

Circular RNA circ-SMAD7 is downregulated in colorectal cancer and suppresses tumor metastasis by regulating epithelial mesenchymal transition

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Abstract. – **OBJECTIVE:** Recently, circular RNAs play a vital role in many diseases including tumor progression. Colorectal cancer (CRC) is one of the most ordinary malignant tumors. The purpose of our study is to detect the potential function of circ-SMAD7 in CRC.

PATIENTS AND METHODS: The level of circ-SMAD7 was detected by Real Time-quantitative Polymerase Chain Reaction (RT-qPCR) in CRC tissue samples. The circ-SMAD7 expression level and the patients' overall survival time were analyzed. Functional experiments were conducted to identify the changes of the biological behaviors in CRC cells after the overexpression of circ-SMAD7. The transwell assay, the Matrigel assay, and the Wound healing assay were conducted. The Western blotting was performed to analyze the effect of circ-SMAD7 on the epithelial-to-mesenchymal transition process.

RESULTS: In the research, the expression level of circ-SMAD7 was significantly increased in CRC tissues compared with that in adjacent samples. Circ-SMAD7 expression was positively associated with patients' overall survival time. The expression of circ-SMAD7 was also decreased in CRC cell lines. Overexpression of circ-SMAD7 led to the inhibition of cell migration and invasion in CRC. In addition, the results of further experiments revealed that the EMT-related process was regulated *via* overexpression of circ-SMAD7 in CRC.

CONCLUSION: These results suggest that circ-SMAD7 can inhibit cell migration and invasion of CRC by suppressing the EMT process, which may offer a potential therapeutic target for CRC.

Keywords:

Circular RNA, Circ-SMAD7, Colorectal cancer, Epithelial-to-mesenchymal transition.

Introduction

Colorectal cancer (CRC) is one of the most prevalent malignant tumors in the world, especially in developed countries¹. It is estimated that 1.2 million new cases were diagnosed of CRC in America in 2018 and 50,260 CRC patients died in the same year which accounted for 8.4% of all cancer-related deaths. Most of the patients die of metastasis by the time they are firstly diagnosed. Numerous studies have been carried out to find out the understanding mechanism contributing to the progression of CRC for the past decades. However, there are few improvements in the poor prognosis for the advanced cases². Therefore, it is urgent to have a deeper understanding of the underlying molecular mechanisms of tumorigenesis and progression in colorectal cancer and figure out new therapeutic strategies.

Circular RNAs (circRNAs) represent a novel class of endogenous noncoding RNAs with their 3'- and 5'-ends joined together to form a covalently closed loop. Due to the special structure, circRNAs are more stable than linear RNA isoforms. CircRNAs have recently attracted much research interest due to its wide expression found in many genes. Moreover, it was found that circRNAs functioned as microRNA (miRNA) sponges which were involved in the initiation and progression of different cancers. Consistently, by regulating the expression of LATS1 and sponging miR-424-5p, circ-RNA_LARP4 suppresses the proliferation and invasion of gastric cancer cells³. As a miR-1252 sponge, hsa_circ_0043256 inhibits cell proliferation and induces cell apoptosis in non-small cell lung cancer⁴. By competing with microRNA-150-5p, circRNA ZNF609 enhances

tumor growth and metastasis of nasopharyngeal carcinoma⁵. The knockdown of circ_0025039 inhibits the proliferation, invasion and colony formation ability of melanoma cells⁶. However, the function of circular RNA in CRC and the potential molecular mechanism have not yet been studied so far. To uncover the role of circ-SMAD7 in CRC, its expression was detected in CRC tissues and the related mechanism was researched.

In this study, circ-SMAD7 was remarkably down-regulated in CRC tissues and cell lines. Moreover, circ-SMAD7 inhibited migration and invasion of CRC *in vitro*. Our further experiments also showed that circ-SMAD7 suppressed the epithelial-to-mesenchymal transition (EMT) process of CRC.

Patients and Methods

Tissue Samples

The tumor samples and the adjacent tissues (≥ 5 cm away from the edge of tumor) were gathered from CRC patients ($n = 52$) who underwent surgery at Qingdao Chengyang District People's Hospital from June 2016 to December 2018. Written informed consent was taken before operation. All fresh tissues were preserved at -80°C . This study was approved as the Human Research Ethics Committee from of Qingdao Chengyang District People's Hospital required.

Cell Culture and Transfection

The human CRC cell lines (HCT116, HCT29, SW620, SW480) and non-tumorigenic epithelial cells (NCM460) were obtained from the American Type Culture Collection (ATCC, Manassas, VA, USA). The culture medium consisted of Roswell Park Memorial Institute-1640 (RPMI-1640, Hyclone, South Logan, UT, USA), 10% fetal bovine serum (FBS, Invitrogen, Carlsbad, CA, USA), and penicillin/streptomycin. Besides, the cells were cultured in an incubator containing 5% CO_2 at 37°C . We used the lentivirus targeting circ-SMAD7 (Genechem, Shanghai, China) for the transfection of the CRC cells using Lipofectamine 3000 (Invitrogen, Carlsbad, CA, USA). The transfection efficiency was detected by RT-qPCR.

RNA Isolation and RT-qPCR

After transfection, TRIzol RNA isolation reagent (Invitrogen, Carlsbad, CA, USA) was utilized to extract the total mRNA from tissues and cells. The first-strand complementary deoxyribonucleic acids (cDNAs) was synthesized using the Transcriptor first

strand cDNA synthesis kit (TaKaRa Biotechnology Co., Ltd., Dalian, China) according to the manufacturer's instructions. The primer sequences for RT-qPCR were as follows: circ-SMAD7, forward: 3'-TGAGAAGAGAAATCTATGAAACC-5', circ-SMAD7, reverse: 3'-GGTGGTCCGCTGCTTTA-5'; GAPDH primers for control: forward: CAATGACCCCTTCATTGACC-3' and reverse: GATTTGGAGGGATCTG-3'. The cycling conditions were as follows: 30 sec at 95°C , 5 min at 60°C for 40 cycles at 95°C , 35 sec at 60°C .

Wound Healing Assay

After transfection, the CRC cells were seeded in 6-well plates and incubated in RPMI-1640 medium overnight. Then the cells were scratched with a plastic tip and cultured in serum-free RPMI-1640. Each assay was repeated in triplicate independently. The relative distance was viewed under a light microscope (Olympus Corp., Tokyo, Japan) at 48 h.

Tube Formation Assay

After transfection, 1×10^5 cells in 200 μL serum-free RPMI-1640 were replanted in top chamber (Corning, Inc., Corning, NY, USA). RPMI-1640 and FBS were added to the lower chamber. Then, they were cultured overnight in an incubator supplemented with 5% CO_2 at 37°C . The top surface of the chambers was treated by methanol for 30 min after wiped by cotton swab. Next, they were stained in crystal violet for 20 min. Five fields were randomly chosen under a Leica DMI4000B microscope (Leica Microsystems, Heidelberg, Germany).

Matrigel Assay

After transfection, 1×10^5 cells in 200 μL serum-free RPMI-1640 were replanted in the top chamber (Corning, Inc., Corning, NY, USA) with 50 μg Matrigel (BD, Bedford, MA, USA). RPMI-1640 and FBS were added to the lower chamber. Then, they were cultured overnight in an incubator supplemented with 5% CO_2 at 37°C . The top surface of the chambers was treated by methanol for 30 min after being wiped by cotton swab. Next, they were stained in crystal violet for 20 min. Five fields were randomly chosen under a Leica DMI4000B microscope (Leica Microsystems, Heidelberg, Germany).

Western Blot Analysis

The reagent radio immunoprecipitation assay (RIPA, Beyotime, Beijing, China) was utilized to extract the protein from cells. The bicinchoninic

acid (BCA) protein assay kit (TaKaRa, Otsu, Shiga, Japan) was chosen for quantifying the protein concentrations. The target proteins were separated by dodecyl sulfate, sodium salt-polyacrylamide gel electrophoresis (SDS-PAGE). Then, they were incubated with antibodies after that the polyvinylidene difluoride (PVDF) membranes (Millipore, Billerica, MA, USA) was replaced. The Cell Signaling Technology (CST, Danvers, MA, USA) provided us the rabbit anti-GAPDH and rabbit anti-E-cadherin, rabbit anti-N-cadherin, rabbit anti-Vimentin, as well as goat anti-rabbit secondary antibody. The Image J (Media Cybernetics, Silver Springs, MD, USA) software was applied for the assessment of the protein expression.

Statistical Analysis

The Statistical analysis was conducted by the Statistical Product and Service Solutions (SPSS) 17.0 (SPSS Inc., Chicago, IL, USA). GraphPad 4.0 (GraphPad Software, Inc., La Jolla, CA, USA) helped presenting these consequences. The Kaplan-Meier method and the independent-sample *t*-test was used when appropriate. The quantitative data was presented as mean \pm SD (standard deviation). Moreover, $p < 0.05$ was considered to indicate a statistically significant difference.

Results

The Association Between Circ-SMAD7 Expression and the Prognosis of CRC Patients

Firstly, based on the median expression, the CRC patients were divided into two groups, low

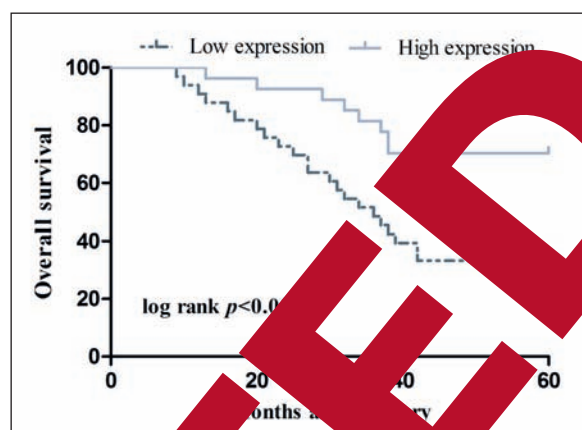


Figure 1. The association between circ-SMAD7 expression level and the prognosis of CRC patients. The expression levels of circ-SMAD7 were positively associated with patients' overall survival ($p < 0.05$).

and high circ-SMAD7 groups. The CRC patients in the low circ-SMAD7 expression group had a poor overall survival compared with those in the high circ-SMAD7 expression group ($p < 0.05$; Figure 1).

Circ-SMAD7 Expression Level Was Lower in Tumor Tissues and Cells

The circ-SMAD7 expression was detected via RT-qPCR in 52 CRC patients' tissue samples and matched adjacent samples. The results showed that circ-SMAD7 was significantly lower-expressed in tumor tissue samples than that in the adjacent tissues (Figure 2A). The circ-SMAD7 expression in human CRC cell lines and NCM460 was also detected. The circ-SMAD7

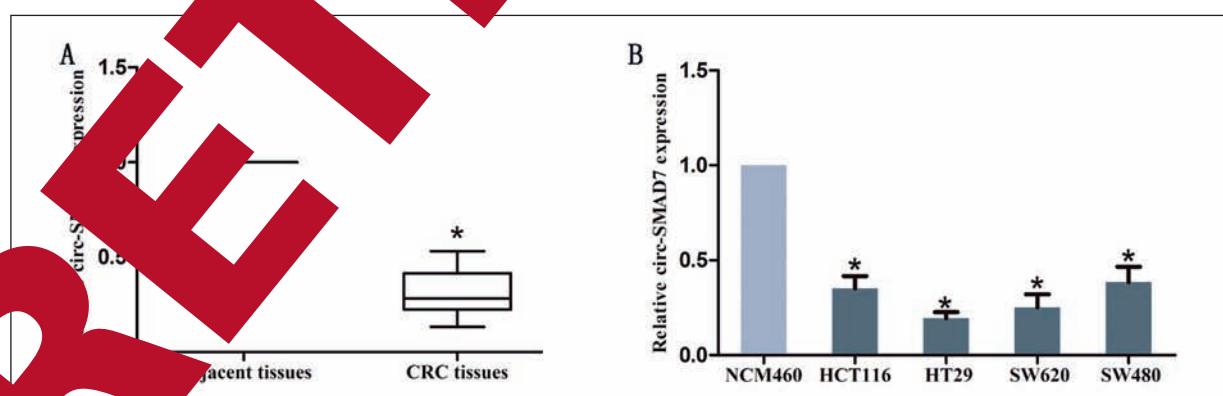


Figure 2. The expression levels of circ-SMAD7 were decreased in CRC tissues and cell lines. **A**, Circ-SMAD7 expression was significantly decreased in the CRC tissues compared with adjacent tissues. **B**, The expression level of circ-SMAD7 relative to GAPDH was determined in the human CRC cell lines and normal human colonic epithelial cells (NCM460) by RT-qPCR. GAPDH was used as an internal control. The data are presented as the mean \pm standard error of the mean. $*p < 0.05$.

expression level was lower in CRC cells than that in NCM460 (Figure 2B). The results suggested that circ-SMAD7 might function in the development of CRC.

Circ-SMAD7 Overexpression Inhibited Cell Migration and Invasion in CRC Cells

In this study, we chose HT29 cells for the overexpression of circ-SMAD7 and the transfection efficiency was detected by RT-qPCR (Figure 3A). To explore how circ-SMAD7 affected the cell migration of CRC cells, the Wound healing assay and the transwell assay were performed. As shown in Figure 3B, the migrated length of the CRC cells was reduced after circ-SMAD7 was overexpressed. As shown in Figure 3C, the number of migrated cells was remarkably decreased after circ-SMAD7 was overexpressed in CRC cells. To explore how circ-SMAD7 affected cell invasion of CRC cells, the Matrigel assay was performed. As shown in Figure 3D, after circ-SMAD7 was overexpressed, the number of the invaded cells was remarkably decreased.

Circ-SMAD7 Overexpression Inhibited EMT Process in CRC

Previous studies have reported the key role of EMT process in cancer metastasis. In this study, the effect of circ-SMAD7 on EMT process was further studied. The EMT-related proteins including E-cadherin, N-cadherin, and Vimentin were detected. Previous studies identified that E-cadherin was downregulated, and N-cadherin and Vimentin were upregulated when the EMT process was activated. Wound healing assay showed that the expression of E-cadherin in CRC cells was higher in circ-SMAD7 overexpression group than that in control group, and the expression of N-cadherin and Vimentin in CRC cells was lower in circ-SMAD7 overexpression group than that in the control group (Figure 4A). The Western blot assay showed that the protein level of E-cadherin in CRC cells was upregulated in circ-SMAD7 overexpression group compared with that in the control group, and the expression of N-cadherin and Vimentin in CRC cells was downregulated in circ-SMAD7 overexpression group compared with that in the control group (Figure 4B).

Discussion

Many of the functions of circRNAs have been elucidated over the past few years. The dysregulated expression of circRNAs has been reported

as an important factor in the progression of CRC. For instance, the overexpression of circ_0000069 enhances cell proliferation and migration in CRC⁷. Hsa_circ_001910 is significantly down regulated in CRC and may be a novel potential biomarker and therapeutic target for the CRC cases⁸. By promoting the expression of p16, the downregulation of hsa_circ_001471 inhibits tumor growth in colorectal cancer⁹. Circ_0071589 promotes carcinogenesis via the miR-600/EZH2 axis in colorectal cancer¹⁰. By sponging miR-101, circ_0000069 is overexpressed in CRC which serves as a novel gene for CRC¹¹.

Generated from chromosomal DNA, circRNA SMAD7 is a novel circRNA which has been reported to be overexpressed in the esophageal squamous cell carcinoma and it inhibits tumor proliferation and migration¹². To further determine whether circ-SMAD7 participated in the regulation of CRC metastasis, circ-SMAD7 was overexpressed in CRC cells. The Wound healing assay and the transwell assay were conducted in the overexpressed cells. The results showed that circ-SMAD7 overexpression repressed the cell migrated ability of CRC cells. Besides, the Matrigel invasion assay was also conducted and the results showed that circ-SMAD7 overexpression repressed the migrated ability of the CRC cells. The above data indicated that circ-SMAD7 inhibited cell migration and invasion of CRC.

The epithelial-to-mesenchymal transition (EMT) is a crucial biological process involved in a multitude of developmental and pathological events. EMT is characterized by the progressive loss of the cell-to-cell contacts resulting in filopodia formation and mesenchymal gene expression which enable cell migration and invasion. EMT process could be regulated by circular RNAs. EMT is an important biological process in the progression of multitude cancers and characterized by the progressive loss of the cell-to-cell contacts which enables cell migration and invasion. Consistently, URG11 promotes cell proliferation and EMT in benign prostatic hyperplasia cells through RhoA/ROCK1 pathway¹³. Through the activation of ZEB1 and the interaction with miR-139-5p, lncRNA HCP5 enhances epithelial-mesenchymal transition in colorectal cancer¹⁴. Circ-10720 participates in the Twist1-mediated regulation of EMT and promotes the progression of hepatocellular carcinoma¹⁵. Moreover, circMTO1 inhibits tumor metastasis in bladder cancer by serving as miR-221 sponge and restraining EMT¹⁶.

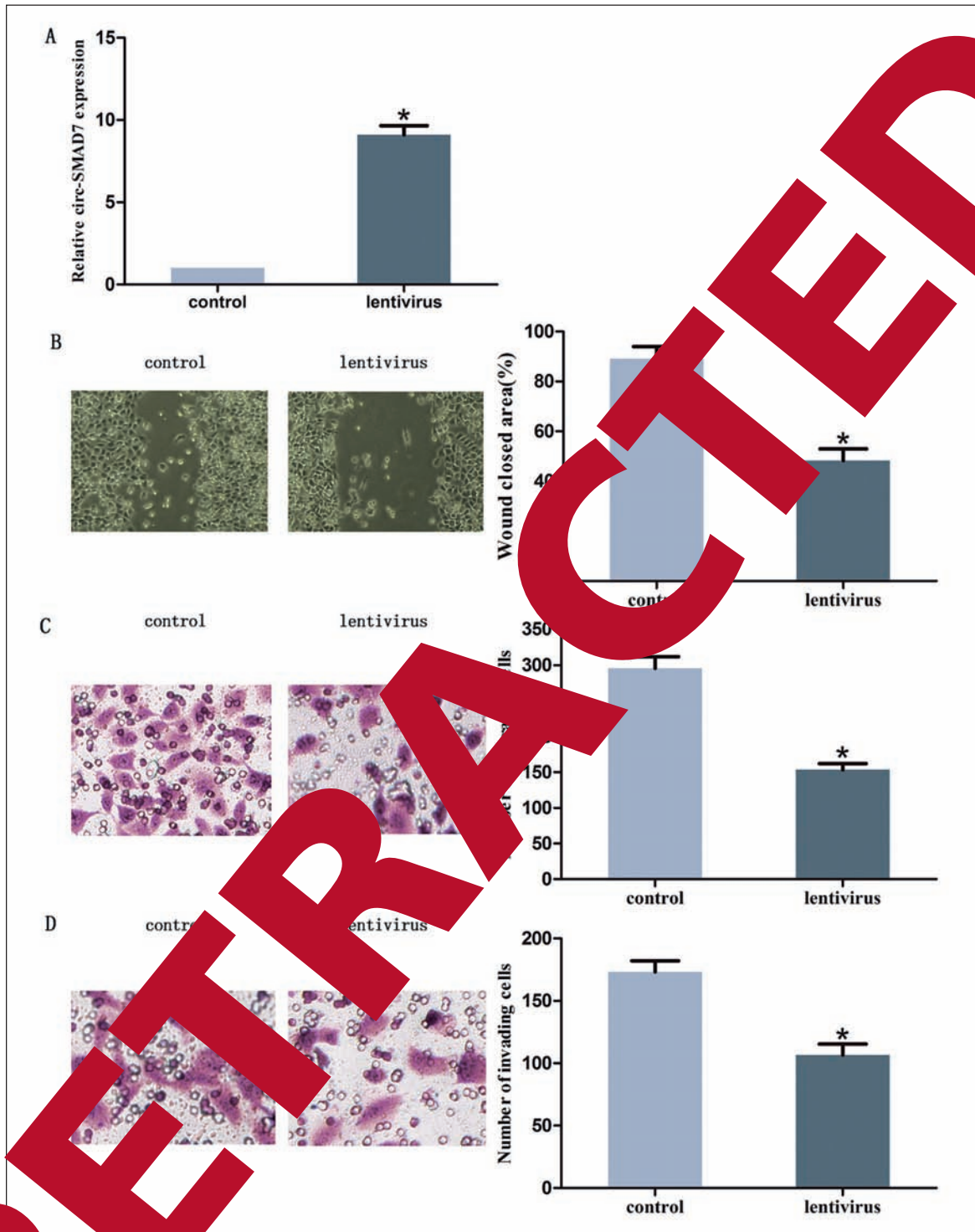


Fig. 3. The overexpression of circ-SMAD7 inhibited CRC cell migration and invasion. **A**, Circ-SMAD7 expression in CRC cells treated with circ-SMAD7 lentivirus (lentivirus) or control was detected by RT-qPCR. GAPDH was used as an internal control. **B**, The Wound healing assay showed that the migrated length of the cells in circ-SMAD7 lentivirus group significantly decreased compared with the control group in CRC cells (magnification: 40 \times). **C**, The transwell assay showed that overexpression of circ-SMAD7 significantly repressed cell migration in CRC cells (magnification: 40 \times). **D**, The Matrigel assay showed that overexpression of circ-SMAD7 significantly repressed cell invasion in CRC cells (magnification: 40 \times). The results represent the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$, as compared with the control cells.

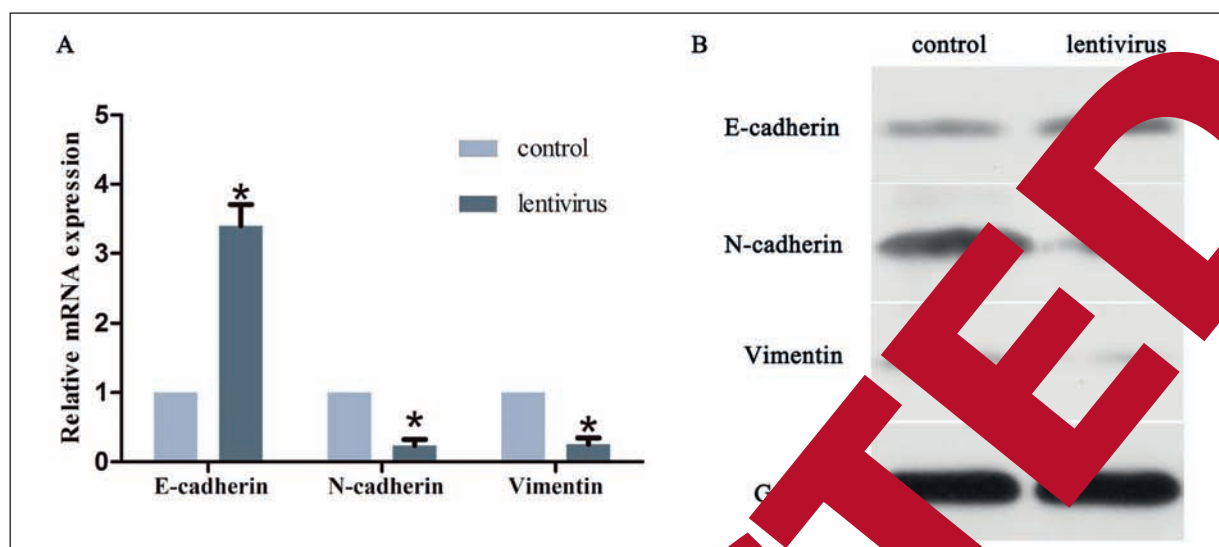


Figure 4. Circ-SMAD7 overexpression inhibited EMT process of CRC cells. **A**, RT-qPCR assay was used to detect the mRNA expression of E-cadherin, N-cadherin, and Vimentin of CRC cells in circ-SMAD7 lentivirus group and control group. **B**, The Western blot assay was used to detect the protein level of E-cadherin, N-cadherin, and Vimentin of CRC cells in circ-SMAD7 lentivirus group and control group. The data are presented as the mean \pm standard error of mean. * $p < 0.05$.

In the present study, the potential interaction between the EMT process and circ-SMAD7 was firstly studied. E-cadherin, N-cadherin, and vimentin are vital proteins in the EMT process. By detecting the expression of those proteins in CRC cells, we found that those proteins could be regulated by the overexpression of circ-SMAD7. These results indicated that circ-SMAD7 could inhibit the EMT process of CRC cells.

Conclusion

The results of the present study identified that circ-SMAD7 was negatively downregulated in CRC tissues and was associated with the prognosis of the CRC patients. Circ-SMAD7 inhibited cell migration and invasion of CRC by inhibiting EMT process. These findings suggest that circ-SMAD7 may serve as a prospective therapeutic target for CRC.

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

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