

miR-206 Inhibits Cell Proliferation, Migration, and Invasion by Targeting BAG3 in Human Cervical Cancer

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miR-206 and Bcl-2-associated athanogene 3 (BAG3) have been suggested as important regulators in various cancer types. However, the biological role of miR-206 and BAG3 in cervical cancer (CC) remains unclear. We investigated the expressions and mechanisms of miR-206 and BAG3 in CC using *in vitro* and *in vivo* assays. In the present study, miR-206 expression was expressed at a lower level in CC tissues and cells than adjacent normal tissues and NEECs. By contrast, BAG3 mRNA and protein were expressed at higher levels in CC tissues and cells. Furthermore, miR-206 overexpression repressed cell proliferation, migration, and invasion *in vitro*, and the 3'-untranslated region (3'-UTR) of BAG3 was a direct target of miR-206. miR-206 overexpression also inhibited EGFR, Bcl-2, and MMP2/9 protein expression, but promoted Bax protein expression. Besides, BAG3 overexpression partially abrogated miR-206-inhibited cell proliferation and invasion, while BAG3 silencing enhanced miR-206-mediated inhibition. *In vivo* assay revealed that miR-206 repressed tumor growth in nude mice xenograft model. In conclusion, miR-206 inhibits cell proliferation, migration, and invasion by targeting BAG3 in human CC. Thus, miR-206-BAG3 can be used as a useful target for CC.

Key words: MicroRNA-206 (miR-206); B-cell lymphoma 2-associated athanogene 3 (BAG3); Cervical cancer

INTRODUCTION

Cervical cancer (CC) has been reported to be the fifth most common type of cancer in women in China^{1,2}. To date, some types of the human papilloma virus, such as HPV 16 and HPV 18, have been demonstrated as important risk factors for CC patients. Despite the great advances in clinical operations, patients with CC still suffer from metastasis and recurrence, which remain the major causes of cancer-related deaths³⁻⁵. It should be noted that other factors are also involved in the development and progression of CC because not all patients have been infected by the human papilloma virus^{6,7}. Thus, it is essential to explore molecular alterations in the progression of CC.

MicroRNAs (miRNAs) have been reported to be a type of noncoding RNAs, with a length of approximately 19–23 nucleotides⁸⁻¹⁰. In recent decades, miRNAs act as oncogenes or tumor suppressor genes in many malignant tumors. Mechanically, miRNAs inhibit the transcription

of tumor-related genes and downregulate their expression via binding to complementary 3'-untranslated region (3'-UTR) sequences on the corresponding mRNAs¹¹⁻¹³. Previous reports also suggested that miR-206 can regulate different target genes to function in diverse cell processes, such as cell differentiation, proliferation, and apoptosis¹⁴⁻¹⁶. In addition, B-cell lymphoma 2 (Bcl-2)-associated athanogene 3 (BAG3) is also involved in multiple biological processes of CC, including cell proliferation, migration, and invasion¹⁷. However, the expression and role of the miR-206/BAG3 pathway in human CC are still elusive.

In this study, we aimed to detect the expression of miR-206 and BAG3 in CC tissues and cells, and then we explored the role of miR-206 and BAG3 on CC cell proliferation, migration, and invasion by *in vitro* and *in vivo* assays. Finally, we evaluated whether BAG3 is an effective target of miR-206.

MATERIALS AND METHODS

Patients and Tissues

Fifty cases of CC specimens were obtained from patients during surgery at Shandong Provincial Hospital Affiliated to Shandong University (Jinan, Shandong, P.R. China). All samples were confirmed by pathological diagnosis. The corresponding normal cervical epithelial tissues were obtained at least 5 cm from the edge of tumors. All tissue samples were frozen in liquid nitrogen immediately after the resection and stored at -80°C until RNA extraction. The study was approved by Shandong Provincial Hospital Affiliated to Shandong University, and written informed consent was obtained from all participants.

Cell Culture and Transfection

Normal human endocervical epithelial cells (NEECs) were generated from human endocervical samples obtained from biopsies of women (22–23 years of age) who underwent surgery for minor gynecological issues in our hospital and had no underlying endocervical pathology. None of them had received hormonal therapy in the 3 months preceding sample collection. Samples were minced into fragments <1 mm and subjected to mild collagenase digestion. NEECs were cultured to confluence in a steroid-depleted medium composed of 75% Dulbecco's modified Eagle's medium (DMEM) and 25% MCDB-105 (Sigma-Aldrich, St. Louis, MO, USA) supplemented with antibiotics, 10% human albumin, and 5 mg/ml insulin (Sigma-Aldrich). Cell lines SiHa and HeLa were obtained from the KeyGEN Company (Shanghai, P.R. China) and cultured in DMEM, 10% fetal bovine serum (FBS; Gibco, Grand Island, NY, USA), and 1% penicillin–streptomycin (Gibco) at 37°C in a humidified atmosphere under 5% CO_2 . The medium was replaced every 3 days.

Double-stranded RNAs that mimic endogenous precursor miR-206 (Invitrogen–Life Technologies, Carlsbad, CA, USA) as well as negative oligonucleotide control were transfected into cells using Oligofectamine (Thermo Scientific, Waltham, MA, USA) according to the manufacturer's instruction.

Quantitative Real-Time Reverse Transcriptase Polymerase Chain Reaction (qRT-PCR)

Total RNA was extracted using TRIzol Reagent kit (Invitrogen), and cDNA was synthesized with oligo (dT) primers using the Reverse Transcription Kit (Takara, Shiga, Japan). PCR amplification was performed using SYBR Green PCR Master Mix Kit (Qiagen, Valencia, CA, USA). U6 and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) were used as internal controls.

The PCR primers (Shanghai Sangon Biotech, Shanghai, P.R. China) were designed as follows: miR-206, 5'-CCG GAATTCATGGT-3' (forward) and 5'-CCGATCGATTT

AACTTTT-3' (reverse); U6, 5'-GCTTCGGCAGCACAT ATACTAAAAT-3' (forward) and 5'-CGCTTCACGAAT TTGCGTGTTCAT-3' (reverse); BAG3, 5'-CATTGATGT CCCAGGTCAAG-3' (forward) and 5'-ATCGGTTCCG AGTCTGATTT-3' (reverse); GAPDH, 5'-GTCGGTGTG AACGGATTT-3' (forward) and 5'-ACTCCACGACGTA CTCAGC-3' (reverse).

Western Blot Analysis

The total protein was extracted from cultured cells of each group. The protein concentration was measured using a bicinchoninic acid (BCA) assay kit (Thermo Fisher Scientific, Rockford, IL, USA) and adjusted to the same protein concentration in all groups. Subsequently, 5× sodium dodecyl sulfate (SDS; Sigma-Aldrich) loading buffer was added, and protein denaturation was performed at 95°C for 5 min. The samples were electrophoresed using SDS-polyacrylamide gel electrophoresis, transferred to a membrane, and blocked using 5% skim milk overnight. After washing the membrane with Tris-buffered saline plus Tween 20 (TBST; Sigma-Aldrich), primary antibodies (EGFR, Bcl-2, Bax, MMP2, MMP9, or β -actin) were added to the samples and incubated at 4°C overnight. Subsequently, the samples were rinsed in TBST supplemented with a horseradish peroxidase (HRP)-conjugated secondary antibody (Abcam, Cambridge, MA, USA) and cultured for 1 h at 37°C . After rinsing the membrane in TBST, enhanced chemiluminescence was employed in order to develop HRP, and HRP was recorded using scanning. The gray value of the target band was analyzed using the ImageJ software (NIH, Bethesda, MD, USA). The experiment was repeated three times independently.

Cell Proliferation Assay

Cell proliferation was measured using the cell counting kit-8 (CCK-8) according to the manufacturer's instructions (Dojindo, Kumamoto, Japan). Cells (2×10^3 cells/well) were incubated in 96-well plates for 24, 48, and 72 h. CCK-8 solution (10 μl) was added to each well, the plates were incubated for 1 h at 37°C , and absorbance at 450 nm wavelength (OD450) was measured in a microplate reader (Bio-Rad, Hercules, CA, USA).

Cell Migration and Wound Healing Assays

Cell migration was analyzed using a Transwell chamber assay (Corning Inc., Cambridge, MA, USA). Cells (2.0×10^5) in 200 μl of serum-free medium were added to the top chamber, while 600 μl of medium containing 10% FBS was added to the lower chamber. Cells that migrated into the lower chambers were fixed in 4% paraformaldehyde, stained with 1% crystal violet (Sinopharm Chemical Reagent Co., Shanghai, P.R. China) after 24 h, and counted in six random fields. For the wound healing assay, 5×10^5 cells were seeded in six-well plates and

cultured for 24 h. The cell monolayers were wounded with a pipette tip. The wound closure was observed every 24 h.

Luciferase Reporter Assay

The 3'-UTR of the human BAG3 gene was cloned into the pGL3 luciferase reporter plasmid (Promega, Madison, WI, USA) downstream of the luciferase gene. QuikChange Site-Directed Mutagenesis Kit (Stratagene, La Jolla, CA, USA) was used to mutate the sequence of BAG3 3'-UTR, which was the complementary binding site of miR-206 in the recombinant luciferase reporter plasmid. Cells were seeded into 48-well plates overnight before cotransfection with luciferase reporter plasmids, pRL-TK *Renilla* luciferase plasmids (Promega), and miR-206 using Lipofectamine 2000 (Invitrogen). Twenty-four hours later, luciferase reporter activities were measured using a Dual-Luciferase Reporter Assay Kit (Promega).

In Vivo Tumorigenesis

Specific pathogen-free (SPF)-grade male BALB/c nude mice were housed at an SPF environment in the Animal Laboratory Unit, School of Medicine, Shandong University (Jinan, Shandong, P.R. China). Cells (5×10^6 per mouse, three mice per group) with miR-206 mimics or miR-NC (negative control) were subcutaneously injected into the right flanks of mice. At 14 days after cell

injection, animals were sacrificed, and xenograft tumors were excised and weighted. The diameters of each tumor including the length (L) and width (W) were measured every 5 days with calipers, and the volume was calculated using the formula $(W+L)/2 \times W \times L \times 0.5236$.

Statistical Analysis

Experiments were repeated at least three times, and the experimental data were represented as mean \pm SD. Differences between groups were analyzed using the Graph Pad Prism 5 software (www.graphpad.com; GraphPad Software, La Jolla, CA, USA) with two-tail Student's t -test and ANOVA methods. A value of $p < 0.05$ was considered to be statistically significant.

RESULTS

The Expression of miR-206 and BAG3 in CC Tissues

In order to characterize the expression of miR-206 and BAG3 in human CC tissues, we detected the expressions of miR-206 and BAG3 in 50 CC tumor tissues and paired adjacent normal tissues. Here miR-206 expression was expressed at a lower level in CC tissues than in matched nontumor tissues ($p < 0.01$) (Fig. 1a). However, BAG3 mRNA was expressed at a higher level in CC tissues than in matched normal tissues ($p < 0.01$) (Fig. 1b). Likewise, the BAG3 protein expression was

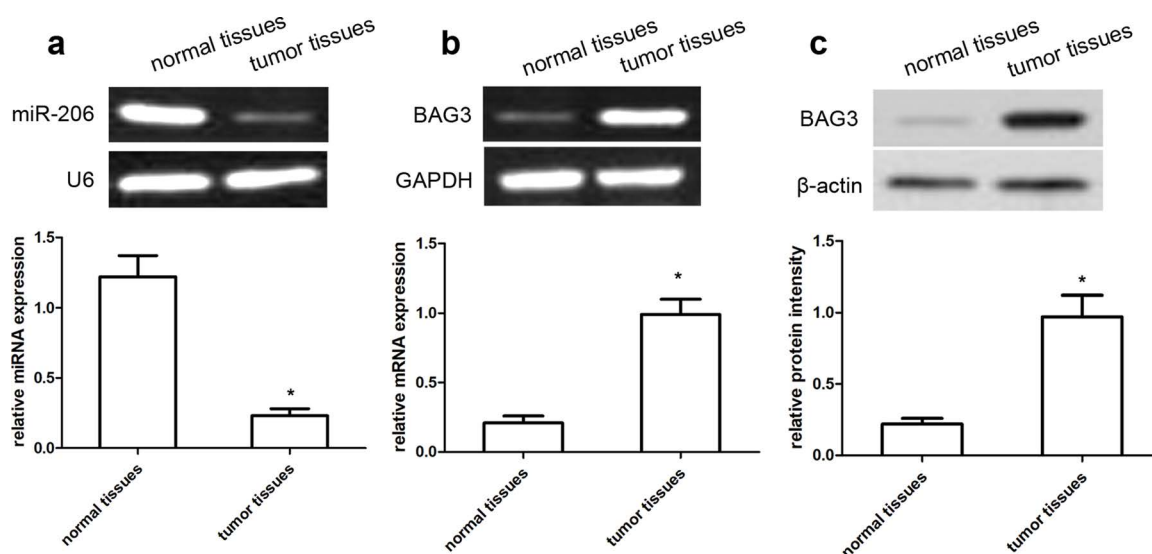


Figure 1. The expression of microRNA-206 (miR-206) and B-cell lymphoma 2 (Bcl-2)-associated athanogene 3 (BAG3) in cervical cancer (CC) tissues. The quantitative real-time reverse transcriptase polymerase chain reaction (qRT-PCR) analysis of miR-206 (a) and BAG3 mRNA (b) expression was conducted in cancer tissues and matched nontumor tissues. Quantification analysis was defined as the relative density of miR-206 and BAG3 mRNA to the internal controls U6 and glyceraldehyde 3-phosphate dehydrogenase (GAPDH), respectively. Results shown are the mean \pm SD of repeated independent experiments. (c) The expression of BAG3 protein was examined in cancer tissues and matched nontumor tissues using Western blot. The average BAG3 protein expression was normalized to β -actin. Results shown are the mean \pm SD of three repeated independent experiments. * $p < 0.01$, compared with normal tissues, Student's t -test.

also identified to be obviously higher in CC tissues than in matched normal tissues ($p < 0.01$) (Fig. 1c).

The Expression of miR-206 and BAG3 in CC Cell Lines

In this study, qRT-PCR analysis was used to detect the expressions of miR-206 and BAG3 mRNA, and Western blot analysis was used to detect the expression of BAG3 protein. Our data showed that the miR-206 expression was obviously reduced in SiHa and HeLa cells compared with normal NEECs (both $p < 0.01$) (Fig. 2a). On the other hand, the expression of BAG3 mRNA and protein was obviously increased in SiHa and HeLa cells compared to normal NEECs (both $p < 0.01$) (Fig. 2b and c).

miR-206 Has an Inhibitory Effect on CC Cell Proliferation

In the present study, miR-206 mimics or miR-NC were transfected into SiHa and HeLa cells, and then cell proliferation was subjected to CCK-8 assay analysis. CCK-8 assay revealed that miR-206 overexpression effectively decreased the number of viable SiHa and HeLa cells compared with the miR-NC group (both $p < 0.01$) (Fig. 3a). These results indicated that transfection of miR-206 mimics obviously inhibited SiHa and HeLa cell proliferation. At the same time, we used Western blot assay to detect cell proliferation-related proteins, involving EGFR, Bcl-2, and Bax proteins. Our data showed that the expression of EGFR and Bcl-2 protein was obviously reduced in SiHa and HeLa cells with miR-206 transfection compared with those in the miR-NC group (both $p < 0.01$) (Fig. 3b). Inversely, Bax protein was expressed at a higher level in SiHa and HeLa cells with miR-206 mimics than in the miR-NC group (both $p < 0.01$) (Fig. 3b). These results

suggested that miR-206 expression affected cell proliferation in the progression of CC.

miR-206 Has an Inhibitory Effect on CC Cell Migration and Invasion

In order to elucidate the effect of miR-206 on cell migration and invasion, we transfected miR-206 mimics or miR-NC into SiHa and HeLa cells, and then we conducted the wound healing and Transwell assays. The wound healing analysis revealed that miR-206 overexpression obviously inhibited SiHa or HeLa cell migration compared with the miR-NC group (both $p < 0.01$) (Fig. 4a). Additionally, Transwell assay analysis revealed that miR-206 overexpression obviously inhibited SiHa and HeLa cell invasion compared with miR-NC (both $p < 0.01$) (Fig. 4b). Subsequently, we used Western blot to explore alterations of cell invasion-related proteins and found that miR-206 mimics obviously reduced the expression of MMP2 and MMP9 proteins in SiHa and HeLa cells compared with miR-NC (both $p < 0.01$) (Fig. 4c). These findings suggested that miR-206 exerts the inhibitory effects on CC cell migration and invasion.

The 3'-UTR of BAG3 Is a Direct Target of miR-206

To determine whether the 3'-UTR of BAG3 is a direct target of miR-206, we used three miRNA databases to predict common and putative miR-206-binding sequences located in the 3'-UTR of BAG3 mRNA (Fig. 5a). We then inserted a 3'-UTR [wild type (wt)/mutant (mut)] sequence of BAG3 mRNA into a luciferase reporter vector to analyze the luciferase density. We also detected the expression level of BAG3 protein in SiHa cells using Western blot analysis. Our results showed that miR-206 mimics

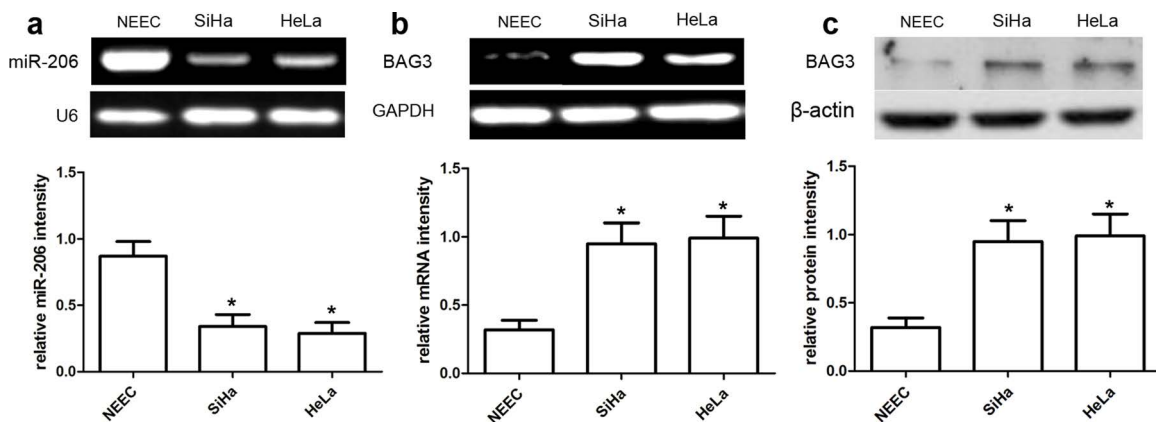


Figure 2. The expression of miR-206 and BAG3 in CC cell lines. qRT-PCR analysis of miR-206 (a) and BAG3 (b) expression in CC SiHa and HeLa cell lines. Quantification analysis was defined as the relative density of miR-206 and BAG3 mRNA to the internal controls U6 and GAPDH, respectively. (c) The expression of BAG3 protein was examined in the CC cell lines SiHa and HeLa using Western blot. The BAG3 expression was normalized to β -actin expression. Results shown are the mean \pm SD of three repeated independent experiments. * $p < 0.01$, compared with normal human endocervical epithelial cells (NEECs), one-way ANOVA.

significantly reduced the luciferase intensity of SiHa cells with BAG3-3'UTR-wt in a dose-dependent manner ($p < 0.01$) (Fig. 5b), while miR-206 mimics did not change the luciferase intensity of SiHa cells with BAG3-3'UTR-mut ($p > 0.05$) (Fig. 5c). Most importantly, the expression of BAG3 protein was reduced in SiHa cell lines cotransfected with miR-206 mimics and 3'-UTR-wt compared with the miR-206 mimics and 3'-UTR-mut-cotransfected SiHa cell lines. These findings indicated that the 3'-UTR of BAG3 is a direct target of miR-206.

BAG3 Overexpression Partially Abrogates miR-206-Inhibited Effects

To further elucidate the role of BAG3 in miR-206-induced signaling pathways in the development of CC, we cotransfected the pcDNA3.1(+)-BAG3 plasmids

and miR-206 mimics into SiHa and HeLa cells. We found that BAG3 plasmids effectively improved the expression of BAG3 protein in SiHa and HeLa cells. Furthermore, CCK-8 assay analysis revealed that overexpression of BAG3 facilitated cell proliferation of SiHa and HeLa cells (both $p < 0.01$) (Fig. 6a). Additionally, Transwell assay analysis revealed that BAG3 overexpression in SiHa and HeLa cells with miR-206 mimics promoted SiHa and HeLa cell invasion more than their controls (both $p < 0.01$) (Fig. 6b).

Inhibition of BAG3 Partially Promotes miR-206-Inhibited Effects

To identify the effect of inhibition of BAG3 expression on miR-206-mediated development of CC, the BAG3 siRNAs were cotransfected into SiHa and HeLa cells with miR-206 mimics. We found that BAG3 siRNAs

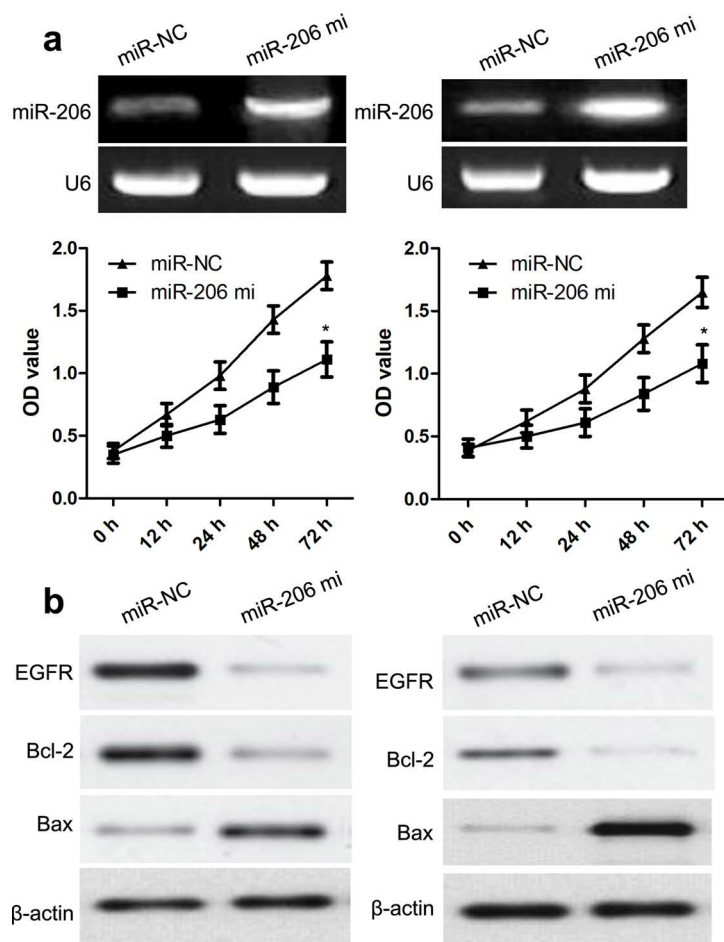


Figure 3. miR-206 inhibits CC cell proliferation. (a) Cells were transfected with miR-206 mimics and identified by qRT-PCR. Cell proliferation was measured using a cell counting kit-8 (CCK-8) assay. SiHa and HeLa cells were transfected with miR-206 mimics or scramble control. (b) Relative EGFR, Bcl-2, and Bax expression in SiHa and HeLa cells was measured after the cells were transfected with miR-206 mimics or negative control (NC) miRNA using Western blot. Results shown are the mean \pm SD of three repeated independent experiments. * $p < 0.01$, compared with miR-NC, one-way ANOVA.

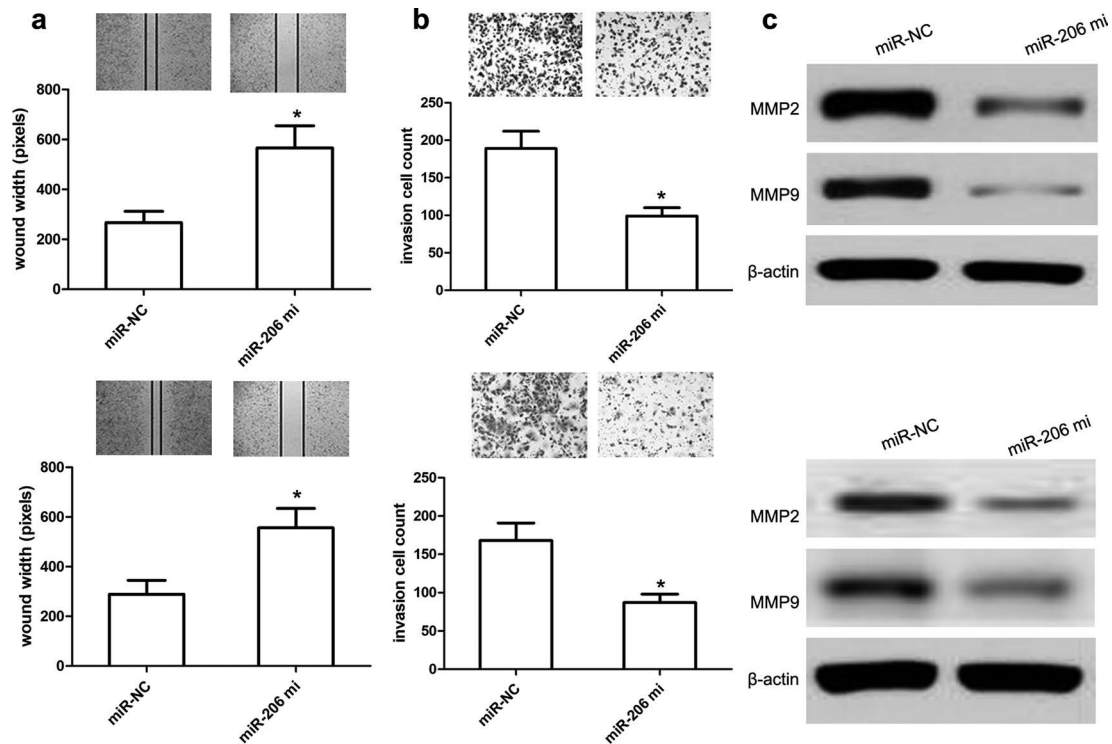


Figure 4. miR-206 reduces CC cell migration and invasion. (a) Wound healing assay performed with SiHa and HeLa cells over 48 h. Cells and wounds were pretreated as described above. Wound healing within the scrape line was recorded every day. Representative scrape lines are shown at day 3; dashed line indicates the margin of the scratch at day 1. (b) Representative fields (magnification: 10×) showing invasive cells after 24-h culture in Matrigel invasion chambers. Panels show SiHa and HeLa cell invasion after transfection with miR-206 mimics or miR-NC. Quantitative analysis of cell invasion experiments demonstrates that miR-206 decreases SiHa and HeLa cell invasion compared to miR-NC. (c) Relative MMP2/9 expressions in SiHa and HeLa cells were measured after the cells were transfected with miR-206 mimics or miR-NC using Western blot. Results shown are the mean \pm SD of three repeated independent experiments. * $p < 0.01$, compared with miR-NC, Student's *t*-test.

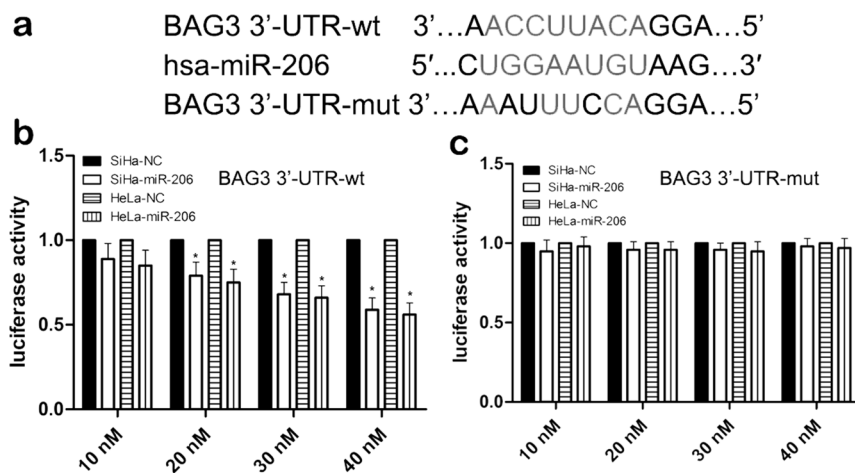


Figure 5. BAG3 is a direct target of miR-206. (a) The wild type (wt) and mutant (mut) of the 3'-untranslated region (3'-UTR) of BAG3 mRNA contain the binding sequences of miR-206. (b, c) The miR-206 mimic inhibited the luciferase activity controlled by wt BAG3-3'-UTR, but miR-206 mimic did not affect the luciferase activity controlled by mut BAG3-3'-UTR in SiHa and HeLa cells. Results shown are the mean \pm SD of three repeated independent experiments. * $p < 0.01$, compared with miR-NC, one-way ANOVA.

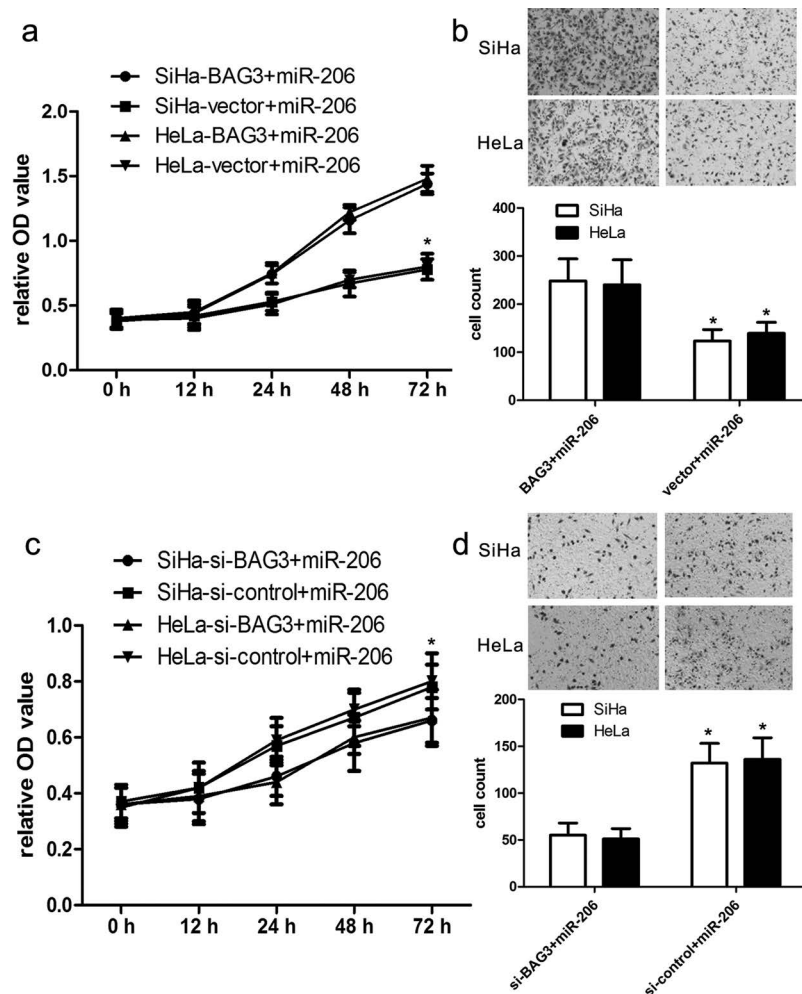


Figure 6. BAG3 modifies the effect of miR-206 on cell proliferation and invasion. (a) The proliferation capacity of miR-206-overexpressing SiHa and HeLa cells was partially improved when cells were transfected with BAG3 plasmids in comparison with miR-NC. (b) The invasion capacity of miR-206-overexpressing SiHa and HeLa cells were effectively improved when cells were transfected with BAG3 plasmids. $*p < 0.01$, versus vector. (c) The proliferation capacity of miR-206-overexpressing SiHa and HeLa cells was partially inhibited when cells were transfected with short interfering BAG3 (si-BAG3) compared with si-control. (d) The invasion capacity of miR-206-overexpressing SiHa and HeLa cells was effectively reduced when cells were transfected with si-BAG3. $*p < 0.01$, versus si-control.

significantly inhibited the expression of BAG3 protein. CCK-8 assay analysis showed that decreased BAG3 expression inhibited SiHa and HeLa cell proliferation (both $p < 0.01$) (Fig. 6c). In addition, Transwell assay analysis showed that BAG3 siRNAs in SiHa and HeLa cells with miR-206 mimics inhibited SiHa and HeLa cell invasion compared with their controls (both $p < 0.01$) (Fig. 6d).

miR-206 Inhibits In Vivo Growth of Engrafted Tumors

In this study, all nude mice that were administered with intratumor injection of miR-206 mimics or miR-NC survived normally after 14 days. First, we demonstrated that miR-206 mimics or miR-NC has no toxic effects on nude mice. Afterward, all engrafted

tumors were resected, weighted, and analyzed. Our data showed that miR-206 mimics or si-BAG3 significantly inhibited the expression of BAG3 compared with the miR-NC or the si-control group, respectively (both $p < 0.01$) (Fig. 7a). Additionally, miR-206 mimics and si-BAG3 commonly repressed the expression of BAG3 protein ($p < 0.01$) (Fig. 7b). According to tumor weight analysis, the weight of the miR-206 mimic-transfected tumor mass was obviously lower than that of their controls ($p < 0.01$) (Fig. 7c). Tumor volume analysis further revealed that the volume of the miR-206 mimic-transfected tumor mass was also obviously smaller than that of their controls at 14 days ($p < 0.01$) (Fig. 7d), suggesting that miR-206 mimics inhibited the growth of SiHa-engrafted tumors.

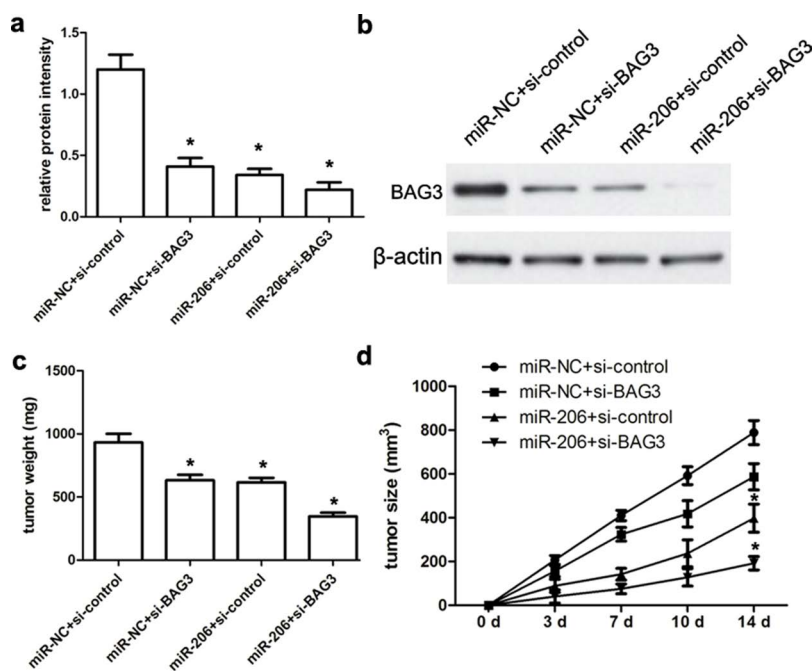


Figure 7. miR-206 inhibits the growth of SiHa-engrafted tumors. (a, b) The expression of BAG3 protein was detected using Western blot assay. (c, d) Tumor size was measured every week using a caliper. At 14 days after cell injection, animals were sacrificed and xenograft tumors were excised and weighed. We identified that miR-206 mimics could repress the SiHa-engrafted tumor growth and volume compared with miR-NC-transfected SiHa-engrafted tumors. Results shown are the mean \pm SD of three repeated independent experiments. * $p < 0.01$, compared with miR-NC, one-way ANOVA.

DISCUSSION

It has been reported that BAG3 signaling pathway plays an important role in many types of tumors and is involved in many biological processes, such as stem cell migration and invasion, and inflammation induction¹⁸. In addition, the BAG3 signaling pathway was also implicated in the progression of many tumors, including cell growth and metastasis^{19,20}. miRNAs were identified to be downregulated in many types of tumors and could mediate tumorigenesis by targeting their tumor suppressor genes¹³. However, the expression and the role of miR-206 in CC have not been clearly reported until now. In our study, we identified that the expression of BAG3 is involved in the initiation and progression of human CC.

First, our study demonstrated that the expression of miR-206 was obviously decreased in CC tissues compared with that in matched normal cervical epithelial tissues. However, BAG3 mRNA and protein showed much higher expression in CC tissues than in matched normal cervical epithelial tissues. Consistent with these findings, Xiao et al. also found that the expression of miR-206 was obviously decreased in clear cell renal cell carcinoma, and miR-206 functions as a novel cell cycle regulator and tumor suppressor in clear cell renal cell carcinoma²¹. We

further demonstrated that miR-206 overexpression plays a suppressive role in cancer cell proliferation, migration, and invasion. Finally, we used bioinformatics analysis and transfection assay to validate that miR-206 had a tumor suppressor effect via downregulation of the target gene BAG3. To our knowledge, this is the first study to explore the posttranscriptional regulation of BAG3 by miR-206 in human CC.

A recent study indicated that EGF and its receptor EGFR play an essential role in human CC, which further mediates CC cell proliferation, apoptosis, and metastasis²². Additionally, matrix metalloproteinases are reported to be implicated in cervical cell invasion, metastasis, and angiogenesis and can cause dynamic alterations of CC cells²³. In the present study, our work revealed that SiHa and HeLa cells transfected with miR-206 mimics indeed decreased the expression of EGFR, MMP2, and MMP9 proteins more than their controls, indicating that miR-206 reduced CC cell proliferation and invasion probably via inhibition of EGFR, MMP2, and MMP9 expression. These effects need to be further identified in the future.

In conclusion, our work demonstrated that miR-206 inhibits cell proliferation, migration, and invasion by targeting BAG3 in human CC. Therefore, the miR-206–BAG3 pathway may be recommended as a useful and effective therapeutic target for the treatment of CC patients.

ACKNOWLEDGMENT: The authors are thankful to other members in their laboratory for their suggestions. The authors declare no conflicts of interest.

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