues. Compared to normal embryonic pituitary cells, the level of miR-16 was decreased, while the expressions of p-ERK1/2, Survivin, and Cyclin D1 along with cell proliferation or S or G2/M phase ratio were up-regulated in the group of HP75. Transfection of miR-16 mimic or si-MEK1 remarkably suppressed the expressions of MEK1, p-ERK1/2, Survivin or Cyclin D1 in HP75 cells, inhibited cell proliferation and induced apoptosis and cycle arrest.

CONCLUSIONS: MiR-16 inhibited ERK/MAPK signal pathway via the suppression of MEK1 expression, and further suppressed proliferation of pituitary tumor cells.

Key Words:

MiR-16, MEK1, ERK/MAPK, Pituitary tumor, Cell cycle, Proliferation, Apoptosis.

Introduction

Pituitary adenoma (PA) belongs to the group of endocrine tumors derived from anterior pituitary or anterior pituitary residual cells from cranio-pharyngeal canal epithelium¹. PA is a type of common intracranial carcinoma and occupies about 10-20% of primary intracranial tumors, which represents the third common one after glioma and meningioma. Recently, PA incidence is increasing in years²⁻⁵.

Mitogen-activated protein kinase (MAPK) signal pathway is widely distributed in multiple tissues and cells, and plays important roles in mediating cell survival, proliferation, cycle, apoptosis, migration, and invasion^{6,7}. Abnormal activation of MAPK signal pathway is closely correlated with occurrence, progression, and metastasis of various tumors^{8,9}. In many cancers (e.g., melanoma), a defect in the ERK/MAPK pathway results in uncontrolled growth, suggesting its essential role in modulating life activities. Many compounds are accordingly developed to potential drugs for treating cancer via the inhibiting steps in the MAP/ERK pathway. An extracellular signal-regulated kinase (ERK) induced MAPK pathway and mainly deploy the function of MAPK. In this pathway, Ras/Raf/MEK/ERK is the major transduction module for ERK/MAPK signal pathway^{10,11}. MAPK kinase 1 (MEK1) presents as a dual specific protein kinase and functions the upstream of ERK, as it can activate ERK by phosphorylation on Thr/Tyr amino acid residues of ERK protein. Numerous studies¹²⁻¹⁴ showed aberrantly elevation of MEK1 protein expression in onset, progression, metastasis, and prognosis of multiple tumors. A previous study¹⁵ also indicated the correlation between improving function of MEK1 and PA occurrence. MicroRNA (miR) is characterized as a group of endogenous sin-

gle-stranded non-coding small molecule RNA with 20-24 nucleic acids length, and can bind with 3'-untranslated region (3'-UTR) of target gene mRNA to interrupt mRNA stability, leading to mRNA degradation or translation inhibition, thus giving rise to negative regulation on gene expression at post-transcriptional level¹⁶. Abnormal expression or dysfunction of miR has become a research focus on tumor pathogenesis¹⁷⁻¹⁹. Accumulative studies^{20,21}, for instance, demonstrated significant decreasing level of miR-16 in PA tumor tissues, indicating its potential tumor-suppressing role in PA pathogenesis. Thus, this investigation concerns the role of miR-16 as well as the mechanism involved in PA cell proliferation and/or apoptosis.

Patients and Methods

Clinical Information

A total of 39 PA patients who received treatment in the Second Affiliated Hospital of Bengbu Medical College from May 2016 to December 2016 were recruited in this study. Tumor tissues were collected during surgery. There were 19 males and 20 females in the patient group, ranging between 33 and 57 years (average age = 41.5 years). Another cohort of 15 normal pituitary samples collected from brain contusion surgery were recruited as the control group. They consisted of 7 males and 8 females, aged from 31 to 58 years (average age = 42.6 years). All sample collections have obtained informed consent from the participants, and this investigation was approved by the Ethical Committee of the Second Affiliated Hospital of Bengbu Medical College.

Major Reagent and Materials

Human PA cell line HP75 was purchased from Sciencell (Carlsbad, CA, USA). Dulbecco's Modified Eagle's medium (DMEM) medium, penicillin-streptomycin were acquired from Gibco (Waltham, MA, USA). Horse serum and fetal bovine serum (FBS) were obtained from Gibco (Waltham, MA, USA). miR-NC, miR-16 mimic and miR-16 inhibitor were designed and synthesized by Gima (Shanghai, China). Rabbit anti-MEK1, ERK1/2, p-ERK1/2 were procured from Abcam (Cambridge, MA, USA). Mouse anti-tubulin D1, Survivin, and beta-actin antibody were got from GeneTex Inc (Irvine, CA, USA). Dual-luciferase Reporter Assay System and pMIR plasmid were from Promega (Madison,

WI, USA). Transfection reagent FuGENE6 was gained from Roche (Indianapolis, IN, USA). Total RNA extraction reagent TRIzol Universal was purchased from Tiangen Biochem (Beijing, China). Real-time qPCR reagent TransScript One-Step qRT-PCR SuperMix was bought from Quanshijin Bio (Beijing, China). Click-iT Edu Alexa Fluor 488 Flow Cytometry Kit was collected from Molecular Probes (Eugene, OR, USA). RIPA lysis buffer and cell apoptosis kit were from Beyotime (Beijing, China).

Cell Culture

Human PA cell line HP75 was inoculated in DMEM medium containing 10% fetal bovine serum (FBS) and horse serum. Cells were incubated in a 37°C chamber with 5% CO₂. Culture medium was changed every 3 days, and cells at log-growth phase with satisfactory status were used for further experiments.

Separation and Culture of Embryonic Pituitary Cells

Six embryos were collected from water balloon abortion at 6th gestation month, without abnormal development. The embryo was cut into pieces and was digested in 0.1% type I collagenase at 37°C for 2 h. The digestion was quenched in culture medium containing 10% FBS. Undigested tissue debris was filtered out, and the filtrate was centrifuged at 1600 rpm for 8 min to obtain the precipitation, which was re-suspended in DMEM medium containing 10% FBS and 1% penicillin-streptomycin. Cells were inoculated in culture dish and were incubated at 37°C with 5% CO₂. Culture medium was changed every 3 days, and cells at log-growth phase with satisfactory status were used for further experiments.

Dual Luciferase Reporter Gene Assay

Using HEK293T cell genome as the template, full-length fragment of 3'-UTR of MEK1 gene was amplified and was ligated into luciferase reporter pMIR plasmid for transforming DH5 α competent bacteria. Positive clones with correct sequences were screened out by sequencing. Those clones with correct sequences were named as pMIR-MEK1-3'-UTR-wt or pMIR-MEK1-3'-UTR-mut. FuGENE6 was used to co-transfect pMIR-MEK1-3'-UTR-wt (or pMIR-MEK1-3'-UTR-mut) and miR-16 mimic (or miR-NC or miR-16 inhibitor) into HEK293T cells. After 48 h incubation, cells were rinsed twice in PBS. Pas-

sive Lysis Buffer from Dual-Luciferase Reporter Assay System kit was added for complete lysis at 4°C. 10 µL lysate supernatant was added into 96-well plate, followed by the addition of Stop&Glo buffer. Dual luciferase activity was measured on a microplate reader.

Cell Transfection and Grouping

In vitro cultured HP75 cells were divided into four groups: miR-NC transfection, miR-16 mimic transfection, si-NC transfection, and si-MEK1 groups. One day before transfection, cells were sub-grouped into culture plate. At the day of transfection, cells should reach 60-70% confluence. 100 µL serum-free and dual antibiotic-free basic medium was used to dilute 10 µL FuGENE6 Reagent, followed by the addition of 20 nmol/L miR-NC, miR-161 mimi, si-NC or si-MEK1. After gentle mixture, 20 min room temperature incubation was performed. After discarding original culture medium from the plate, transfection mixture was added for gentle mixture and further incubation. 6 h later, DMEM containing 10% FBS and 1% streptomycin-penicillin was added for 72 h continuous incubation. Cells were collected for assays of cell proliferation, apoptosis, and expression of related indexes.

Quantitative Reverse Transcription-Polymerase Chain Reaction (qRT-PCR) for Gene Expression

TransScript Green One-Step qRT-PCR SuperMix was used to test relative expression level of target genes using RTA and TaqMan Universal kit as the template for one-step qRT-PCR. In a 20 µL reaction system, there were 1 µg RNA template, 0.5 µM forward and reverse primers, 10 µL 2X TransStart Tip Green qPCR SuperMix, 4 µL RT Enzyme Mix, 0.4 µL Dye II and distilled water. qRT-PCR conditions were: 45°C for 5 min for reverse transcription, followed by 94°C for 30 s and 40 cycles each containing 94°C for 5 s, 60°C for 30 s. Gene expression was measured by Bio-Rad CFX96 quantitative PCR (Hercules, USA) recording fluorescent data.

Western Blot

Cells were lysed by RIPA lysis buffer at 4°C incubation for 30 min. After 10000 g centrifugation for 10 min, the supernatant was saved, and 40 µg samples were loaded and were separated in 10% separating sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separating gel (40 V for 300 min). Proteins were transferred to

polyvinylidene difluoride (PVDF) membrane by electrophoresis (250 mA, 120 min). The membrane was blocked in 5% defatted milk powder for 60 min at room temperature. Primary antibody (anti-survivin at 1:4000, ERK1/2 at 1:3000, p-ERK1/2 at 1:3000, cyclin D1 at 1:3000, and β-actin at 1:10000) was added for 4°C overnight incubation. The membrane was rinsed in PBST for three times, and horseradish peroxidase (HRP) conjugated secondary antibody (1:25000) was added for 1 h at room temperature incubation. The membrane was rinsed in PBST for three times, an enhanced diaminobenzidine tetrahydrochloride (ECL) substrate solution was added for 2-3 min incubation. The membrane was exposed in the dark and scanned for image analysis.

Cell Apoptosis Assay

Cells were digested and collected with trypsin. After suspension in Binding Buffer, 5 µL Annexin V-fluoresceine isothiocyanate (FITC) and 5 µL PI buffer was added for staining. Beckman Coulter CytoFLEX flow cytometry (Brea, CA, USA) was used to test cell apoptosis.

Flow Cytometry for Cell Proliferation

Cells were re-suspended in complete culture medium. Cell proliferation was measured by Click-iT EdU Alexa Fluor 488 Flow Cytometry Assay Kits. In brief, cells were treated in 10 µM EdU for 2 h, and were incubated for 48 h furthermore. Cells were digested with trypsin. After centrifugation, fixation, and permeabilization, reaction buffer containing Alexa Fluor 488 labels was added for 30 min dark incubation at room temperature. By centrifugation and washing, Beckman Coulter (Brea, CA, USA) CytoFLEX flow cytometry was used to test cell proliferation.

Flow Cytometry for Cell Cycle

Cells were digested in trypsin and were fixed in 70% ethanol. Phosphate buffered solution (PBS) containing 25 µg/mL PI, 25 µg/mL RNase A, 0.1% Triton X-100 was added for 4°C dark incubation for 30 min. Beckman FC 500 MCL/MPL flow cytometry (Brea, CA, USA) was added for measuring cell cycle.

Statistical Analysis

SPSS 18.0 (SPSS Inc., Chicago, IL, USA) was used for data analysis. Measurement data were presented as mean±standard deviation (SD). Student *t*-test was used to compare measurement data between groups. A statistical significance was defined when $p < 0.05$.

Results

Targeted Regulation Between miR-16 and MEK1

Bioinformatics analysis revealed complementary binding sites between miR-16 and 3'-UTR of MEK1 (Figure 1A). Dual luciferase gene reporter assay further validated that transfection of miR-16 mimics significantly suppressed relative luciferase activity in HEK293T cells, whilst transfection of miR-16 inhibitor elevated relative luciferase activity (Figure 1B), indicating the regulating effect of miR-16 on MEK1 mRNA.

Abnormal Expression of miR-16 and MEK1 in PA Tumor Tissues

qRT-PCR showed that, compared to that in normal pituitary tissues, the level of miR-16 was significantly decreased while MEK expression was statistically up-regulated in PA tumors ($p < 0.05$) (Figure 2A). Western blot results also showed significantly higher MEK1 protein expression in PA tumor tissue compared to that in normal pituitary tissues (Figure 2B), indicating potential role of miR-16 in regulation of MEK1 protein expression and PA occurrence.

MiR-16 Down-Regulation and MEK1 Up-regulation in PA Tumor Cells

We also determine the level of miR-16 and MEK1 in PA tumor cells. qRT-PCR results showed that, compared to normal embryonic pituitary cells, in PA cells miR-16 levels were statistically reduced with concomitant up-regulation of MEK1, Cyclin D1, and Survivin mRNA levels (Figure 3A). Concomitantly, the expression of MEK1, p-ERK1/2, Cyclin D1 and Survivin were remarkably elevated at protein level by Western blotting

detection (Figure 3B). Flow cytometry showed that HP75 cells performed significantly higher proliferation potency (Figure 3C) and S or G2/M phase ratio (Figure 3D) than normal embryonic pituitary cells did, whilst G0/G1 phase ratio was getting lower correspondingly. These results showed that down-regulation of miR-16 might be involved in the rise of MEK1 protein expression and PA pathogenesis.

MiR-16 Over-expression Inhibited PA Tumor Cells Proliferation and Induced Cell Apoptosis or Cell Cycle Arresting

We further evaluate the overexpression of miR-16 on the proliferation of PA tumor cells. Intriguingly, our data demonstrated that the transfection of miR-16 mimic or si-MEK1 significantly suppressed levels of MEK1, p-ERK1/2, Cyclin D1 and Survivin (Figure 4A and 4B), and impeded cell proliferation potency (Figure 4E), with facilitating effect on cell apoptosis (Figure 4C) or cell cycle arresting at G0/G1 phase (Figure 4D).

Discussion

MAPK signal transduction pathway is widely distributed in eukaryotic cells with important signal transduction function and further activates multiple transcriptional factors in nucleus and protein kinase, to regulate transcription and expression of related target genes, eventually mediating various pathological and biological processes including cell survival, proliferation, migration, apoptosis, angiogenesis, and immune response^{22,23}. ERK-induced MAPK signal pathway is the classical signal transduction pathway, and is the major pathway for MAPK to exert its

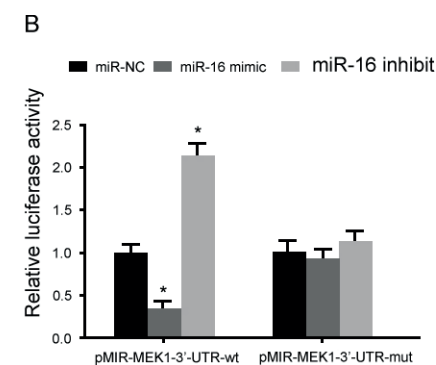
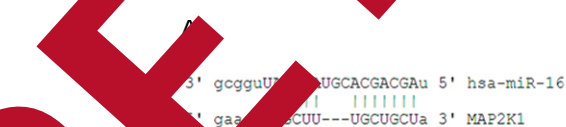


Figure 1. Targeted regulation between miR-16 and MEK1. (A) Binding sites between miR-16 and 3'-UTR of MEK1 mRNA; (B) Dual luciferase reporter gene assay. *, $p < 0.05$ compared to miR-NC group.

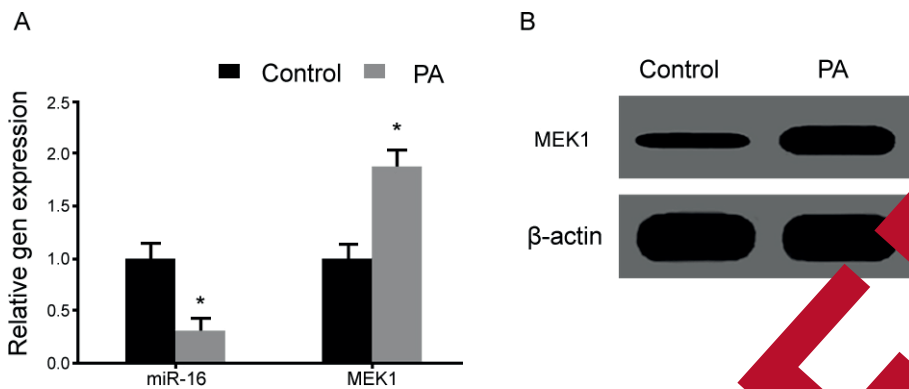


Figure 2. Abnormal expression of miR-16 and MEK1 in PA tumor tissues. (A) qRT-PCR for gene expression; (B) Western blot for protein expression. *, $p < 0.05$ compared to control group.

functions^{9,24}. Accumulative evidence showed that abnormal activation of ERK/MAPK signal pathway was correlated with occurrence and progression of multiple tumors including gastric cancer²⁵, gallbladder carcinoma⁶, and colon cancer²². Therefore, in this paper, we identified the possible mechanism of miR-16 on PA tumor that was also associated with ERK/MAPK signal pathway. MEK1 represents a type of dual-specific

protein kinase, and functions at the upstream of ERK protein to phosphorylate and activate tyrosine/serine/threonine (Tyr/Thr) residues of ERK protein, thus activating ERK/MAPK signal pathway. The previous study¹⁵ showed the correlation between MEK1 and PA pathogenesis. Interestingly, our *in silico* bioinformatics analysis showed complementary target sites between miR-16 and 3'-UTR of MEK1 mRNA, the relation of which was

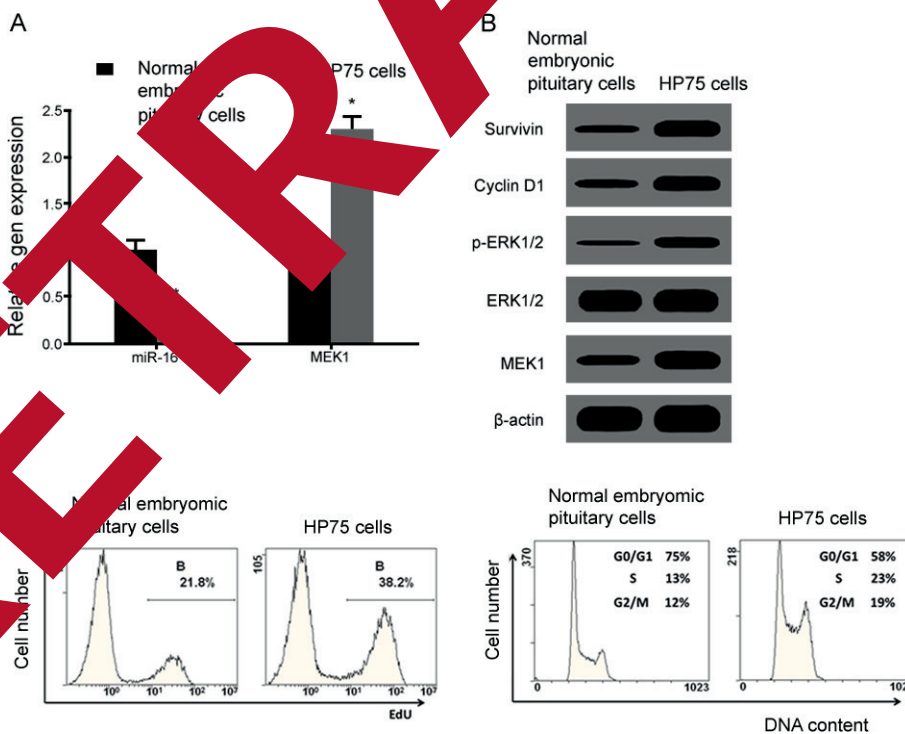


Figure 3. MiR-16 down-regulation and MEK1 up-regulation in PA tumor cells. (A) RT-PCR for gene expression; (B) Western blot for protein expression; (C) Flow cytometry for cell proliferation; (D) Flow cytometry for cell cycle. *, $p < 0.05$ compared to normal embryonic pituitary cells.

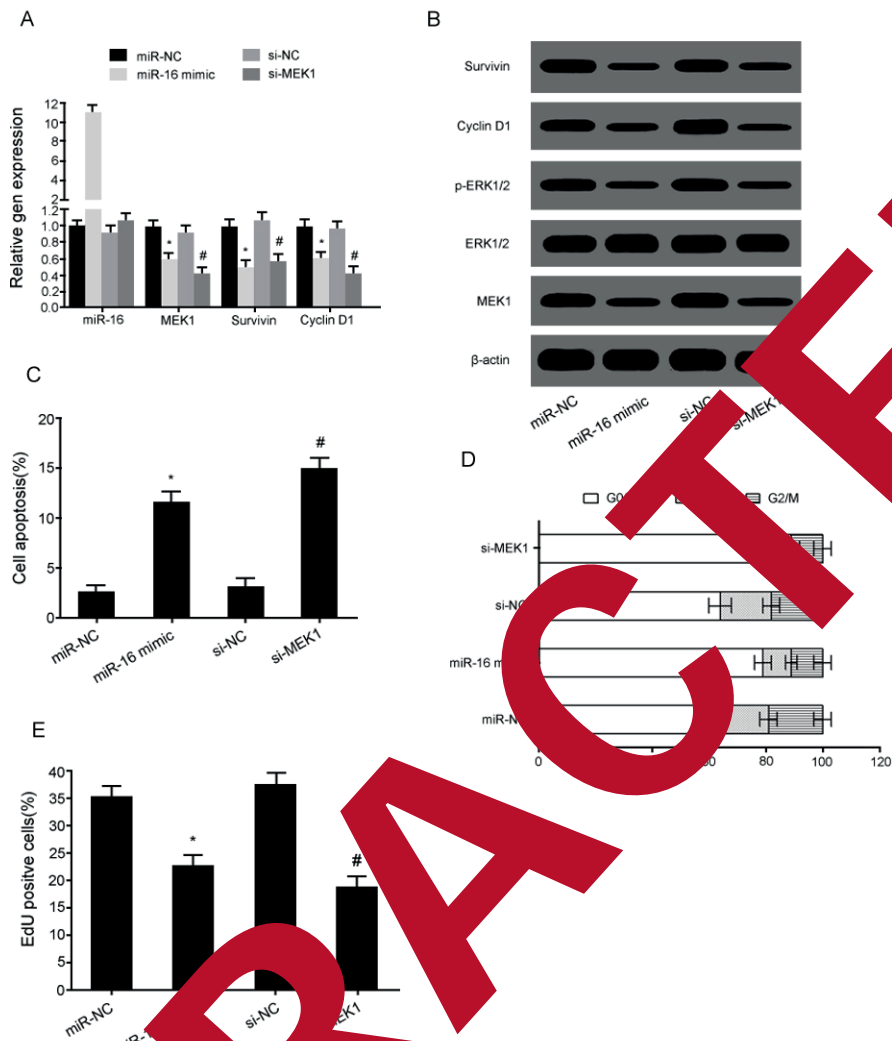


Figure 4. MiR-16 over-expression in PA cells inhibited proliferation and induced cell apoptosis or cell cycle arrest. (A) qRT-PCR for gene expression; (B) Western blot for protein expression; (C) Flow cytometry for cell apoptosis; (D) Flow cytometry for cell cycle; (E) Flow cytometry for cell proliferation. a, $p < 0.05$ comparing between miR-16 mimic and miR-NC; b, $p < 0.05$ comparing between si-MEK1 and si-NC.

further verified by dual luciferase gene reporter assays. Our preliminary data showed that the miR-16 expression in PA patient tumor tissues was significantly decreased with growing level of MEK1. Along with the evidence that miR-16 expression inhibited PA tumor cells proliferation, we speculated the involvement of ERK/MAPK signal pathway in the regulation of miR-16 expression.

MicroRNAs exert essential regulatory function on proliferation and apoptosis of pituitary tumor cells. Amaral et al²⁰ showed that, compared to that in normal pituitary tissues, significantly lower miR-16 expression was found in PA tumor tissues. Bottoni et al²¹ found remarkably lower miR-16

expression in PA tissues, and its correlation with tumor lesion size, as lower miR-16 expression was accompanied with larger tumor volume. Renjie et al²⁷ also showed that, compared to normal pituitary tissues, PA lesion gave rise to significantly lower expression of miR-16 in GH3 and MNQ cells. Compared to non-invasive pituitary tissues, dramatically lower miR-16 expression was detected in invasive PA tumor tissues, indicating that miR-16 down-regulation was correlated with PA progression and peripheral invasion. Consistently, in this study, reduction of miR-16 level was observed in both PA patient tumor tissues and PA cell line HP75, supporting studies performed by Amaral et al²⁰, Bottoni et al²¹, and Renjie et al²⁷.

Dworakowska et al¹⁵ found that, compared to normal pituitary tissues, in PA tumor tissues, the level of MEK1 was significantly increased, which resulted in the induction of ERK/MAPK signal pathway. In this study, we observed that in PA tumor cells, MEK1 expression and ERK/MAPK pathway activity were abnormally potentiated, as similar with Dworakowska et al¹⁵. Further study showed that transfection of miR-16 mimic or si-MEK1 significantly suppressed MEK1, p-ERK1/2, Cyclin D1, and Survivin expression in HP75 cells, inhibited the cell proliferation potency, indicating that miR-16 could weaken malignant biological property of PA cells via targeted inhibition on MEK1 expression based on the finding of *in silico* prediction and luciferase gene reporter assay. Moreover, Renjie et al²⁷ showed that over-expression of miR-16 could weaken clonal formation or invasion potency of PA cells, which were similar with our observation that miR-16 antagonized malignant biological characteristics of PA cells. However, *in vivo* study is further required for the evaluation of miR-16 on PA cell growth or tumor formation potency within animal model.

Conclusions

MiR-16 is down-regulated, while ERK/MAPK signal pathway is activated in pathogenesis of PA. Over-expression of miR-16 down-regulated the proliferation potency of PA tumor cells, induced cell cycle arrest, and cell apoptosis via targeted inhibition of MEK1 expression.

Conflict of Interest

The Authors declare that there is no conflict of interest.

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