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ORIGINAL RESEARCH

RETRACTED ARTICLE: miR-136 targets MIEN1 and involves the metastasis of colon cancer by suppressing epithelial-to-mesenchymal transition

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Abstract: MIEN1 is a novel oncogene, and it involves tumor progression in various cancer types, including colon cancer. However, the definite molecular mechanisms of MIEN1 in colon cancer progression remain to be completely elucidated. In the present study, bioinformatics prediction showed that miR-136 could be an upstream regulator of MIEN1; a luciferase assay and Western blot assay revealed that miR-136 negatively regulates MIEN1 expression via directly targeting its 3′-untranslated region sequence. Moreover, a functional assay using wound healing and transwell invasion showed that overexpressed miR-136 inhibited cell migration and invasion, and overexpression of MIEN1 partly rescued the above-mentioned effects of miR-136 in colon cancer cells. Additionally, a clinical sample assay showed that miR-136 expression was generally downregulated in colon cancer tissue, which was inversely correlated with MIEN1 expression. Furthermore, we found that miR-136 suppressed the Akt/NF-κB signaling pathway and epithelial-to-mesenchymal transition in colon cancer. These results suggest that miR-136, as a tumor suppressor, acts in tumor metastasis by suppressing MIEN1 expression in colon cancer, providing a novel target for the treatment of colon cancer.

Keywords: colon cancer, miR-136, MIEN1, migration, invasion

Introduction

Colon cancer is one of the most frequent causes of cancer death worldwide.[1] Despite recent advances of diagnosis and treatment strategies in clinical and experimental oncology,[2] the mortality rate of colon cancer remains high. Therefore, it is urgent to investigate the molecular mechanisms underlying the progression of colon cancer and to identify novel therapeutic targets for early diagnosis and treatment of colon cancer.

MIEN1, a novel oncogene located in the 17q12–21 region of the human chromosome,[3] is often dysregulated in various cancer types.[4–6] MIEN1 expression is upregulated in different stages and grades of prostate cancer phenotypes and involves tumor progression of prostate cancer.[3,7,8] MIEN1 was also upregulated and can be used as a novel breast cancer biomarker in patients with metastatic progression to lung and liver, and siRNA-mediated knockdown of MIEN1 induces apoptosis of breast cancer cells.[4,9] Recently, MIEN1 was reported to be overexpressed in colorectal cancer tissue, and MIEN1 expression level was closely associated with tumor serosal invasion, lymph node metastasis, and an advanced Dukes stage.[10] However, the role of MIEN1 in colon cancer progression remains unknown.

MicroRNA (miRNA) is an abundant group of small noncoding RNA (with about 22 nucleotides); it controls expression of the target gene by binding to the 3′ untranslated

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region (UTR) of their target genes and plays an important role in a variety of biological processes, including cell proliferation, apoptosis, differentiation, invasion, migration, and so on.[11–14] A growing number of studies have found that miRNAs are dysregulated in a variety of cancer types, and that these play a critical role in tumorigenesis.[15–20] Recent studies demonstrated that some miRNAs are critical regulators in the development and progression of cancer, including colon cancer.[21–23] Therefore, identification of novel miRNAs that are involved in colon cancer progression may contribute to the development of prognostic biomarker and therapeutic strategy for colon cancer.

miR-136 has been reported to be dysregulated in various cancer types and involves tumor progression.[24] It was overexpressed in murine lung cancers via miRNA microarray expression profiling.[25] Moreover, upregulated miR-136 was also observed in human non-small-cell lung cancer (NSCLC).[26] miR-136 also functions as a tumor suppressor and suppresses mesenchymal metastasis in triple-negative breast cancer.[27] However, the expression and biological function of miR-136 in colon cancer remain to be established.

In this study, we for the first time identified MIEN1 as a direct target of miR-136, which revealed the deregulated expression of miR-136 in colon cancer and investigated the function of miR-136 on cell migration and invasion in the progression of colon cancer. In conclusion, miR-136 acts as a tumor suppressor and may serve as a potential therapeutic target in colon cancer.

Materials and methods

Human tissue specimens

Paired tissue specimens of colon cancer and matched normal tissues were obtained, with informed consent from 30 colon cancer patients between 2010 and 2015 at the People's Hospital of Weifang. The tissues obtained from the surgery were stored in liquid nitrogen immediately until use. The Institute Research Medical Ethics Committee of People's Hospital of Weifang granted approval for this study.

Cell culture and transfection

Human colon cancer cell lines (SW-480 and SW-620) purchased from ATCC were grown in Dulbecco's Modified Eagle's Medium (DMEM) supplemented with 10% (vol/vol) fetal bovine serum and 2 mM of L-glutamine. Cultures were maintained at 37°C in a humidified atmosphere with 5% CO_2.

SW-480 and SW-620 cells were seeded in 12-well plates and transiently transfected with miR-136 mimic, miR-136 inhibitor, mimic negative control (mimic control), and inhibitor negative control (inhibitor control) sequences using Lipofectamine 2000 (Thermo Fisher Scientific, Waltham, MA, USA). SW-480 and SW-620 cells were contransfected with miR-136 mimic and MIEN1 plasmid. The cells were harvested at 24 h for further assay.

Quantitative real-time polymerase chain reaction

We used Trizol solution (Sigma-Aldrich, St Louis, MO, USA) to extract RNA from cells and human colon cancer tissue, which was then reverse-transcripted to obtain complementary DNA (cDNA; PrimeScript RT Reagent kit, Takara, Japan) according to the manufacturer's instructions. The expression levels of miRNA and mRNA were then detected by SYBR Premix Ex Taq II (Takara, Japan) using the CFX96™ Real-Time PCR Detection System (Bio-Rad Laboratories, Hercules, CA, USA). The primer sequences of miR-136 and MIEN1 were described previously.[26,28–30]

Luciferase reporter gene assays

The 3′-UTR of MIEN1 was amplified and subcloned into pGL3 luciferase promoter vector (Promega, Madison, WI, USA), and the mut-MIEN1 was built by mutating the binding site of miR-136 on the 3′-UTR of MIEN1 as previously described.[31] The MIEN1/pGL3 or mut-MIEN1/pGL3 was cotransfected with miR-136 mimics or inhibitors into HEK293 cells. The cells were harvested at 48 h, and a dual-luciferase reporter assay kit (Promega) was used to detect the relative luciferase activity. All experiments were performed at least three times.

Western blotting analysis

We used radioimmunoprecipitation assay (Thermo Fisher Scientific) to get the whole cell extracts, and then, the protein samples were separated by sodium dodecyl sulfate–polyacrylamide gel electrophoresis (10%) and incubated with polyclonal (rabbit) anti-MIEN1, anti-Akt, anti-p-Akt, and anti-p-NF-κB antibody (Santa Cruz Biotechnology, Santa Cruz, CA, USA) overnight at 4°C, and with goat anti-rabbit IgG (Pierce, Rockford, IL, USA) secondary antibody for 1 h at room temperature. ECL detection systems (SuperSignal West Femto, Pierce, Rockford, IL, USA) were used for detection.

Invasion and migration assay

A transwell invasion assay was used here to detect invasion capability of NSCLC cells. Cells were transferred to the upper chamber and incubated at 37°C containing 5% CO_2. Then, we observed the procedures of cellular growth at 72 h. The transwell migration chambers were used to evaluate cell invasion.

A wound healing assay was also used to detect cell migration capability as described previously.[32]

Statistical analysis

Each experiment was repeated at least three times. Data were shown as mean ± standard deviation (SD) and analyzed using SPSS 19.0. Statistical comparisons between groups were made using Student's *t*-test and a two-tailed test, where $P<0.05$ was considered to be statistically significant.

Results

MIEN1 is a direct target of miR-136 in colon cancer

In this study, we used TargetScan, PicTar, and miRanda and found that the 3′-UTR of MIEN1 has a binding site for miR-136 (Figure 1A). Next, we used a luciferase reporter assay to confirm this prediction. As shown in Figure 1B, miR-136 mimics significantly decreased the luciferase activity of the wide-type MIEN1/pGL-3, whereas miR-136 inhibitors observed reverse effects. Moreover, both miR-136 mimics and miR-136 inhibitors failed to affect the luciferase activity of the mutant-type MIEN1/pGL-3.

To further characterize the effects of miR-136 on MIEN1 expression, we transfected the mimics or inhibitors of miR-136 into SW-480 and SW-620 cells to overexpress or knockdown miR-136, and then analyzed the MIEN1 expression levels by quantitative real-time polymerase chain reaction (qRT-PCR) and Western blot assay. As shown in Figure 1B, miR-136 mimics significantly decreased MIEN1 expression at both the mRNA and protein levels in colon cancer cells. In contrast, miR-136 inhibitors increased MIEN1 expression in colon cancer cell lines. These data

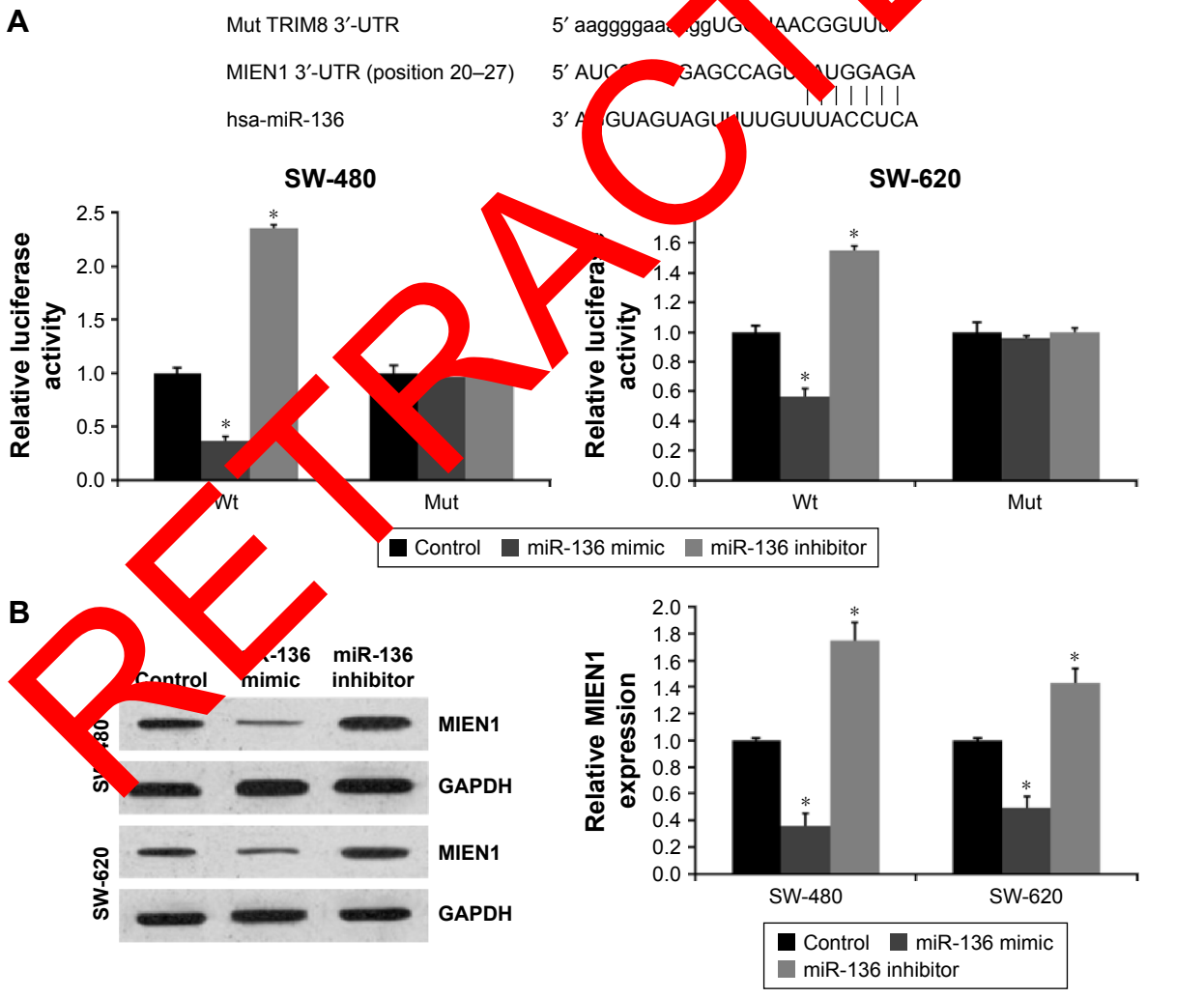

Figure 1 miR-136 represses MIEN1 expression by targeting MIEN1 3′-UTR in colon cancer cells.
Notes: (**A**) Sequence alignment of miR-136 and 3′-UTR of MIEN1 using mirco-RNA.org. Luciferase reporter assay. SW-480 and SW-620 cells were transiently cotransfected with Wt/Mut 3′-UTR with miRNAs as indicated. (**B**) The effects of miR-136 on the expression of MIEN1 at both protein and mRNA levels in SW-480 and SW-620 cells. Data are presented as mean ± SD from three independent experiments. *$P<0.01$ vs control group.
Abbreviations: miRNA, microRNA; SD, standard deviation; UTR, untranslated region; Wt, wild type; Mut, mutation type.

demonstrated that miR-136 suppressed MIEN1 expression by directly targeting the 3′-UTR of MIEN1.

miR-136 is negatively associated with MIEN1 expression in colon cancer

Furthermore, we analyzed the expression pattern of miR-136 and MIEN1 in colon cancer tissues. A qRT-PCR assay was used to detect the expression levels of miR-136 and MIEN1 mRNA in 30 pairs of colon cancer tissues and matched normal colon tissues. As shown in Figure 2A and B, the expression level of miR-136 was markedly decreased in colon cancer tissues compared with the corresponding normal tissue. Next, we analyzed the clinicopathological significance of miR-136 in colon cancer tissues (Table 1). Our results showed that there was no significant association between miR-136 expression and the parameters, including age and gender, but we found that the miR-136 levels were negatively associated with tumor size, lymph node invasion, TNM stage, and metastasis. Consistent with previous studies,[10] we also confirmed that MIEN1 was overexpressed in colon cancer tissue samples. Additionally, we investigated the relationship of miR-136 expression with MIEN1 expression (Figure 2C). As expected, miR-136 expression was negatively correlated with that of MIEN1 in colon cancer samples (R=–0.739), suggesting that miR-136 negatively regulated MIEN1 expression.

miR-136 represses the invasion, migration, and EMT of colon cancer cells by inhibiting MIEN1

To further analyze the function of miR-136 and MIEN1 in colon cancer progression, we upregulated miR-136 and MIEN1 to detect the migratory and invasive capability of colon cancer cells. We first used miR-136 mimics to upregulate miR-136 expression, and miR-136 inhibitors to downregulate miR-136 expression and transfected miR-136 mimics with MIEN1 to rescue MIEN1 expression (Figure 1A and B) as shown in Figure 2C, the wound healing assay showed that knockdown of miR-136 by miR-136 inhibitors promoted cell migration in both SW-480 and SW-620 cells. The overexpressed miR-136 by miR-136 mimics in both SW-480 and SW-620 cells obviously inhibited cell migration,

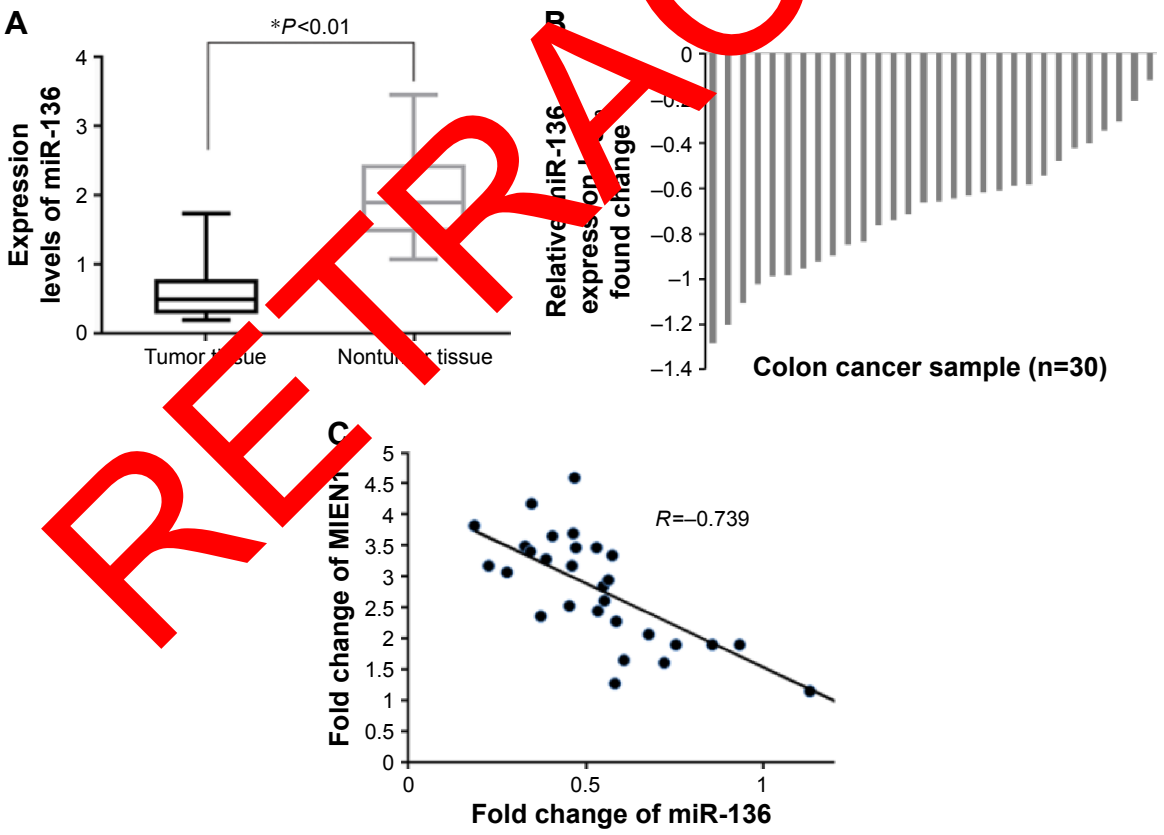

Figure 2 miR-136 expression in colon cancer.

Notes: (**A**) Statistical analysis of relative miR-136 expression levels in colon cancer and compared normal tissues. (**B**) The expression of miR-136 in 30 pairs of colon cancer tissues and compared normal tissues was detected by qRT-PCR. Data are shown as $\log_{10}$ of relative ratio change of colon cancer tissues relative to the adjacent normal tissues. Data are presented as mean ± SD from three independent experiments. *P<0.01 vs normal tissues. (**C**) Correlation of miR-136 levels with MIEN1 mRNA levels was examined by qRT-PCR in 30 cases of colon tissues. Statistically significant differences are indicated: *P<0.01 vs paired non-tumorous tissues.

Abbreviations: SD, standard deviation; qRT-PCR, quantitative real-time polymerase chain reaction.

Table 1 Relationship between miRNA-136 and clinicopathological parameters in 30 colon cancer patients

Clinicopathological parameters	All cases	miR-136 expression		*P*-value
		High	Low	
Age (years)				0.224
<60	18	9	9	
≥60	12	6	6	
Gender				0.385
Male	16	7	9	
Female	14	8	6	
Tumor size (cm)				0.004
≤5	12	5	7	
>5	18	5	13	
Degree of differentiation				<0.01
Well and moderate	19	7	12	
Poor	9	6	3	
Lymph node invasion				<0.01
Absent	12	8	4	
Present	18	7	11	
TNM stage				<0.01
Stage I+II	13	9	4	
Stage III+IV	17	6	11	
Metastasis				<0.01
No	16	6	10	
Yes	14	9	5	

which was rescued by overexpression of MIEN1. Consistent with the above-mentioned results, transfection of miR-136 mimics significantly decreased the invasion capabilities of colon cancer cells, which was rescued by overexpression of MIEN1, while an miR-136 inhibitor showed the opposite effect of miR-136 mimics (Figure 3D). These data strongly suggested that miR-136 inhibits the migratory and invasive ability of colon cancer cells by targeting MIEN1.

The epithelial-to-mesenchymal transition (EMT) is crucial to cancer progression and metastasis. In this study, to reveal the potential of miR-136 in the EMT process, we detected the expression levels of E-cadherin, N-cadherin, and Vimentin (EMT-related proteins) using a Western blot assay. As shown in Figure 3E, miR-136 mimics evidently induced E-cadherin expression in the miR-136 mimics group, while the inhibition of miR-136 mimics was reversed by contransfecting with MIEN1 in colon cancer cells. Moreover, miR-136 remarkably reduced N-cadherin and vimentin expression, which was attenuated by contransfecting with MIEN1. These indicated that miR-136 represses EMT by targeting MIEN1.

miR-136 suppressed the Akt/NF-κB signaling pathway in colon cancer

Previous studies suggest that MIEN1 plays an important regulatory role in phosphorylation of AKT,[6] which subsequently activated the NF-κB signaling pathway.[5] Here, we speculated that miR-136 might regulate the expression of downstream effectors of MIEN1. As shown in Figure 4A–C, miR-136 evidently decreased p-AKT and p-NF-κB protein expression levels in colon cancer. Conversely, miR-136 inhibitors-induced miR-136 knockdown increased p-AKT and p-NF-κB expression.

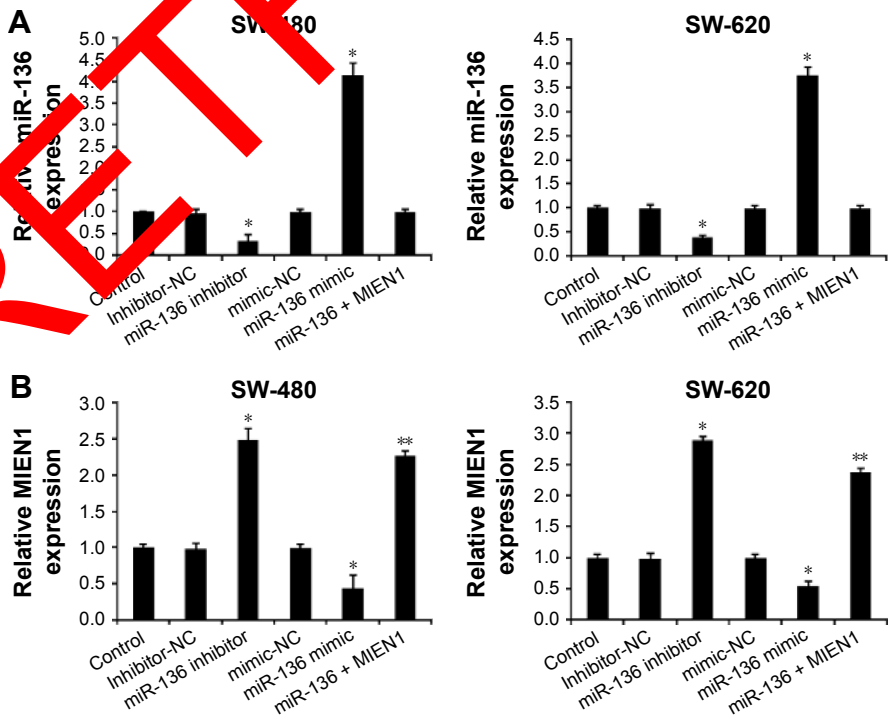

Figure 3 (*Continued*)

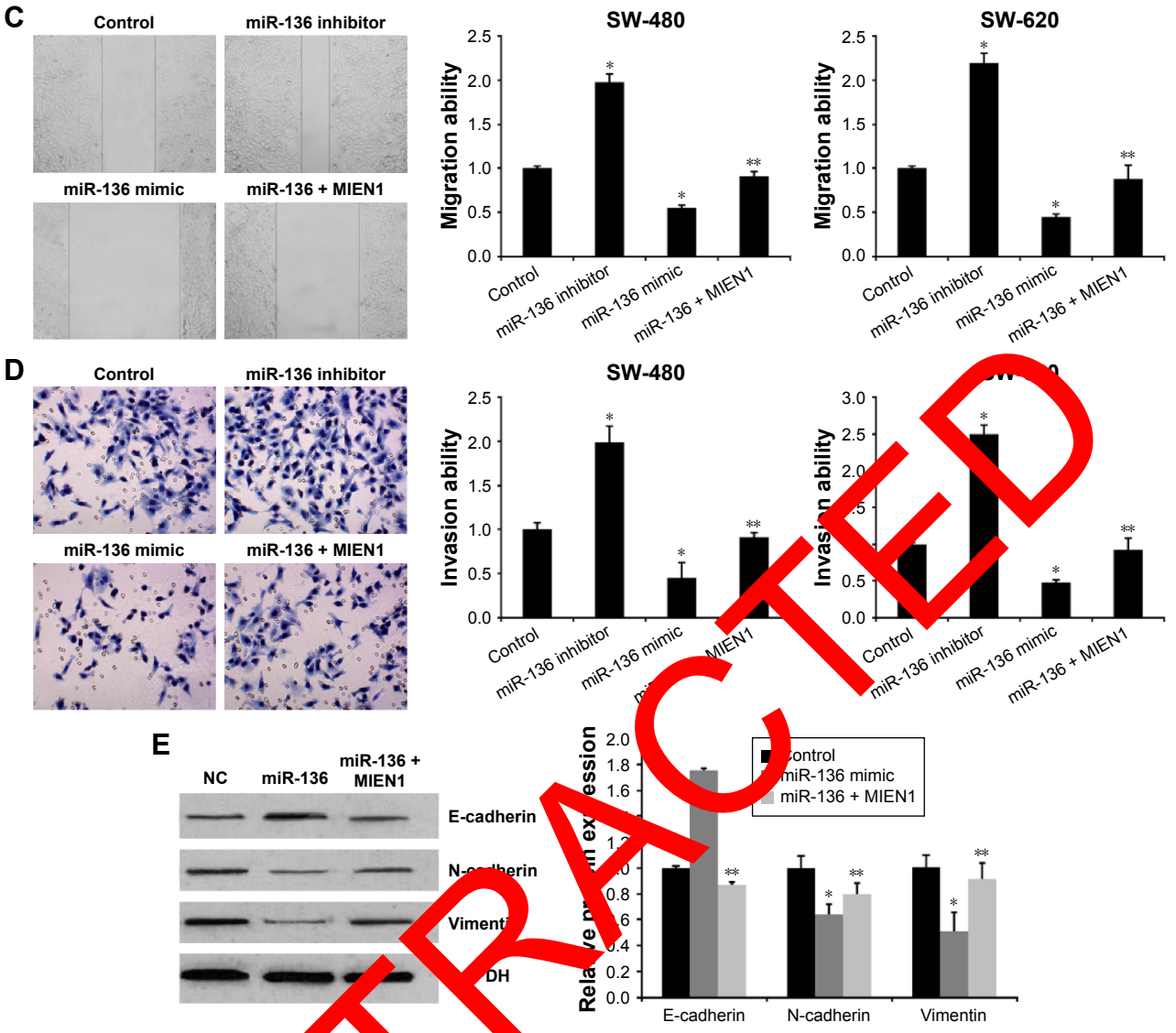

Figure 3 miR-136 represses the invasion, migration, and EMT of colon cancer cells by inhibiting MIEN1.
Notes: (**A**) A qPCR assay revealed the effects of miR-136 mimic, miR-136 inhibitor, and ectopic MIEN1 on miR-136 expression in colon cancer cells. (**B**) qPCR assay revealed the effects of miR-136 mimic, miR-136 inhibitor, and ectopic MIEN1 on MIEN1 expression in colon cancer cells. Data are presented as mean ± SD from three independent experiments. *$P<0.01$ vs control group, mimics-NC group and inhibitor-NC group. (**C**) Wound healing assay revealed the effects of miR-136 and MIEN1 on cell migration in colon cancer cells. (**D**) Transwell invasion assay revealed the effects of miR-136 and MIEN1 on cell migration in colon cancer cells. (**E**) Western bolt assay revealed the effects of miR-136 and MIEN1 on EMT in colon cancer cells. Data are presented as mean ± SD from three independent experiments. *$P<0.01$ vs control group, **$P<0.01$ vs miR-136 mimic group.
Abbreviations: EMT, epithelial-to-mesenchymal transition; miRNA, microRNA; NC, native control; SD, standard deviation; UTR, untranslated region; qPCR, quantitative real-time polymerase chain reaction.

Discussion

MIEN1 located in the 17q12 region of the human chromosome, next to the Her-2/neu loci,[3] has reported to be dysregulated in various cancer types.[4–6] For example, MIEN1 was reported to be overexpressed in colorectal cancer tissue and closely associated with tumor serosal invasion, lymph node metastasis, and an advanced Dukes stage.[10] However, only a few studies have investigated the potential molecular mechanism of MIEN1 in colon cancer progression. Here, we for the first time demonstrated that MIEN1 was a direct target of miR-136, which is involved in colon cancer invasion, migration, and EMT by repressing MIEN1 expression.

Many recent studies have demonstrated the critical role of miRNAs in tumorigenesis and progression via regulating target gene expression.[33,34] MIEN1 as a novel oncogene was also reported to be regulated by miRNAs in several cancer types.[8,30] Here, bioinformatics databases predict that miR-136, as an upstream miRNA, binds to the 3′-UTR of MIEN1 directly, which was also confirmed by luciferase assay. Moreover, miR-136 mimics significantly inhibited

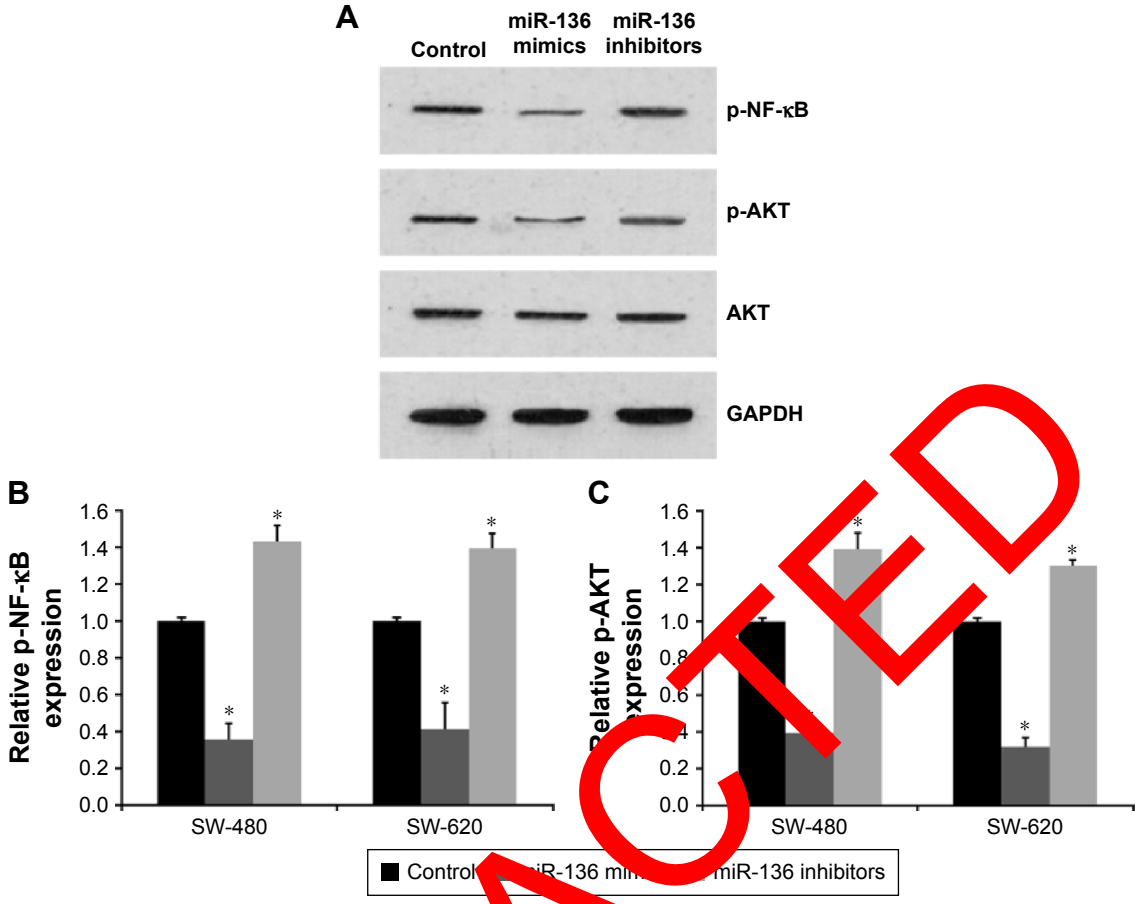

Figure 4 miR-136 affects the AKT/NF-κB signaling pathway in colon cancer cells.
Notes: (**A**) Expression of the downstream targets of MIEN1 transfected with miR-136 mimics or inhibitors in colon cancer cells detected by Western blotting. qPCR showing the expression of p-AKT (**B**) and p-NF-κB (**C**) of 95D transfected with miR-136 mimics or inhibitors. *$P<0.01$ vs control group.
Abbreviation: qPCR, quantitative real-time polymerase chain reaction.

MIEN1 expression, whereas miR-136 inhibitors significantly increased MIEN1 expression.

miR-136 functions as a regulator, dysregulated in various cancer types, and involves tumor progression.[24] MiRNA microarray expression profiling showed that miR-136 was prominently overexpressed in murine lung cancers.[25] miR-136 was also reported to be significantly upregulated in human SCLC primary tumors.[26] These studies demonstrated miR-136 as an oncogene. However, other study showed that miR-136 functions as a tumor suppressor by suppressing mesenchymal invasion and metastasis in triple-negative breast cancer.[27] Therefore, the expression and role of miR-136 are controversial, as they vary in different types of cancer. Here, we found that the expression level of miR-136 was markedly decreased in colon tissues, and its expression level was negatively associated with tumor size, lymph node invasion, TNM stage, and metastasis in the clinicopathological characteristic assay, indicating the important role of miR-136 in the progression of colon cancer. Additionally, these results were further confirmed by statistical analysis that the expression level of miR-136 was negative with that of MIEN1 in colon cancer. Similarly, Yang et al showed that miR-136 may play a tumor-suppressive role by repressing EMT via targeting Smad2 and Smad3 in lung adenocarcinoma.[35]

Next, the functional assay showed that miR-136 mimics decreased cell invasion, migration, and EMT. In addition, the Akt/NF-κB signaling pathway, the downstream regulator of MIEN1, was regulated by miR-136. miR-136 repressed colon cancer invasion and migration, which was rescued by overexpressed MIEN1.

Taken together, this study demonstrated that miR-136 suppressed colon cancer cell invasion, migration, and EMT progression by directly targeting MIEN1. Moreover, the expression of miR-136 was downregulated in colon cancer tissues, and miR-136 expression level was negatively associated with tumor size, lymph node invasion, and TNM stage of colon cancer. In conclusion, we demonstrated the regulatory mechanism underlying MIEN1 upregulation in

colon cancer and indicated the miR-136/MIEN1 pathway as new potential therapeutic targets for colon cancer.

Disclosure

The authors report no conflicts of interest in this work.

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