



MiR-424-5p Inhibits Proliferation, Invasion and Promotes Apoptosis and Predicts Good Prognosis in Glioma by Directly Targeting BFAR

Zhe Cheng¹ · Hansheng Shu¹ · Ying Cui¹ · Qiuqian Zhang¹ · Biao Zhao¹ · Didi Pan¹ · Qing Chao¹ · Dawei Wang¹

Received: 10 January 2020 / Accepted: 21 May 2020 / Published online: 1 June 2020
© Arányi Lajos Foundation 2020

Abstract

The biological function of miRNA (miR)-424-5p in glioma has not been clarified. This study was to explore the roles of miR-424-5p/Bifunctional apoptosis regulator (BFAR) axis in glioma. Ninety-six pairs of human glioma tissues and their adjacent non-cancer tissues were collected. The levels of BFAR and miR-424-5p were detected by quantitative polymerase chain reaction (qPCR) in glioma tissues and cell lines. Moreover, the biological roles of miR-424-5p and BFAR in glioma cells were assessed. We found a miR-424-5p binding site in the 3'UTR of BFAR by using TargetScan 7.2 online database. The miR-424-5p level was dramatically decreased in glioma tissues and cell lines, and the BFAR expression was significantly increased. The BFAR expression was negatively related to the miR-424-5p level in glioma tissues. Compared to patients with high miR-424-5p levels in glioma tissues, patients with low miR-424-5p levels had significantly lower survival rate ($\chi^2 = 13.728$ and $P < 0.001$). Compared to patients with high BFAR levels in glioma tissues, patients with low BFAR levels had significantly higher survival rate ($\chi^2 = 5.516$ and $P = 0.027$). Furthermore, up-regulation of miR-424-5p obviously restrained glioma cells proliferation and invasion, and promoted apoptosis. Besides, knockdown of BFAR also could markedly inhibit the proliferation and invasion, and promote apoptosis. Finally, overexpression of BFAR in glioma cells partially reversed the inhibited effects of miR-424-5p mimic. Knockdown of miR-424-5p restrained glioma cell apoptosis and promoted invasion and proliferation via regulation of BFAR.

Keywords Glioma · Bifunctional apoptosis regulator · Prognosis · MicroRNA

Introduction

Glioma is one of the most common primary intracranial tumors [1]. Glioma treatment includes surgical resection / radiation therapy / chemotherapy. However, all of these treatment strategies have been shown to be unable to completely inhibit glioma cells, which is an important reason for the extremely high recurrence rate of glioma patients [2]. Studies have shown that the 1-, 2-, and 5-year survival rates of glioma patients are 66.0%, 45.3%, and 24.5% [3].

Previous reports demonstrated that altered microRNA (miR) expression has participated in tumorigenesis [4–8]. Many miRs have been confirmed to be dysregulated in glioma, including miR-93-5p, miR-181, miR-125a, miR-454-3p and 199a-5p [9–13]. Up to now, the correlation of miR-424-5p on glioma cell proliferation, invasion and apoptosis, and its prognostic value were unexplored. Therefore, we investigated the functional roles and its mechanisms and prognostic value of miR-424-5p in glioma.

Bifunctional apoptosis regulator (BFAR) is characterized by a winged helix DNA-binding domain and is essential for embryogenesis [14]. It is reported that the BFAR functions as an oncogene in colorectal cancer, neuroblastoma and melanoma [15–17]. Moreover, we found a miR-424-5p binding site in the 3'UTR of BFAR by using TargetScan 7.2 online database. Therefore, we investigated the prognostic value of miR-424-5p in 96 glioma patients. Then, in order to investigate the functional role of miR-424-5p in glioma, we detect the miR-424-5p level in glioma tissues and cell lines. Next, we predicted that miR-424-5p directly targeted BFAR according to the

Zhe Cheng and Hansheng Shu contributed equally to this work.

✉ Qing Chao
hnfw12a@163.com

✉ Dawei Wang
yu_geng16@yeah.net

¹ Department of Neurosurgery, The Second Affiliated Hospital of Bengbu Medical College, No. 220 Hongye Road, West of Longzi Lake, Bengbu, Anhui Province, People's Republic of China

online database TargetScan 7.2. At last, the effects of miR-424-5p or BFAR on apoptosis, invasion and proliferation of glioma cells were determined.

Material and Methods

Human Tissue Samples Collection

Ninety-six pairs of human glioma tissues and their adjacent non-cancer tissues were collected between October 2015 and July 2017. This study was approved by the Ethical Committee of The Second Affiliated Hospital of Bengbu Medical College (BM20150117013). Written informed consent was provided in accordance with the Declaration of Helsinki.

Twenty Four-Month Follow-Up

Ninety-six patients with glioma included in our study were followed up for 24 months. The follow-up date is until June 2019.

Cell Culture

The human glioma cell lines such as U251, U373, U87, HS683, sw1783 and the human brain normal glial cell line (HEB) were purchased from the Shanghai Institutes for Biological Sciences. All the cells were cultured in the DMEM medium containing 10% FBS (GIBCO, USA) at 37 °C in a humidified atmosphere of 5% CO₂.

Transient Transfection

The BFAR-overexpression plasmid was generated by inserting BFAR cDNA into a pcDNA3.1 vector (pcDNA-BFAR). The miR-424-5p mimics, miR-424-5p inhibitors, si-NC, si-BFAR, pcDNA3.1 vector and pcDNA-BFAR were transfected using Lipofectamine 3000 reagent.

CCK-8

In each group, 5×10^3 cells were seeded in a 96-well plate, and 10 μ L of CCK-8 solution was added to each well at different time periods (0 h, 24 h, 48 h, and 72 h) and cultured for 2 h. Enzyme-linked immunosorbent assay was used to determine the optical density (A) at a wavelength of 570 nm.

Apoptosis Detection

Apoptosis detection was performed as described in earlier study [14]. The detection instrument was FACS Calibur flow cytometer.

Transwell Invasion Assay

Transwell invasion assay was performed as described in earlier study [6]. The migrated cells in random three visual fields were photographed and counted under a microscope (Olympus, Tokyo, Japan).

Quantitative Polymerase Chain Reaction (qPCR) Analysis

QPCR was used to measure RT-cDNA with SYBR Green PCR Kit (QIAGEN, Shanghai, China), as described in earlier study [6]. Prime sequences are shown in Table 1.

Western Blot Analysis

Western blot was used as described in earlier study [6]. Glioma tissues and transfected cells were lysed with RIPA lysis buffer. The primary antibodies including rabbit monoclonal BFAR, MMP-2, MMP-9, ki-67, cleaved caspase-3, GAPDH and the secondary anti-rabbit antibody, were purchased from the Institute of Cell Research, Wuhan University.

Luciferase Reporter Assay

The pGL3-BFAR-3'UTR WT and pGL3-BFAR-3'UTR MUT were synthesized by GenePharma. Glioma cells were transfected with pGL3-BFAR-3'UTR WT or pGL3-BFAR-3'UTR MUT, along with miR-424-5p mimics or miR-NC using Lipofectamine 3000.

Immunohistochemical Staining

Glioma tissue wax section was incubated with BFAR monoclonal antibody, then incubated with alkaline phosphatase secondary antibody for 1 h.

Table 1 Primer sequences of miR-424-5p, BFAR, U6 and GAPDH

RNA	Primer sequence (5'—3')
miR-424-5p Forward primer	ATAGAGCTCTCCTGTACGT
miR-424-5p Reverse primer	CAGGCATACCAGGGAGTACA
BFAR Forward primer	CTCCTTCAGCTTCGGCAGCACATA
BFAR Reverse primer	AACGCTTCACGAACATAGAGTCGT
U6 Forward primer	ATAGAGGCATTACGACCAGCT
U6 Reverse primer	GAGCCAGTTCGGATCGATTCT
GAPDH Forward primer	GTGTCATAGAGCTCTTCGTCTCTGT
GAPDH Reverse primer	GAACCAGGCCCTTCGAGG

Statistical Analysis

Student's *t* test and χ^2 test were used for measurement or counting data. K–M method was used to calculate the statistical difference between survival curves. Inspection level $\alpha = 0.05$.

Results

Expression Levels of miR-424-5p and BFAR in Glioma Tissues and their Correlation with Patients' Prognosis

The miR-424-5p level in glioma tissues was lower than that in the adjacent non-cancer tissues ($P < 0.05$, Fig. 1a). Next, our data further confirmed that the gene and protein levels of BFAR were obviously higher in glioma tissues than that in the adjacent non-cancer tissues ($P < 0.05$, Fig. 1b and c). Correlation analysis showed that the level of miR-424-5p was significantly correlated with the expression level of BFAR in glioma tissues ($r = -0.549$, $P < 0.001$, Fig. 1d).

In this study, 50 patients died during 24-month following. We divided patients into four groups (high/low miR-424-5p or BFAR levels) according to the median of miR-424-5p and BFAR levels in glioma tissues, respectively. Compared to patients with high miR-424-5p levels in glioma tissues, patients with low miR-424-5p levels had significantly lower survival rate ($\chi^2 = 13.728$ and log-rank $P < 0.001$, Fig. 1e).

Compared to patients with high BFAR levels in glioma tissues, patients with low BFAR levels had significantly higher survival rate ($\chi^2 = 5.516$ and log-rank $P = 0.027$, Fig. 1f).

MiR-424-5p Directly Targeted BFAR 3'UTR

We detected the gene expression levels of miR-424-5p and BFAR in U251, U373, U87, HS683, sw1783 and HEB cell lines. Our data found that the miR-424-5p level was lowest and the BFAR level was highest in HS683 than that in the other four glioma cell lines (Fig. 2a and b). Therefore, HS683 cell was used in the following experiments.

Actually, we found a miR-424-5p binding site in the 3'UTR of BFAR by using TargetScan 7.2 online database (Fig. 2c). Then, we validated BFAR, a critical oncogene, is a direct target of miR-424-5p by luciferase reporter assay. Introduction of miR-424-5p significantly suppressed WT BFAR reporter activity but not the activity of the mutated reporter construct in HS683 cell, suggesting that miR-424-5p could specifically target the BFAR 3'UTR by binding to the seed sequence (Fig. 2d). Up-regulation of miR-424-5p could obviously reduce BFAR expression (Fig. 2e). These results suggested that miR-424-5p directly targeted BFAR through 3'UTR sequence binding. After transfection with miR-424-5p mimic or inhibitor, or pcDNA-BFAR or si-BFAR, the results showed that the miR-424-5p or BFAR level was significantly up-regulated or down-regulated compared to a NC or si-NC group (Fig. 2f and g), respectively.

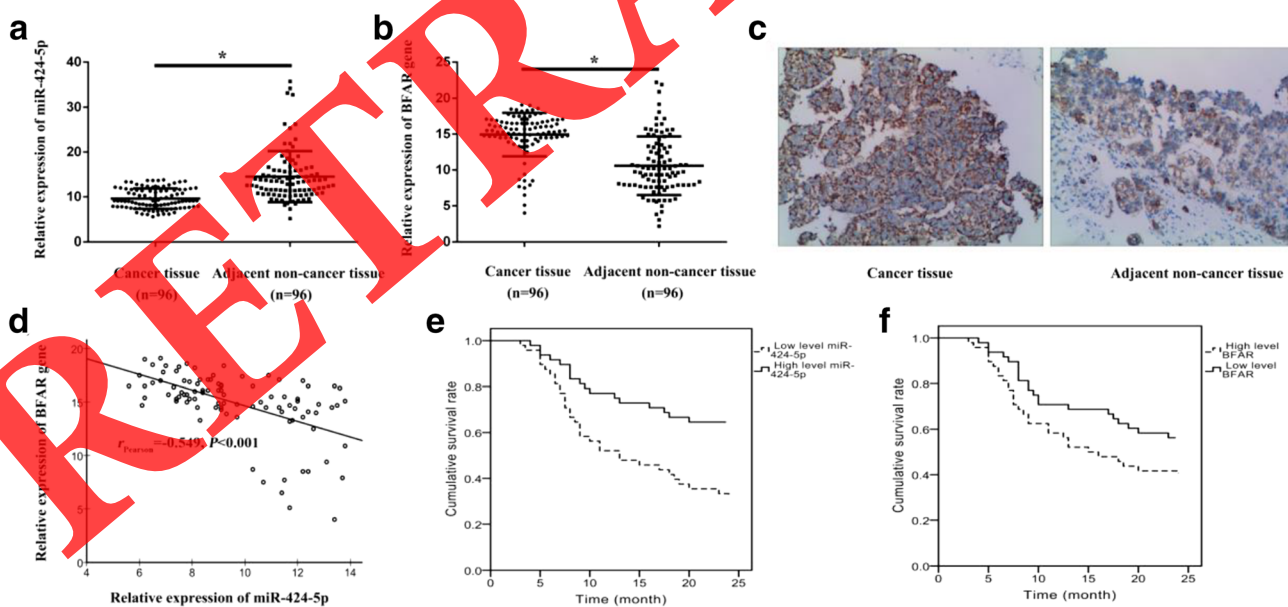
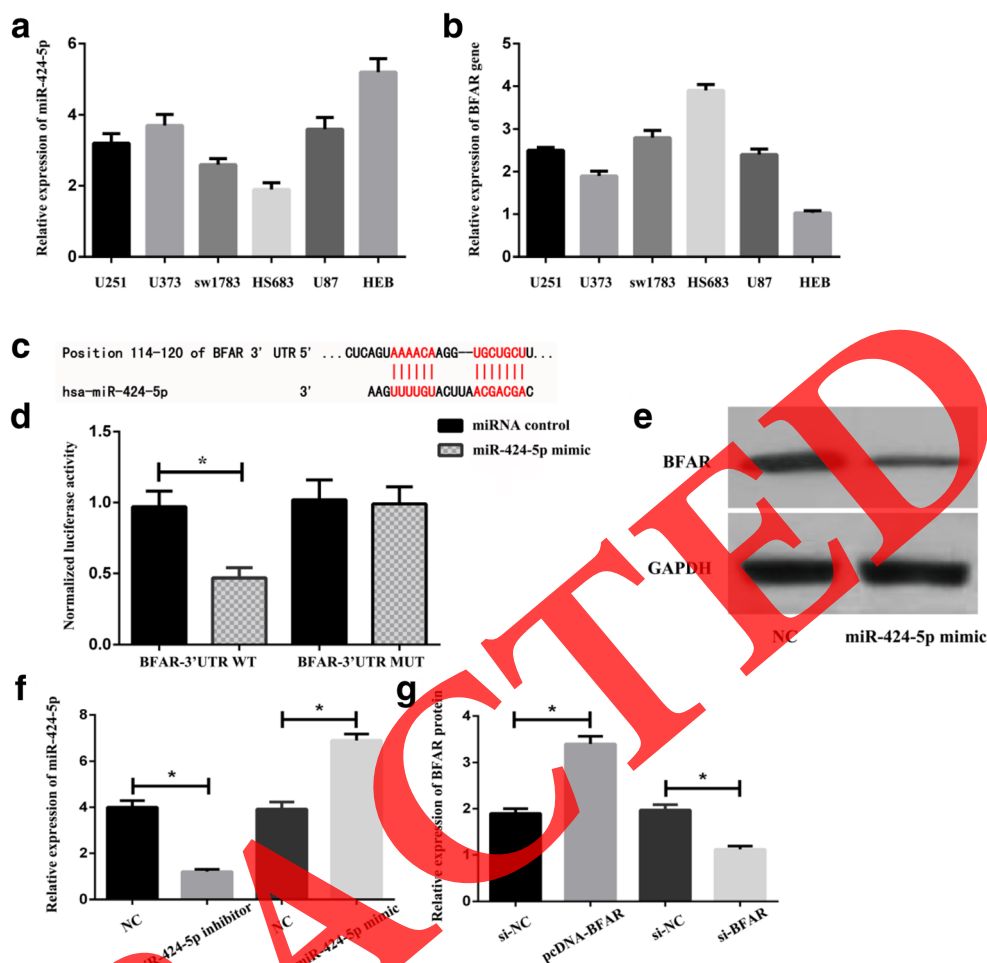


Fig. 1 The expression levels of miR-424-5p and BFAR in glioma tissues and their correlation with patients' prognosis. **a**: Quantitative polymerase chain reaction analysis of miR-424-5p level in glioma tissues and adjacent non-cancer tissues ($n = 96$). Transcript levels were normalized to U6 level; **b** Quantitative polymerase chain reaction analysis of BFAR level in glioma tissues and adjacent non-cancer tissues ($n = 96$). Transcript levels were normalized to GAPDH level; **c** Detection of

BFAR protein level in glioma tissues and adjacent non-cancer tissues by immunohistochemistry; **d**: Correlation analysis between the level of miR-424-5p and BFAR in glioma tissues; **e** Relationship between the level of miR-424-5p in glioma tissues and patients' two-year survival rate; **f** Relationship between the level of BFAR in glioma tissues and patients' two-year survival rate. * $P < 0.05$

Fig. 2 BFAR is a direct target of miR-424-5p. **a–b** The miR-424-5p level was lowest and the BFAR level was highest in HS683 than that in the other four glioma cell lines; **c** Schematic representation of BFAR 3'UTRs showing putative miR-424-5p target site; **d** The analysis of the relative luciferase activities of BFAR-WT and BFAR-MUT. **e** The protein expressions of BFAR were determined via Western blot assay. **f** The level of miR-424-5p was determined via quantitative polymerase chain reaction assay. **g** The level of BFAR was determined via Western blot assay. * $P < 0.05$



The Effects of miR-424-5p on Apoptosis, Invasion, and Proliferation in Glioma Cells

To study the role of miR-424-5p in regulating HS683 cells apoptosis, our results suggested that introduction of miR-424-5p significantly promoted HS683 cells apoptosis (Fig. 3a and b). However, transfection with miR-424-5p inhibitor suppressed the cells apoptosis of HS683 compared with the NC group (Fig. 3a and b). Result of western blot showed that inhibiting miR-424-5p expression in HS683 suppressed expression of cleaved caspase-3 (Fig. 3f and j). Compared to the NC group, the results from Transwell assays showed that increased miR-424-5p level significantly decreased the number of invading glioma cells (Fig. 3c and d). In addition, down-regulation of miR-424-5p had opposite effects on regulating the invasion of glioma cells (Fig. 3c and d). Result of western blot also showed that inhibiting miR-424-5p expression in HS683 promoted expressions of MMP-2 and MMP-9 (Fig. 3f, g and h). To investigate the functional roles of miR-424-5p in HS683 cells proliferation, CCK-8 assay was performed. CCK-8 results were

shown in Fig. 3e. At 0 h, there was no significant difference in the proliferation capacity of HS683 cells between the three groups ($P > 0.05$). At 24 h, 48 h, and 72 h, compared with the NC group, the cell proliferation ability in miR-424-5p mimic group was significantly decreased, and was significantly increased in the miR-424-5p inhibitor group ($P < 0.05$). Result of western blot also showed that inhibiting miR-424-5p expression in HS683 promoted expression of ki-67 (Fig. 3f and i). Taken together, we demonstrated that miR-424-5p could inhibit the progression of glioma by promoting apoptosis and repressing invasion and proliferation.

Knockdown of BFAR Inhibited Glioma Cells Proliferation and Invasion, and Promoted Apoptosis

To investigate the functional roles of BFAR in glioma cells, the apoptosis, invasion, and proliferation of glioma cells were detected after transfection with si-BFAR, pcDNA3.1 vector or pcDNA-BFAR. We found that silencing BFAR evidently promoted the apoptosis of HS683 cell (Fig. 4a and b). Result of

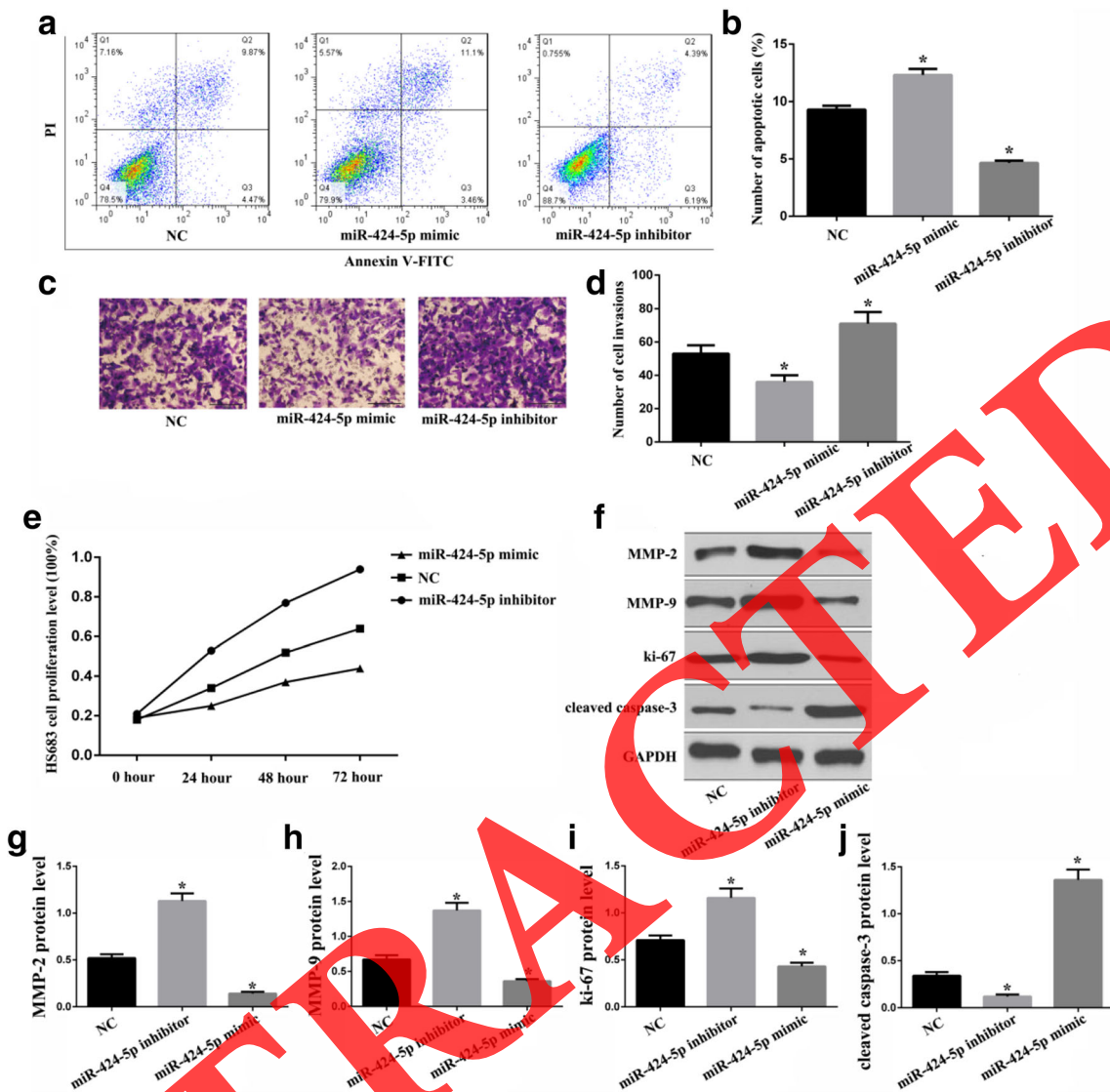


Fig. 3 The effects of miR-424-5p on apoptosis, invasion, proliferation and related molecules expressions in glioma cell. **a-b** The apoptosis was assessed by flow cytometer. **c-d** The invasion was assessed by Transwell

assay. **e** The proliferation was assessed by CCK-8. **f-j** The protein expressions of MMP-2, MMP-9, ki-67, and cleaved caspase-3 were examined by Western blot assay. * $P < 0.05$, vs. NC

western blot showed that inhibiting BFAR expression in HS683 promoted expression of cleaved caspase-3 (Fig. 4f and i). Next, transwell assay revealed that decreased BFAR expression restrained invasion of HS683 cell (Fig. 4c and d). Result of western blot showed that inhibiting BFAR expression in HS683 inhibited expressions of MMP-2 and MMP-9 (Fig. 4f, g, and h). CCK-8 results were shown in Fig. 4e. At 0 h, there was no significant difference in the proliferation capacity of HS683 cells between the three groups ($P > 0.05$). At 24 h, 48 h, and 72 h, compared with the NC group, the cell proliferation ability in si-BFAR group was significantly decreased, and was significantly increased in the pcDNA-BFAR group ($P < 0.05$). Result of western blot also showed that inhibiting BFAR expression in HS683 inhibited expression of ki-67 (Fig. 4f and j).

MiR-424-5p Markedly Inhibited the Proliferation and Invasion, and Promoted Apoptosis of Glioma Cells through Regulating BFAR Expression

To determine whether miR-424-5p regulated the apoptosis, invasion, and proliferation of glioma cells by directly targeting BFAR, we cotransfected NC or miR-424-5p mimic with pcDNA3.1 or pcDNA-BFAR into HS683 cells (Fig. 5a and b). Overexpression of BFAR abrogated the promoted effect of miR-424-5p mimic on cell apoptosis (Fig. 5c and d). Next, the data showed that BFAR overexpression partially reversed the invasion and proliferation of HS683 cell restrained by miR-424-5p mimic (Fig. 5e, f, and g). Western blot results further confirmed our results (Fig. 5h-l). Hence, the effects of miR-424-5p mimic were reversed by overexpression of BFAR.

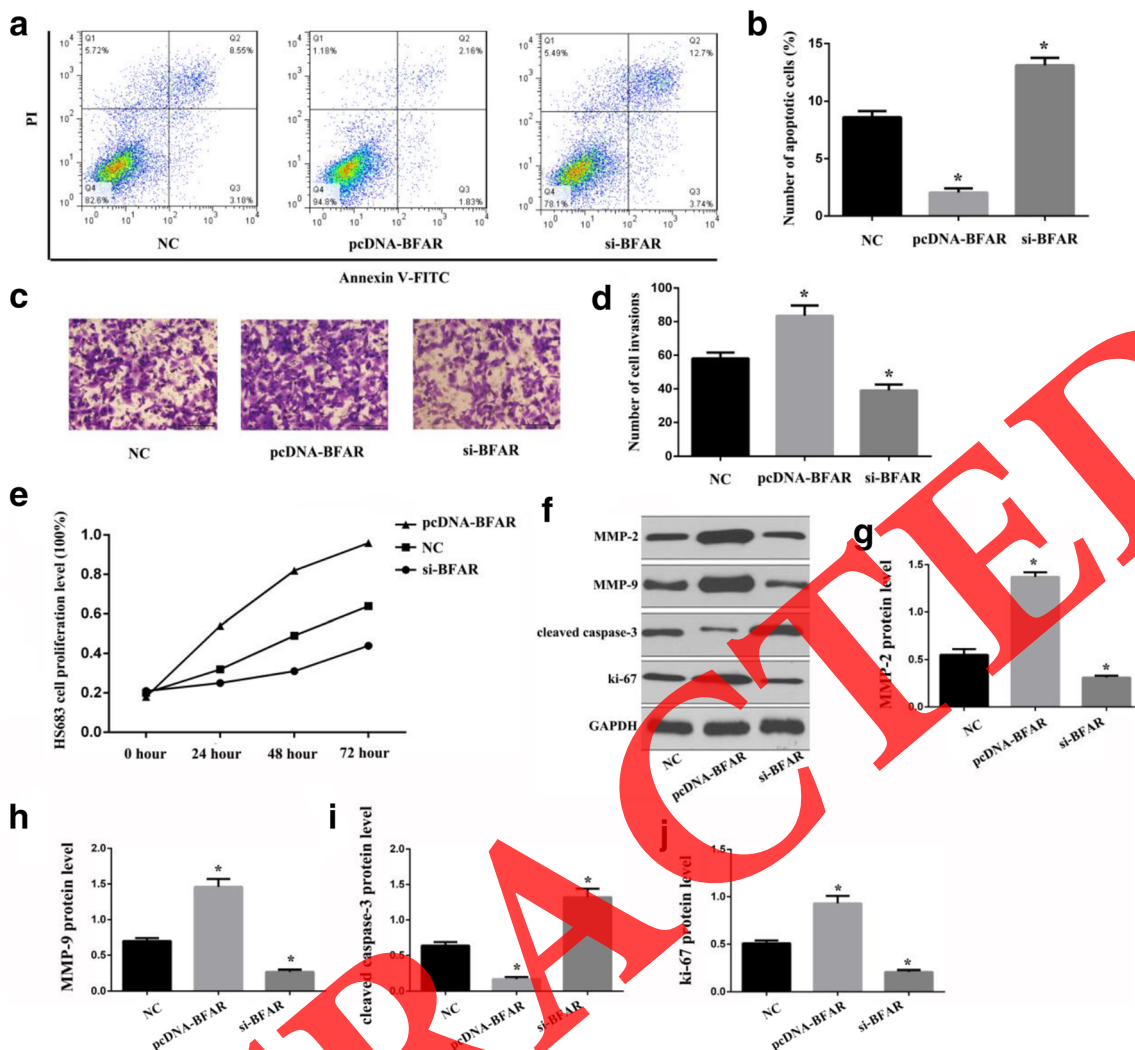


Fig. 4 Knockdown of BFAR inhibited glioma cells proliferation and invasion, and promoted apoptosis. **a–b** The apoptosis was assessed by flow cytometer. **(c–d)** The invasion was assessed by Transwell assay. **e**

The proliferation was assessed by CCK-8. **f–j** The protein expressions of MMP-2, MMP-9, ki-67, and cleaved caspase-3 were examined by Western blot assay. * $P < 0.05$, vs. NC

Altogether, all above results suggested that overexpression of miR-424-5p inhibited the proliferation and invasion, and promoted apoptosis of glioma cells via directly down-regulating BFAR expression.

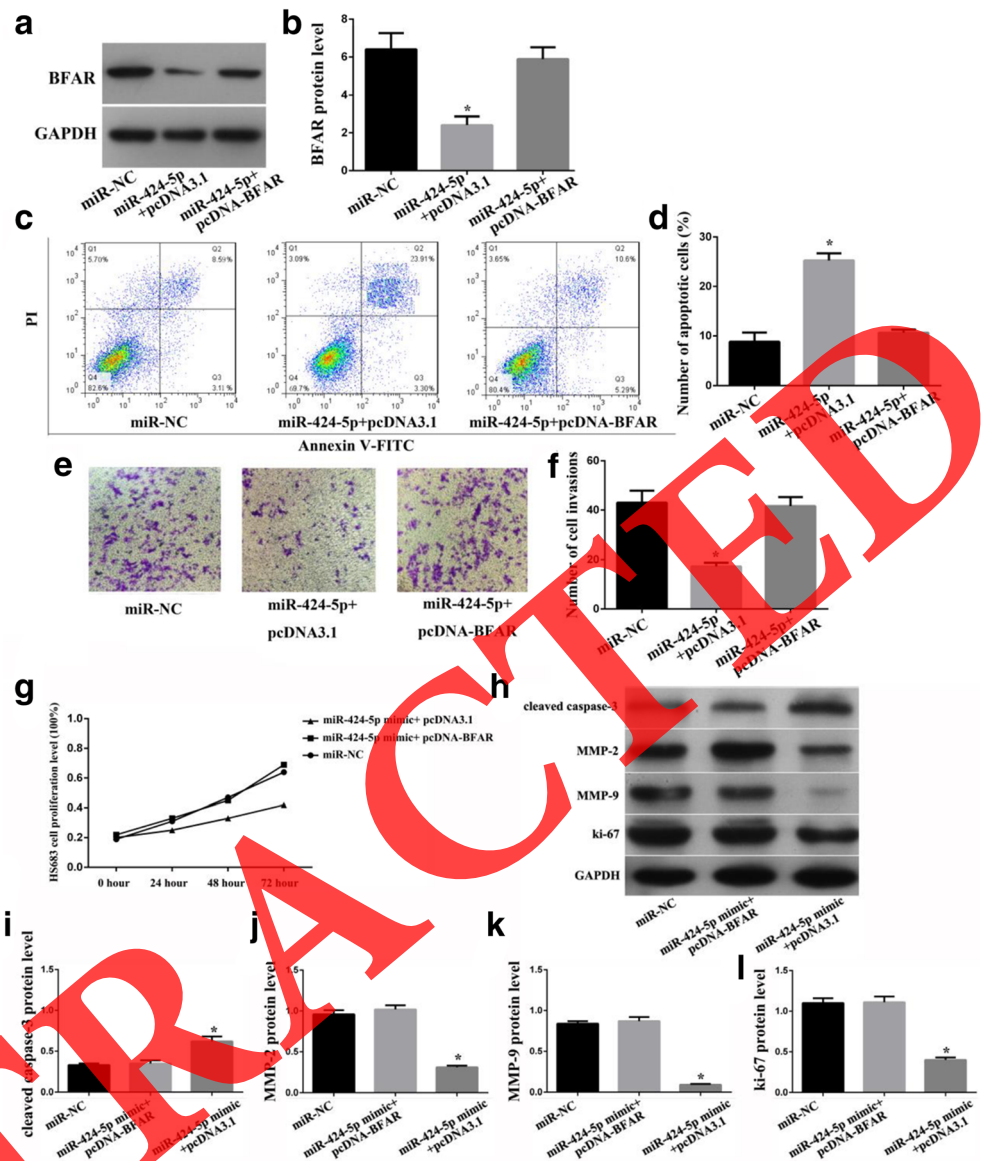
Discussion

Glioma still has no available curative treatment [18–20]. It is extremely necessary to identify novel molecular signatures that can predict the clinical outcome and response to treatment of Glioma. MiRs serve as important regulatory factors, which affects glioma progression. Wu et al. [9] reported that miR-93-5p inhibits glioma proliferation and metastasis by targeting MMP2. Yin et al. [21] indicated that miR-125a-3p suppresses glioma by targeting the anti-oxidative gene Nrg1. Numerous

studies have found that miR-424-5p not only affected cell apoptosis and invasion, but also was closely associated with prognosis in cancers including intrahepatic cholangiocarcinoma, colorectal cancer, hepatocellular carcinoma and ovarian carcinoma [22–25].

In this study, our results showed that the miR-424-5p level was down-regulated in glioma tissues compared with the adjacent normal tissues, and patients with low miR-424-5p levels had significantly lower survival rate. And miR-424-5p level was also down-regulated in glioma cell lines compared with HEB cells. Moreover, we for the first time explored the functional roles of miR-424-5p in glioma cell. Firstly, we found that overexpression of miR-424-5p significantly promoted glioma cell apoptosis than the cells transfected with NC, whereas down-regulation of miR-96-5p inhibited the apoptosis of glioma cell. Invasion is one process of metastasis.

Fig. 5 Introduction of BFAR promoted cell invasion, proliferation, and inhibited cell apoptosis in miR-424-5p-overexpressing glioma cells. **a-b** The protein expression of BFAR was examined by Western blot assay. **c-d** The apoptosis was assessed by flow cytometer. **e-f** The invasion was assessed by Transwell assay. **g** The proliferation was assessed by CCK-8. **h-l** The protein expressions of MMP-2, MMP-9, ki-67, and cleaved caspase-3 were examined by Western blot assay. * $P < 0.05$, vs. miR-NC



Here, the data indicated that increased or decreased miR-424-5p level significantly inhibited or enhanced the invasive ability of HS683 cell compared with the control group. The proliferation process has been confirmed to be critical in cell invasion in types of cancer [26]. At the molecular level, proliferation is characterized by up-regulation of ki-67 [27, 28]. We found that introduction of miR-424-5p inhibited the proliferation of glioma cell by decreasing ki-67 expressions. All above results indicated that miR-424-5p restrained cell invasion and proliferation of glioma.

Moreover, we found that BFAR might be the functional target gene of miR-424-5p. Furthermore, increased expression or knockdown of miR-424-5p significantly inhibited or promoted BFAR expression, respectively. BFAR is an apoptosis-regulating molecule that acts through cysteine proteases, and it is an oncogene and participated in the

development and progression of multiple cancers [15–17]. We also observed that BFAR expressions were frequently at high expression in glioma tissues when compared with the adjacent non-cancer tissues, which agreed with previous studies in melanoma, colorectal cancer, and neuroblastoma [15–17]. Hence, we found that BFAR expression may play a cardinal role in tumorigenesis of glioma. Besides, miR-424-5p level was inversely correlated with BFAR expression in glioma. Moreover, the data showed that silencing BFAR could restrain the invasion and proliferation, and prompts the apoptosis of glioma cell. Next, our results showed that overexpression of BFAR inhibited the invasion and proliferation, and prompted the apoptosis of glioma cell caused by up-regulation of miR-424-5p. Our findings demonstrated that miR-424-5p might act as a tumor suppressor gene in glioma by directly targeting BFAR.

Conclusions

Altogether, the miR-424-5p level was dramatically down-regulated and the BFAR expression was significantly up-regulated in glioma tissues. Introduction of miR-424-5p promoted apoptosis, and inhibited invasion and proliferation of glioma cells by directly down-regulating BFAR expression. Hence, these findings suggested important roles for miR-96-5p/BFAR axis in glioma therapy.

Author Contributions Qing Chao, Zhe Cheng and Dawei Wang conceived the study. Zhe Cheng, Hansheng Shu, Ying Cui, Qiuqian Zhang, and Biao Zhao were involved in protocol development, gaining ethical approval, patient recruitment and data analysis. Zhe Cheng, Hansheng Shu, Didi Pan and Dawei Wang wrote the first draft of the manuscript. All authors reviewed and edited the manuscript and approved the final version of the manuscript.

Funding Information This research was funded by the Natural Science Foundation of Anhui Province (1908085QH334), the Science and Technology Development Foundation of Bengbu Medical College (BYKY17107) and the Bengbu Medical College Translational Medicine Key Special Project (BYTM2019047).

Compliance with Ethical Standards

Conflict of Interest The authors declare that they have no conflict of interest.

Ethical Approval This study was approved by the Ethical Committee of The Second Affiliated Hospital of Bengbu Medical College (BM20150117013).

Informed Consent Written informed consent was provided in accordance with the Declaration of Helsinki.

References

- Chen J, Wu X, Xing Z, Ma C, Xiong W, Zhu X, He X (2018) FOXG1 expression is elevated in Glioma and inhibits Glioma cell apoptosis. *J Cancer* 9:778–783
- Jansen E, Hamisch C, Ruess D, Heiland DH, Goldbrunner R, Ruge MI, Schnell O, Grau SJ (2019) Observation after surgery for low grade glioma: long-term outcome in the light of the 2016 WHO classification. *J Neuro-Oncol* 145:501–507
- Chapman CH, Hara JH, Molinaro AM, Clarke JL, Oberheim Bush NA, Taylor JW, Butowski NA, Chang SM, Fogh SE, Sneed PK, Nakamura JL, Raleigh DR, Braunstein SE (2019) Reirradiation of recurrent high-grade glioma and development of prognostic scores for progression and survival. *Neurooncol Pract* 6:364–374
- Gorbea C, Mosbrugger T, Cazalla D (2017) A viral Sm-class RNA base-pairs with mRNAs and recruits microRNAs to inhibit apoptosis. *Nature* 550:275–279
- Khan AQ, Ahmed EI, Elareer NR, Junejo K, Steinhoff M, Uddin S (2019) Role of miRNA-regulated Cancer stem cells in the pathogenesis of human malignancies. *Cells* 8:840
- Qin WJ, Wang WP, Wang XB, Zhang XT, Du JD (2019) MiR-1290 targets CCNG2 to promote the metastasis of oral squamous cell carcinoma. *Eur Rev Med Pharmacol Sci* 23:10332–10342
- Buonfiglioli A, Efe IE, Guneykaya D, Ivanov A, Huang Y, Orłowski E, Krüger C, Deisz RA, Markovic D, Flüh C, Newman AG, Schneider UC, Beule D, Wolf SA, Dzaye O, Gutmann DH, Semtner M, Kettenmann H, Lehnardt S (2019) Let-7 MicroRNAs regulate microglial function and suppress Glioma growth through toll-like receptor 7. *Cell Rep* 29:3460–3471
- Guo X, Zhang M, Li Q, Zhao J, Wang B, Wang J, Mao P, Song J (2020) Evaluation of genetic variants in MIR3142HG in susceptibility to and prognosis of Glioma. *Am J Clin Oncol* 43:1–8
- Wu H, Liu L, Zhu JM (2019) MiR-93-5p inhibited proliferation and metastasis of glioma cells by targeting MMP2. *Eur Rev Med Pharmacol Sci* 23:9517–9524
- Xu CH, Xiao LM, Zeng EM, Chen LK, Zheng SY, Li DH, Liu Y (2019) MicroRNA-181 inhibits the proliferation, drug sensitivity and invasion of human glioma cells by targeting Selenoprotein K (SELK). *Am J Transl Res* 11:6632–6640
- Hou L, Luo P, Ma Y, Jia C, Yu F, Ly Z, Wu C, Fu D (2017) MicroRNA-125a-3p downregulation correlates with tumorigenesis and poor prognosis in patients with non-small cell lung cancer. *Oncol Lett* 14:4441–4448
- Shao N, Wang L, Xue L, Wang R, Lan Q (2015) Plasma miR-454-3p as a potential prognostic indicator in human glioma. *Neurol Sci* 36:309–313
- Wang G, Li Y, Li J, Zhang D, Luo C, Zhang B, Sun X (2019) microRNA-199a-5p suppresses glioma progression by inhibiting MAGT1. *J Cell Biochem* 120:15248–15254
- Kaminski A, Gupta KH, Goldufsky JW, Lee HW, Gupta V, Shafikhani SH (2018) *Pseudomonas aeruginosa* ExoS induces intrinsic apoptosis in target host cells in a manner that is dependent on its GAP domain activity. *Sci Rep* 1:14047
- Bianchini M, Levy E, Zucchini C, Pinski V, Macagno C, De Sanctis P, Valvassori L, Carinci P, Mordoh J (2006) Comparative study of gene expression by cDNA microarray in human colorectal cancer tissues and normal mucosa. *Int J Oncol* 29:83–94
- Barbagallo I, Parenti R, Zappalà A, Vanella L, Tibullo D, Pepe F, Onni T, Li Volti G (2015) Combined inhibition of Hsp90 and heme oxygenase-1 induces apoptosis and endoplasmic reticulum stress in melanoma. *Acta Histochem* 117:705–711
- Lee B, Galli S, Tsokos M (2007) Sensitive Ewing sarcoma and neuroblastoma cell lines have increased levels of BAD expression and decreased levels of BAR expression compared to resistant cell lines. *Cancer Lett* 247:110–114
- Litak J, Mazurek M, Grochowski C, Kamieniak P, Roliński J (2019) PD-L1/PD-1 Axis in Glioblastoma Multiforme. *Int J Mol Sci* 20:5347
- McCarthy BJ, Shibui S, Kayama T, Miyaoka E, Narita Y, Murakami M, Matsuda A, Matsuda T, Sobue T, Palis BE, Dolecek TA, Kruchko C, Engelhard HH, Villano JL (2012) Primary CNS germ cell tumors in Japan and the United States: an analysis of 4 tumor registries. *Neuro-Oncology* 14:1194–1200
- Johnson DR, O'Neill BP (2012) Glioblastoma survival in the United States before and during the temozolomide era. *J Neuro-Oncol* 107:359–364
- Yin F, Zhang JN, Wang SW, Zhou CH, Zhao MM, Fan WH, Fan M, Liu S (2015) MiR-125a-3p regulates glioma apoptosis and invasion by regulating Nrg1. *PLoS One* 10:e0116759
- Wu J, Yang B, Zhang Y, Feng X, He B, Xie H, Zhou L, Wu J, Zheng S (2019) miR-424-5p represses the metastasis and invasion of intrahepatic cholangiocarcinoma by targeting ARK5. *Int J Biol Sci* 15:1591–1599
- Sahami-Fard MH, Kheirandish S, Sheikha MH (2019) Expression levels of miR-143-3p and -424-5p in colorectal cancer and their clinical significance. *Cancer Biomark* 24:291–297
- Wang S, Zhang JH, Wang H, Yang L, Hong S, Yu B, Guo JC, Liu J, Zhu YB (2019) A novel multidimensional signature predicts

- prognosis in hepatocellular carcinoma patients. *J Cell Physiol* 234: 11610–11619
25. Cha SY, Choi YH, Hwang S, Jeong JY, An HJ (2017) Clinical impact of microRNAs associated with Cancer stem cells as a prognostic factor in ovarian carcinoma. *J Cancer* 8:3538–3547
 26. Song ZB, Yang HP, Xu AQ, Zhan ZM, Song Y, Li ZY (2020) Connective tissue growth factor as an unfavorable prognostic marker promotes the proliferation, migration, and invasion of gliomas. *Chin Med J* 6:670–678
 27. Zhang HY, Zhang BW, Zhang ZB, Deng QJ (2020) Circular RNA TTBK2 regulates cell proliferation, invasion and ferroptosis via miR-761/ITGB8 axis in glioma. *Eur Rev Med Pharmacol Sci* 24: 2585–2600
 28. Fan R, Wang H, Zhang L, Ma T, Tian Y, Li H (2020) Nanocrystallized Oleanolic acid better inhibits proliferation, migration and invasion in intracranial Glioma via Caspase-3 pathway. *J Cancer* 11:1949–1958

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

RETRACTED