

Circular RNA circ-SMAD7 promoted glioma cell proliferation and metastasis by upregulating PCNA

C.-Y. ZUO, W. QIAN, C.-J. HUANG, J. LU

Department of Neurosurgery, The Ninth People's Hospital of Suzhou, Suzhou, China

Abstract. – **OBJECTIVE:** Recent studies have discovered a class of circular RNAs (circRNAs), which are dysregulated in various tumors and participate in the regulation of tumor progression. In our research, we aim to research the function of circ-SMAD7 in the progression of glioma.

PATIENTS AND METHODS: Circ-SMAD7 expression was detected by quantitative Real Time Polymerase Chain Reaction (qRT-PCR) in glioma tissue patients. Pearson's Chi-square test was used to determine the association of circ-SMAD7 expression with several pathological factors. Besides, cell proliferation assay, cell cycle assay, transwell assay, and Matrigel assay were conducted to detect the function of circ-SMAD7 in glioma. In addition, the interaction between circ-SMAD7 and proliferating cell nuclear antigen (PCNA) in glioma was studied by performing RT-PCR and Western blot assay.

RESULTS: Circ-SMAD7 expression was observed in glioma tissues was compared with adjacent samples. The expression of circ-SMAD7 was associated with patients' WHO stage and KPS score. Cell proliferation was inhibited and cell cycle was regulated after circ-SMAD7 was downregulated in glioma cells. Besides, cell migration and invasion were inhibited after circ-SMAD7 was downregulated in glioma cells. In addition, the mRNA and protein expression of PCNA was repressed after circ-SMAD7 was knocked down in glioma cells. Furthermore, PCNA expression level positively correlated with circ-SMAD7 expression level in glioma samples.

CONCLUSION: Our study suggests that circ-SMAD7 promotes proliferation and metastasis of glioma cells by upregulating PCNA. Circ-SMAD7/PCNA might be a novel therapeutic strategy in glioma.

Key Words:

Circular RNAs, Circ-SMAD7, Glioma, PCNA.

Introduction

Glioma remains one of the most ordinary subtypes of malignant intracranial cancers globally and one of the most fatal and aggressive types of cancers¹. Glioma exerts heterogeneous characteristics which brings a huge challenge to the current treatments². Despite therapeutic treatment developed for the last decades, the five-year survival rate for patients remains the poorest among all cancers^{3,4}. Therefore, the severe situation underscores the urgency of figuring out effective therapeutic interventions for the glioma.

Circular RNAs (circRNAs) are characterized with evolutionary conservation, enormous abundance and relative stability in cytoplasm. Recently, circRNAs play an important role in the initiation and progression of several cancers through sponging microRNAs (miRNAs) to regulate miRNAs' downstream genes or acting as competing endogenous RNAs (ceRNAs) for encoding RNAs. For example, the upregulation of hsa_circ_100395 significantly inhibits cell proliferation and reduces cell migration and invasion in lung cancer by targeting TCF21⁵. Circ_001988 is markedly down regulated in colorectal cancer which may be a novel potential biomarker and therapeutic target for colorectal cancer cases⁶. Circ_0067934 functions as an oncogene in cervical cancer by regulating the miR-545/EIF3C axis⁷. Through downregulating the expression of RhoA and circRNA_000839, miR-200b inhibits cell invasion and cell migration in hepatocellular carcinoma⁸. Upregulation of circ-ITCH inhibits cell proliferation and cell metastasis in triple-negative breast cancer through regulating the Wnt/ β -catenin pathway⁹. Recently, circ-SMAD7 is reported to be as a novel oncogene in cancers. However, how

circ-SMAD7 functions in the proliferation and metastasis of glioma and the underlying mechanism remain unexplored.

In our work, circ-SMAD7 was remarkably upregulated in glioma tissues and cell lines. Circ-SMAD7 enhances cell proliferation and metastasis in glioma cell *in vitro*. Moreover, we further explored the underlying mechanism how circ-SMAD7 functioned in glioma development and found its function in tumorigenesis was associated with proliferating cell nuclear antigen (PCNA), which was reported to be an oncogene in many cancers including glioma.

Patients and Methods

Tissue Specimens

Paired tissues were sequentially enrolled from 46 glioma patients undergoing surgery in The Ninth People's Hospital of Suzhou from April 2016 to December 2018. This investigation was approved by the Ethics Committee of The Ninth People's Hospital of Suzhou. Signed written informed consents were obtained from all participants before the study.

Cell Culture

Human glioma cell lines (U87, U373, U251, and T98) and one normal human astrocyte cell line were maintained in the culture medium consisted of 10% fetal bovine serum (FBS; Thermo Fisher Scientific, Inc., Waltham, MA, USA), penicillin as well as Dulbecco's Modified Eagle's Medium (DMEM; Thermo Fisher Scientific, Waltham, MA, USA) at 37°C in humidified atmosphere with 5% CO₂.

Lentivirus Expression of Short-Hairpin RNA and Cell Transfection

Lentiviruses expressing short-hairpin RNA (shRNA) directed against circ-SMAD7 were provided by Genesharma (Shanghai, China). The complementary DNA encoding circ-SMAD7 was amplified and inserted into pcDNA3.1 (Genesharma, Shanghai, China), which were then for the infection of glioma cells with Lipofectamine 3000 (Invitrogen, Carlsbad, CA, USA). The detection of circ-SMAD7 expression level in these cells was conducted using quantitative real-time polymerase chain reaction (qRT-PCR).

RNA Extraction and QRT-PCR

Total RNA from tissues and cells were separated by using TRIzol reagent (Invitrogen, Carlsbad,

CA). Then, the total RNA was reverse-transcribed to complementary deoxyribose nucleic acids (cDNAs) through reverse Transcription Kit (TaKaRa Biotechnology Co., Ltd., Dalian, China). Thermocycling conditions were as follows: 30 s at 95°C, 5 s for 40 cycles at 60°C, 35 s at 60°C. The 2^{-ΔΔCt} method was utilized for calculating relative expression. The primer sequences are as follows: circ-SMAD7, forward 5'-GAGAAATCTATTGGAG-3', circ-SMAD7 reverse 5'-GGTTTCGCTCGCTGCTT-3', β-actin, forward 5'-CGAAGCGTCAGAGGCT-3' and reverse 5'-CACTTCTTGGAATGC-3'. The relative expression was calculated by performing the 2^{-ΔΔCt} method.

Western Blot Analysis

Total proteins were collected from cells *via* radioimmunoprecipitation assay (RIPA) buffer and then quantified by using a protein assay (bicinchoninic acid method; Beyotime, Shanghai, China). The target proteins were separated by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE). Then, they were incubated with antibodies after replaced by the polyvinylidene difluoride (PVDF) membrane (Roche, Basel, Switzerland). Then, the rabbit anti-β-actin (Cell Signaling Technology, CST, Danvers, MA, USA) and rabbit anti-PCNA (Cell Signaling Technology, CST, Danvers, MA, USA) were used for incubation of these membranes. The Pierce enhanced chemiluminescence (ECL) was utilized for visualizing Western blotting Substrate Immunoreactive bands (Santa Cruz Biotechnology, Santa Cruz, CA, USA).

Cell Counting Kit-8 (CCK-8) Assay

Cell proliferation of these treated cells was monitored by CCK-8 (Beyotime Institute of Biotechnology, Shanghai, China). Briefly, 5 mg/mL CCK-8 was added at each point (0, 24, 48, and 72 h). OD450 was measured using Spectrophotometer (Thermo-Fisher Scientific, Waltham, MA, USA) after the cells were incubated for 1 h.

Cell Cycle Assay

2×10⁵/mL cells were diluted by RNase A in 75% ice-cold ethanol overnight. And these cells were stained with propidium iodide (PI; 50 mg/mL; MultiSciences Biotech Co., Ltd, Hangzhou, China) in the dark for 30 min at 4°C. Then, they were measured with flow cytometer (FACScan, BD Bioscience, Franklin Lakes, NJ, USA).

Transwell Assay and Matrigel Assay

After transfection, 1×10^5 cells in 200 μ L serum-free DMEM were replanted in top chamber (Corning, Inc., Corning, NY, USA) with or without 50 μ g Matrigel (BD, Franklin Lakes, NJ, USA). DMEM and FBS was added to the lower chamber. Next, they were cultured overnight in an incubator supplemented with 5% CO₂ at 37°C. The top surface of chambers was treated by methanol for 30 min after wiped by cotton swab. Then they were stained in crystal violet for 20 min. Five fields were randomly chosen under a Leica DMI4000B microscope (Leica Microsystems, Heidelberg, Germany).

Statistical Analysis

Data analysis was performed using Statistical Product and Service Solutions (SPSS) 18.0 (SPSS Inc., Chicago, IL, USA). Graph PAD 5.0 (GraphPad Software, Inc., La Jolla, CA, USA) helped presenting these consequences. The difference between two groups were compared by Student's *t*-test. The statistically significance was defined as $p < 0.05$.

Results

Circ-SMAD7 Expression Level in Glioma Tissues and Cells

The circ-SMAD7 expression was detected via qRT-PCR in 46 glioma patients' tissue samples and matched adjacent tissues. As shown in Figure 1A, circ-SMAD7 was significantly

ulated in tumor tissue samples compared with adjacent tissues. As shown in Table I, the expression of circ-SMAD7 was associated with patients' WHO stage and KPS score. Moreover, circ-SMAD7 level of glioma cells was higher than that of normal human astrocyte 1800 cell line (Figure 1B). The results suggested that upregulation of circPSMC3 might be associated with glioma development.

Knockdown of Circ-SMAD7 Inhibited Cell Proliferation in Glioma Cells

We chose U251 cells to knockdown of circ-SMAD7. Then, qRT-PCR was utilized for detecting the circ-SMAD7 expression in treated cells (Figure 2A). To explore how circ-SMAD7 affected glioma proliferation, CCK8 assay was performed and results showed that after circ-SMAD7 was knocked down, the cell growth ability of U251 cells was significantly repressed (Figure 2B). Besides, the effect of circ-SMAD7 on glioma cell cycle was also researched. As was shown in Figure 2C, the percentage of G0/G1 cells was increased and the percentage of S cells was reduced after knockdown of circ-SMAD7 in U251 cells.

Knockdown of Circ-SMAD7 Inhibited Cell Migration and Invasion in Glioma Cells

To explore how circ-SMAD7 affected glioma migration and invasion, transwell assay and Matrigel assay were performed. The results of transwell assay revealed that after circ-SMAD7 was knocked down, the migrated ability of glioma cells was sig-

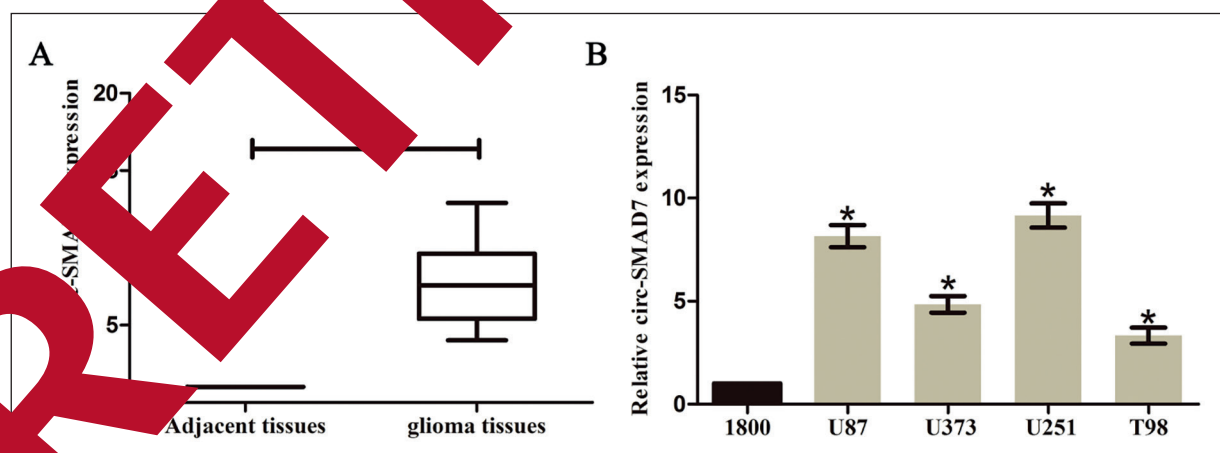


Figure 1. Expression levels of circ-SMAD7 were increased in glioma tissues and cell lines. **A**, QRT-PCR results showed that circ-SMAD7 expression was significantly increased in the glioma tissues compared with adjacent tissues. **B**, Expression levels of circ-SMAD7 relative to β -actin were determined in the human glioma cell lines and normal human astrocyte 1800 cell line by qRT-PCR. Data are presented as the mean \pm standard error of the mean. * $p < 0.05$.

Table 1. Correlation between circ-SMAD7 expression and clinicopathological characteristics in glioma patients.

Characteristics	Patients	Expression of circ-SMAD7		
		Low group	High group	
Total	46	20	26	
Age (years)				0.978
≤ 50	16	7	9	
> 50	30	13	17	
Gender				0.923
Male	20	7	13	
Female	26	13	13	
WHO stage				0.014
II	25	15	10	
III-IV	21	5	16	
KPS score				0.0002
≥ 90	20	15	5	
< 90	26	5	21	

$p < 0.05$ is considered statistically significant.

nificantly repressed (Figure 3A). In addition, Matrigel assay also revealed that after circ-SMAD7 was knocked down in glioma cells, the number of invaded cells was remarkably decreased (Figure 3B).

The Interaction Between circ-SMAD7 and PCNA in Glioma

qRT-PCR results showed that expression level of PCNA in glioma cells was lower in circ-

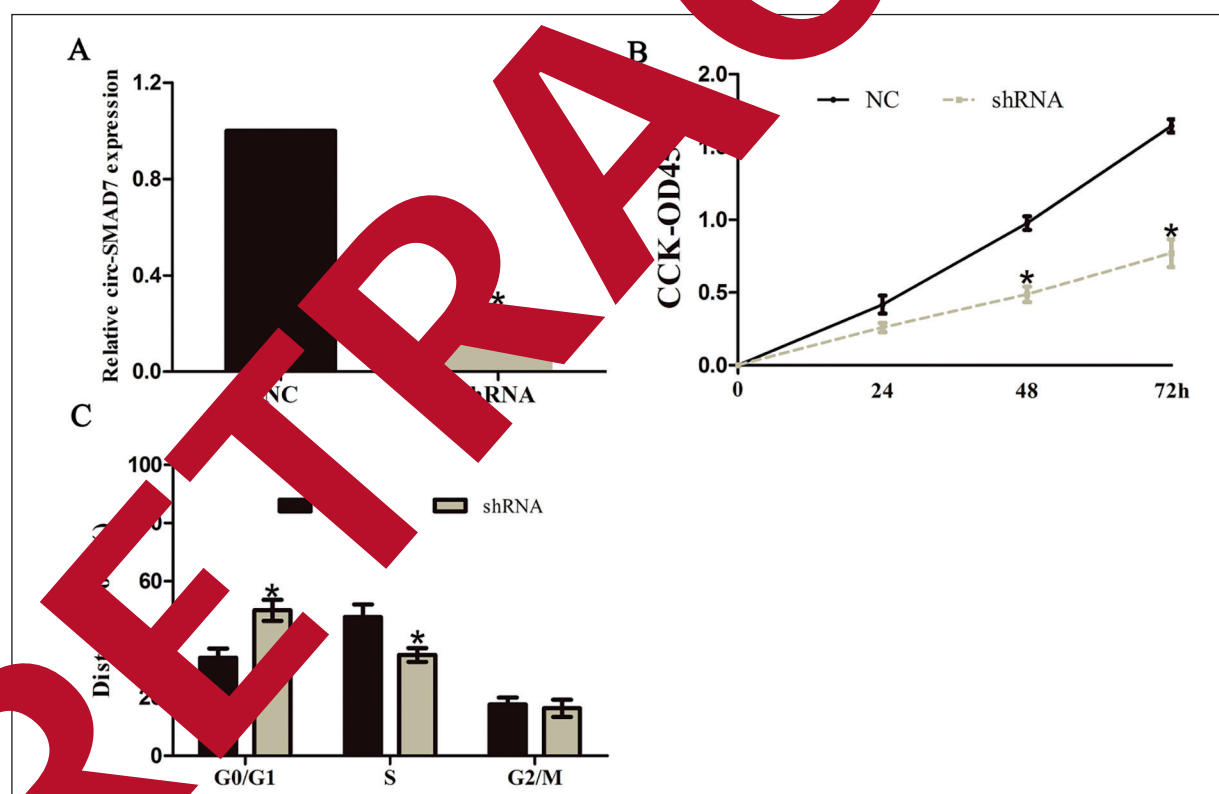


Figure 2. Knockdown of circ-SMAD7 inhibited glioma cell proliferation. **A**, Circ-SMAD7 expression in U251 glioma cells transfected with circ-SMAD7 shRNA (shRNA) and negative control (NC) was detected by qRT-PCR. β -actin was used as an internal control. **B**, CCK-8 assay showed that knockdown of circ-SMAD7 significantly inhibited cell growth in glioma cells. **C**, Percentage of G0/G1 cells was increased and the percentage of S cells was reduced after knockdown of circ-SMAD7 in glioma cells. 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.

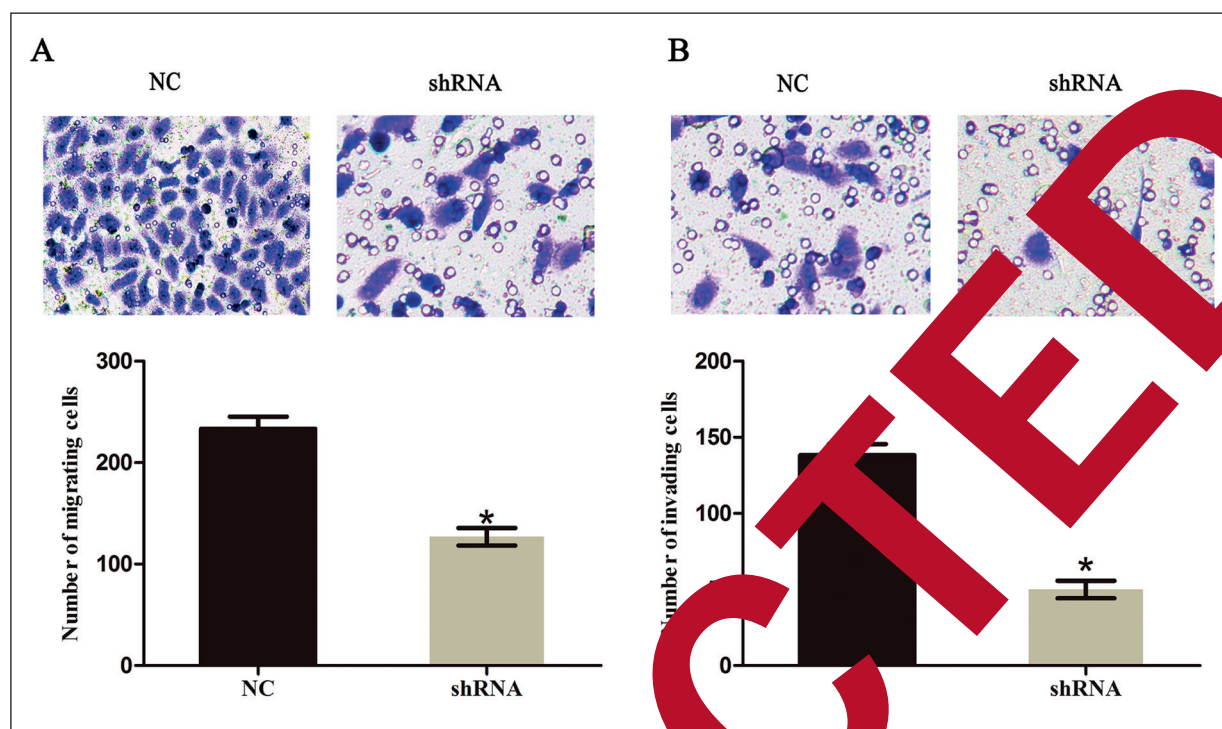


Figure 3. Knockdown of circ-SMAD7 inhibited glioma cell migration and invasion. **A**, Transwell assay showed that knockdown of circ-SMAD7 significantly decreased cell migration of glioma cells (magnification: 40×). **B**, Matrigel assay showed that number of invaded cells was significantly decreased after knockdown of circ-SMAD7 in glioma cells (magnification: 40×). The results represent the average of three independent experiments (mean ± standard error of the mean). * $p < 0.05$, as compared with the control cells.

SMAD7 shRNA (shRNA) group compared with the PCNA level in negative control (NC) group (Figure 4A). Western blot assay found that after circ-SMAD7 was knocked down, PCNA could be downregulated at protein level (Figure 4B). We further found that PCNA expression of glioma tissue was significantly higher compared with that of adjacent tissues (Figure 4C). Correlation analysis revealed that the positive association was seen between PCNA expression level and circ-SMAD7 expression in glioma tissue (Figure 4D).

Discussion

A number of researches has identified that circRNAs are dysregulated in glioma and participate in the process of tumor development. Increasing evidence has proved that circRNAs are potential indicators and therapeutic target for glioma. For instance, circ_0001649 is downregulated in glioma which predicts poor prognosis in glioma¹⁰. Circ-ITCH suppresses cells prolifera-

tion and induces cells apoptosis in epithelial glioma which is associated with prolonged overall survival¹¹. Circ_0074362 enhances cell proliferation, cell migration, and cell invasion in glioma¹². Circ_LARP4 is significantly down-regulated in glioma which may serves as a potential biomarker for prognosis of glioma patients¹³. CircRNA TTBK2 functions as an oncogene in glioma via regulating miR-217/HNF1β/Derlin-1 pathway¹⁴. Circ-001567 is upregulated in glioma and promotes cell proliferation and cell invasion¹⁵.

CircRNA SMAD7, located in chromosomal 18, is reported to be overexpressed in esophageal squamous cell carcinoma and participate in regulating tumor development¹⁶. Our study showed that circ-SMAD7 was upregulated in glioma samples and cell lines. The expression of circ-SMAD7 was associated with patients' WHO stage and KPS score. After circ-SMAD7 was knocked down in glioma cells, glioma cell proliferation was found to be inhibited and cell cycle distribution was regulated. Moreover, glioma cell migration and invasion were also found to be inhibited after circ-SMAD7 was knocked

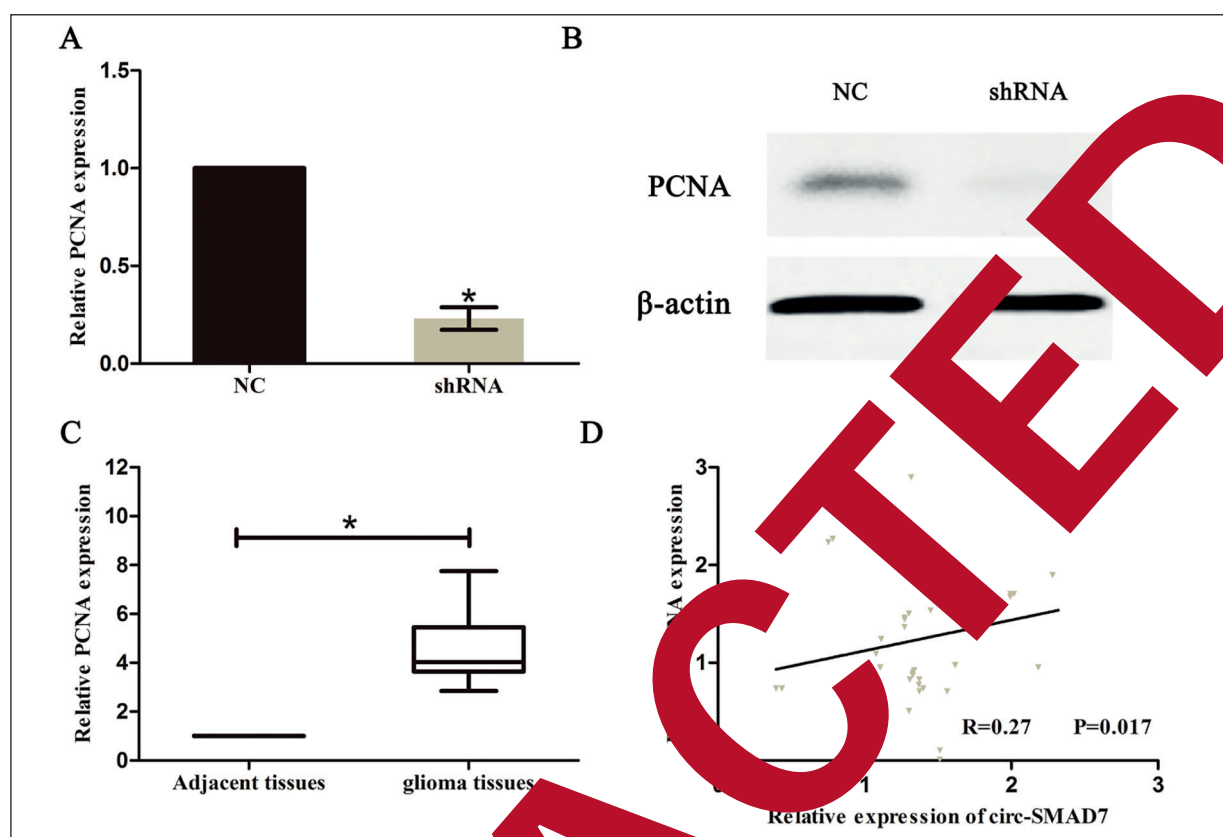


Figure 4. Interaction between circ-SMAD7 and PCNA in glioma cells. **A**, QRT-PCR results showed that PCNA expression was lower in circ-SMAD7 shRNA (shRNA) group compared with the NC group. β -actin was used as an internal control. **B**, Western blot assay revealed that PCNA protein expression was decreased in circ-SMAD7 shRNA (shRNA) group compared with the NC group. **C**, PCNA expression was significantly upregulated in glioma tissues compared with adjacent tissues. **D**, Linear correlation between the expression of PCNA and circ-SMAD7 in glioma tissues. The results represent the average of three independent experiments and are presented as the mean \pm standard error of the mean. * $p < 0.05$.

down. Above results indicated that circ-SMAD7 promoted tumorigenesis of glioma and might act as an oncogene.

Then, we further explored the potential target proteins of circ-SMAD7 using bio-informative methods and experiments. Results showed that the potential target protein, proliferating cell nuclear antigen (PCNA), was significantly up-regulated in glioma tissue samples. Known as an oncogene, PCNA takes part in the regulation of various biological processes in many carcinomas. For example, upregulating PCNA is correlated to poor prognosis of patients with osteosarcoma¹⁷. The positive expression rates of PCNA were 73% in breast cancer tumor tissues and could be utilized for evaluating the prognosis of breast cancer¹⁸. PCNA is significantly up-regulated in colorectal cancer, especially in those with liver metastasis, and can help evaluating liver metastasis in patients with colorectal

cancer¹⁹. In the present work, PCNA expression could be downregulated *via* knockdown of circ-SMAD7, while PCNA protein level could also be downregulated *via* knockdown of circ-SMAD7. Moreover, PCNA expression in glioma tissues was positively related with circ-SMAD7 expression. All the results above suggested that circ-SMAD7 might promote tumorigenesis of glioma *via* upregulating PCNA.

Conclusions

Circ-SMAD7 was remarkably higher-expressed in glioma tissues and cells. Besides, circ-SMAD7 could enhance glioma proliferation, migration, and invasion through targeting PCNA. These findings suggest that circ-SMAD7 may contribute to therapy for glioma as a candidate target.

Conflict of Interest

The Authors declare that they have no conflict of interests.

References

- 1) AVGEROPOULOS NG, BATCHELOR TT. New treatment strategies for malignant gliomas. *Oncologist* 1999; 4: 209-224.
- 2) KALPATHY-CRAMER J, GERSTNER ER, EMBLEM KE, ANDRONESI O, ROSEN B. Advanced magnetic resonance imaging of the physical processes in human glioblastoma. *Cancer Res* 2014; 74: 4622-4637.
- 3) PENAS-PRADO M, GILBERT MR. Molecularly targeted therapies for malignant gliomas: advances and challenges. *Expert Rev Anticancer Ther* 2007; 7: 641-661.
- 4) DEMUTH T, BERENS ME. Molecular mechanisms of glioma cell migration and invasion. *J Neurooncol* 2004; 70: 217-228.
- 5) CHEN D, MA W, KE Z, XIE F. CircRNA hsa_circ_100395 regulates miR-1228/TCF21 pathway to inhibit lung cancer progression. *Cell Cycle* 2018; 17: 2080-2090.
- 6) WANG X, ZHANG Y, HUANG L, ZHANG J, PAN F, LI B, YAN Y, JIA B, LIU H, LI S, ZHENG W. Decreased expression of hsa_circ_001988 in colorectal cancer and its clinical significances. *Int J Clin Exp Pathol* 2015; 8: 16020-16025.
- 7) HU C, WANG Y, LI A, ZHANG J, XUE F, ZHU L. Up-regulated circ_0067934 acts as an oncogene and facilitate cervical cancer progression via the miR-545/EIF3C axis. *J Cell Physiol* 2019; 134: 9225-9232.
- 8) WANG BG, LI JS, LIU Y, LI Q. MicroRNA-200b suppresses the invasion and migration of hepatocellular carcinoma by down-regulating PCNA and circRNA_000339. *Tumour Biol* 2017; 39: 1010428317727777.
- 9) WANG ST, LI JB, LIU Y, WANG YF, XIE F, LI Q, WANG R, WEI Q, WANG YH, ZHANG R, FENG XH. Circ-ITCH regulates triple-negative breast cancer progression through the Wnt/beta-catenin pathway. *Neoplasia* 2019; 66: 232-239.
- 10) WANG Y, SUI X, ZHAO H, CONG L, LI Y, XIN T, GUO M, HAO W. Decreased circular RNA hsa_circ_0001649 predicts unfavorable prognosis in glioma and exerts oncogenic properties in vitro and in vivo. *Gene* 2018; 676: 117-123.
- 11) LUO L, GAO Y, SUN X. Circ-ITCH correlates with small tumor size, decreased FIGO stage and prolonged overall survival, and it inhibits cells proliferation while promotes cells apoptosis in epithelial ovarian cancer. *Cancer Biomark* 2019; 25: 505-513.
- 12) DUAN X, LIU D, WANG J, CHEN Z. Circular RNA circ_0074362 promotes glioma cell proliferation, migration, and invasion by inhibiting the inhibition of miR-125b-3p on hsa_circ_0074362 expression. *DNA Cell Biol* 2019; 37: 917-923.
- 13) ZOU T, WANG J, GAO Y, LIANG Y. Circular RNA LARP1 promotes ovarian cancer progression as a potential biomarker for ovarian cancer prognosis. *Eur Rev Med Pharmacol Sci* 2018; 22: 7178-7182.
- 14) LIU Y, LIU X, XUE Y, LI W, MA J, XI Z, QUE Z, LIU Y. TTBK2 circular RNA promotes glioma malignancy by regulating miR-217/HNF1beta/Derlin-1 pathway. *Hematol Oncol* 2017; 10: 52.
- 15) TIAN L, BAO L, ZHONG J, PANG L. Upregulation of circular RNA VPS13C-hsa-circ-001567 promotes ovarian cancer cell proliferation and invasion. *Cancer Biother Biopharm* 2019; 34: 110-118.
- 16) ZHANG Y, WANG Q, ZHU D, RONG J, SHI W, CAO X. Up-regulation of circ-SMAD7 inhibits tumor proliferation and migration in esophageal squamous cell carcinoma. *Biomed Pharmacother* 2019; 111: 596-601.
- 17) WANG X, WANG D, YUAN N, LIU F, WANG F, WANG B, ZHOU D. The prognostic value of PCNA expression in patients with osteosarcoma: a meta-analysis of 16 studies. *Medicine (Baltimore)* 2017; 96: e8254.
- 18) GUO JL, GU SQ, LI Y, ZHANG XY. Evaluation of clinical significance of endoglin expression during breast cancer and its correlation with ER and PCNA. *Eur Rev Med Pharmacol Sci* 2017; 21: 5402-5407.
- 19) YUE SQ, YANG YL, DOU KF, LI KZ. Expression of PCNA and CD44mRNA in colorectal cancer with venous invasion and its relationship to liver metastasis. *World J Gastroenterol* 2003; 9: 2863-2865.