

MiR-101 affects proliferation and apoptosis of cervical cancer cells by inhibition of JAK2

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Abstract. – **OBJECTIVE:** JAK2 expression and dysfunction play a role in tumor pathogenesis. Bioinformatics analysis revealed a targeted binding site between miR-101 and the 3'-UTR of JAK2 mRNA. This study investigated the role of miR-101 in regulating JAK2 expression and affecting the proliferation and apoptosis of cervical cancer cells.

PATIENTS AND METHODS: The tumor tissues and adjacent tissues of patients with cervical cancer were collected. The expression of miR-101 and JAK2 was detected by qPCR. The dual luciferase reporter gene assay validated the targeting relationship between miR-101 and JAK2. The cervical cancer Caski cells were cultured *in vitro*, and divided into miR-NC group and miR-101 mimic group. The expression of JAK2 and p-JAK2 was detected by Western blot, cell apoptosis was detected by flow cytometry, and cell proliferation was detected by EdU staining.

RESULTS: Compared with adjacent tissues, miR-101 expression was significantly increased, and JAK2 expression was increased in cervical cancer tissues. There was a targeted regulatory relationship between miR-101 and JAK2. Compared with Caski cells, miR-101 expression in HeLa and Caski was significantly decreased, and the expression of JAK2 and p-JAK2 was significantly increased. Transfection of miR-101 mimic significantly reduced the expression of JAK2 and p-JAK2 in Caski cells, reduced cell proliferation and increased cell apoptosis.

CONCLUSION: The decrease of miR-101 expression and the increase of JAK2 expression play a role in cervical cancer, while the increase of miR-101 expression can inhibit the proliferation and promote the apoptosis of cells by inhibiting the expression of JAK2.

Keywords:

miR-101, JAK2, Cervical cancer.

Introduction

Cervical carcinoma is a common female malignant tumor. The incidence rate is second only to breast cancer, ranking second in female malignant tumors¹, posing a serious threat to the lives and health of patients^{2,3}.

The tyrosine kinase (JAK)-signal transducer and activator of transcription (STAT) signaling pathway is widely expressed in various tissues and cells, and the abnormal activation of JAK-STAT signaling pathway is associated with the occurrence, progression, metastasis and drug resistance of various tumors⁴⁻⁷. JAK2, an important regulator of the JAK-STAT3 signaling pathway, is a signaling pathway kinase that plays an important role in activating the JAK-STAT signaling pathway. A number of studies⁸⁻¹⁰ have shown that the abnormal expression and function of JAK2 play an important regulatory role in the occurrence and progression of various tumors such as breast cancer, liver cancer and gastric cancer.

MicroRNA is an endogenous non-coding small-molecule single-stranded RNA in eukaryotes with a length of about 22-25 nucleotides, which binds to the 3'-UTR of the target gene mRNA by complementary pairing, resulting in degradation or inhibition of translation. MicroRNAs that regulate the expression of target genes, which account for 1% of human genes, regulate the expression of more than 1/3 human genes¹¹. Several studies have found that miR-101 is an important tumor suppressor gene that plays a role as a tumor suppressor gene in the development and progression of various tumors of gastric cancer, bladder cancer and prostate cancer¹²⁻¹⁴. A number

of studies have shown that the decreased expression of miR-101 is associated with the occurrence and progression of cervical cancer¹⁵⁻¹⁷. Bioinformatics analysis revealed a targeted binding site between miR-101 and the 3'-UTR of JAK2 mRNA. This study was to detect the expression profiles of miR-101 and JAK2 in tumor tissues and paracancerous tissues of cervical cancer patients, and investigate whether miR-101 regulates JAK2 expression and affects cell proliferation and apoptosis of cervical cancer cells.

Patients and Methods

Patients

Thirty-six patients with cervical cancer who were treated in our hospital from April 2018 to September 2018 were enrolled. The specimens of cervical cancer tissue confirmed by histopathological examination were collected and the paracancerous tissues which were located at least 2 cm away from the tumor were collected as a control. This study was approved by the Ethics Committee of our hospital and informed consents were obtained from all patients.

Main Reagents and Materials

Human normal cervical epithelial HcerEpic cells, HEK293T cells were purchased from Beijing Beina Biological (Beijing, China); Human Cervical Cancer HeLa, Caski cells were purchased from Guangzhou Youbao Bio (Guangzhou, China); RPMI-1640 medium, Anti-MiR-101 serum medium purchased from Gibco (Grand Island, NY, USA); Fetal Bovine Serum (FBS) was purchased from Shanghai Shengsheng (Shanghai, China); Lipofectamine 2000 were purchased from Invitrogen (Carlsbad, CA, USA); qRT-PCR SuperMix was purchased from Beijing TransGen Biotech (Beijing, China); miR-101 mimic, miR-NC, EdU Cell Proliferation Assay Kit were purchased from Guangzhou Rui (Guangzhou, China); rabbit anti-human JAK2, p-JAK2 polyclonal antibody was purchased from Cell Signaling Technology (Danvers, MA, USA); rabbit anti-human β -actin polyclonal antibody was purchased from Shanghai Shenggong Bio (Shanghai, China); HRP-conjugated secondary antibody was purchased from Jackson ImmunoResearch (West Grove, PA, USA); pMIR plasmid Purchased from Changsha Youbao Bio (Changsha, China); Dual-Luciferase Reporter Assay System was purchased from Promega (Madison, WI, USA).

Cell Culture

HcerEpic, HeLa, and Caski cells were cultured in RPMI-1640 medium containing 10% FBS at a 37°C 5% CO₂ cell culture incubator. After the cells were over, 0.125% trypsin digestion was performed to collect the cells followed by a sub-culture at a ratio of 1:4 to 1:5. Cells in log phase were selected for experiment.

Construction of Luciferase Reporter Gene Vector

The PCR product containing full-length 3'-UTR fragment of the JAK2 gene and the fragment containing the mutant was cloned into the pMIR vector and designated as pMIR-JAK2-WT. A luciferase reporter vector containing the 3'-UTR mutant of JAK2 gene was also constructed and designated as pMIR-JAK2-MUT. pMIR-JAK2-WT and pMIR-JAK2-MUT was transfected into HEK293T cells with miR-101 mimic (or miR-NC) using Lipofectamine 2000 reagent, and cultured for 48 h followed by measuring the relative luciferase activity according to the Dual-Luciferase Reporter Assay System kit instructions.

Cell Transfection and Grouping

Caski cells cultured *in vitro* were divided into two transfection groups: miR-NC transfection group and miR-101 mimic transfection group. The general procedure for transfection was to dilute Lipofectamine 2000, miR-NC, miR-101 mimic with Opti-MEM. After incubation for 5 min at room temperature, gently mixing Lipofectamine 2000 with miR-NC and miR-101 mimic for 20 min incubation at room temperature followed by addition of the transfectants to the cell culture medium. After 72 hours of culture, cells were collected for analysis.

qRT-PCR Detection of Gene Expression

The RNA was extracted using TRIzol reagent, and the relative expression of the gene was detected by one-step qRT-PCR using TransScript Green One-Step qRT-PCR SuperMix in the 20 μ L reaction system including: 1 μ g of Template RNA, 0.2 μ M of pre-primer, 0.2 μ M of post-primer, 10 μ L of 2 \times TransStart Tip Green qPCR SuperMix, 0.4 μ L of One-Step RT Enzyme Mix, 0.4 μ L of Passive Reference Dye II, and RNase-free water. The qRT-PCR reaction conditions were: 45°C, 5 min; 94°C, 30 s; (94°C, 5 s; 60°C, 30 s) \times 40 cycles, and gene expression was detected on a Bio-Rad CFX96 Real-time PCR instrument (Hercules, CA, USA).

Western Blot

The cells were lysed by SDS lysate, and the total protein was extracted. After boiling at 100 °C for 5 min, the protein concentration was determined by BCA method. 40 µg protein was separated by 10% sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) separation gel and 5% concentrated gel, transferred to the polyvinylidene difluoride (PVDF) membrane (300 mA, 100 min), blocked with 5% skim milk powder at room temperature, and incubated with the primary antibody at 4°C overnight (the dilution ratios of JAK2, p-JAK2, and β-actin were 1:2000, 1:800, 1:8000, respectively). After washing times with PBST, the membrane was incubated with the horseradish peroxidase (HRP)-labeled secondary antibody (1:10000 dilution) at room temperature followed by washing the membrane 3 times with PBST, addition of ECL luminescent solution for 1-3 min, exposing and developing.

Flow Cytometry Detection of Apoptosis

The two miR-NC and miR-101 mimic transfected cells were collected by trypsinization and resuspended in 100 µL Annexin V Binding Buffer according to the instructions following the addition of 5 µL FITC Annexin V and 10 µL PI. After incubation for 15 min at room temperature, 400 µL Annexin V Binding Buffer was added to stop the reaction and cell apoptosis was measured using a Beckman Coulter FC500 flow cytometer (Brea, CA, USA).

Flow Cytometry Detection of Cell Proliferation

The two miR-NC and miR-101 mimic transfected cells were harvested by trypsinization, and resuspended in complete medium containing 10% FBS. After incubation with 10 µM of EdU at 37°C for 2 h, cells were further cultured for 48 h. After the cells were collected by enzymatic digestion, cells were washed by centrifugation, fixed, and permeabilized, and then stained with solution containing Alexa Fluor 488 label. After the mixture was incubated at room temperature for 30 minutes under dark and cell proliferation was measured by flow cytometry.

Statistical Analysis

Statistical analysis of the data was performed by SPSS 18.0 software (SPSS Inc., Chicago, IL, USA). The measurement data were expressed as mean ± standard deviation (SD). The comparison

between the measurement data of two groups was performed by Student's *t*-test. The difference of multiple groups was assessed by ANOVA with Newman-Keuls multiple comparison post-hoc analysis. *p* < 0.05 was considered statistically significant.

Results

A Targeting Relationship between miR-101 and JAK2 mRNA

Bioinformatic analysis revealed a complementary binding site between miR-101 and the 3'-UTR of JAK2 mRNA (Figure 1A). The dual luciferase gene reporter assay showed that transfection of miR-101 mimic significantly reduced relative luciferase activity in pMIR-JAK2-WT transfected HEK293T cells compared to miR-NC transfected cells, while transfection miR-NC and miR-101 mimic had no significant effect on relative luciferase activity in pKIR-JAK2-MUT transfected HEK293T cells (Figure 1B), indicating that miR-101 can target 3'-UTR of JAK2 mRNA.

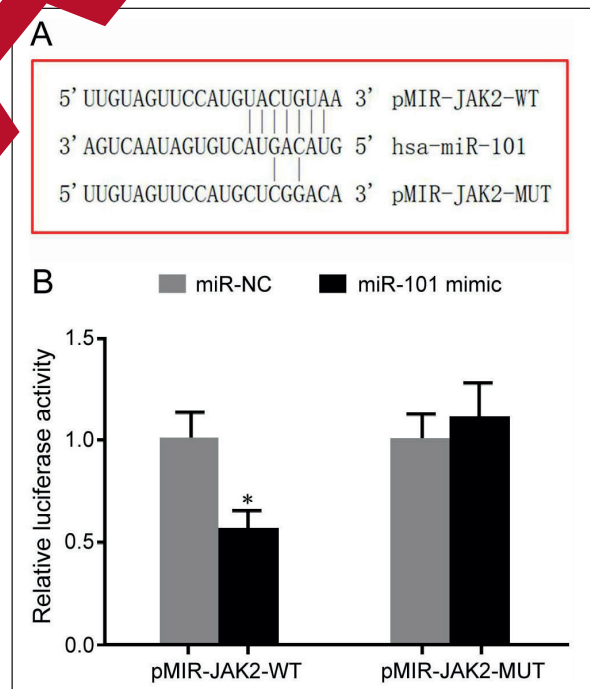


Figure 1. There is a targeting relationship between miR-101 and JAK2 mRNA. (A) Schematic diagram of the site of action between miR-101 and the 3'-UTR of JAK2 mRNA; (B) Dual luciferase gene reporter assay. *Represents *p* < 0.05 compared to miR-NC.

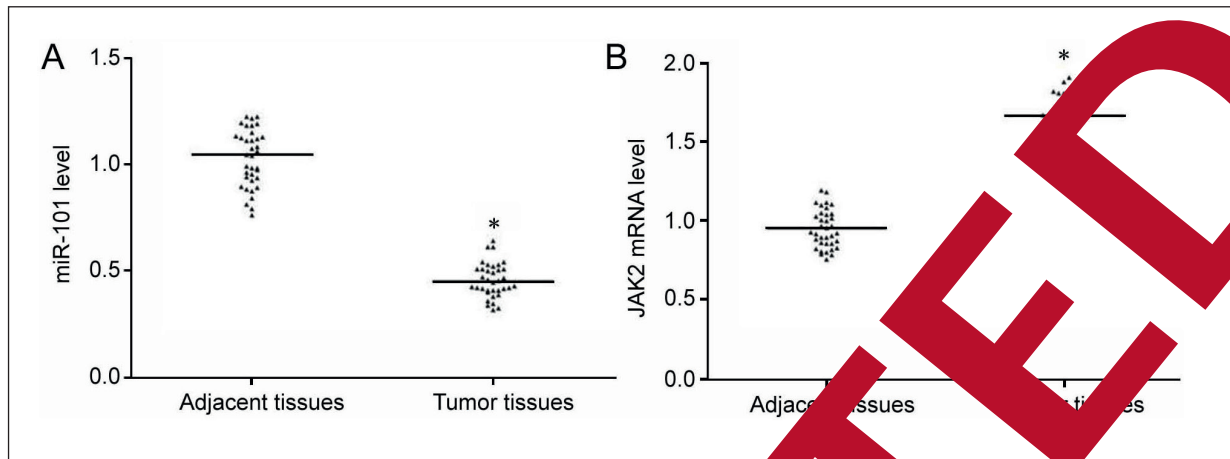


Figure 2. Abnormal expression of miR-101 and JAK2 in cervical cancer. **(A)** qRT-PCR detection of miR-101 expression in cervical cancer tissues; **(B)** qRT-PCR detection of JAK2 mRNA expression in cervical cancer tissues. *Represents $p < 0.05$ compared to the two groups.

Abnormal Expression of MiR-101 and JAK2 in Cervical Cancer

The results of qRT-PCR showed that the expression of miR-101 was significantly decreased in tumor tissues of patients with cervical cancer compared with adjacent tissues ($p < 0.05$) (Figure 2A), while the expression of JAK2 mRNA was significantly increased in tumor tissues ($p < 0.05$) (Figure 2B).

Increased MiR-101 and Increased JAK2 Expression in Cervical Cancer Cells

The results of qRT-PCR showed that the expression of miR-101 was significantly decreased in HeLa and Caski cells compared with normal cervical epithelial HcerEpic cells ($p < 0.05$) (Figure 3A). Western blot analysis showed that the expression of JAK2 and p-JAK2

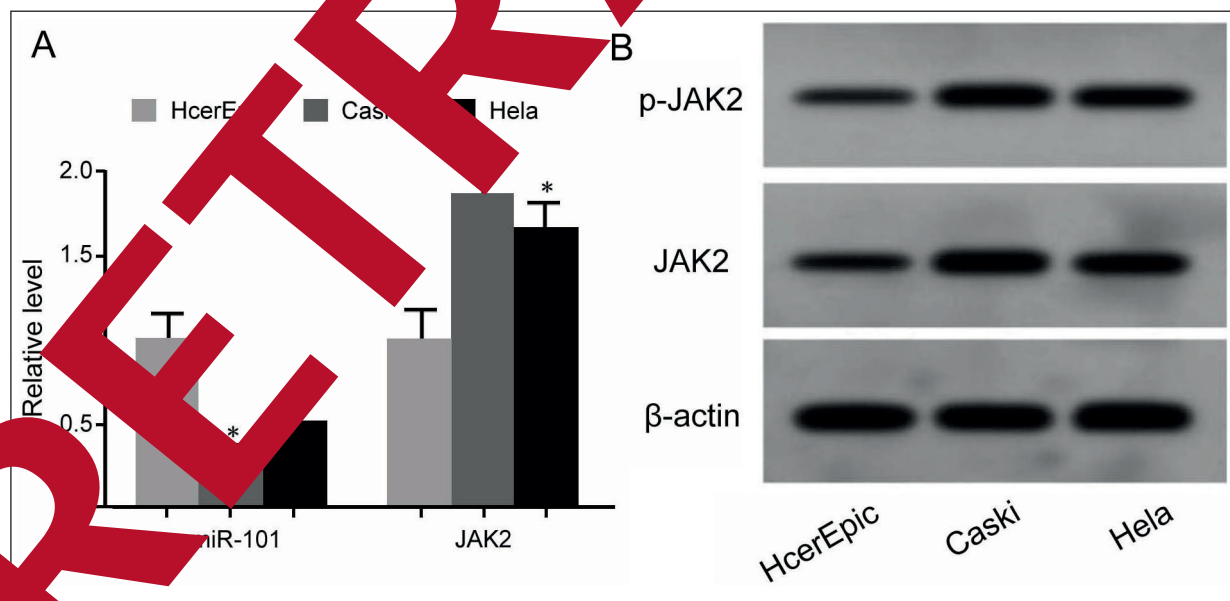


Figure 3. Increased expression of miR-101 in cervical cancer cells and increased expression of JAK2. **(A)** qRT-PCR detection of miR-101, JAK2 mRNA expression in cervical cancer cells; **(B)** Western blot analysis of JAK2, p-JAK2 protein expression in cervical cancer cells. *Represents $p < 0.05$ compared to HcerEpic cells.

protein in HeLa and Caski cells was significantly higher than those in normal cervical epithelial HcerEpic cells (Figure 3B).

Increased MiR-101 Inhibits JAK2 Expression and Proliferation of Cervical Cancer Cells, Induces Cell Apoptosis

The qRT-PCR assay showed that miR-101 mimic transfection significantly up-regulated the expression of miR-101 in Caski cells compared to the miR-NC group ($p < 0.05$) (Figure 4A), resulting in a significant decrease in JAK2 mRNA expression (Figure 4A). Western blot analysis showed that the expression of JAK2 and p-JAK2 protein in Caski cells was significantly decreased in miR-101 mimic transfection group compared with miR-NC group ($p < 0.05$) (Figure 4B). Flow cytometry analysis showed that transfection of miR-101 mimic significantly increased apoptosis in Caski cells (Figure 4C) and attenuated cell proliferation (Figure 4D).

Discussion

The JAK-STAT signaling pathway is widely expressed in various tissues and cells, and is involved in the regulation of various biological processes such as cell survival, proliferation, cell apoptosis, migration and invasion, and abnormal activation of JAK-STAT signaling pathway are related to the occurrence, progression, metastasis and resistance of several tumors⁴⁷. JAK2, an important regulator of the JAK-STAT signaling pathway, is a signaling pathway kinase that plays an important role in the activation of the JAK2-STAT signaling pathway. In response to ligand binding, the receptors form a homodimer or heterodimer and phosphorylate the JAK2 kinase, and the activated JAK2 phosphorylates the tyrosine residue of STAT, causing STAT to complement STAT via the SH2 domain to the tyrosine phosphorylation site of the receptor complex, at which the JAK kinase is spatially adjacent to STAT and phosphorylates its hydroxytyrosine. Phosphorylated STAT is dissociated from the receptor complex, forms a dimer and is translocated from the cytoplasm to the nucleus, where it acts on specific DNA fragments, and regulates gene transcription and expression¹⁸⁻²⁰. Several studies²¹⁻²⁴ have shown that the abnormal expression of miR-101 is related to the occurrence, progression and metastasis of various tumors such as lung cancer, gastric cancer and pancreatic cancer.

This study investigated whether miR-101 plays a role in regulating JAK2 expression and affecting the biological processes of proliferation and apoptosis of cervical cancer cells.

Analysis of the clinical samples in this work showed that compared with normal tissues, miR-101 expression in cervical cancer patients was significantly decreased, while the expression of JAK2 was significantly increased. Compared with normal cervical epithelial HcerEpic cells, miR-101 expression in cervical cancer HeLa and Caski cells was significantly decreased, while the expression of JAK2 was significantly increased. The results showed that the expression of miR-101 expression was associated with increased expression of JAK2, and the abnormalities of miR-101 and JAK2 were associated with the pathogenesis of cervical cancer. In this paper, the dual luciferase reporter assay showed that transfection of miR-101 mimic significantly reduced the relative luciferase activity of pMIR-JAK2-WT transfected HEK293T cells compared to miR-NC transfection group. Transfection of miR-NC or miR-101 mimic had no significant effect on the relative luciferase activity of pMIR-JAK2-MUT transfected HEK293T cells, revealing the target relationship between miR-101 and JAK2 mRNA. In the study of the relationship between miR-101 and cervical cancer, Huang et al²⁵ found that the expression of miR-101 in cervical cancer HeLa cells was significantly abnormal, and overexpression of miR-101 in HeLa cells inhibits cell proliferation, attenuates cell invasion, and induces apoptosis through inhibiting the expression of COX-2. Jiang et al¹⁵ observed that compared with normal cervical mucosa tissue, miR-101 expression in cervical cancer patients is significantly reduced. In addition to tumor tissue, the expression of miR-101 was decreased in peripheral blood of cervical cancer patients, and was associated with FIGO clinical stage and lymph node metastasis. Compared with those with higher expression of miR-101, the survival rate and prognosis of patients with lower miR-101 expression were lower and worse. Lin et al²⁶ detected that miR-101 expression was abnormal in tumor tissues of cervical cancer patients compared with the control by using gene expression microarray and RT-PCR. LNA-ISH further showed that the positive rate of miR-101 expression in cervical mucosa was 80%, while the positive rate of miR-11 expression in cervical cancer tissues was only 8%, and the positive rate of target gene COX-2 was significantly increased.

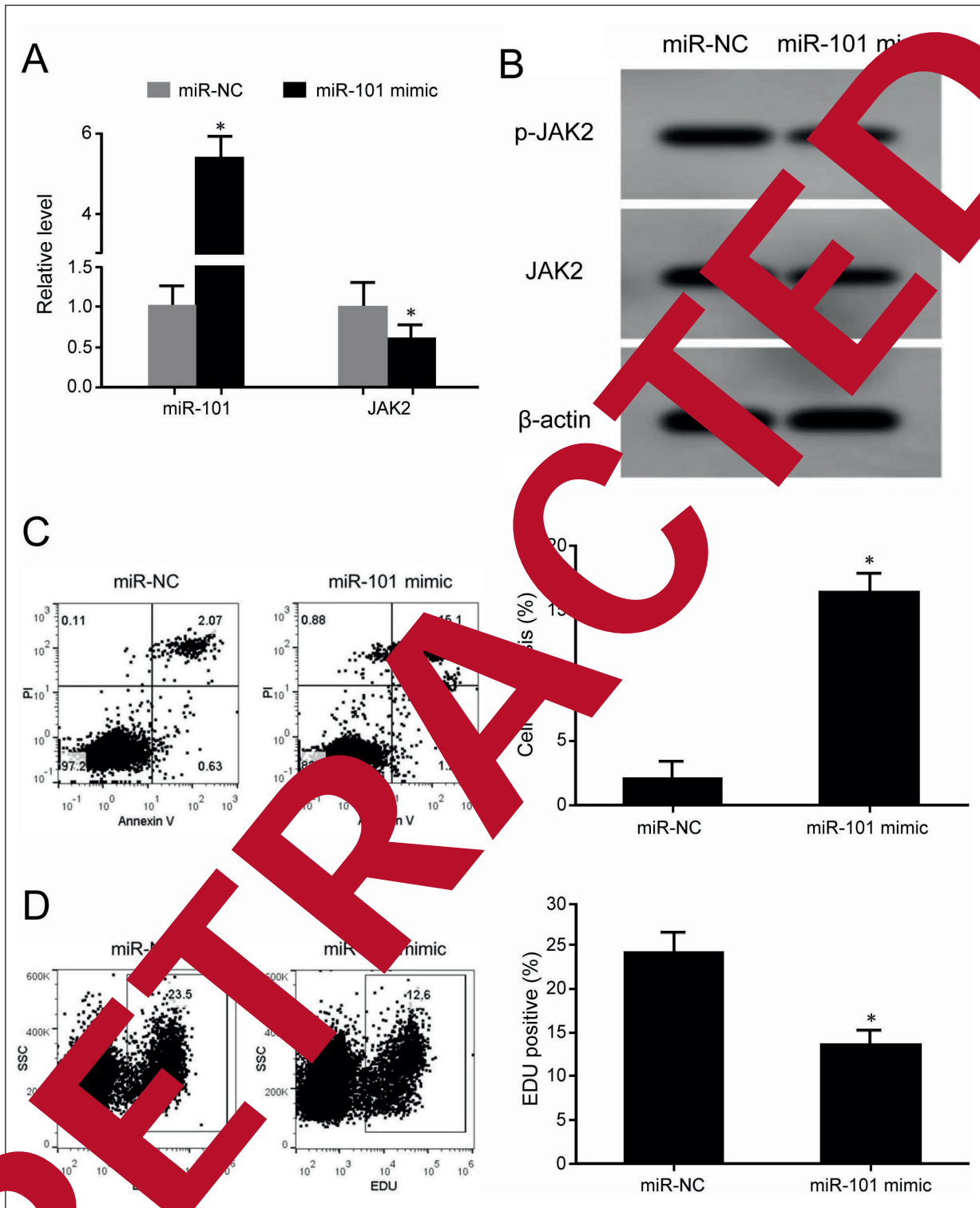


Figure 1 miR-101 inhibits JAK2 expression and proliferation of cervical cancer cells, induces apoptosis. **(A)** qRT-PCR detection of miR-101, JAK2 mRNA expression; **(B)** Western blot analysis of JAK2, p-JAK2 protein expression; **(C)** flow detection of apoptosis; **(D)** flow detection of cell proliferation. * represents $p < 0.05$ compared to miR-NC group.

Liu et al²⁷ demonstrated that miR-101 expression was significantly decreased in cervical cancer tissues compared with normal cervical tissues. In this study, miR-101 expression was significantly decreased in cervical cancer tissues and tumor cells, indicating that miR-101 plays a role as a tumor suppressor gene in the pathogenesis of cervical cancer, which was consistent with Jiang et al¹⁵ and Lin et al²⁶.

Further studies showed that transfection of miR-101 mimic significantly reduced the expression of JAK2 and p-JAK2 in cervical cancer Caski cells, which significantly attenuated cell proliferation and increased cell apoptosis. In the study of the relationship between miR-101 and the biological effects of cervical cancer cells, Liang et al¹⁶ showed that there is a targeted regulatory relationship between miR-101 and Fos gene in cervical cancer HeLa cells, overexpression miR-101 can block the G1/S phase of the cell cycle by inhibition of Fos expression. Lin et al²⁸ observed that miR-101 plays a role as a tumor suppressor gene in cervical cancer. Overexpression of miR-101 in cervical cancer SiHa cells can inhibit cell proliferation, reduce cell invasion and increase cell apoptosis, and inhibition of COX-2 gene expression. Liu et al²⁷ showed that overexpression of miR-101 in cervical cancer SiHa cells significantly inhibited cell proliferation and cell cycle arrest, and promoted apoptosis. Shen et al¹⁷ showed that the expression of miR-101 was increased in relation to cervical cancer. The overexpression of miR-101 could inhibit the proliferation of cervical cancer cells and decrease growth and tumorigenicity in animals by inhibition of CXCL6 expression. This study combines miR-101 targeting regulation between miR-101 and JAK2, revealing that the decreased expression of miR-101 and the increased expression of JAK2 play a role in cervical cancer, while the expression of miR-101 is decreased. It has a negative anti-cancer effect on the malignant biological characteristics of cervical cancer cells. However, whether miR-101 regulates the biological effects of JAK2 on cervical cancer cells *in vivo* remains unclear and requires further investigations.

Conclusions

This study showed that the decrease of miR-101 expression and the increase of JAK2 expression play a role in cervical cancer, while the increase

of miR-101 expression can inhibit the proliferation of cells and promote the apoptosis of cells by inhibiting the expression of JAK2.

Conflict of Interest

The Authors declare that they have no conflicts of interests.

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