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ORIGINAL RESEARCH

RETRACTED ARTICLE: DICER1-AS1 Promotes the Malignant Behaviors of Colorectal Cancer Cells by Regulating miR-296-5p/STAT3 Axis

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Background: Long non-coding RNA (lncRNA) exerts a regulatory role in the occurrence and progression of tumors. This study aimed at probing into the function and mechanism of lncRNA DICER1 antisense RNA 1 (DICER1-AS1) in colorectal cancer (CRC).

Methods: The expressions of DICER1-AS1, miR-296-5p and STAT3 mRNA were tested by quantitative real-time polymerase chain reaction (qRT-PCR). Cell counting kit-8 (CCK-8) assay was employed to detect cell proliferation and Transwell was used to detect cell migration and invasion. In addition, the expressions of apoptosis-related proteins Bax and Bcl2 were detected by Western blot. Interactions between DICER1-AS1 and miR-296-5p, and miR-296-5p and STAT3 were predicted and determined by bioinformatics analysis, luciferase reporter assay and RNA binding protein immunoprecipitation (RIP) assay.

Results: The expressions of DICER1-AS1 and STAT3 mRNA were significantly up-regulated while miR-296-5p expression was remarkably down-regulated in CRC tissues and cell lines. Overexpression of DICER1-AS1 or transfection of miR-296-5p inhibitors could promote the proliferation, migration and invasion and inhibit apoptosis of CRC cells, whereas knockdown of DICER1-AS1 or transfection of miR-296-5p mimics had the opposite effects. Additionally, DICER1-AS1 could down-regulate miR-296-5p expression via sponging it. DICER1-AS1 also enhanced the expression of STAT3, which was identified as a target gene of miR-296-5p.

Conclusion: DICER1-AS1 acts as an oncogenic lncRNA in CRC via modulating miR-296-5p/STAT3 axis. Our results provide a new direction for the diagnosis and treatment of CRC.

Keywords: DICER1-AS1, miR-296-5p, CRC, proliferation, metastasis

Background

Colorectal cancer (CRC) is one of the most common tumors in the world, whose mortality rate ranks fourth among cancer-related deaths.[1] Currently, the most important treatment methods for CRC consist of surgery, chemotherapy and target therapy. Despite the continuous improvement of these treatment methods in clinical practice, the 5-year survival rate of patients with stage IV CRC is still only around 10%.[2] Therefore, a more effective therapeutic strategy is urgently needed.

Long non-coding RNA (lncRNA) is a kind of RNA molecule with a length of over 200 nucleotides and no protein-coding ability. LncRNA is involved in a variety of biological processes, including X chromosome imprinting, chromatin remodeling, RNA selective splicing and decay, cell differentiation, cell fate control and so on. Meanwhile, it is also implicated in cancer cell proliferation, metastasis

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and drug resistance.[3,4] In recent years, cancer-related lncRNAs has received high attention. For example, PCA3, PCGEM1 and PCAT1 are known to be overexpressed in prostate cancer and to promote cancer cell proliferation and colony formation.[5] Moreover, lncRNA-ATB is found to be abnormally expressed in a variety of malignancies, including hepatocellular carcinoma, gastric cancer, lung cancer and CRC, and its overexpression promotes proliferation, migration and invasion of cancer cells.[6] As a lncRNA, DICER1 antisense RNA 1 (DICER1-AS1) is transcribed from human chromosome 14q32.13. Its expression is up-regulated in osteosarcoma and DICER1-AS1 has the potential to be a biomarker for cancer diagnosis and prognosis.[7] However, its function and mechanism in CRC are unclear.

MicroRNAs (miRNAs), which also belong to non-coding RNA (ncRNA), are highly conserved non-coding RNA molecules with a length of 21–25 nucleotides, and they could regulate cell differentiation, metabolism, proliferation and apoptosis.[8] With the deepening of the study of tumor molecular biology, an increasing number of studies show that miRNAs are involved in the progression of cancer.[9,10] It can lead to the degradation of target mRNAs, inhibiting the translation to corresponding proteins, thus playing a regulatory role in the biological behaviors of cancer cells.[11,12] MiR-296-5p was generated from the precursor RNA of the transcription of human chromosome 20q13.32. Studies demonstrate that the expression of miR-296-5p is down-regulated in a variety of tumors, including non-small cell lung cancer (NSCLC) and liver cancer.[13,14] However, the role of miR-296-5p in the development of CRC needs further study.

Signal transducer and activator of transcription 3 (STAT3) is one of the important members of the family of signal transducer and activator of transcription (STAT), and it is also a vital nuclear transcription factor. At present, it is found that STAT3 is excessively activated in many tumors, suggesting that it is closely related to tumorigenesis. STAT3 is at the intersection of multiple carcinogenic signaling pathways.[15] It is proved that PIPKI facilitates PI3K-Akt-mTOR signaling pathway activation to increase STAT3 phosphorylation levels, thus triggering tumor-associated macrophage recruitment.[16] Another study reports that STAT3 is highly expressed in CRC and high STAT3 expression is markedly associated with a poor prognosis in patients with CRC.[17]

Bioinformatics analysis (Starbase/TargetScans) showed that DICER1-AS1 could probably adsorb miR-296-5p, and miR-296-5p may target the 3′ UTR of STAT3 mRNA. This study aimed to explore the expression patterns, functions and regulatory mechanisms of DICER1-AS1, miR-296-5p and STAT3 in the progression of CRC, so as to provide clues for clinical diagnosis and treatments of CRC.

Materials and Methods

Tissue Samples

Our study was endorsed by the Research Ethics Committee of Central Hospital of Linyi and the informed consent of all patients involved was also obtained. The cancer tissues of 52 patients with CRC who had undergone CRC resection in our hospital from March 2017 to March 2018 were selected, and none of them received neoadjuvant therapy such as chemotherapy and radiotherapy prior to the experiment. In the control group, the specimens were from adjacent tissues of the same patient (at least 3 cm away from the surgical margin), and no cancer cells were found by pathological examination. All specimens were removed during surgery and immediately stored in liquid nitrogen at –196°C for the following experiments.

Cell Culture and Cell Transfection

Human normal colorectal epithelial cell line NCM460 and CRC cell lines (SW620, HT-29, HCT-8, and HCT-116) were purchased from American Type Culture Collection (ATCC, Rockville, MD, USA). These cells were cultured in RPMI-1640 medium (Thermo Fisher Scientific, MA, USA) supplemented with 10% fetal bovine serum (FBS, Thermo Fisher Scientific, MA, USA) and antibiotics (100 μg/mL streptomycin and 100 units/mL penicillin) (Gibco, Grand Island, NY, USA) in an incubator at 37°C in 5% CO_2. Overexpressing DICER1-AS1 plasmid (pcDNA3.1-DICER1-AS1), knockdown plasmid (pcDNA3.1-DICER1-AS1 shRNA), mimics and inhibitors of miR-296-5p, and corresponding negative control (NC) were obtained from GenePharma (Shanghai, China). HT-29 and HCT-8 cells were inoculated into 24-well cell culture plate at the density of 3×10^5 cells/well. In compliance with the supplier's instructions, HT-29 and HCT-8 cells were transfected using Lipofectamine® 3000 (Invitrogen; ThermoFisherScientific, Inc.). The transfection efficiency was detected by quantitative real-time polymerase chain reaction (qRT-PCR).

qRT-PCR

The total RNA of tissue or cell was extracted by TRIzol reagent (Invitrogen, Waltham, MA, USA). Nanodrop-spectrophotometer was used to detect RNA concentration

and purity. According to the manufacturer's instructions, we used PrimeScript-RT Kit (Madison, WI, USA) to synthesize complementary DNA (cDNA) from 1 μg total RNA, and then we used SYBR®Premix-Ex-Taq™ (Takara, Dalian, China) and ABI7300 systems for qRT-PCR. The total volume of the PCR system was 30 μL, and each sample contained 300 ng of DNA. The amplification procedure was initially denatured for 10 min at 95°C, followed by 45 cycles, namely, 95°C for 10 s, 60°C for 30 s and 85°C for 20 s. GAPDH was the internal parameter of DICER1-AS1 and STAT3, and U6 was the internal parameter of miR-296-5p. $2^{-\Delta\Delta CT}$ method was adopted to calculate the relative expressions of DICER1-AS1, miR-296-5p and STAT3. The primers were designed and synthesized by Guangzhou (RiboBio Co., LTD). The sequence of the degenerate primer pair is as follows: DICER1-AS1 forward, 5′-TGACCAGTCTTACC CCTCCT-3′; DICER1-AS1 reverse, 5′-CTGAAGCACCTG AAATGCG-3′. miR-296-5p forward, 5′-GTATCCAGT GCAGG GTCCGA-3′; miR-296-5p reverse, 5′-CGACGA GGGCCCCCCCT-3′. STAT3 forward, 5′ CTCAACTTCAG ACCCGTCAACA 3′; STAT3 reverse, 5′ GCTCCACG ATTCTCTCCTCCA 3′.

Immunohistochemical Stain

Paraffin blocks containing CRC tissues were sliced and dewaxed, followed by being dehydrated and rehydrated. Then, the sections were incubated with primary antibody (anti-STAT3, abcam, ab119352, 1:200) for 12 h and then secondary antibody for 30 min at room temperature, respectively. Subsequently, the sections were washed gently with PBS buffer. Following that, DAB (Beijing Airan Biotechnology Co., Ltd.) was used to terminate the reaction before the color was developed. Ultimately, the staining was scored by two pathologists independently. The results of IHC were scored according to tumor positive cell rate and staining intensity. After evaluating staining intensity (0, no staining; 1, weak staining; 2, moderate staining; 3, intense staining) and the proportion of stained cells (0, no staining; 1, 1–25% staining; 2, 26–50% staining; 3, 51–75% staining; 4, 75–100% staining), the two scores were added up. The ultimate score was used to represent the expression of STAT3: 0 points, negative; 1–4 points, weak positive; 5–6 points, strong positive.

Cell Counting Kit-8 (CCK-8) Assay

HT-29 and HCT-8 cells in logarithmic growth phase were resuspended and inoculated into 96-well plate with a density of 1×10^3/well (100 μL/well). After the culture for 24 h, 48 h, 72 h and 96 h, respectively, 10 μL CCK-8 solution (Beyotime Biotechnology, Shanghai, China) was added into each well. Then the cells were incubated in the incubator for 1 h, and the absorbance value at 450 nm of the cells was measured by a microplate reader.

Transwell Assay

CRC cell migration and invasion were detected by Transwell chambers (Corning, Beijing, China). Matrigel (BD, San Jose, CA, USA) was used in invasion experiment, but not in migration experiment. 5×10^4 cells resuspended with serum-free medium were placed in the upper chamber and 400 μL medium with 10% FBS was added in the lower chamber. After the incubation at 37°C for 24 h, the cells that failed to migrate or invade were removed from the membrane of the chambers. Then the cells passing through the membrane were fixed with 4% paraformaldehyde for 10 min and stained with 0.5% crystal violet. After being washing with tap water, the cells were counted under a microscope.

Dual-Luciferase Reporter Gene Assay

Dual-luciferase reporter gene assay was used to validate the targeting relationship between miR-296-5p and DICER1-AS1 or 3′-UTR of STAT3. The wild-type (WT) DICER1-AS1 sequence or the WT STAT3 3′-UTR fragment containing predicted binding sites of miR-296-5p was amplified and inserted into the pmirGLO dual-luciferase RNA target expression vector (Promega, Madison, WI, USA) to construct the report vector pmirGLO-DICER1-AS1-WT or pmirGLO-STAT3-WT. The presumed binding sites in DICER1-AS1 or STAT3 3′-UTR were mutated using GeneArt™ Site-Directed Mutagenesis PLUS System (cat. no. A14604; Thermo Fisher Scientific, Inc.). Mutant (MUT) DICER1-AS1 or MUT STAT3 3′-UTR was also inserted into pmirGLO vector to generate report vector pmirGLO-DICER1-AS1-MUT or pmirGLO-STAT3-MUT. The corresponding reporter vectors and miR-296-5p or NC mimics were co-transfected into HEK293 cells and incubated for 48 h. Luciferase activity was then measured employing Dual-Luciferase Reporter Assay System (Promega, Madison, WI, USA).

Western Blot

The cells were collected and washed with cold PBS for 3 times, and then RIPA lysate (Beyotime Biotechnology, Shanghai, China) was added to extract the protein. After that, the protein concentration was determined by Bradford method, and 10–20 μg protein was loaded in each well for Western blot analysis. The equivalent proteins taken from

each group were separated by 10% SDS-PAGE, and the proteins on the gel were then transferred to polyvinylidene fluoride (PVDF) membrane (Millipore, Bedford, MA, USA). After the block with 5% skim milk for 1 h at room temperature, the membrane was incubated with primary antibody at 4°C for 8 h. After washing the membrane twice with TBST, cells were incubated with secondary antibodies at room temperature for 1 h. After being washed three times, the membrane was exposed with ECL chemiluminescent reagent (Millipore, Bedford, MA, USA), and imaging was performed with a membrane scanning machine. Antibodies used in this study including anti-STAT3 antibody (ab119352, 1:1000), anti-p-STAT3 (ab76315, 1:500), anti-GAPDH (ab181602, 1:2000), anti-bax (ab32503, 1:1000), anti-bcl-2 (ab59348), and secondary antibody (ab7090, 1:2000) were purchased from Abcam (Shanghai, China).

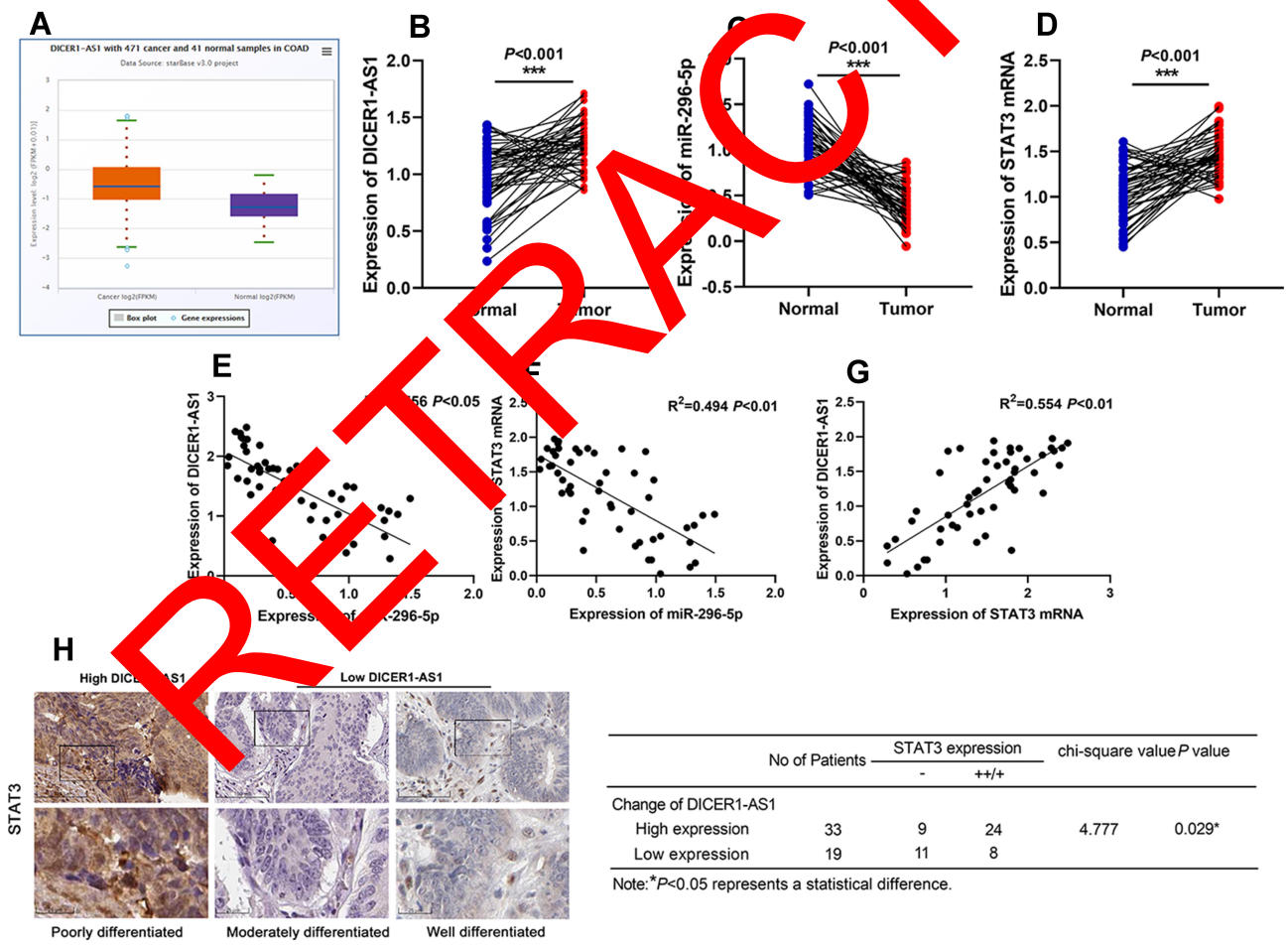
Statistical Methods

SPSS 16.0 software (SPSS Inc., Chicago, IL, USA) was used for statistical analysis, and the results were expressed as mean±SD (x±s). Student's *t*-test was used to compare the data between the two groups. The comparisons among the three groups were performed by ANOVA (parametric) test. If the results showed a significant difference, the Student's Newman-Keuls analysis was used to test the difference between the two groups. $P < 0.05$ was considered statistically significant.

Results

Expression and Correlation of DICER1-AS1, miR-296-5p and STAT3 mRNA in CRC Patients

Through StarBase database (http://starbase.sysu.edu.cn/panGeneDiffExp.php#), we found that expression level



	No of Patients	STAT3 expression		chi-square value	*P* value
		-	++/+		
Change of DICER1-AS1					
High expression	33	9	24	4.777	0.029*
Low expression	19	11	8		

Note: *$P<0.05$ represents a statistical difference.

Figure 1 The expressions of DICER1-AS in CRC tissues. (**A**) The expression of DICER1-AS1 in CRC patients from the StarBase database. (**B**–**D**) The expressions of DICER1-AS1, miR-296-5p and STAT3 mRNA in CRC tissues were detected by qRT-PCR. (**E**–**G**) Person's correlation analysis among DICER1-AS1, miR-296-5p and STAT3 mRNA. (**H**) The representative images of the immunohistochemistry staining were shown, and the association between STAT3 protein expression and DICER1-AS1 expression in CRC tissues was analyzed. ***$P < 0.001$.

of DICER1-AS1 was up-regulated in CRC tissues (Figure 1A). We then detected the expressions of DICER1-AS1, miR-296-5p and STAT3 mRNA in CRC tissues by qRT-PCR. As shown, the expressions of DICER1-AS1 and STAT3 mRNA in CRC tissues were up-regulated, while the expression of miR-296-5p was down-regulated (Figure 1B–D). We further examined the relationship among DICER1-AS1, miR-296-5p and STAT3 in CRC tissues. The results of Person's correlation analysis showed that there were negative correlations between miR-296-5p and DICER1-AS1 expressions, and miR-296-5p and STAT3 mRNA in CRC (Figure 1E and F) and that there was a positive correlation between DICER1-AS1 and STAT3 (Figure 1G). Correspondingly, immunohistochemical analysis exhibited that STAT3 protein expression in CRC tissues was positively correlated with the expression of DICER1-AS1 (Figure 1H). We also analyzed the correlation between the expression level of DICER1-AS1 and the clinicopathological indexes of CRC patients. According to the median method, the patients were divided into a high DICER1-AS1 expression group and a low DICER1-AS1 expression group. The results showed that the high expression of DICER1-AS1 was significantly related to the increase of tumor size, low tissue differentiation and higher TNM stage (Table 1). Additionally, the data from

Table 1 Correlation Between DICER1-AS1 Expression and Clinical Features (n=52)

Parameters	Group	N	DICER1-AS1 Expression		*P* value
			Low=26	High=26	
Gender	M Fema	30 22	18 8	12 14	0.092
Age (years)	<60 ≥60	11 31	5 16	11 15	0.777
Tumor size	≦5cm >5cm	20 32	14 12	6 20	0.023*
Differentiation grade	Medium/ Low High	29 23	9 17	20 6	0.002*
Lymph node metastasis	Positive Negative	32 22	14 12	18 8	0.254
TNM stage	I II III	12 17 23	9 10 7	3 7 16	0.029*

Note: *Presents $P < 0.05$.

The Cancer Genome Atlas (TCGA) indicated that high expression of DICER1-AS1 was associated with shorter survival time of CRC patients (Supplementary Figure 1).

Effects of DICER1-AS1 on Proliferation, Metastasis and Apoptosis of CRC Cells

We further detected the expression of DICER1-AS1 in normal colorectal epithelial cell and CRC cell lines. qRT-PCR results displayed that the expression level of DICER1-AS1 was significantly up-regulated in CRC cell lines compared with NCM460 cells (Figure 2A). To figure out the effects of DICER1-AS1 on proliferation, metastasis and apoptosis of CRC cells, we chose HT-29 with the lowest expression of DICER1-AS1 and HCT-8 cell line with the highest expression. The cell models of overexpression and low expression of DICER1-AS1 were successfully constructed by overexpressing DICER1-AS1 plasmid and DICER1-AS1 shRNA, respectively (Figure 2B and C). We used CCK-8 assay to detect cell proliferation and Transwell assay to detect migration and invasion. Compared with the control group, the proliferation, migration and invasion of the cells in DICER1-AS1 overexpression group were significantly promoted, while these processes in DICER1-AS1 knockdown group were significantly inhibited (Figure 2D–G). We further detected the apoptosis-related factors of cells by Western blot. After overexpression of DICER1-AS1, the expression level of Bax was down-regulated, while the expression level of Bcl2 was up-regulated in HT-29 cells, and the knockdown of DICER1-AS1 led to the opposite effect in HCT-8 cells (Figure 2H).

MiR-296-5p Was a Target of DICER1-AS1

Considering the reverse relationship between miR-296-5p and DICER1-AS1 in expression characteristics, we were curious whether there was a targeting relationship between miR-296-5p and DICER1-AS1. Interestingly, StarBase database analysis demonstrated that there were complementary base binding sites between miR-296-5p and DICER1-AS1 (Figure 3A). To further verify the targeting relationship between them, we carried out dual-luciferase reporter assay. As shown, compared with NC, miR-296-5p could significantly reduce the luciferase activity of wild-type DICER1-AS1 reporter plasmid, but had no significant effect on mutant DICER1-AS1 reporter plasmid (Figure 3B). Additionally, nuclear and cytoplasmic RNAs were separated in CRC cells, and qRT-PCR showed that DICER1-AS1 was mainly located in the cytoplasm of CRC cells, suggesting its potential as a molecular sponge (Supplementary Figure 2). To

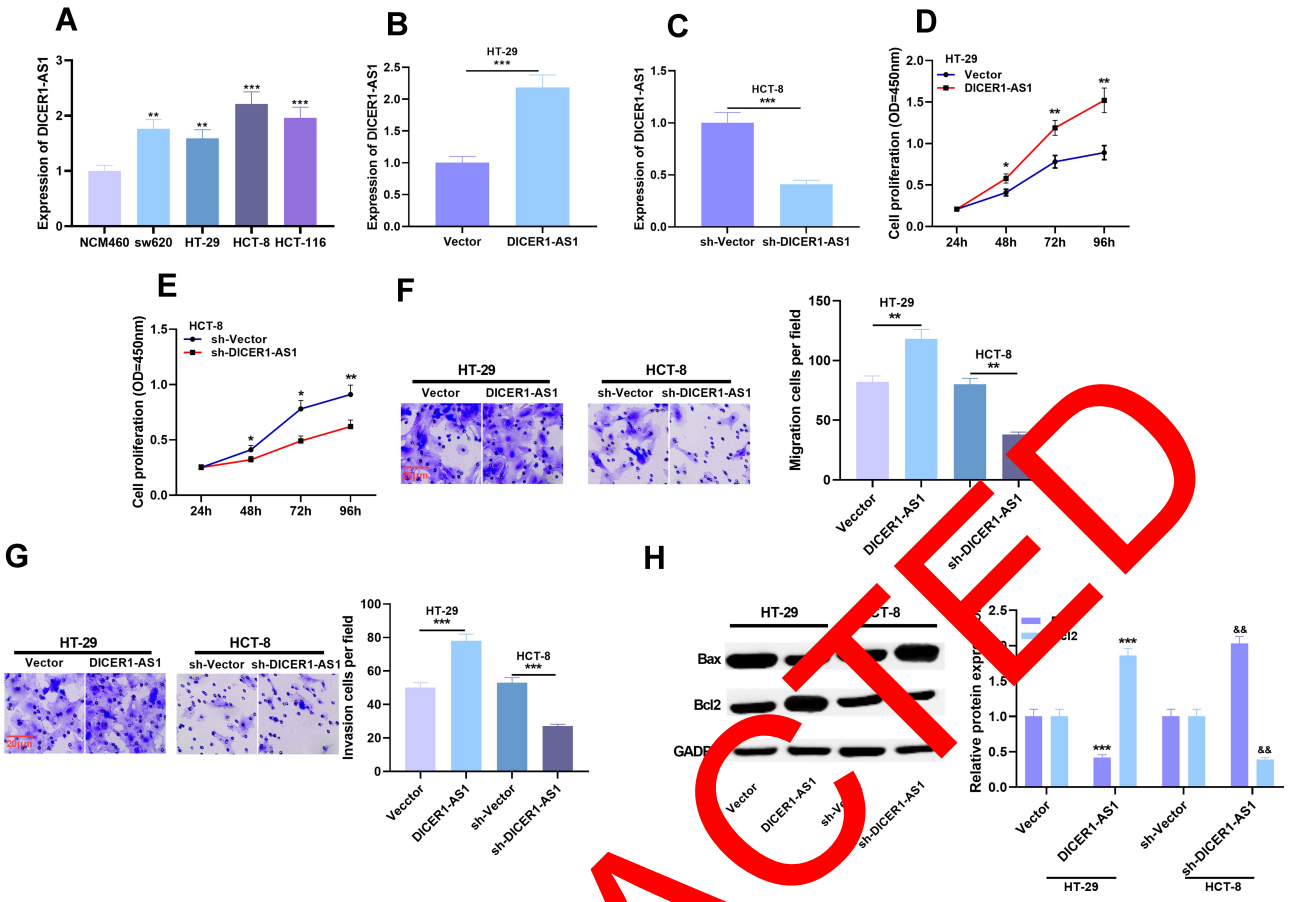


Figure 2 Effects of overexpression or knockdown of DICER1-AS1 on proliferation, migration and invasion of CRC cells. (**A**) The expression of DICER1-AS1 in CRC cell lines was detected by qRT-PCR. (**B** and **C**) The transfection efficiency of DICER1-AS1 knockdown and overexpression was verified by qRT-PCR analysis. (**D**–**G**) Cell proliferation, migration and invasion were detected by CCK-8 assay and Transwell assay. (**H**) The protein expressions of Bax and Bcl2 were detected by Western blot. *P < 0.05, **P < 0.01, ***P < 0.001, and $^{\&\&}$ P < 0.01.

further verify the relationship between DICER1-AS1 and miR-296-5p in CRC cell lines, we examined the level of miR-296-5p in colorectal epithelial cell line and CRC cell lines. The expression of miR-296-5p was significantly down-regulated in CRC cell lines (Figure 3C). In addition, qRT-PCR results displayed that overexpression and low expression of DICER1-AS1 could decrease and increase the expression level of miR-296-5p in CRC cells, respectively (Figure 3D). However, transfection of miR-296-5p mimics and inhibitors exerted no significant effect on the expression level of DICER1-AS1 (Figure 3E). These results validated that miR-296-5p was a downstream target of DICER1-AS1, and could be negatively regulated by DICER1-AS1.

Effects of miR-296-5p on Proliferation, Metastasis and Apoptosis of CRC Cells

To further explore the effects of miR-296-5p on proliferation, metastasis and apoptosis of CRC cells, we used miR-296-5p mimics and inhibitors to promote and inhibit the expression of miR-296-5p in HCT-8 and HT-29 cells, respectively (Figure 4A and B). The results of CCK-8 assay showed that the proliferation of HCT-8 cells transfected with miR-296-5p mimics was remarkably slower than that of NC group, while the proliferation of HT-29 cells transfected with miR-296-5p inhibitor was significantly promoted (Figure 4C and D). Transwell assay demonstrated that the ability of migration and invasion of cells was remarkably decreased after the transfection of miR-296-5p mimics, while the transfection of miR-296-5p inhibitors had the opposite effect (Figure 4E and F). Western blot displayed that compared with in control group, the expression level of Bax in miR-296-5p mimics group was up-regulated, while the expression level of Bcl2 was down-regulated; Bax expression level was down-regulated and Bcl2 expression level was up-regulated in the cells transfected with miR-296-5p inhibitors (Figure 4G). These findings further clarified that miR-296-5p was

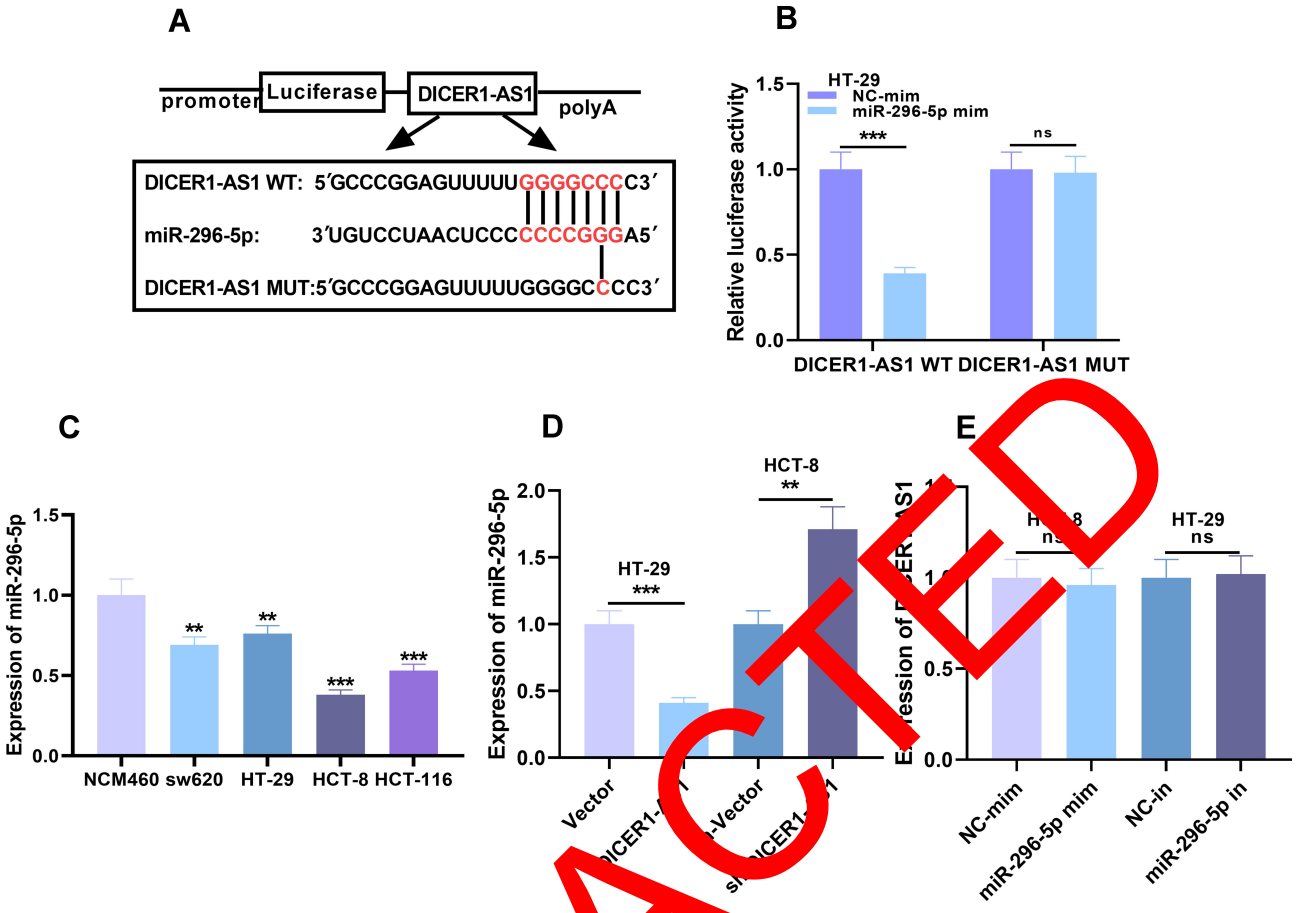


Figure 3 The targeting relationship between DICER1-AS1 and miR-296-5p in CRC. (**A**) The potential binding site between DICER1-AS1 and miR-296-5p was obtained from StarBase database. (**B**) The targeting relationship between DICER1-AS1 and miR-296-5p was validated by dual-luciferase reporter assay. (**C**) The expression of miR-296-5p in CRC cell lines was detected by qRT-PCR. (**D**) Effect of DICER1-AS1 on miR-296-5p expression in CRC was examined by qRT-PCR. (**E**) Effect of miR-296-5p on DICER1-AS1 expression in CRC was examined by qRT-PCR. $^{**}P < 0.01$ and $^{***}P < 0.001$.

associated with the malignant phenotype of CRC and probably could function as a tumor suppressor.

STAT3 Was the Functional Target of miR-296-5p

TargetScan (http://www.targetscan.org/vert_72/) showed that the 3′ region of miR-296-5p was complementary to the 3′UTR of STAT3 mRNA, suggesting that STAT3 could be a target gene of miR-296-5p (Figure 5A). Dual-luciferase reporter assay showed that the miR-296-5p mimics could decrease the luciferase activity of luciferase reporter containing STAT3 3′ UTR-WT, but had no significant effect on the luciferase activity of STAT3 3′ UTR-MUT (Figure 5B). We further tested the expression level of STAT3 mRNA in CRC cell lines. The expression level of STAT3 mRNA in CRC cells was significantly higher than that in normal colorectal epithelial cells (Figure 5C). Western blot showed that STAT3 and p-STAT3 expressions were down-regulated and up-regulated, respectively, after the transfection of miR-296-5p mimics and inhibitors in CRC cells; after overexpression and knocking down the expression level of DICER1-AS1 in cells, the expressions of STAT3 and p-STAT3 were up-regulated and down-regulated, respectively (Figure 5D and E). Collectively, STAT3 was identified as a target of miR-296-5p and positively regulated by DICER1-AS1.

DICER1-AS1 Promoted the Malignant Phenotypes of CRC Cells Through Regulating miR-296-5p

Next, we transfected miR-296-5p mimics into HT-29 cells overexpressing DICER1-AS1. qRT-PCR demonstrated that after the transfection of miR-296-5p mimics, the expression level of DICER1-AS1 in HT-29 cells had no significant change, but the expression level of STAT3 mRNA

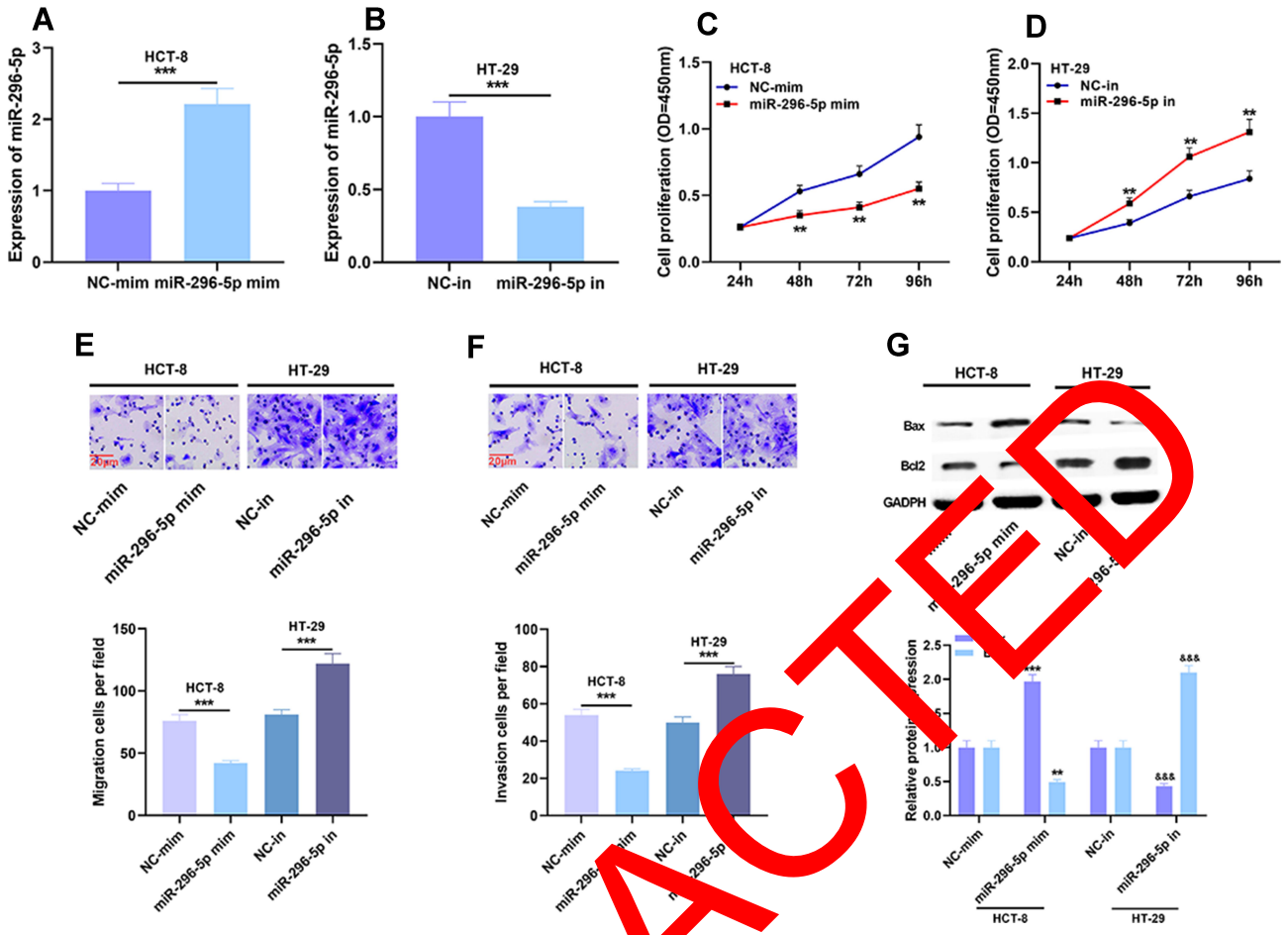


Figure 4 Effects of miR-296-5p on proliferation, migration and invasion of CRC cells. (**A** and **B**) The transfection efficiency of miR-296-5p mimics and miR-296-5p inhibitors was verified by qRT-PCR analysis. (**C**–**F**) Cell proliferation, migration and invasion were detected by CCK-8 assay and Transwell assay. (**G**) The protein expressions of Bax and Bcl2 were detected by Western blot after transfection. $^{**}P < 0.01$ and $^{***}P < 0.001$ and $^{\&\&\&}P < 0.01$.

was significantly down-regulated (Figure 6A and C). Then the proliferation, migration and invasion of HT-29 cells were detected by CCK-8 and Transwell assays. Compared with in DICER1-AS1 group, cell proliferation, migration and invasion in DICER1-AS1/miR-296-5p mimics group were significantly inhibited (Figure 6D–F). Western blot showed that after the transfection of miR-296-5p mimics, the promotion of Bcl-2 expression and inhibition of Bax expression in HT-29 cells induced by DICER1-AS1 over-expression were reversed (Figure 6G). The above results further verified the existence of DICER1-AS1/miR-296-5p/STAT3 axis in CRC.

Discussion

The investigation on the molecular mechanism related to proliferation, metastasis and apoptosis of CRC cells will help to identify potential therapeutic targets.[18] The current study provided a new axis involved in CRC progression, namely DICER1-AS1/miR-296-5p/STAT3. We firstly observed that the expression of DICER1-AS1 was up-regulated in CRC tissues and cells, and further verified that DICER1-AS1 promoted the progression of CRC by targeting miR-296-5p to up-regulate the expression of STAT3.

It is reported that abnormal expression of lncRNAs is involved in the tumorigenesis and progression of CRC. For example, lncRNA CRNDE can regulate the chemoresistance of CRC cells by regulating the expression level of miR-181a-5p and the activity of Wnt/β-catenin signaling.[19] In addition, lncRNA BFAL1 mediates the carcinogenesis of enterotoxic Bacillus fragilis-associated CRC through regulating RHEB/mTOR pathway.[20] In this study, we found that the expression of DICER1-AS1 was up-regulated in CRC tissues and cell lines. In vitro experiments showed that DICER1-AS1 could promote the proliferation, migration and invasion of CRC cells and inhibit their apoptosis. To our best knowledge, this is the first work to investigate the expression and function of DICER1-AS1 in CRC.

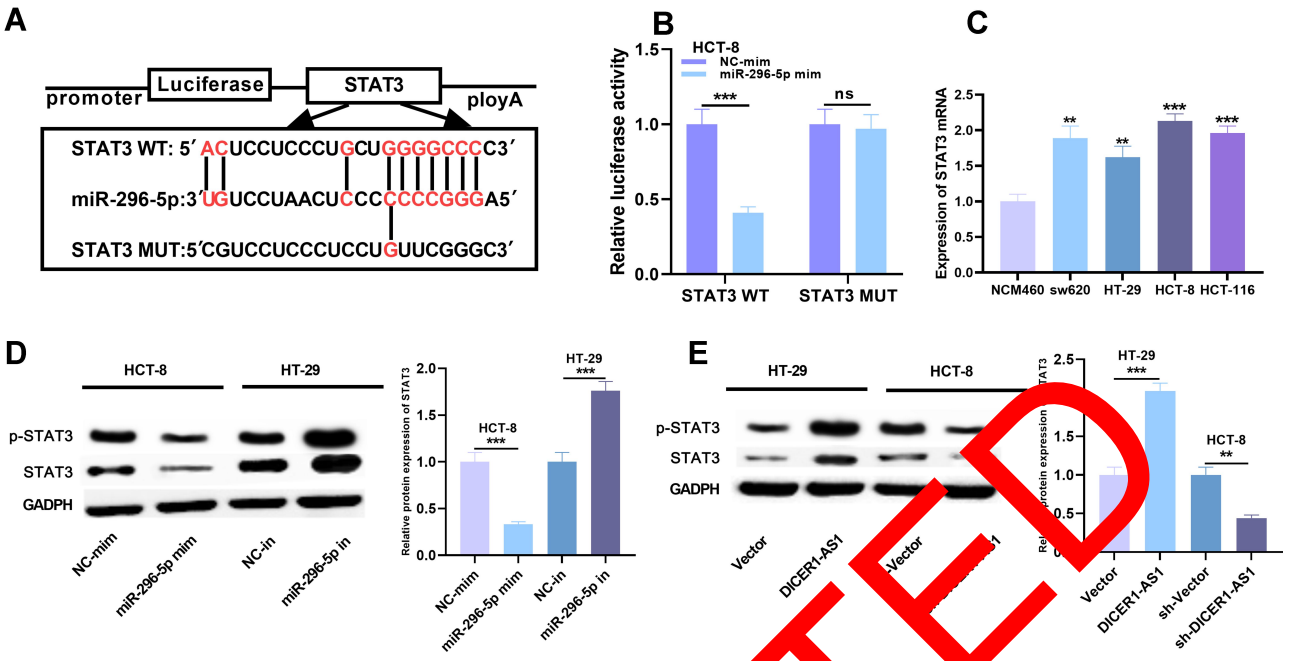


Figure 5 The targeting relationship between miR-296-5p and STAT3 in CRC. (**A**) The potential binding site between miR-296-5p and STAT3 was obtained from TargetScan database. (**B**) The targeting relationship between miR-296-5p and STAT3 was verified by dual-luciferase reporter assay. (**C**) The expression of STAT3 mRNA in CRC cell lines was detected by qRT-PCR. (**D** and **E**) The protein expression of STAT3 and p- STAT3 was detected by Western blot after transfection. $^{**}P < 0.01$ and $^{***}P < 0.001$.

Existing studies authenticate the role of miR-296-5p as a tumor suppressor. For example, the expression of miR-296-5p is down-regulated in hepatocellular carcinoma and miR-296-5p suppresses the epithelial-mesenchymal transition of cancer cells by targeting neuropilin-1, ERB-B2 receptor tyrosine kinase-2 and ERB-B3 receptor tyrosine kinase-3.[12] Similarly, its expression is down-regulated in NSCLC tissues and cell lines and miR-296-5p targets polo-like kinase-1 to regulate the progression of NSCLC.[11] The expression and function of miR-296-5p in CRC are also confirmed: down-regulation of miR-296-5p in CRC tissues can facilitate the proliferation of CRC cells by activating the Wnt/β-catenin/cyclin D1 signaling pathway.[21] Our work indicates that the overexpression of miR-296-5p could inhibit the proliferation, invasion and migration of CRC cells, and promote the apoptosis of CRC cells. This finding is consistent with the above reports supporting that miR-296-5p exerts a tumor-suppressive role in tumors.

An increasing number of studies manifest that lncRNAs can function as ceRNAs of miRNAs, and they can inhibit miRNAs as molecular sponges. For example, lncRNA SNHG14 promotes the tumorigenesis and metastasis of CRC through the miR-32-5p/SKIL axis;[22] in CRC, lncRNA PVT1 regulates the expression of Y-box binding protein 1 by acting as ceRNA of miR-216a-5p, thereby promoting cancer progression.[23] To further pinpoint the molecular mechanism of CRC, we screened the potential downstream target miR-296-5p of DICER1-AS1 through StarBase database. We made a hypothesis that miR-296-5p might play a role as a downstream molecule of DICER1-AS1 in CRC. Next, the luciferase reporter assay confirmed the targeted binding relationship between DICER1-AS1 and miR-296-5p. Overexpression and knockdown of DICER1-AS1 decreased and increased the expression of miR-296-5p, respectively, and the transfection of miR-296-5p mimics reduced the increase of proliferation, migration and invasion of cancer cells caused by DICER1-AS1 overexpression. These data confirmed that miR-296-5p participated in the development of CRC as a downstream molecule of DICER1-AS1.

STAT3 is a crucial signal conducting molecule in cells and regarded as a potential target for cancer therapy, and it mediates a variety of cellular functions, including proliferation, differentiation, migration, invasion, angiogenesis, apoptosis and immune response.[24] Moreover, it is identified as a molecular link between chronic inflammatory bowel disease and tumorigenesis of CRC.[25] Previous researches elucidate that it can increase the expressions of a series of oncogenes including cyclin D2, hypoxia-inducible factor 1α, vascular endothelial growth factors and so on.[26–28] Its activation also endows CRC cells with 5-FU resistance and radioresistance.[26,29] A recent study

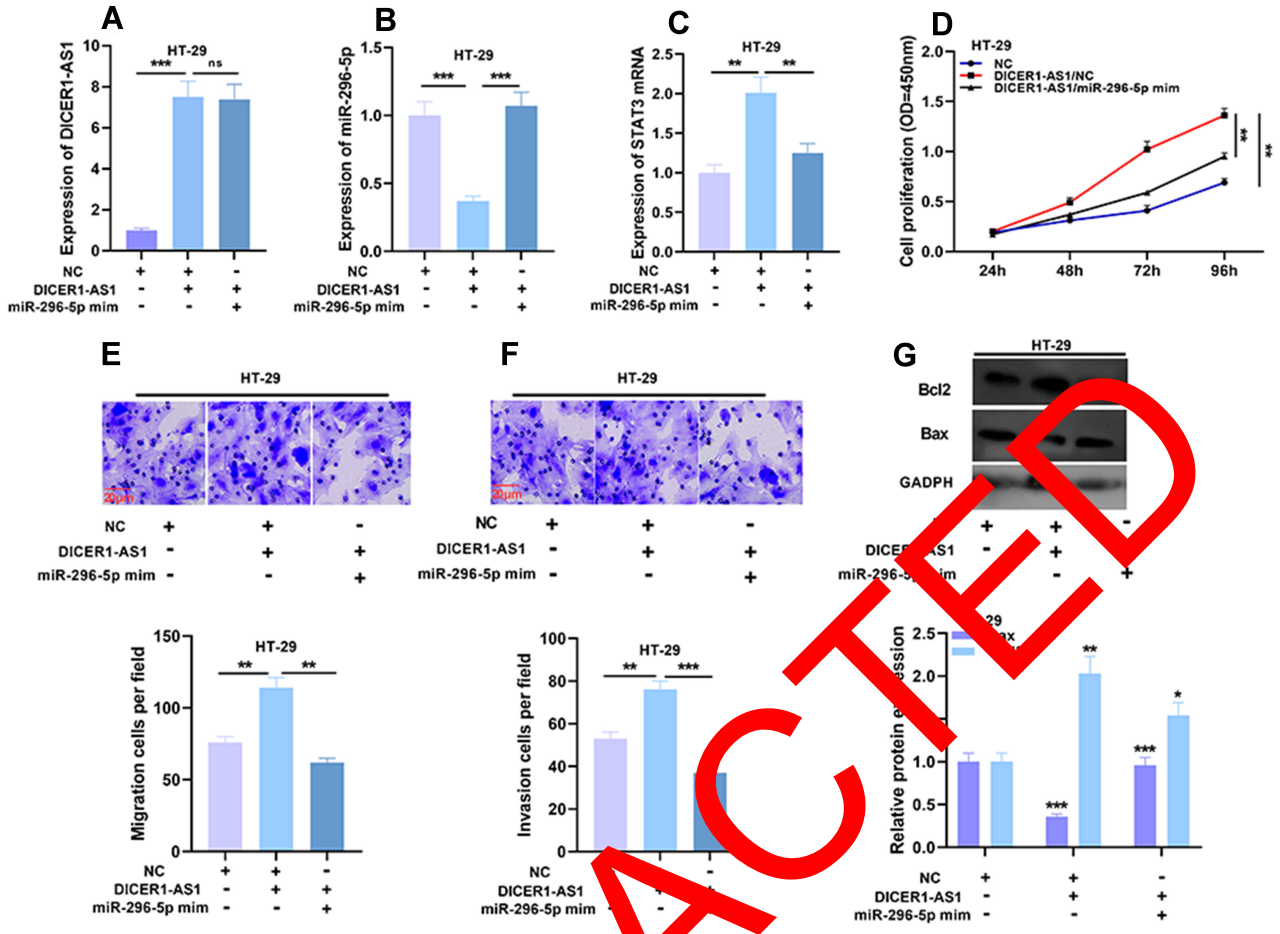


Figure 6 Effects of DICER1-AS1 and miR-296-5p on proliferation, migration and invasion of CRC cells. (**A**–**C**) The co-transfection efficiency was verified by qRT-PCR analysis. (**D**–**F**) Cell proliferation, migration and invasion were detected by CCK-8 assay and Transwell assay. (**G**) The protein expressions of Bax and Bcl2 were detected by Western blot after transfection. *$P < 0.05$, **$P < 0.01$ and ***$P < 0.001$.

indicates that miR-296-5p inhibits the malignant phenotypes of esophageal squamous cell carcinoma by suppressing STAT3.[30] In this work, we determined the interaction between miR-296-5p and STAT3 in CRC. We first confirmed that miR-296-5p could negatively regulate the expression of STAT3 in CRC cells, which was consistent with the previous work.[30] In addition, overexpression and knockdown of DICER1-AS1 could increase and decrease the expression of STAT3 protein, respectively. These data revealed that in CRC, DICER1-AS1 played an oncogenic role partly by regulating the expression of STAT3.

Conclusion

To sum up, our study provides the first evidence that upregulation of DICER1-AS1 is associated with CRC progression. In terms of mechanism, DICER1-AS1 can regulate miR-296-5p/STAT3 axis. This work may provide new molecular targets for clinical trials.

Abbreviations

LncRNA, Long non-coding RNA; CRC, colorectal cancer; DICER1-AS1, DICER1 antisense RNA 1; STAT3, signal transducer and activator of transcription 3; ceRNA, competing endogenous RNA; qRT-PCR, real-time polymerase chain reaction; CCK-8, Cell counting kit-8.

Data Sharing Statement

The data used to support the findings of this study are available from the corresponding author upon request.

Ethics Approval and Consent to Participate

The collection and use of patient tissue samples were approved by the Linyi Central Hospital Ethics Committee. All patients involved gave informed consent to the study and signed a written consent form.

Consent for Publication

All the authors reviewed the final edition of this manuscript and agreed to submit.

Author Contributions

All authors contributed to data analysis, drafting or revising the article, have agreed on the journal to which the article will be submitted, gave final approval of the version to be published, and agree to be accountable for all aspects of the work.

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Disclosure

The authors declare that they have no competing interests for this work.

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