

UCA1 Regulates the Growth and Metastasis of Pancreatic Cancer by Sponging miR-135a

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Pancreatic cancer (PC) is a devastating malignant disease with a poor prognosis. This study aimed to investigate the role of urothelial carcinoma associated 1 (UCA1) in the progression of PC. Our results revealed that long noncoding RNA (lncRNA) UCA1 was overexpressed in PC tissues compared with adjacent histologically normal tissues. A downregulated level of UCA1 was also detected in five human PC cell lines (SW1990, BxPC-3, MiaPaCa-2, PANC-1, and CAPAN-1) compared with normal pancreatic duct epithelial HPDE cells. The proliferation of PC cells was inhibited after UCA1 was suppressed by a lentiviral vector. The cell apoptosis rate was largely promoted by downregulating UCA1. Further research revealed that microRNA (miRNA)-135a is a direct target of UCA1. The expression of miR-135a was decreased in PC tissues and cell lines compared with control groups. In addition, the decreased level of miR-135a was elevated by adding miR-135a mimic in SW1990 cells transfected with lncRNA UCA1. Similarly, an upregulated level of miR-135a was downregulated by adding miR-135a inhibitor in SW1990 cells transfected with UCA1 siRNA. Luciferase activity assay further confirmed the targeting relationship between UCA1 and miR-135a. Moreover, miR-135a reversed the effect of UCA1 on cell apoptosis rate and cell viability in SW1990 cells. The migration and invasion capacities of PC cells were suppressed by UCA1. siRNA was then enhanced by the miR-135a inhibitor. In vivo, UCA1 siRNA effectively suppressed tumor growth and the expression of migration markers. Taken together, our research revealed that UCA1 works as an oncogene by targeting miR-135a. The UCA1–miR-135a pathway regulated the growth and metastasis of PC, providing new insight in the treatment of PC.

Key words: Urothelial carcinoma associated 1 (UCA1); miR-135a; Pancreatic cancer (PC); Growth; Metastasis

INTRODUCTION

Pancreatic cancer (PC) is a highly aggressive malignant tumor with a characteristic of hepatic metastasis. About 43,000 new cases and a similar number of deaths (36,800) are diagnosed in the US every year^{1,2}. Pancreatic ductal adenocarcinoma (PDAC) accounts for more than 90% of PCs³. Although many cancer therapeutics have been tried, the median survival of PC is still less than 6 months⁴. Treatment of PC is largely ineffective due to a lack of reliable early detection markers and effective therapies, leaving PC with the fourth highest death rate among cancers in the US⁵. Thus, it is urgent to get a better understanding of the molecular mechanism of PC in order to develop an effective diagnosis and treatment strategy.

In recent years, accumulating evidence has indicated that a group of long noncoding RNAs (lncRNAs) play an essential regulatory role in a series of biological processes, such as cell proliferation, differentiation, apoptosis, and

cancer metastasis^{6,7}. Urothelial carcinoma associated 1 (UCA1), located on human chromosome 19, is a kind of lncRNA and was first explored in human bladder cancer^{8,9}. Overexpressed UCA1 in bladder cancer was proven to promote cell proliferation and migration and enhance drug resistance¹⁰. In addition, upregulated UCA1 has been reported to exert a carcinogenic effect in several other cancers such as breast cancer¹¹, non-small cell lung cancer¹², gastric cancer¹³, colorectal cancer¹⁴, and hepatocellular carcinoma¹⁵. A recent study mentioned that UCA1 promoted tumorigenesis in PC¹⁶. However, we are still far from a complete understanding of the possible mechanism of UCA1 in PC tumorigenesis and metastasis.

MicroRNAs (miRNAs) have been identified to play a crucial role in regulating different cellular processes in cancers by binding its seed sequence to the 3'-untranslated region (3'-UTR) of specific target mRNAs^{17,18}. Recently, many studies have revealed the potential role of miRNAs

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in diagnosis, prediction, and prognosis of PDAC, including miR-21¹⁹, miR-194²⁰, miR-217²¹, and miR-135a²². miR-135a acts as a tumor suppressor in the cell proliferation and clonogenicity of PDAC, but few studies have mentioned the interaction between miR-135a and lncRNAs in PDAC.

In this study, we aimed to explore the mechanism of UCA1 in the metastasis of PC. A high expression of UCA1 was detected in PC tissues and cell lines. The synthesized small interfering RNA (siRNA) UCA1 inhibited the migration and invasion of PC in vivo and in vitro. miR-135a was identified as a direct target of UCA1 and miR-135a and counteracted the role of UCA1 in facilitating proliferation and inhibiting apoptosis in SW1990 and PANC-1 cells. The UCA1-miR-135a pathway may serve as a site for exploring new therapy for PC.

MATERIALS AND METHODS

Clinical Sample Collection

Fifty pairs of human PC and adjacent normal tissues were collected from the Affiliated Shengjing Hospital of China Medical University. The specimens were preserved in liquid nitrogen after removal and stored at -80°C until use. All the methods in our study were in line with the licensed guidelines, and all the experimental protocols were approved by the clinical research ethics committees of the Affiliated Shengjing Hospital of China Medical University.

Cell Line Culture

Five human PC cell lines (SW1990, BxPC-3, MiaPaCa-2, PANC-1, and CAPAN-1) and normal human pancreatic duct epithelial (HPDE) cells were purchased from the American Type Culture Collection (Manassas, VA, USA). All cell lines were maintained routinely in RPMI-1640 media (Cat. No. 11875-093; Gibco) supplemented with 10% fetal bovine serum (FBS; Life Technologies, Inc., Grand Island, NY, USA) and grown at 37°C in a 5% CO₂ cell culture incubator.

Quantitative Reverse Transcription Polymerase Chain Reaction (qRT-PCR)

Total RNA was extracted from tissue specimens and cell lines using the TRIzol reagent (Invitrogen, Carlsbad, CA, USA) according to the protocol. RNA was reverse transcribed into cDNA using the SuperScript VILO cDNA Synthesis Kit (Life Technologies). qRT-PCR was performed on a Fast Real-Time PCR 7500 System according to the manufacturer's protocol (Applied Biosystems, Foster City, CA, USA). The RT-PCR primers for UCA1 and miR-135a were purchased from GeneCopoeia (San Diego, CA, USA). The specific primers were as follows: UCA1, 5'-GACCCTACCCGGTCATTTATAG-3' (forward)

and 5'-CTGATGGGCATGGCTTTATTC-3' (reverse); miR-135a, 5'-CCCAGGGTCTGGTGCAGGAGA-3' (forward) and 5'-CAGGGGCTGAGCGGTGAGGG-3' (reverse). The expression levels of UCA1 and miR-135a were normalized by the level of the internal control β -actin, respectively. Fold change of UCA1 or miR-135a was calculated by the comparative 2^{- $\Delta\Delta$ Ct} method.

Northern Blotting

The expression levels of UCA1 and miR-135a in PC tissues, adjacent normal tissues, PC cell lines (SW1990, BxPC-3, MiaPaCa-2, PANC-1, and CAPAN-1), and normal HPDE cells were further determined by Northern blot assay. Northern blot analysis was performed as previously described²³. β -Actin (Beyotime, Shanghai, P.R. China) was used as an endogenous reference.

Cell Transfection

Mimics and inhibitors specific for miR-135a and siRNA fragments targeting UCA1 were designed and purchased from Invitrogen. The mock and fragments were designed as the negative control of miR-135a and UCA1, respectively. The SW1990 and PANC-1 cells were seeded into 24-well plates at 1×10^5 cells/well. UCA1 siRNA and UCA1 scramble were amplified using Primer STAR premix (TaKaRa, Dalian, P.R. China) and cloned into lentivirus plasmid according to the manufacturer's protocol. SW1990 and PANC-1 cells were transfected with recombinant lentivirus. Mimics and inhibitors specific to miR-135a and mock were transfected into SW1990 and PANC-1 cells using Lipofectamine 2000 (Invitrogen). Cells were harvested for subsequent experiments after transfection for 48 h.

Cell Viability Analysis

Cell viability was identified using a methylthiazole-tetrazolium (MTT) assay. Briefly, SW1990 and PANC-1 cells were seeded into 96-well plates (3,000 cells/well). MTT dye solution (20 μ l; 5 mg/ml; Sigma) and 150 μ l of dimethyl sulfoxide (DMSO) were added to each well, and incubation was continued for 4 h. Finally, the OD was determined with a microplate spectrophotometer (ELx800; Bio-TEK, Winooski, VT, USA) at 570 nm. Experiments were done in triplicate.

Tumor Sphere Formation Assay

SW1990 and PANC-1 cells were transfected with UCA1 scramble or UCA1 siRNA, respectively. Single-cell suspension was plated into 24-well ultra-low attachment plates (Corning Inc., Tewksbury, NY, USA) in serum-free media: low-glucose (1 g/L) DMEM supplemented with L-glutamine, sodium pyruvate, 100 U/ml penicillin/streptomycin (Wisent Inc., Quebec, Canada), 20 ng/ml basic fibroblast growth factor, 20 ng/ml epidermal growth factor, 4 μ g/ml heparin calcium salt (Fisher,

Pittsburgh, PA, USA), and 1× B27 (Invitrogen, Grand Island, NY, USA). Spheres were observed after 14 days using microscopy and were dissociated by trypsinization every 5–7 days and split to 1:3 ratio. Sphere sizes were measured by ImageJ software. Tumor spheres were stained in DiI cell-labeling solution (5 µl/ml; Thermo Fisher Scientific, Inc., Waltham, MA, USA).

Flow Cytometric Analysis of Cell Apoptosis

Cells in each group were harvested at 48 h posttransfection. For the apoptosis analysis, cells were resuspended (1×10^6) and fixed, and then stained using the annexin V–fluorescein isothiocyanate (FITC) and PI apoptosis detection kits (Annexin-V–FITC Apoptosis Detection Kit; eBioscience). The apoptosis rates were then analyzed using the FACSCaliber II sorter and CellQuest FACS system (BD Biosciences, San Jose, CA, USA) according to the manufacturer's protocol. The flow cytometry analysis was repeated at least three times.

Wound Healing Assay

To determine the effect of UCA1 siRNA on the migration of SW1990 and PANC-1 cells in vitro, cells transfected with UCA1 siRNA or UCA1 scramble were seeded at 2.5×10^5 cells/well into six-well plates and grown to about 90% confluence after 24 h. Medium was removed, and cell monolayers were scratched off with a sterile P200 micropipette tip. The destroyed cells were washed with PBS three times, and cells were then cultured in serum-free medium for 24 h at 37°C. The wound areas were photographed with a phase-contrast microscope (Leica DM IL; Leica Microsystems, Wetzlar, Germany) equipped with a digital camera (Leica DFC300FX).

Transwell Invasion Assay

For the invasion assays, SW1990 and PANC-1 cells pretransfected with UCA1 siRNA or UCA1 scramble (2×10^4 cells/well) were placed in Transwell cell culture chambers (8-mm pore size; Merck Millipore Corp, Billerica, MA, USA) coated with Matrigel (Becton-Dickinson, NJ, USA). Cell suspension was placed in the upper chamber of the insert, and the lower chamber was filled with complete medium (containing 20% FBS) as a chemoattractant. Cells were incubated for another 24 h. Noninvading cells on the upper membranes were removed, and the invasive cells were fixed in 95% ethanol and stained with hematoxylin. Cells were examined, photographed, and quantified under a light microscope at 100× in five random fields per membrane. Each sample was assayed in triplicate.

Luciferase Activity Assay

The Luc-UCA1-WT and Luc-UCA1-MUT were constructed as follows. The wild-type (WT) 3'-UTR and

mutant (MUT) 3'-UTR (modified miR-135a binding site) were amplified by chemical synthesis and were inserted into a luciferase reporter vector (pGL4.74) to generate Lnc-UCA1-WT and Lnc-UCA1-MUT constructs, respectively. SW1990 cells were cotransfected with 0.1 µg of Lnc-UCA1-WT or Lnc-UCA1-MUT, together with 40 nM miR-135a mimic or 40 nM negative control for 24 h. Luciferase activity was detected by a dual-luciferase reporter system according to the manufacturer's instructions (E2920; Promega, Madison, WI, USA). The experiments were performed in triplicate.

Subcutaneously Xenografted Mouse Model

All animal experiments were carried out in accordance with a protocol approved by the Institutional Animal Care and Use Committee (IACUC). SW1990 cells were transfected with UCA1 scramble or UCA1 siRNA for 24 h. Next, 4×10^6 cells were subcutaneously inoculated into 6- to 8-week-old male athymic nude mice. After tumors ($100\text{--}150\text{ mm}^3$) had established, the tumor volume was measured every 5 days with a caliper and calculated using the formula: $\text{length} \times (\text{width}^2)/2$.

Immunohistochemistry

Formalin-fixed paraffin-embedded sections (5 µM) from tissue microarrays were prepared. They were deparaffinized in xylene, rehydrated, and then incubated in 30% H₂O₂ to quench the activity of endogenous peroxidase. The sections were then incubated with primary antibodies directed against matrix metalloproteinase-2 (MMP-2) and MMP-9 overnight at 4°C. Proteins were visualized under light microscopy.

Statistical Analysis

All results are presented as mean ± SD and evaluated with a Student's *t*-test. A value of $p < 0.05$ was considered statistically significant. All experiments were performed at least three times.

RESULTS

lncRNA UCA1 Is Highly Expressed in PC Tissues and Cell Lines

To determine the role of UCA1 in the development of PC, the relative expression of UCA1 in PC tissue and cell lines was detected through qPCR and Western blotting. The expression of UCA1 was significantly increased in PC tissues (mean: threefold) compared with the normal tissue ($p < 0.01$) (Fig. 1A). In addition, the level of UCA1 RNA in a panel of human PC cell lines and HPDE cells was measured by qRT-PCR. By comparison with normal cell lines (HPDE), the expression of UCA1 was largely increased in PC cell lines (SW1990, BxPC-3, MiaPaCa-2, PANC-1, and CAPAN-1) ($p < 0.05$, $p < 0.01$) (Fig. 1B). Moreover, the expression of UCA1 in

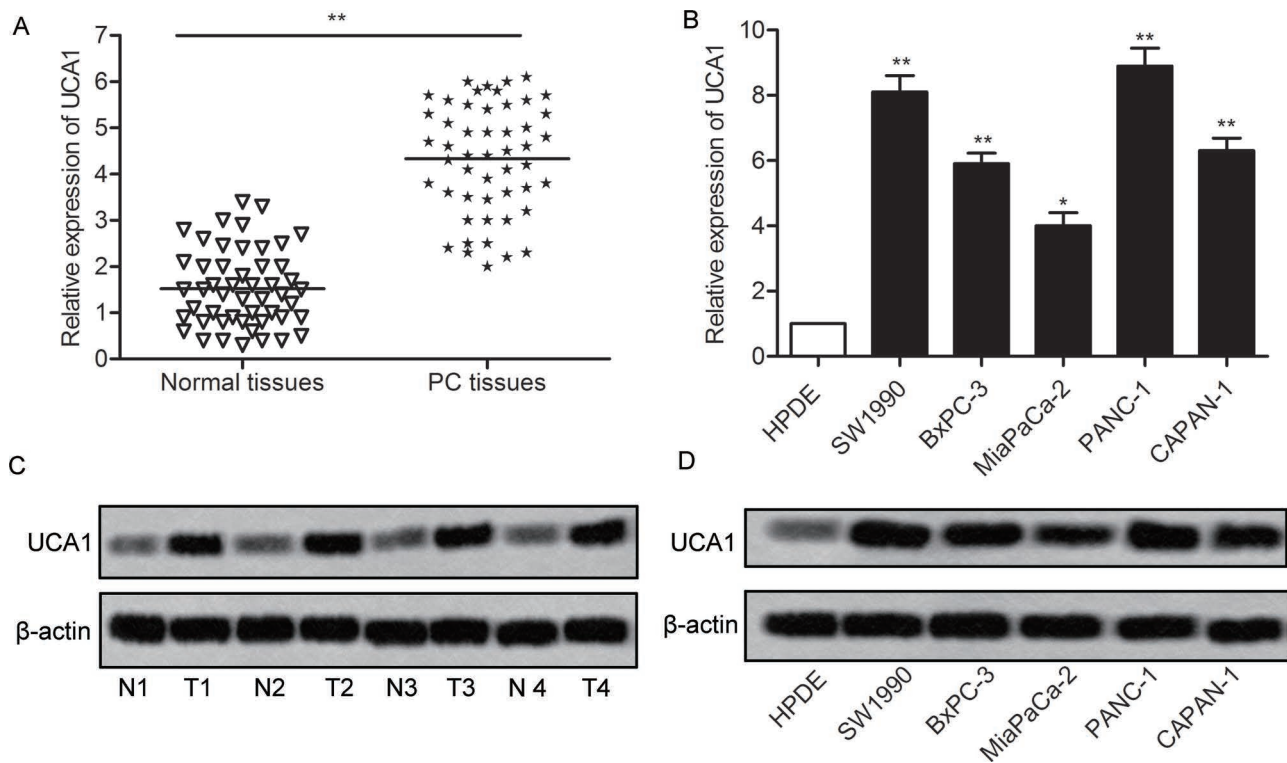


Figure 1. Urothelial carcinoma associated 1 (UCA1) is overexpressed in pancreatic cancer (PC) tissues and cell lines. (A) Relative expression of UCA1 in PC tissues and in adjacent histologically normal tissues was detected by quantitative reverse transcription polymerase chain reaction (qRT-PCR) (** $p < 0.01$ vs. normal tissues). (B) Relative expression of UCA1 in human PC cell lines (SW1990, BxPC-3, MiaPaCa-2, PANC-1, and CAPAN-1), and HPDE cells was detected through qRT-PCR (* $p < 0.05$, ** $p < 0.01$ vs. HPDE). (C) The expression of UCA1 in PC tissues and adjacent histologically normal tissues was detected by Western blotting. (D) The expression of UCA1 in related cell lines mentioned above was detected by Western blotting. GAPDH was used as an endogenous reference. The bars show means \pm SD of three independent experiments.

PC tissue and cell lines was further evaluated through Western blotting (Fig. 1C and D). The results revealed that the expression of UCA1 in tumor tissue and cell lines was largely increased when compared with normal tissue and cell lines. These results suggest that UCA1 is highly expressed in PC.

UCA1 Promotes the Proliferation of PC

To further investigate the impact of UCA1 on the proliferation of PC cells, we verified whether UCA1 was capable of affecting apoptosis and cell viability. SW1990 and PANC-1 cells were transfected with UCA1 scramble or UCA1 siRNA, respectively. The relative expression of UCA1 was largely decreased by UCA1 siRNA in SW1990 and PANC-1 cells ($p < 0.001$) (Fig. 2A). Meanwhile, the downregulated UCA1 largely suppressed cell proliferation of SW1990 and PANC-1 cells, which was detected through MTT assay ($p < 0.05$) (Fig. 2B and C). Tumor sphere formation assay exhibited that the growth rate of SW1990 and PANC-1 cells was significantly decreased by UCA1 siRNA (Fig. 2D). Flow cytometric analysis

further indicated that the apoptosis rate was obviously elevated with the overexpression of UCA1 ($p < 0.001$) (Fig. 2E and F). These results indicate that UCA1 promotes cell proliferation in PC.

UCA1 Promotes the Migration and Invasion of Pancreatic Cancer

To elucidate the role of UCA1 in regulating migration and invasion in PC cells, we transfected SW1990 and PANC-1 cells with UCA1 siRNA or UCA1 scramble, respectively. The wound healing assay showed that the closing rate of scratch wounds was significantly decreased by UCA1 siRNA compared with the UCA1 scramble ($p < 0.05$) (Fig. 3A and B). Similar conclusions were drawn from the Transwell invasion assay. The statistical results showed that the number of invasive cells in the UCA1 siRNA group was largely decreased compared with the UCA1 scramble group ($p < 0.001$) (Fig. 3C and D). Integrating these results, we concluded that UCA1 siRNA may inhibit the migration and invasion of PC.

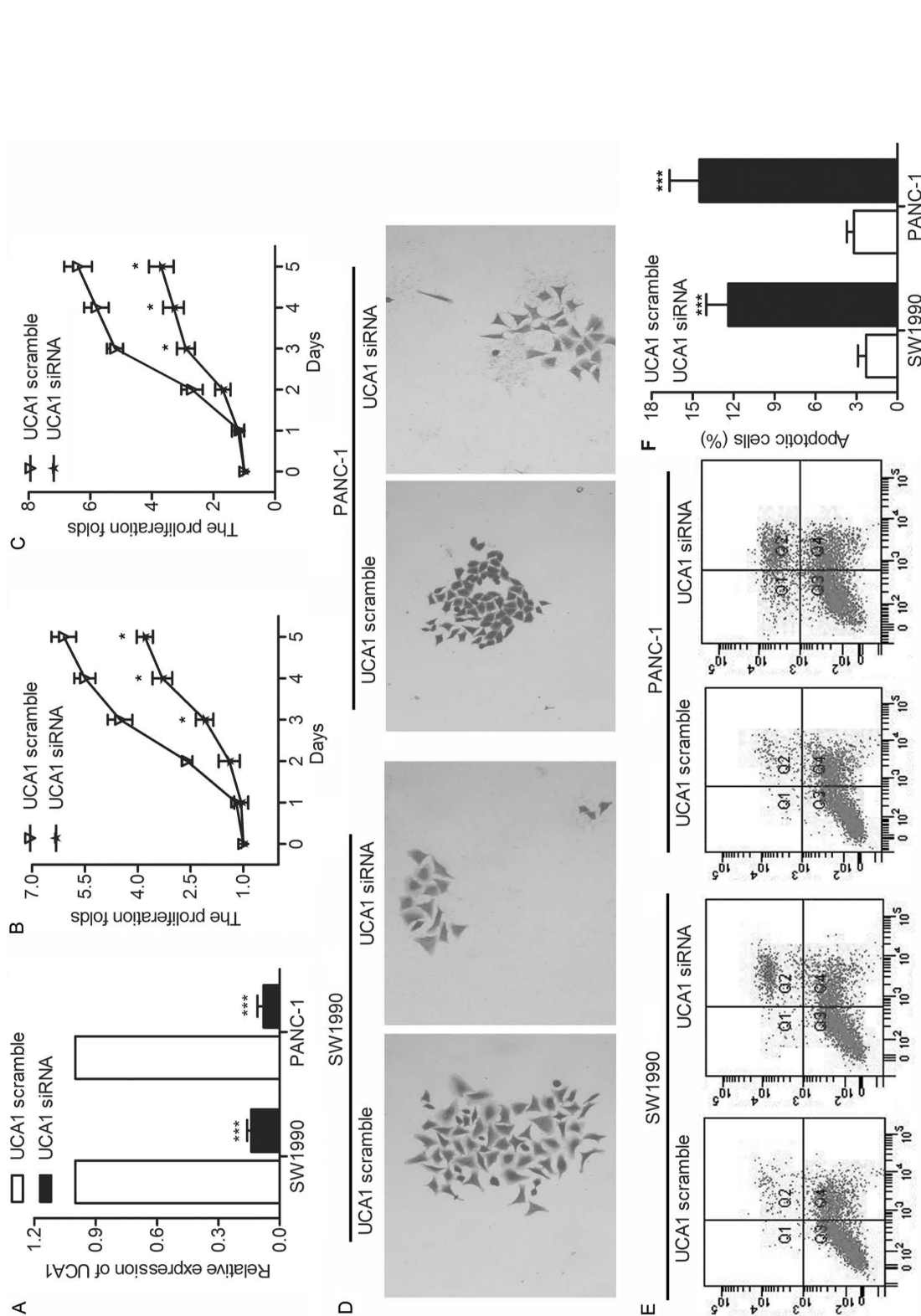


Figure 2. UCA1 promotes the proliferation of PC. SW1990 and PANC-1 cells were transfected with UCA1 siRNA or UCA1 scramble, respectively. (A) Relative expression of UCA1 in SW1990 and PANC-1 cells was detected through qRT-PCR ($***p < 0.001$ vs. UCA1 scramble). (B, C) Cell proliferation rates in SW1990 and PANC-1 cells were detected through MTT assay ($*p < 0.05$ vs. UCA1 scramble). (D) Cell proliferation of SW1990 and PANC-1 cells was exhibited by tumor sphere assay. (E) Flow cytometry was performed to determine the percentages of apoptosis in SW1990 and PANC-1 cells. (F) Histogram represents the statistical analysis of flow cytometry ($***p < 0.001$ vs. UCA1 scramble).

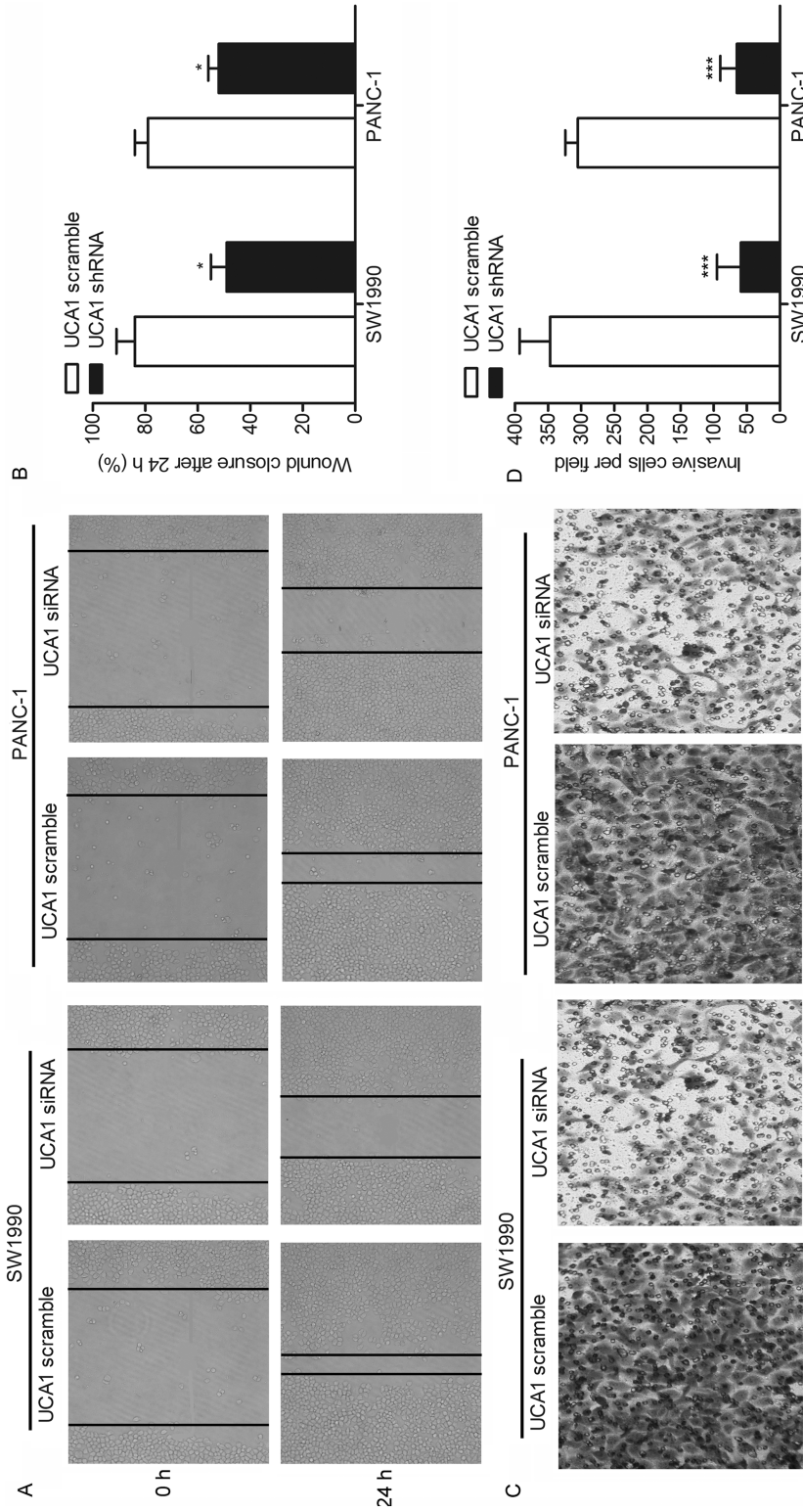


Figure 3. UCA1 promotes the migration and invasion of PC. SW1990 and PANC-1 cells were transfected with UCA1 scramble or UCA1 siRNA, respectively. (A) Migration rate of SW1990 and PANC-1 cells detected through wound healing assays. (B) Histogram represents the statistical analysis of wound healing assays (* $p < 0.05$ vs. UCA1 scramble). (C) Transwell invasion assays were conducted to observe the invasive cells in SW1990 and PANC-1 cells. (D) Histogram represents the statistical analysis of wound healing assay (*** $p < 0.001$ vs. UCA1 scramble).

miR-135a Is a Target of UCA1

miR-135a has been identified as an important tumor suppressor in inhibiting cell proliferation and clonogenicity, and inducing G₁ arrest and apoptosis of PDAC, but few studies mentioned the interaction between miR-135a and lncRNA in the treatment of PDAC. Through bioinformatics analysis, we learned that two complementary sites of miR-135a in UCA1 RNA exist (Fig. 4A). The expression of miR-138 was found to be significantly decreased in tumor tissue and cell lines (SW1990, BxPC-3, MiaPaCa-2, PANC-1, and CAPAN-1) compared with normal tissue and normal HPDE cells ($p < 0.01$) (Fig. 4B and C). The result was further identified through Western blotting analysis in the above tissues and cell lines (Fig. 4D and E). These results revealed that miR-135a was overexpressed in PC tissue and cell lines. To further investigate the targeting relationship between UCA1 and miR-135a, PANC-1 cells were transfected with lncRNA UCA1 or UCA1 siRNA in combination with miR-135a mimic or miR-135a inhibitor. The results showed that a decreased level of miR-135a was elevated by adding miR-135a mimic in PANC-1 cells transfected with lncRNA UCA1. Similarly, the upregulated level of miR-135a was downregulated by adding an miR-135a inhibitor in PANC-1 cells transfected with UCA1 siRNA (Fig. 4F and G). A luciferase activity assay was conducted to further verify the targeting relationship. Luciferase reporter assays showed that relative luciferase activity in Lnc-UCA1-WT miR-138 mimic recombinant vector was significantly decreased compared with the control groups ($p < 0.01$) (Fig. 4H). All the results above illustrate the fact that miR-135a is a direct target of UCA1.

miR-135a Offsets the Role of UCA1 on the Viability and Motility of PC Cells

The targeting relationship between miR-135 and UCA1 has already been identified above, so we set out to explore the effect of the two on the viability and motility of PC cells. Compared with the control group, the elevated cell apoptosis rate in UCA1 siRNA-transfected PANC-1 cells was suppressed by adding an miR-135a inhibitor ($p < 0.01$) (Fig. 5A and B). The MTT assay further indicated that miR-135a inhibitor reduced the inhibiting role of UCA1 siRNA on cell proliferation ($p < 0.01$) (Fig. 5C). Compared with the control groups, the decreased number of invasive cells and the lowered cell migration rate in PANC-1 cells transfected with UCA1 siRNA were both cut down by cotransfecting with an miR-135a inhibitor ($p < 0.01$) (Fig. 6A–C). The negative correlation between the relative expression of UCA1 and miR-135a further proved the targeting relationship between the two (Fig. 6D). These results indicate that miR-135a offsets the role of UCA1 on the viability and motility of PC cells as a direct target.

UCA1 Enhances Tumor Growth and Metastasis In Vivo

To investigate the role of UCA1 in regulating migration and invasion on PANC-1 cells in vivo, PANC-1 UCA1 siRNA and PANC-1 UCA1 scramble recombinant cell lines were established. A xenograft mouse model was created by injecting recombinant cell lines into SPF nude mice subcutaneously. Average tumor volume was obviously smaller in the PANC-1 UCA1 siRNA group than in the PANC-1 UCA1 scramble group (Fig. 7A and B). In addition, the suppressed expression of UCA1 and the upregulated level of miR-135a in the UCA1 siRNA PANC-1 group of mice further verified the targeting relationship between UCA1 and miR-135a in vivo (Fig. 7C and D). Moreover, the expression level of migration marker proteins MMP-2 and MMP-9 was significantly decreased in the PANC-1 UCA1 siRNA group compared with the control group through immunohistochemistry (IHC) analysis (Fig. 7E). On the basis of the above results, we deduced that UCA1 enhances tumor growth and metastasis in vivo.

DISCUSSION

In recent studies, UCA1 has been identified to possess an oncogenic role in tumor growth and metastasis, and it acts as a potential biomarker and therapeutic target in various kinds of human cancers. In accordance with these facts, overexpressed UCA1 was detected in human PC tissues and cell lines in this study. However, the underlying mechanism of UCA1 in PC is less well characterized, and the treatment of PC is largely ineffective due to the lack of effective diagnosis strategies and treatment regimens. Therefore, it is of great significance to get a better understanding of the mechanism of UCA1 in PC. In this study, for the first time, we revealed that UCA1 regulates the growth and metastasis of PC by targeting miR-135.

Previous research convinced us that the high expression of UCA1 was first found in bladder cancer, and the dysregulation of UCA1 was subsequently found in some other cancers²⁴. Overexpressed UCA1 showed an extensive potential in cell proliferation, migration, invasion, and drug resistance through different mechanisms. For example, upregulated expression of UCA1 enhanced cell proliferation and 5-fluorouracil resistance in colorectal cancer by inhibiting the relative expression of miR-204-5p²⁵. In addition, the expression of UCA1 was significantly increased in renal cell carcinoma tissues and cells, and overexpressed UCA1 regulated cellular proliferation, migration, and apoptosis²⁶. Similarly, in our study highly expressed UCA1 was found in PC tissues and cell lines, compared with adjacent histologically normal tissues and cell lines. To verify the role of UCA1 in PC cell lines, SW1990 and PANC-1 cells were transfected with UCA1 siRNA and UCA1 scramble, respectively. Downregulated

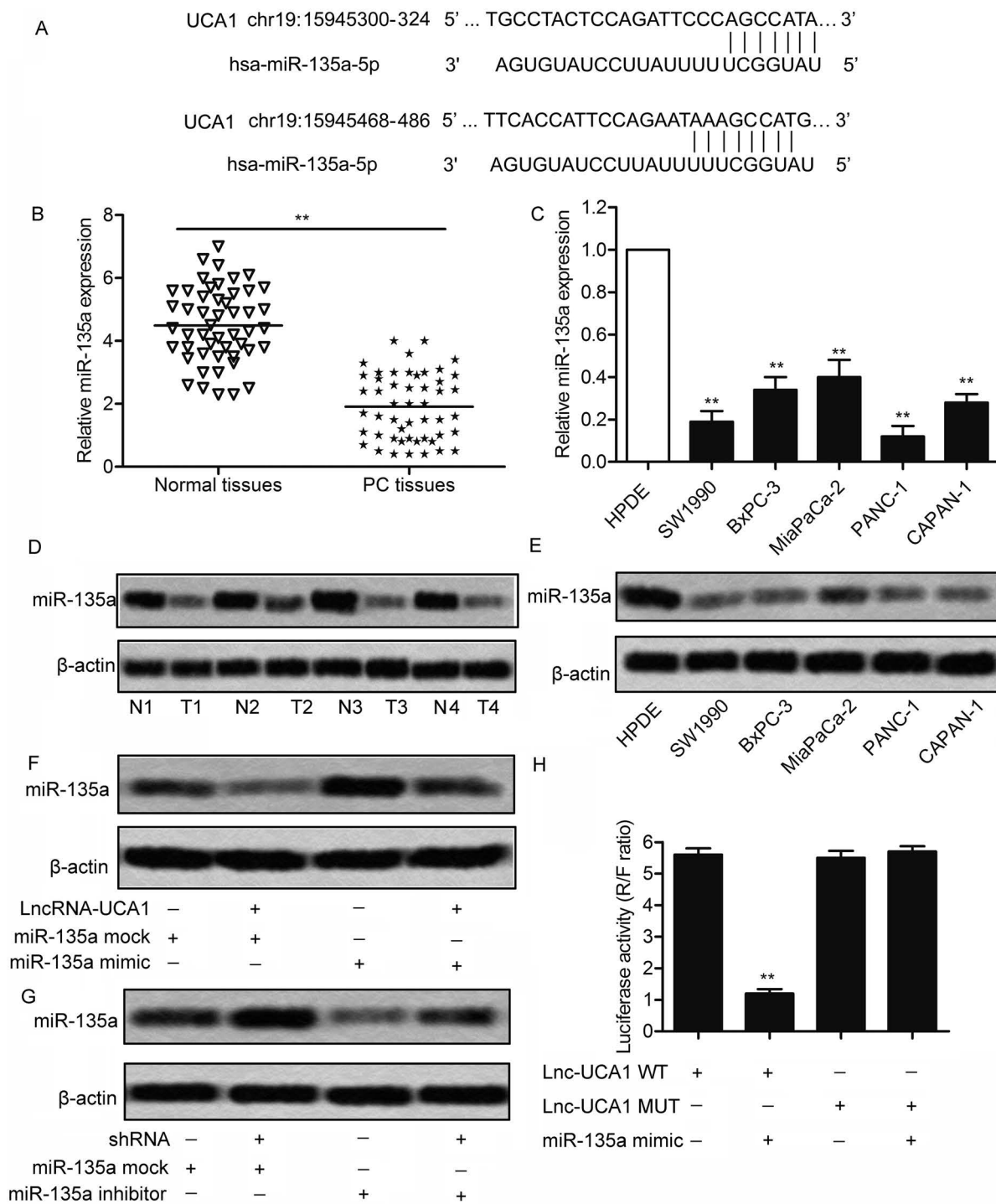


Figure 4. microRNA (miR)-135a is a target of UCA1. (A) The targeting relationship between miR-135a and UCA1 was predicted through bioinformatics. (B) Relative expression of miR-135a in PC tissues and normal tissues was detected through qPCR (** $p < 0.01$). (C) Relative expression of miR-135a in human PC cell lines (SW1990, BxPC-3, MiaPaCa-2, PANC-1, and CAPAN-1) and HPDE cells were detected through qRT-PCR (** $p < 0.001$ vs. HPDE group). (D) Expression of miR-135a in PC tissues and normal tissues was detected by Western blotting. (E) Expression of miR-135a in related cell lines was detected by Western blotting. β -Actin was used as an endogenous reference. (F) The expression of miR-135a was measured by Western blotting in SW1990 cells transfected with long noncoding RNA (lncRNA) UCA1 and/or miR-135a mimic or mock. (G) The expression of miR-135a was measured through Western blotting in SW1990 cells transfected with UCA1 siRNA and/or miR-135a inhibitor or mock, respectively. (H) The wild-type (Lnc-UCA1-WT) or mutant (Lnc-UCA1-MUT) luciferase reporter was cotransfected into SW1990 cells with miR-NC or miR-135a mimic. The luciferase reporter assay was conducted to detect the luciferase activity in SW1990 cells (** $p < 0.001$ vs. Lnc-UCA1-WT group).

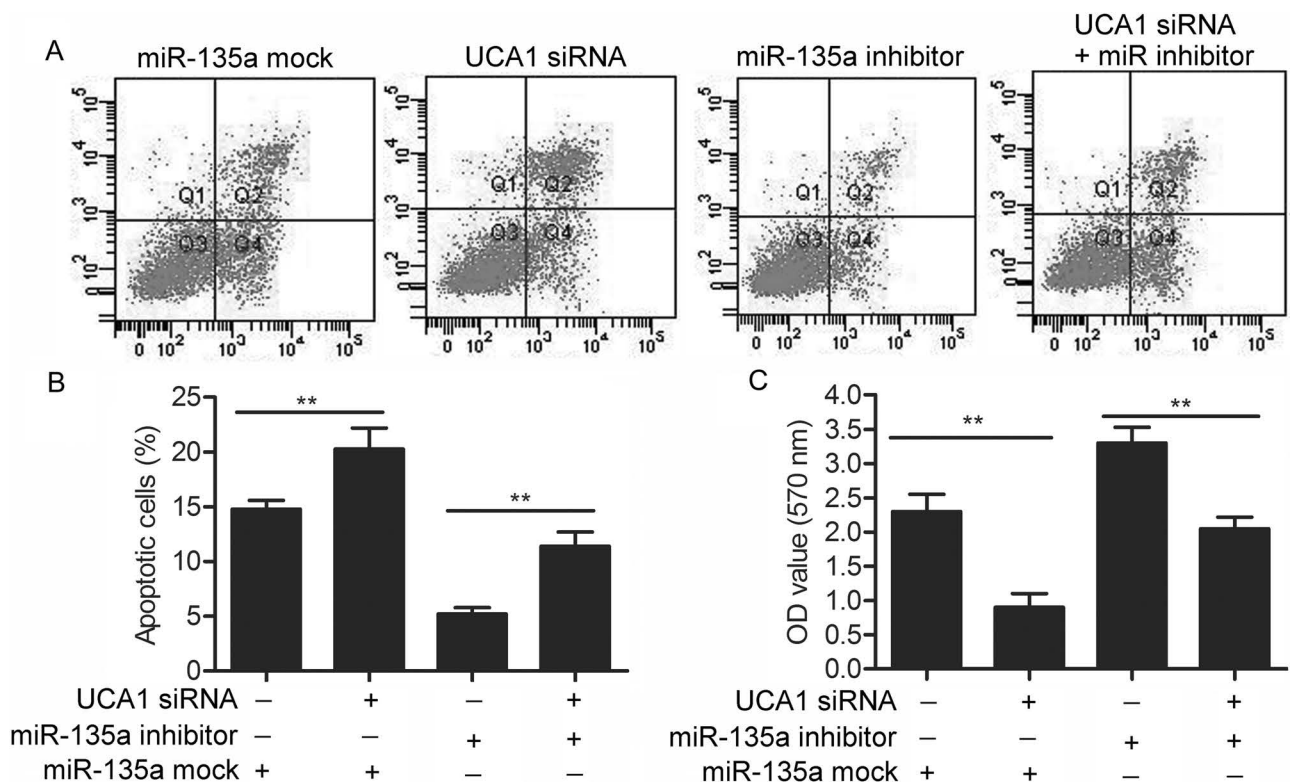


Figure 5. miR-135a offsets the role of UCA1 on cell proliferation and apoptosis. SW1990 cells were transfected with UCA1 siRNA and/or miR-135a inhibitor or mock, respectively. (A) Flow cytometry was performed to determine the percentages of cell apoptosis in SW1990 cells. (B) The histogram represents the statistical analysis of flow cytometry (** $p < 0.01$). (C) Cell viability was detected through MTT assay in SW1990 cells (** $p < 0.01$).

UCA1 was identified to suppress cell proliferation in SW1990 and PANC-1 cells through the MTT and tumor sphere assays. Moreover, flow cytometry showed that the cell apoptosis rate was significantly raised by UCA1 siRNA compared with the control group. These results suggested that the expression of UCA1 is upregulated in PC tissues and cell lines, and overexpressed UCA1 inhibits cell proliferation and induces cell apoptosis in PC cells.

Previous studies also reported the influence of UCA1 on the invasion and migration of cancer cells. For example, UCA1 promoted cell migration and invasion in bladder cancer through the hsa-miR-145-ZEB1/2-FSCN1 pathway²⁷. UCA1 also acted as a poor prognostic factor and suppressed UCA1, inhibiting the migration of endometrial cancer cell²⁸. In our study, wound healing and Transwell invasion assays were conducted to verify whether UCA1 played a similar role in PC. The results suggested that the migration and invasion abilities of PC cells were both largely suppressed by UCA1 siRNA. The above research revealed the promoting role of UCA1 in cell migration and invasion of PC.

Recently, an increasing number of research has revealed that miRNAs act as tumor suppressors or oncogenes in

many human cancers^{29,30}. Previous studies proved that miR-135a was downregulated in human primary gastric cancer and that miR-135a mimic inhibited proliferation and promoted the apoptosis of GC cells by targeting KIFC1³¹. Other research showed that miR-135a inhibited migration and invasion of lung cancer cells and regulated epithelial-mesenchymal transition-related marker genes by targeting a transcription factor KLF8³². However, the possible relationship between miR-135a and lncRNAs has not been elucidated until now. In our study, the targeting relationship between UCA1 and miR-135a was first predicted by bioinformatics analysis. In addition, the relative expression of miR-135a was found to be largely upregulated in PC samples and cell lines compared with normal tissues and cell lines. What is more, the level of miR-135a was upregulated by UCA1 siRNA and was suppressed by lncRNA-UCA1 in SW1990 cells. The luciferase activity assay showed that the intensity of the fluorescence signal was largely weakened by miR-135a mimic in the lncRNA-UCA1 WT group. Subsequently, miR-135a was identified as offsetting the role of UCA1 on the viability and motility of PC cells. The relative expression of miR-135a had a positive correlation with the expression of UCA1 in 50 pairs of PC tissues. The

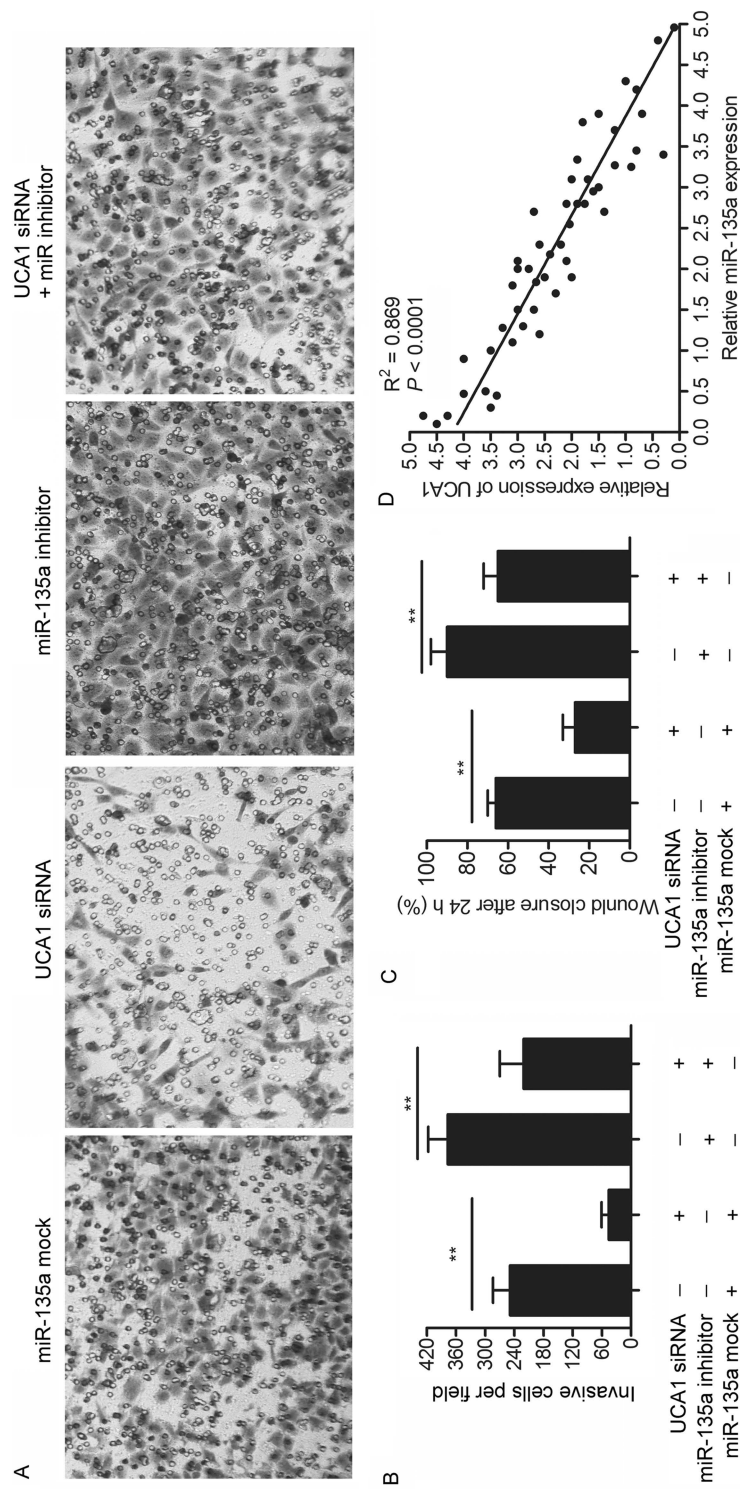


Figure 6. miR-135a offsets the role of UCA1 on cell migration and invasion. SW1990 cells were transfected with UCA1 siRNA and/or miR-135a inhibitor or mock, respectively. (A) The Transwell invasion assay was conducted to observe the invasive cells in SW1990 cells. (B) The histogram represents the statistical analysis of Transwell invasion assay (** $p < 0.01$). (C) The histogram represents the statistical analysis of cell migration rate detected through wound healing assay (** $p < 0.01$). (D) The correlation analyses were performed between the relative expression of UCA1 and miR-135a in 50 pairs of PC samples from the Affiliated Shengjing Hospital of China Medical University.

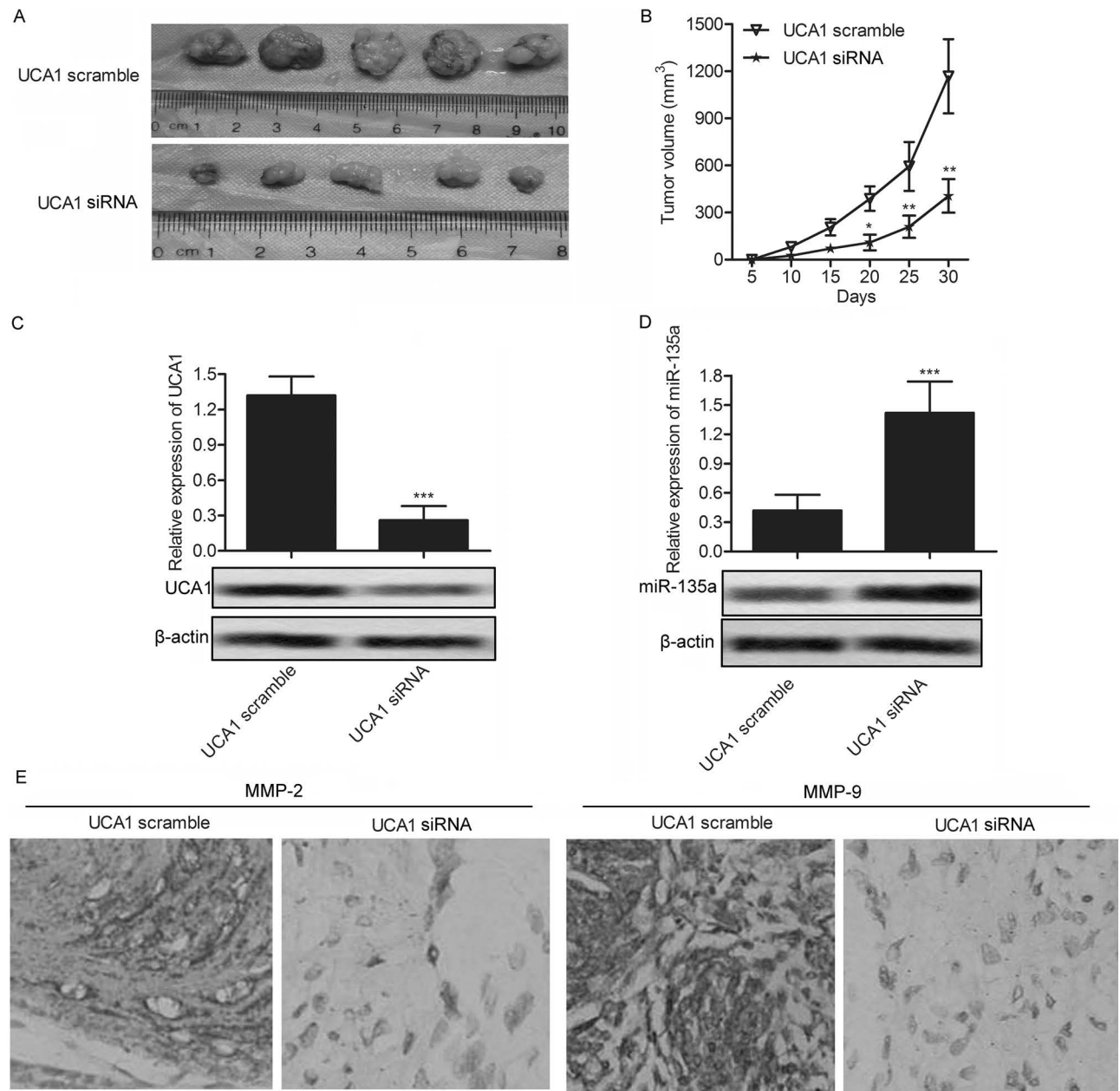


Figure 7. UCA1 siRNA suppresses tumor growth and metastasis in vivo. Xenograft mouse model was created by subcutaneous injection of SW1990 cells pretreated with UCA1 scramble or UCA1 siRNA to SPF nude mice. (A) Representative tumors from two groups of mice are shown ($n=5$). (B) Tumor growth trend in UCA1 scramble or UCA1 siRNA group mice is shown ($*p<0.05$, $**p<0.01$ vs. UCA1 scramble group). (C, D) The expression of UCA1 and miR-135a in UCA1 scramble and UCA1 siRNA group mice was detected through qRT-PCR and Western blotting ($***p<0.001$ vs. UCA1 scramble). (E) Expression of migration markers MMP-2 and MMP-9 in formalin-fixed, paraffin-embedded tumors from UCA1 scramble or UCA1 siRNA group mice was detected through immunohistochemistry (IHC) analysis.

above results indicate that UCA1 regulates the proliferation and migration of PC by targeting miR-135a.

Having identified that UCA1 promotes the proliferation of PC cells in vitro, we further explored the effect of UCA1 in vivo. According to previous reports, UCA1 was identified to be correlated with tumor growth in

hepatoma carcinoma³³, breast cancer³⁴, and colon cancer³⁵. In keeping with previous studies, downregulated expression of UCA1 was found to significantly suppress tumor growth in lncRNA-UCA1 model mice. UCA1 siRNA also reduced the expression level of miR-135a in vivo. Moreover, the expression of migration marker

proteins MMP-2 and MMP-9 was decreased by UCA1 siRNA in vivo. These results indicate that UCA1 siRNA inhibits PC growth and metastasis in vivo.

In conclusion, our research found that UCA1 was overexpressed in PC tissue and cell lines. Downregulated UCA1 was verified to suppress cell proliferation and migration in PC cell lines. Further research revealed that miR-135a was a direct target of UCA1. Moreover, UCA1 siRNA was verified to suppress PC growth and metastasis in vivo. Our research is the first to reveal the possible link between miR-135a and UCA1 in PC. The UCA1-miR-135a pathway provides a new insight for PC treatment.

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