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ORIGINAL RESEARCH

RETRACTED ARTICLE: Circ_0005576 Promotes Malignant Progression Through miR-874/CDK8 Axis in Colorectal Cancer

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Purpose: To investigate the function of circ_0005576 in colorectal cancer (CRC) progression.

Patients and Methods: Circ_0005576 expression in CRC patients was detected by quantitative real-time polymerase chain reaction (qRT-PCR) and in situ hybridization (ISH). CRC cells were transfected using Lipofectamine 2000 reagent. CRC cell proliferation was researched by Cell Counting Kit-8 (CCK-8) assay and 5-ethynyl-2-deoxy-uridine (EdU) incorporation experiment. Cell cycle and apoptosis were determined by flow cytometry analysis. Luciferase reporter assay was used to explore the relationship between circ_0005576 and miR-874 or between miR-874 and CDK8. qRT-PCR and Western blot were used to detect circ_0005576, miR-874, and CDK8 expression. In vivo experiments were performed using nude mice. CDK8 and Ki67 expression in xenograft tumors was investigated by immunohistochemistry. Tunel assay was conducted to analyze the apoptosis of xenograft tumors.

Results: Circ_0005576 expression was up-regulated in CRC, which was associated with tumor progression ($P < 0.05$ or $P < 0.01$). Circ_0005576 knockdown in CRC cells reduced proliferation, induced apoptosis, increased cells in the G1 phase, and decreased cells in the S phase ($P < 0.01$ or $P < 0.001$). Circ_0005576 promoted CDK8 expression via sponging miR-874. miR-874 knockdown and CDK8 overexpression significantly reversed the inhibitory effect of circ_0005576 knockdown on CRC cells malignant phenotype ($P < 0.05$ or $P < 0.01$). Circ_0005576 knockdown inhibited tumor growth in vivo ($P < 0.01$). Circ_0005576 knockdown reduced CDK8, Ki67 expression, and enhanced apoptosis in xenograft tumors.

Conclusion: Circ_0005576 promoted malignant progression through the miR-874/CDK8 axis in CRC.

Keywords: CRC, circ_0005576, miR-874/CDK8 axis, malignant progression, in vivo study

Introduction

According to the latest statistics, colorectal cancer (CRC) has become the third most common tumor in the world.[1] Around 1.36 million new cases and 694,000 mortalities are attributed to CRC every year.[2] CRC treatment has made rapid progress in recent years, but unexpected recurrence and metastasis are still important reasons for the poor prognosis of patients.[3] Understanding of the progression mechanism of CRC is urgently needed to find new treatment strategies to improve clinical intervention efficiency.

Circular RNAs (circRNAs) are a class of non-coding RNA molecules with covalent closed loops, characterized by highly stable nuclease resistance, species

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conservation, and specific expression in developmental stages.[4] Recent studies have shown that circRNAs function as a "sponge" for miRNAs to block the inhibitory effect of miRNAs on downstream target gene expression.[5,6] Several circRNAs have been confirmed to be involved in the development of diseases through this pathway. In CRC, circ_0009361 has been revealed to inhibit tumor growth and metastasis in vivo and in vitro by regulating the expression of APC2 via sponging miR-582.[7] CRC cell proliferation, migration, invasion in vitro, and tumor growth in vivo could be suppressed by knockdown of circ_000984. Mechanistically, circ_000984 could enhance CDK6 expression via sponging miR-106b, thereby inducing a series of malignant phenotypes of CRC cells.[8] Research also demonstrated that circ_001569 facilitated CRC cell proliferation and invasion by indirectly promoting the expression of E2F5, BAG4, and FMNL2 via sponging miR-145.[9] At present, more and more circRNAs with important regulatory function on CRC have emerged. High stability and specific expression in tissues and diseases make circRNAs potential biomarkers for disease diagnosis and prognosis.[10]

Circ_0005576 is a recently discovered circRNA, which has been found to facilitate cervical cancer progression by acting on the miR-153/KIF20A axis.[11] Circ_0005576 has therefore been proposed as an effective target for the therapeutic intervention in cervical cancer. However, no study has proven the role of circ_0005576 in the development of CRC as well as other human tumors. We speculated that circ_0005576 might be involved in the development of CRC. Hence, in the present work, the function of circ_0005576 in CRC has been explored with miR-874/CDK8 as the axis. As far as we know, this is the first time that circ_0005576 has been studied in CRC. The targeted therapy of human tumors including CRC, has a very important role in improving the prognosis of patients. We hope this study will provide a novel target for the clinical treatment of CRC.

Patients and Methods

Patients and Tissues

Tumor tissues and adjacent normal tissues were collected from 112 patients with CRC. All tissues were immediately frozen in liquid nitrogen. These patients were first diagnosed with CRC in our hospital from 2011.4 to 2014.9, and had never received radiation or chemotherapy before surgery. Clinical data of all patients were collected, including age, gender, tumor size, TMN stage, local invasion, and lymphatic metastasis. In addition, all patients were followed up for 1500 days after treatment. Kaplan–Meier survival analysis was applied to the survival analysis of patients.

All patients volunteered to participate in this study and have signed written informed consent. This study has been approved by the Weifang People's Hospital ethics committee in compliance with the Helsinki Declaration.

In situ Hybridization (ISH)

ISH was performed to detect the expression of circ_0005576 in clinical specimens. Briefly, normal tissues and tumor tissues collected from CRC patients were embedded in paraffin, followed by being made into sections with a thickness of 4 μm. Xylene was used for the dewaxing of sections and gradient ethanol was used to hydrate sections. After washing with phosphate-buffered saline (PBS), sections were incubated with proteinase K (Solarbio, Beijing, China) for 30 min at 58°C. Then, polyoxymethylene (4%) was added into sections for the fixation of sections. These sections were hybridized for 12 h at 55°C by adding 5′-digoxigenin-labeled circ_0005576 probe (20 μL, View Solid Biotechnology, Beijing, China). Subsequently, the sections were subjected to incubation with horseradish peroxidase (HRP) for 30 min at 4°C. Diaminobenzidine (DAB) (Solarbio, Beijing, China) was used for color development. The expression of circ_0005576 in sections was observed under a microscope, and brown particles were circ_0005576 positive expression signals.

Circ_0005576 Structural Stability Test

The structural stability of circ_0005576 was detected by incubating ribonuclease R (RNase-R) with total RNA. In short, clinical tumor tissue samples were ground into powder in liquid nitrogen. Total RNA in tumor tissues was extracted using TRIzol reagent (Thermo Fisher Scientific, Waltham, MA, USA) according to the instructions. Total RNA samples with an amount of 2.5 μg were incubated with 10 U RNase-R (Geneseed Biotech, Guangzhou, China) for 30 min at 37°C. The expression of circ_0005576 and GAPDH in the RNA samples was detected by quantitative real-time polymerase chain reaction (qRT-PCR).

Cell Culture

Normal colonic epithelial cell line (FHC) and CRC cell lines (SW620, SW116, SW480, and LOVO) were provided by the Institute of Biochemistry and Cell Biology of the Chinese Academy of Sciences (Shanghai, China). Cell lines were maintained in Dulbecco's modified Eagle medium (DMEM) with 10% fetal bovine serum (FBS), streptomycin (100 mg/mL), and penicillin (100 units/mL). All cells were incubated in a humidified atmosphere with 5% CO_2 at 37°C.

Transfection

SW620 and SW480 cells were seeded in 6-well plates with serum-free DMEM (1×10^5 cells and 1 mL DMEM per well). shRNA targeting circ_0005576 was used to transfect cells (named sh-circ_0005576 group). Moreover, cells were transfected by shRNA negative control targeting circ_0005576 (named sh-NC group). miR-874 mimics and negative control were respectively transfected into cells (named miR-874 mimics group and miR-NC group, respectively). In addition, cells underwent co-transfection by circ_0005576 shRNA and miR-874 inhibitor (named sh-circ_0005576 + miR-inhibitor group), or by circ_0005576 shRNA and miR-874 negative control (sh-circ_0005576 + miR-NC group), or by circ_0005576 shRNA and pcDNA3.1-CDK8 negative control vector (named sh-circ_0005576 + NC-CDK8 group), or by circ_0005576 shRNA and pcDNA3.1-CDK8 overexpression vector (named sh-circ_0005576 + OE-CDK8 group). shRNA and negative control targeting circ_0005576, miR-874 mimics, miR-874 inhibitor and negative control, pcDNA3.1-CDK8 negative control vector, and pcDNA3.1-CDK8 overexpression vector were all synthesized and provided by Gene Pharma (Shanghai, China). Lipofectamine 2000 reagent (ThermoFisher Scientific, Waltham, MA, USA) was used for the transfection according to the instructions. Successfully transfected cells were collected after 48 h and were cultured in DMEM containing 10% FBS at 37°C, 5% CO_2. The transfection efficiency was determined by qRT-PCR after 24 h of culture.

Cell Counting Kit-8 (CCK-8) Assay

Cells were collected after 48 h of transfection and dispersed in DMEM containing 10% FBS. The density of cell suspension was 1×10^5 cells/mL. In 96-well plates, 100 µL cell suspension was added into each well for 0, 24, 48 and 72 h incubation at 37°C, 5% CO_2. At each time point, 10 µL CCK-8 solution (Solarbio, Beijing, China) was added into each well for 2 h incubation at 37°C. The optical density (OD) value of each well was measured at a wavelength of 450 nm using a microplate reader (Biotek, Winooski, VT, USA). Five duplicate wells were set in each group.

5-Ethynyl-2-Deoxy-Uridine (EdU) Incorporation Experiment

The proliferation of SW620 and SW480 cells was explored by using the EdU incorporation experiment. Cells were seeded in 24-well plates (4×10^4 cells per well) with 600 µL DMEM (10% FBS) for 24 h culture at 37°C, 5% CO_2 so that cells adhered to the bottom of each well. Then, PBS was used to wash cells in each well. EdU solution (10 µmol/L) (RiboBio, Guangzhou, China) was added into cells for 2 h incubation at 37°C. After washing with PBS, cells were fixed and permeabilized in PBS containing 2% formaldehyde and 0.5% Triton X100 (Solarbio, Beijing, China) for 15 min. PBS containing 10% FBS was used to block cells for 30 min. Then, 4′-diamidino-2-phenylindole (DAPI) (Solarbio, Beijing, China) was used to stain cells. Under a fluorescence microscope (Nikon, Tokyo, Japan), EdU positive cells were observed with red fluorescence as positive signals.

Flow Cytometry Analysis

For cell cycle detection, cells were harvested after 48 h of culture, followed by being fixed with 75% ethanol for 24 h at −20°C. After washing twice with PBS, cells were stained with propidium iodide (PI) (Solarbio, Beijing, China) for 30 min at room temperature. Cell cycle distribution features were evaluated by FACS Calibre flow cytometer (BD Bioscience, San Jose, CA, USA) with Cell Quest software (BD Bioscience) for data analysis.

For apoptosis detection, cells were incubated with Annexin V and PI for 30 min in darkness. The apoptosis was assessed using a FACS Calibre flow cytometer with Cell Quest software for data analysis.

Luciferase Reporter Assay

Through TargetScan and miRanda online analysis, we noticed that miR-874 possessed the binding site for circ_0005576 and CDK8. The 3′-UTR segments of circ_0005576 containing the miR-874 binding site were cloned into the pmirGLO luciferase reporter, including wild type (wt)-circ_0005576-luciferase reporter and

mutant type (mut)-circ_0005576-luciferase reporter. Furthermore, the CDK8-3′URT-wt-luciferase reporter and CDK8-3′URT-mut-luciferase reporter containing the miR-874 binding site were also prepared. All luciferase reporters were provided by Gene Pharma (Shanghai, China). SW620 cells were transfected by miR-874 mimics (named miR-874 mimics group) and negative control (named miR-NC group) respectively. Thereafter, the above four kinds of luciferase reporters were used separately to cotransfect SW620 cells of the miR-874 mimics group and miR-NC group. Lipofectamine 2000 reagent was used for the transfection. Cells were cultured at 37°C, 5% CO_2 for 48 h. Dual-Luciferase Reporter Assay System (Promega, Madison, WI, USA) was used for the detection of luciferase activity with sea renal fluorescent as control.

RNA Pull-Down Assay

SW620 and SW480 cells were subjected to transfection with biotinylated miR-874-wild type, biotinylated miR-874-mutant type, and biotinylated miR-874-negative control (Ribobio, Guangzhou, China). Cells were sequentially named Bio-miR-874-Wt group, Bio-miR-874-Mut group, and Bio-NC group. After 48 h of culture, cells of each group were collected and lysed. Notably, 50 μL of each sample was aliquoted for input. According to the manual, the remaining lysate of each sample was incubated with Dynabeads M-280 Streptavidin (Invitrogen, CA, USA). The beads were added into RNase-free solutions. Subsequently, biotinylated miR-874 was added for 10 min incubation at room temperature. EDTA (10 mM) with formamide (95%) was then used to incubate the beads for 5 min at 65°C. Thereafter, Trizol was applied for the purification of the bound circ_0005576. The enrichment of circ_0005576 was detected by qRT-PCR.

qRT-PCR

Tissues that were stored in liquid nitrogen were ground into powder in liquid nitrogen. According to the instructions, total RNA was collected from tissues and cells by using Trizol Reagent (Thermo Fisher Scientific, Waltham, MA, USA). RNA samples were transcribed into cDNA by Primescript RT Reagent kit (Takara, Shiga, Japan). A7500 Real-Time PCR System (Applied Biosystems, Foster City, CA, USA) with Fast Start Universal SYBR Green Master (Roche Applied Science, Mannheim, Germany) was used for qRT-PCR. The PCR procedure for circ_0005576, miR-874, and U6 was as follows: 95°C for 120 s, and 40 cycles of 95°C for 30 s and 60°C for 45 s. The PCR parameters for CDK8 and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) were as follows: 95°C for 120 s, and 40 cycles of 95°C for 15 s, 60°C for 30 s. Primer sequences were designed by Gene Pharma (Shanghai, China) as follows: circ_0005576, forward, 5′-TGCCAAGAACAAACAGAAGC-3′, reverse, 5′-TTTTACCAACAGCACCATCG-3′. miR-874, forward, 5′-TGCGGCTGCCCTGGCCCGAGGGAC-3′, reverse, 5′-CCAGTGCAGGGTCCGAGGT-3′. U6 forward, 5′-GCTTCGGCAGCACATATACTAAAAT-3′, reverse, 5′-CGCTTCACGAATTTGCGTGTC-3′. CDK8, forward, 5′-TCACCTTTGAAGCC-TTAGC-3, reverse, 5′-CTGATGTAGGAAGTGG-CT-3′. GAPDH, forward, 5′-CGGAGTCAACGGA-TTGGTCGT-3′, reverse, 5′-AGCCTTCTCCATG-GGTC-AGAC-3′. U6 was used as the internal control for circ_0005576 and miR-874. GAPDH served as the internal control for CDK8. The relative expression of circ_0005576, miR-874, and CDK8 was analyzed by the $2^{-\Delta\Delta Ct}$ method.

Western Blot

Cells were harvested after 48 h of transfection and lysed with cell lysis. Total protein concentration was measured using the BCA Protein Assay kit (ThermoFisher Scientific, Waltham, MA, USA). An equal amount of total proteins (50 μg) was collected for separation by 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE). And then these proteins were transferred onto a polyvinylidene fluoride (PVDF) membrane. Non-fat milk (5%) was used to block the PVDF membrane for 2 h. Polyclonal rabbit anti-human CDK8 (1:1000, Santa-Cruz Biotechnology, Santa Cruz, CA, USA) was added onto the PVDF membrane for 12 h incubation at 4°C. Tris-buffered saline and Tween 20 (TBST) were used to wash the PVDF membrane three times. The PVDF membrane was subsequently incubated with horseradish peroxidase (HRP)-conjugated secondary antibody (1:5000, Solarbio, Beijing, China) for 2 h at room temperature. The blots were visualized by enhanced chemiluminescence plus reagent (GE Healthcare, Chicago, IL, USA). Quantity One software version (Bio-Rad, Hercules, CA, USA) was used to quantify CDK8 protein expression with GAPDH as the internal control.

In vivo Tumor Growth Assay

Animal experiments were performed with the approval of the Animal Ethics Committee of Weifang People's Hospital. Animal experiments were performed in

accordance with relevant guidelines and regulations of the Animal Care and Use Committees at the Weifang People's Hospital, and a signed document issued by the Animal Care and Use Committees that granted approval was obtained. Twelve nude mice (4 weeks old) were provided by the Shanghai Experimental Animal Center, Chinese Academy of Sciences (Shanghai, China). A total of 1×10^6 SW620 cells transfected by circ_0005576 shRNA and negative control was dispersed in 100 μL PBS. Then, these cells were injected subcutaneously into the back of nude mice. Cells of each group were randomly injected with 6 nude mice. After injection, mice were housed individually in cages with free access to food and water. Tumor size was measured every 7 days. The tumor volume was calculated as follows: $V = (ab^2)/2$. The long (a) and short (b) diameters of tumors were measured using vernier calipers. On the 28th day, mice were deeply anesthetized via intraperitoneal injection of 60 mg/kg pentobarbital. Thereafter, mice were sacrificed by rapid cervical dislocation. Tumor tissues in mice were stripped and weighed.

Immunohistochemistry

Tumor tissues obtained from nude mice were fixed in formalin and embedded in paraffin. Tumor sections with a thickness of 4 μm were prepared. After dewaxing, sections were rehydrated by gradient alcohol and blocked by 0.3% H_2O_2. Antigen retrieval of the sections was performed by adding 0.01 M sodium citrate buffer solution (pH = 6.0) for 15 min incubation at 95°C. After washing by PBS, rabbit anti-Ki67 and rabbit anti-CD34 antibodies (1:100, Solarbio, Beijing, China) were used to incubate sections for 12 h at 4°C. Goat-anti-rabbit IgG-HRP (1:500, Boster, Wuhan, China) was then used to incubate sections for 1 h at room temperature. The staining of sections was performed using diaminobenzidine (DAB) solution and hematoxylin. CD34 and Ki-67 expression was observed under a microscope (Olympus, Tokyo, Japan) with brown particles as positive expression signals.

Tunel Assay

Tumor sections were dewaxed with xylene and hydrated by gradient alcohol. Proteinase K (Solarbio, Beijing, China) was added onto sections for 30 min incubation at room temperature. To block endogenous peroxidase, 0.3% H_2O_2 was used to incubate sections for 10 min at room temperature. Sections were incubated with 100 μL terminal transferase reaction solution (Solarbio, Beijing, China) for 1 h at 37°C in darkness. A total of 50 μL HRP working solution was used to incubate sections for 30 min at 37°C in the dark. Sections were then stained with diaminobenzidine (DAB) and hematoxylin. After dehydration by gradient ethanol, the sections were treated with xylene and sealed in neutral resin. Apoptotic cells were observed under a microscope (Olympus, Tokyo, Japan) with brown particles indicating positive signals.

Statistical Analysis

All experiments were independently repeated at least three times. Data were expressed as mean ± standard deviation (SD) and analyzed by SPSS software (SPSS Inc., Chicago, IL, USA). A comparison of the two groups was carried out by Student's *t* test, and a comparison of at least three groups was evaluated by one-way analysis of variance (ANOVA). The correlation between circ_0005576 expression and CRC patients' clinical pathology was analyzed by Pearson's $\chi 2$ test. Correlation analysis between two genes was performed using Pearson's correlation analysis. $P < 0.05$ meant statistically significant difference.

Results

Circ_0005576 Expression in CRC Patients Was Aberrantly Up-Regulated and Associated with Disease Progression

Circ_0005576 expression in tissues of 112 CRC patients was determined by qRT-PCR in order to investigate the role of circ_0005576 in the development of CRC. The expression of circ_0005576 in tumor tissues was found to be aberrantly up-regulated compared to that in normal tissues ($P < 0.01$) (Figure 1A). Kaplan–Meier survival analysis showed that CRC patients with high circ_0005576 expression had markedly lower percent survival than those with low circ_0005576 expression ($P < 0.05$) (Figure 1B). ISH assay further proved the increased circ_0005576 expression in tumor tissues compared to that in normal tissues (Figure 1C). The structural stability of circ_0005576 was detected by incubating RNase-R with total RNA. The result showed that the incubation with RNase-R did not affect the level of circ_0005576, but significantly reduced GAPDH levels ($P < 0.001$) (Figure 1D). In vitro studies exhibited much higher circ_0005576 expression in CRC cell lines (SW620, SW116, SW480, and LOVO) than that in a normal colonic epithelial cell line (FHC) ($P < 0.05$ or $P < 0.01$) (Figure 1E). Analysis of patients' clinical data showed that high circ_0005576 expression was

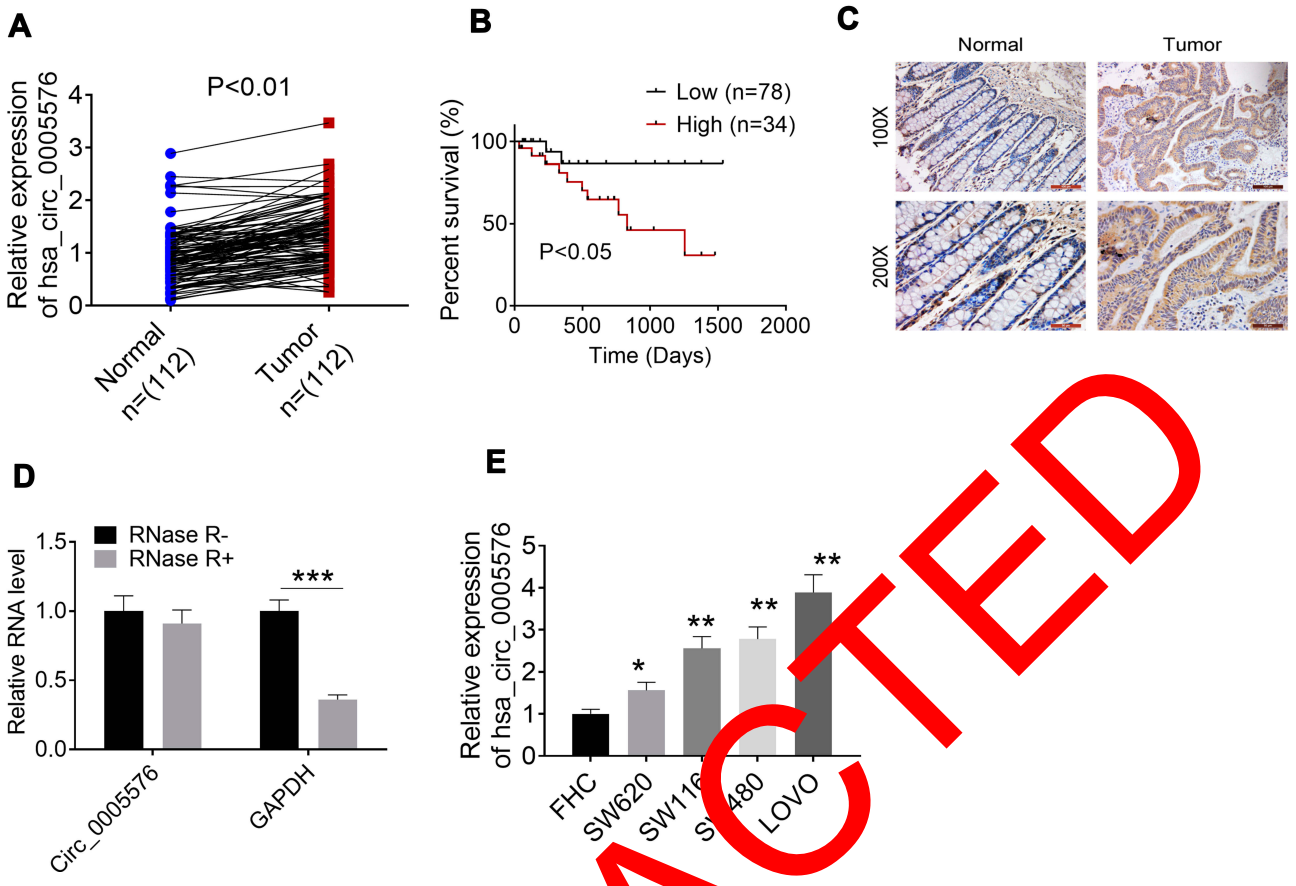

Figure 1 Circ_0005576 expression in CRC patients was aberrantly up-regulated. (**A**) qRT-PCR was performed to detect circ_0005576 expression in normal/tumor tissues of 112 CRC patients. Results indicated that circ_0005576 was aberrantly up-regulated in tumor tissues compared to in normal tissues. (**B**) Kaplan–Meier survival analysis showed that CRC patients with high circ_0005576 expression had markedly lower percent survival than those with low circ_0005576 expression. (**C**) ISH assay proved the increased circ_0005576 expression in tumor tissues than that in normal tissues. (**D**) Circ_0005576 structural stability was researched by incubating total RNA with RNase-R. Data revealed that the circle structure of circ_0005576 could not be destroyed by RNase-R and circ_0005576 could be stably expressed in CRC. ***$P < 0.001$. (**E**) qRT-PCR illustrated that circ_0005576 expression in CRC cell lines (SW620, SW116, SW480 and LOVO) was obviously up-regulated compared to in normal colonic epithelial cell line (FHC). *$P < 0.05$ and **$P < 0.01$ when compared with FHC cells.

Abbreviations: CRC, colorectal cancer; GAPDH, glyceraldehyde-3-phosphate dehydrogenase; qRT-PCR, quantitative real-time polymerase chain reaction; ISH, in situ hybridization.

significantly associated with large tumor size and advanced TMN stage ($P < 0.05$) (Table 1).

Knocking Down of Circ_0005576 Inhibited Proliferation and Promoted Apoptosis of CRC Cells

Circ_0005576 expression in SW620 and SW480 cells was obviously suppressed by transfection with circ_0005576 shRNA ($P < 0.001$) (Figure 2A). A CCK-8 assay and the EdU experiment were performed to explore whether circ_0005576 was responsible for CRC cell proliferation. Results showed prominently lower OD value at 72 h and less EdU positive cells (red fluorescence) of the sh-circ_0005576 group relative to the sh-NC group ($P < 0.01$ or $P < 0.001$) (Figure 2B and C). Moreover, flow cytometry analysis exhibited that, compared with the sh-NC group, SW620 and SW480 cells of the sh-circ_0005576 group had more cells in the G1 phase, fewer cells in the S phase, and more apoptotic cells ($P < 0.01$) (Figure 2D and E).

Circ_0005576 Promoted CDK8 Expression Through Suppressing miR-874 in CRC

The binding site of circ_0005576 and miR-874 obtained by bioinformatics analysis is shown in Figure 3A. Luciferase reporter assay was conducted to confirm miR-874 as a direct target of circ_0005576 using SW620 cells. Compared with SW620 cells cotransfected by miR-874 negative control and wt-circ-Luciferase reporter, the relative luciferase activity of cells cotransfected by miR-874 mimics

Table 1 The Correlation Between Circ_0005576 Expression and Clinicopathological Parameters of CRC Patients

Characteristics	Number of Patients	Low Circ_0005576 Expression (< Median)	High Circ_0005576 Expression (≥ Median)	*P*-value
Number	112	78	34	
Ages (years)				0.400
<60	37	26	11	
≥60	75	52	23	
Gender				0.503
Female	43	30	13	
Male	69	48	21	
Tumor size				0.024
≤5 cm	74	58	16	
>5 cm	38	20	18	
TMN stage				0.034
I–II	64	49	15	
III–IV	48	29		
Local invasion				0.056
T1 + T2	69	51	18	
T3 + T4	43	27	16	
Lymphatic metastasis				0.055
Yes	53	34	19	
No	59	44	15	

Abbreviations: CRC, colorectal cancer; TNM, tumor node metastasis.

and the wt-circ-Luciferase reporter was prominently reduced ($P < 0.001$). However, in comparison with SW620 cells cotransfected by miR-874 negative control and mut-circ-Luciferase reporter, the relative luciferase activity of cells cotransfected by miR-874 mimics and the mut-circ-Luciferase reporter was not obviously changed. RNA pull-down assay presented that SW620 and SW480 cells of the Bio-miR-874 Wt group showed distinctly higher relative circ_0005576 enrichment than that of the Bio-NC group and Bio-miR-874-Mut group ($P < 0.001$) (Figure 3B). Furthermore, relative to the sh-NC group, much higher miR-874 expression occurred in SW620 and SW480 cells of the sh-circ_0005576 group ($P < 0.001$) (Figure 3C). Data from clinical tissues showed markedly lower miR-874 expression in tumor tissues than in normal tissues ($P < 0.01$) (Figure 3D). Circ_0005576 and miR-874 expression level in tumor tissues exhibited a significant negative correlation ($P = 0.0174$) (Figure 3E). Thus, these results supported the hypothesis that circ_0005576 acted as an miR-874 sponge.

Interestingly, we noticed that CDK8 possessed a binding site for miR-874 according to bioinformatics analysis (Figure 3F). Subsequently, whether CDK8 was a direct target of miR-874 was verified via luciferase reporter assay using SW620 cells. As a result, relative to SW620 cells cotransfected by miR-874 negative control and CDK8-3′URT wt, distinctly reduced relative luciferase activity was found in cells cotransfected by miR-874 mimics and CDK8-3′URT wt ($P < 0.001$). However, compared with SW620 cells cotransfected by miR-874 negative control and CDK8-3′URT mut, the changes of relative luciferase activity in cells cotransfected by miR-874 mimics and CDK8-3′URT mut were not statistically significant (Figure 3G). qRT-PCR and Western blot analysis indicated that, relative to the CDK8 mRNA and protein expression in SW620 and SW480 cells of the miR-NC group, it was remarkably decreased in miR-874 mimics group ($P < 0.01$ or $P < 0.001$) (Figure 3H and I). These data supported that CDK8 was directly suppressed by miR-874.

In clinical tissues, dramatically higher CDK8 expression was found in tumor tissues than in normal tissues ($P < 0.01$) (Figure 3J). Notably, the CDK8 expression was negatively correlated with miR-874 in tumor tissues ($P = 0.0015$)

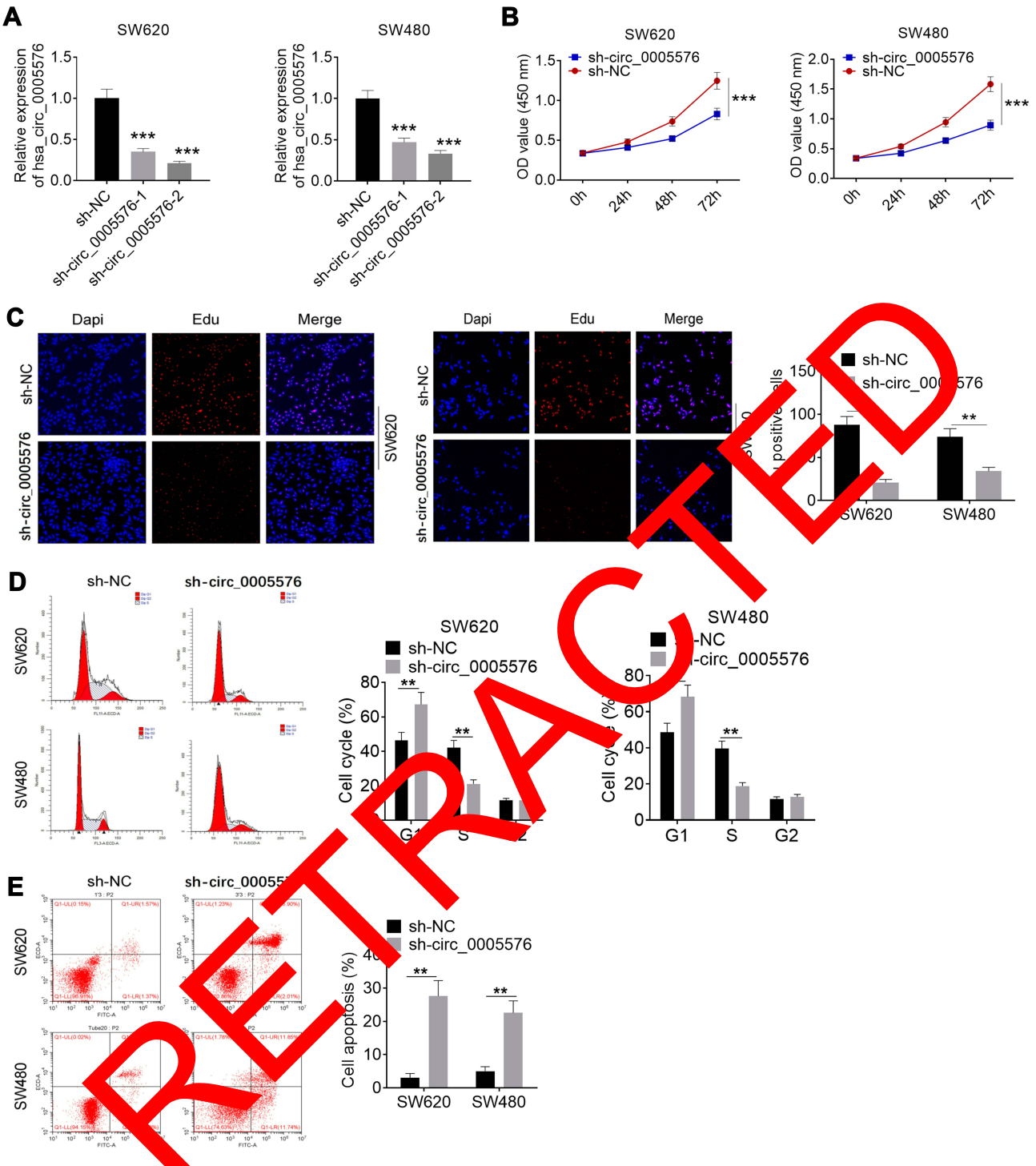

Figure 2 Knocking down of circ_0005576 inhibited proliferation and promoted apoptosis of CRC cells. (**A**) qRT-PCR was performed to detect the transfection efficiency. Results indicated that circ_0005576 expression in SW620 and SW480 cells was obviously regulated by transfection. (**B**) CCK-8 assay showed that knockdown of circ_0005576 prominently inhibited CRC cells proliferation. (**C**) According to EdU experiment, knockdown of circ_0005576 significantly reduced EdU positive cells (red fluorescence). This indicated that knockdown of circ_0005576 obviously inhibited CRC cells proliferation. (**D**) Flow cytometry analysis revealed that knockdown of circ_0005576 markedly increased cells in G1 phase and decreased cells in S phase. (**E**) Flow cytometry analysis indicated that knockdown of circ_0005576 remarkably induced apoptosis of CRC cells. $^{**}P < 0.01$ and $^{***}P < 0.001$.

Abbreviations: NC, negative control; OD, optical density; DAPI, 4′-6-diamidino-2-phenylindole; EdU, 5-ethynyl-2-deoxy-uridine; CRC, colorectal cancer; qRT-PCR, quantitative real-time polymerase chain reaction; CCK-8, Cell Counting Kit-8.

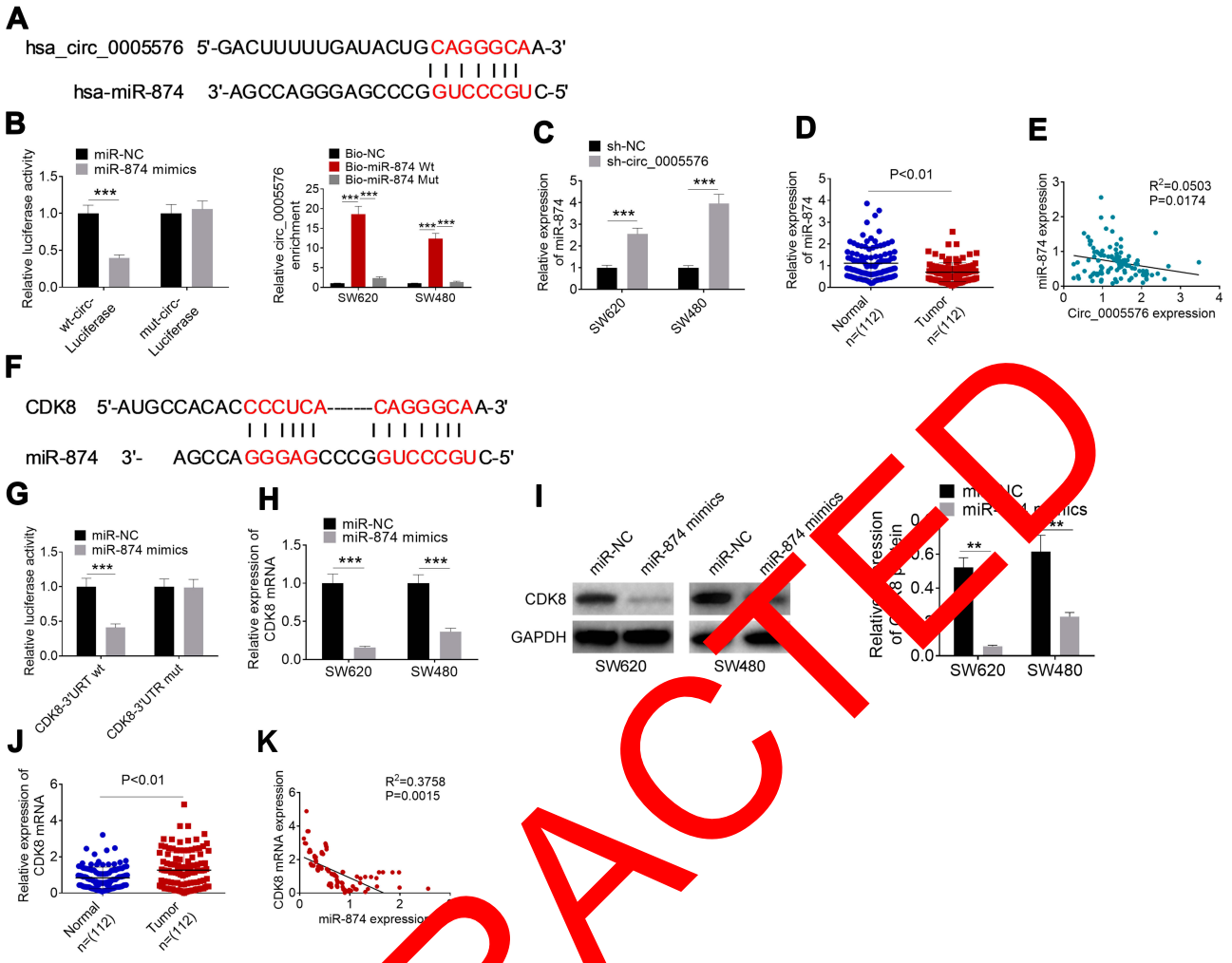

Figure 3 Circ_0005576 promoted CDK8 expression through suppressing miR-874 in CRC. (**A**) The binding site between circ_0005576 and miR-874. (**B**) Luciferase reporter assay and RNA pull-down assay confirmed that circ_0005576 acted as miR-874 sponge. (**C**) qRT-PCR showed that down-regulation of circ_0005576 significantly elevated miR-874 expression in SW620 and SW480 cells. (**D**) According to qRT-PCR, miR-874 expression was markedly declined in CRC tumor tissues than that in adjacent normal tissues. (**E**) Circ_0005576 and miR-874 in CRC tumor tissues exhibited a significant negative correlation. (**F**) CDK8 possessed binding site for miR-874. (**G**) Luciferase reporter assay verified that CDK8 was directly suppressed by miR-874. (**H**) qRT-PCR indicated that miR-874 up-regulation reduced the expression of CDK8 mRNA in SW620 and SW480 cells. (**I**) Western blot analysis revealed that miR-874 up-regulation diminished the expression of CDK8 protein in SW620 and SW480 cells. (**J**) CDK8 expression in CRC tumor tissues was dramatically increased when compared with normal tissues. (**K**) The CDK8 expression was negatively correlated with miR-874 expression in CRC tumor tissues. $^{**}P < 0.01$ and $^{***}P < 0.001$.

Abbreviations: CRC, colorectal cancer; qRT-PCR, quantitative real-time polymerase chain reaction; NC, negative control; wt, wild type; mut, mutant type; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

(Figure 3K). Thus, circ_0005576 promoted CDK8 expression through suppressing miR-874 in CRC.

miR-874 Knockdown and CDK8 Overexpression Reversed the Inhibitory Effect of Circ_0005576 Knockdown on CRC Progression

Rescue experiments were carried out to explore whether the miR-874/CDK8 axis is a direct mediator of circ_0005576 effects on CRC progression. SW620 and SW480 cells of the sh-circ_0005576 group had much lower CDK8 mRNA and protein expression than the sh-NC group ($P < 0.01$). When relative to the sh-circ_0005576 + miR-NC group, SW620 and SW480 of the sh-circ_0005576 + miR-inhibitor group exhibited obviously higher CDK8 mRNA and protein expression ($P < 0.01$). Meanwhile, in comparison with the sh-circ_0005576 + NC-CDK8 group, distinctly higher CDK8 mRNA and protein expression was found in SW620 and SW480 of sh-circ_0005576 + OE-CDK8 group ($P < 0.01$) (Figure 4A). CCK-8 assay exhibited that, compared with the sh-NC group, SW620 and SW480 cells of the sh-circ_0005576 group showed markedly lower OD value at 48 and 72

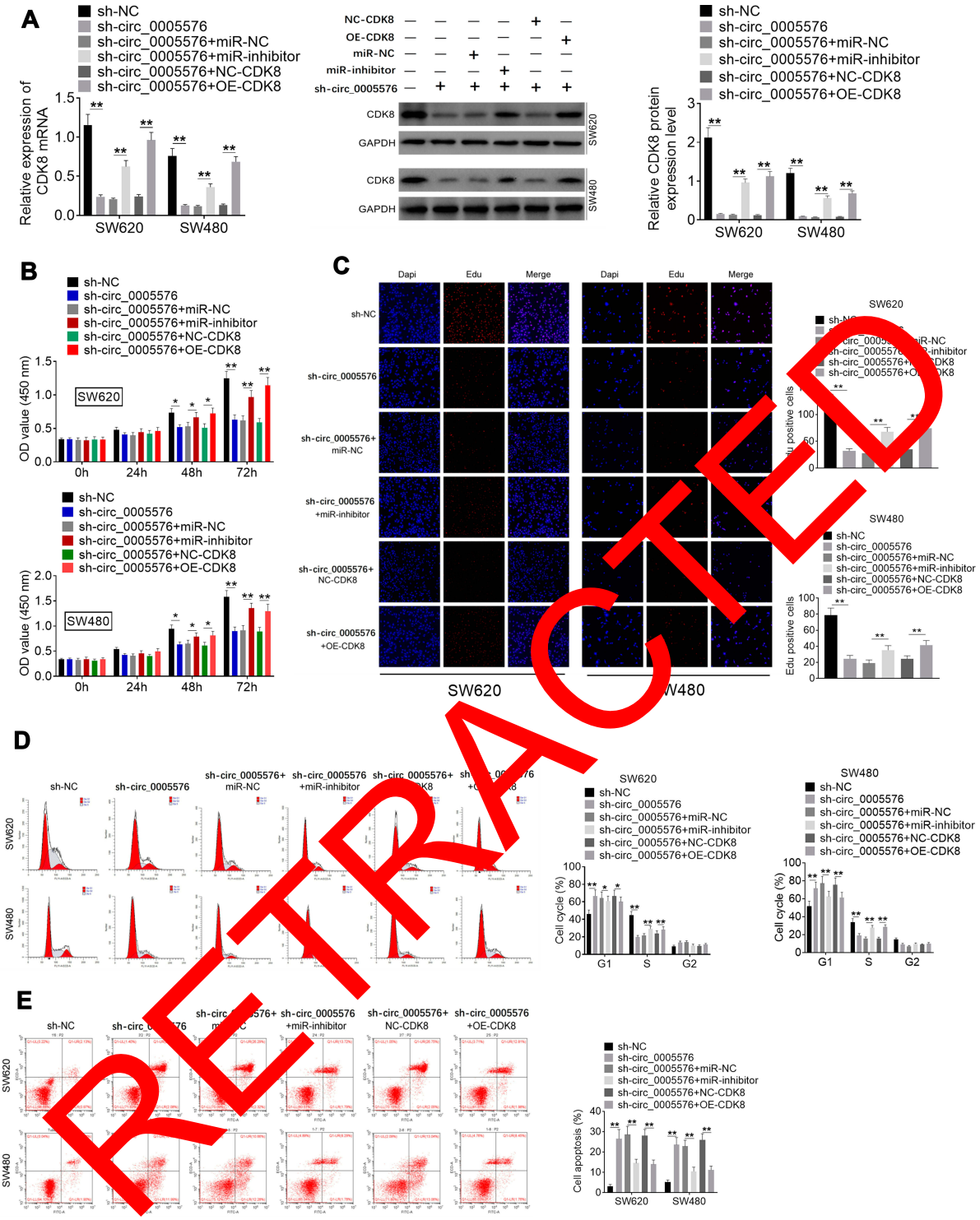

Figure 4 miR-874 knockdown and CDK8 overexpression reversed the inhibitory effect of circ_0005576 knockdown on CRC development. (**A**) qRT-PCR was performed to detect the transfection efficiency. Data illustrated that CDK8 mRNA and protein expression in SW620 and SW480 cells was successfully regulated by transfection. (**B**) CCK-8 assay indicated that circ_0005576 knockdown inhibited SW620 and SW480 cell proliferation. However, miR-874 knockdown and CDK8 overexpression reversed this inhibitory effect. (**C**) EdU experiment revealed that circ_0005576 knockdown inhibited SW620 and SW480 cell proliferation. However, miR-874 knockdown and CDK8 overexpression reversed this inhibitory effect. (**D**) According to flow cytometry analysis, circ_0005576 knockdown arrested SW620 and SW480 cells in G1 phase and reduced cells in S phase. However, miR-874 knockdown and CDK8 overexpression reduced cells in G1 phase and elevated cells in S phase. (**E**) Flow cytometry analysis exhibited that circ_0005576 knockdown induced SW620 and SW480 cells apoptosis. However, miR-874 knockdown and CDK8 overexpression reduced apoptosis of SW620 and SW480 cell. *$P < 0.05$ or **$P < 0.01$.

Abbreviations: CRC, colorectal cancer; qRT-PCR, quantitative real-time polymerase chain reaction; CCK-8, Cell Counting Kit-8; OD, optical density; DAPI, 4′-6-diamidino-2-phenylindole; EdU, 5-ethynyl-2-deoxy-uridine; NC, negative control; GAPDH, glyceraldehyde-3-phosphate dehydrogenase.

h ($P < 0.05$ or $P < 0.01$). However, at 48 and 72 h, much higher OD value was occurred in SW620 and SW480 cells of sh-circ_0005576 + miR-inhibitor group when compared with sh-circ_0005576 + miR-NC group ($P < 0.05$ or $P < 0.01$). At the same time point, SW620 and SW480 cells of sh-circ_0005576 + OE-CDK8 group presented prominently higher OD value than that of the sh-circ_0005576 + NC-CDK8 group ($P < 0.05$ or $P < 0.01$) (Figure 4B). According to results from the EdU experiment, it could be noted that SW620 and SW480 cells of the sh-circ _0005576 group exhibited less EdU positive cells (red fluorescence) than the sh-NC group ($P < 0.01$). Interestingly, more EdU positive cells were observed in SW620 and SW480 cells of sh-circ_0005576 + miR-inhibitor group relative to the sh-circ_0005576 + miR-NC group ($P < 0.01$). Compared with SW620 and SW480 cells of the sh-circ_0005576 + NC-CDK8 group, the EdU positive cells in the sh-circ_0005576 + OE-CDK8 group were obviously increased ($P < 0.01$) (Figure 4C). Data from flow cytometry analysis revealed that, compared with SW620 and SW480 cells of the sh-NC group, more cells in the G1 phase, fewer cells in the S phase, and more apoptotic cells occurred in the sh-circ_0005576 group ($P < 0.01$). In comparison with the sh-circ _0005576 + miR-NC group, SW620 and SW480 cells of the sh-circ_0005576 + miR-inhibitor group showed fewer cells in G1 phase, more cells in S phase and less apoptotic cells ($P < 0.05$ or $P < 0.01$). Relative to the sh-circ _0005576 + NC-CDK8 group, fewer cells in G1 phase, more cells in S phase and fewer apoptotic cells were observed in the sh-circ_0005576 + OE-CDK8 group ($P < 0.05$ or $P < 0.01$) (Figure 4D and E). Therefore, miR-874 knockdown and CDK8 overexpression reversed the inhibitory effect of circ_0005576 knockdown on CRC development.

Circ _0005576 Knockdown Suppressed Tumor Growth and Induced Apoptosis in vivo

Notably, after 28 days of inoculation, knockdown of circ_0005576 significantly reduced tumor volume and weight ($P < 0.01$) (Figure 5A–C). Immunohistochemical results of xenograft tumor tissues showed that knockdown of circ_0005576 significantly reduced CDK8 and Ki67

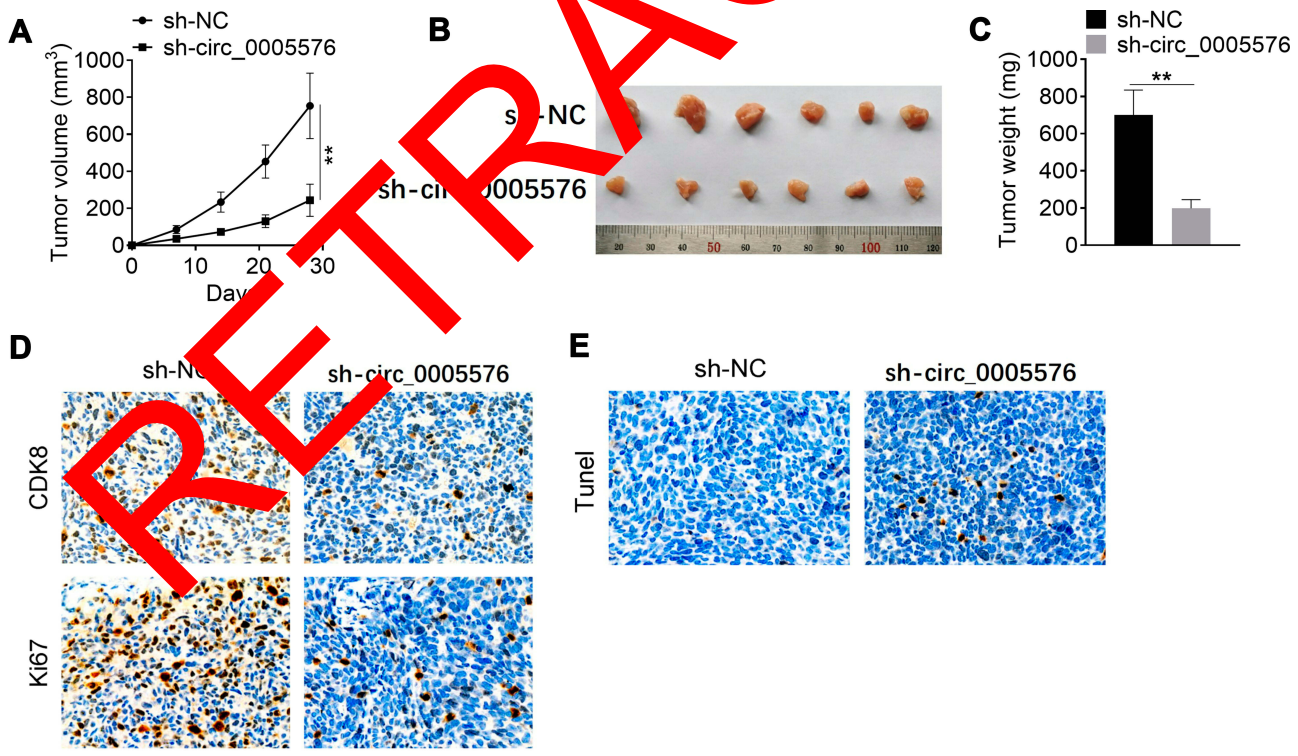

Figure 5 Circ_0005576 knockdown inhibited tumor growth and induced apoptosis in vivo. (**A**) After 28 days of inoculation, knockdown of circ_0005576 significantly reduced xenograft tumor volume. (**B**) Picture of xenograft tumor tissues after 28 days of inoculation. (**C**) Knockdown of circ_0005576 significantly reduced xenograft tumor weight after 28 days of inoculation. (**D**) Immunohistochemical results revealed that, knockdown of circ_0005576 significantly reduced CDK8 and Ki67 expression in xenograft tumor tissues. (**E**) Tunel assay indicated that circ_0005576 knockdown obviously increased cell apoptosis in xenograft tumor tissues. $^{**}P < 0.01$.
Abbreviation: NC, negative control.

expression (Figure 5D). Tunel assay exhibited more apoptotic cells in xenograft tumor tissues by circ_0005576 knockdown (Figure 5E).

Discussion

CircRNAs are a type of non-coding RNA with a covalently closed circular structure, which makes circRNA expression more stable due to their resistance to RNA exonuclease.[12] Increasing evidence indicates that the abnormal expression of circRNAs exerts important regulatory roles in tumorigenesis.[13] CircRNAs are thus considered as potential diagnostic markers and therapeutic targets for human tumors. With the development of high-throughput sequencing technology, the difference in circRNA expression in tumor tissues and adjacent tissues can be easily compared. Up to now, thousands of circRNAs with abnormal expression levels in tumor tissues have been found.[14] In the present research, we initially discovered that circ_0005576 was significantly up-regulated in CRC. The up-regulated circ_0005576 in CRC was closely associated with poor prognosis, including large tumor size and advanced TMN stage. Circ_0005576 was capable of stable expression in CRC because it was resistant to the degradation by RNase. Knockdown of circ_0005576 could inhibit the growth and apoptosis of CRC in vivo and in vitro. Currently, only one study has documented that circ_0005576 mediated the progression of human tumors. It was revealed that circ_0005576 could facilitate the progression of cervical cancer.[11] Unfortunately, more data on circ_0005576 affecting human disease development are not yet available. Our data demonstrate for the first time that circ_0005576 is an oncogene in CRC. It may be served as a potential therapeutic target for CRC.

In this work, circ_0005576 was discovered to be acting as a sponge for miR-874, which suppressed the expression of miR-874 in CRC by directly binding to miR-874. miR-874 has been found to function as a tumor suppressor in human malignant tumors. In hepatocellular carcinoma, the decreased expression of miR-874 was significantly associated with lymph node metastasis and advanced tumor stage. miR-874 was capable of inhibiting metastasis and epithelial–mesenchymal transition of hepatocellular carcinoma cells.[15] Previous data also confirmed that miR-874 could suppress the progression of osteosarcoma, pancreatic ductal adenocarcinoma, and non-small cell lung cancer.[16,18] In CRC, Zhao et al[19] illustrated that miR-874 expression level was prominently reduced in CRC. The suppressed cell growth and enhanced apoptosis of CRC cells could be achieved by up-regulation of miR-874. Research by Han et al[20] also confirmed the down-regulation of miR-874 in CRC. Up-regulation of miR-874 weakened the colony-forming ability of CRC cells and increased the sensitivity of CRC cells to 5-fluorouracil. Wang et al[21] suggested miR-874 to be a novel therapeutic target for CRC, and low expression of miR-874 in CRC was an independent predictor of low survival. Results from this article also revealed that, as a tumor suppressor, miR-874 expression was down-regulated in CRC and was directly inhibited by circ_0005576.

Interestingly, this study also found that CDK8 was a target gene of miR-874 and circ_0005576 indirectly enhanced CDK8 expression by directly inhibiting miR-874 in CRC. CDK8 is a member of the cyclin-dependent kinase family.[22] As a key regulator of the cell cycle, CDK8 was reported to regulate the G1/S phase of the cell cycle by activating Cyclin E.[23,24] In this paper, circ_0005576 knockdown increased CRC cells in G1 phase and decreased cells in S phase. However, the overexpression of CDK8 significantly reversed this effect. Ruiz et al[25] reported that CDK8 has been required for β-catenin-mediated transcription and tumor cell proliferation. Firestein et al[24] also discovered that CDK8 was an oncogene in CRC. The inhibition of CDK8 suppressed CRC cell proliferation characterized by β-catenin hyperactivity. However, abnormal activation of the WNT/β-catenin signaling pathway occurred in almost all CRCs. Results from this study confirmed the carcinogenic effect of CDK8.

There is a limitation in this research. The results should be validated in another CRC cohort. However, we cannot validate the results in another CRC cohort currently due to the limitations of laboratory conditions. Of course, this point will be one of the focuses of our future research.

Conclusion

In summary, this paper identified circ_0005576 as a novel oncogene for CRC. The significantly up-regulated circ_0005576 facilitated the progression of CRC. Mechanically, circ_0005576 promotes malignant progression of CRC via the miR-874/CDK8 axis. Thus, circ_0005576 may be a novel potential target for clinically therapeutic interventions in CRC. Of course, we will perform more research in the future to provide a more solid theoretical basis for the application of circ_0005576 in the clinically targeted therapy of CRC.

Highlights

(1) Circ_0005576 expression in CRC patients was up-regulated.

(2) Knocking down of circ_0005576 inhibited CRC cell proliferation.

(3) Circ_0005576 promoted CDK8 expression via inhibiting miR-874.

(4) Circ_0005576 knockdown inhibited tumor growth in vivo.

(5) Circ_0005576 promoted CRC progression via mediating miR-874/CDK8 axis.

Disclosure

The authors report no conflicts of interest in this work.

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