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miRNA-497 Negatively Regulates the Growth and Motility of Chondrosarcoma Cells by Targeting Cdc25A

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Chondrosarcoma (CHS) is the second most common malignant bone sarcoma with increased risk of invasion and metastasis. However, the regulatory mechanisms of CHS tumorigenesis remain unknown. Here we investigated the novel role of miR-497 in regulating chondrosarcoma cell growth and cell cycle arrest. RT-PCR analysis showed that the expression of miR-497 is aberrantly downregulated in human chondrosarcoma samples and cells. After transfection with miR-497 mimic or antagomir, the proliferation and apoptosis of JJ012 and OUMS-27 chondrosarcoma cells were determined by CCK-8 assay and flow cytometric analysis, respectively. Results showed that the proliferation capacity of JJ012 and OUMS-27 cells was significantly decreased by miR-497 overexpression but increased by miR-497 repression. Apoptosis in both cell types was remarkably enhanced by miR-497 mimic but inhibited by miR-497 antagomir. By bioinformatics and luciferase reporter analysis, Cdc25A was proven to be a direct target of miR-497 in chondrosarcoma cells. Further studies indicated that miR-497 modulates the growth of chondrosarcoma cells by targeting Cdc25A, in which the cell cycle inhibitor p21 is involved through a p53-independent pathway. In conclusion, we demonstrated that miR-497 represents a potential tumor suppressor in human chondrosarcoma that regulates the growth of chondrosarcoma cells by targeting Cdc25A. This may provide a novel therapeutic target for chondrosarcoma.

Key words: miR-497; Chondrosarcoma (CHS); Metastasis; Cdc25A; p21

INTRODUCTION

Chondrosarcoma (CHS) is the second most common malignant bone sarcoma after osteosarcoma, accounting for 20–30% of all malignant tumors of bone (1). CHS usually occurs in adults aged more than 20 years. It is classified as grade I (atypical cartilaginous tumor), grade II, or grade III chondrosarcoma according to the degree of metastatic progression. According to its clinicopathological entities, CHS can also be classified as one of several histological subtypes, including conventional (about 85% of all cases), dedifferentiated (about 9–10% of all cases), mesenchymal and clear-cell chondrosarcoma (<5% of cases) (2). CHS has distinct clinical and genetic features depending on the subtypes, and the overall survival rate of CHS ranges from 29% to 83%, according to the subtype and grade (3). Despite significant improvements in radiotherapy and chemotherapy, the efficiency of these two therapeutic approaches to CHS is very low. Surgery remains the primary treatment approach for chondrosarcoma (4). Thus, knowledge about the mechanisms by which CHS progresses is needed to improve the clinical therapeutic strategies used in human CHS.

MicroRNAs (miRNAs) are endogenous 21–23 nucleotide-long, noncoding, single-stranded RNAs, representing a large family of crucial endogenous regulators for gene expression and cellular activity (5). By binding to specific targets with distinct degrees of complementarity, most miRNAs exhibit a negative regulatory role in the expression of multiple genes at the posttranscriptional level through the inhibition of translation or degradation of target mRNA. There is much evidence that miRNAs are involved in diverse biological processes, including cell growth, differentiation, and apoptosis (6,7).

It is known that a single miRNA can bind and regulate multiple targets to perform different functions. Various studies have suggested that dysregulation of miRNAs contributes to the pathogenesis of cancer and other human diseases (8). In terms of CHS, altered expression of miRNAs has been reported, including miR-100, miR-134, miR-138, miR-145, miR-335, miR-497, let-7a, and miR-181a. These miRNAs play significant roles in CHS progression (9–11). Aberrant expression of miR-497 has also been reported in various cancers (12). In hepatocellular carcinoma, miR-497 is downregulated, and the

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expression of multiple cell cycle regulators is integrally altered by deregulation of miR-497 expression, contributing to the aberrant cell proliferation in carcinogenesis (13). Downregulation of miR-497 in osteosarcoma cells was also proven to be involved in cell growth and modulates the sensitivity of cells to cisplatin through the PI3K/Akt pathway (14). On the other hand, overexpressed miR-497 was found to be associated with the postnatal quiescence of skeletal muscle stem cells by targeting cell cycle genes Cdc25 and Ccnd (15). However, the precise role of miR-497 in CHS is not well defined.

Cell division cycle 25 A (Cdc25A) belongs to the Cdc25 family of proteins, which are highly conserved phosphatases. Overexpression of Cdc25A positively regulates cell cycle progression by dephosphorylating and activating cyclin-dependent kinase (CDK) complexes (8). Inactivation of Cdc25A occurs upon DNA damage that fosters checkpoint activation, contributing to the delay in cell cycle and DNA repair or apoptosis. In the present study, we determined the novel role of miR-497 in regulating chondrosarcoma cell growth and metastasis via Cdc25A. miR-497 was found to be downregulated in CHS and negatively regulates cell growth by directly targeting Cdc25A. Our data demonstrated a potential role of miR-497 deregulation in CHS tumorigenesis, which might represent a novel therapeutic target for CHS.

MATERIALS AND METHODS

Human Chondrosarcoma Samples and Cell Cultures

Twenty-two primary human chondrosarcoma tissues and 18 normal adjacent tissues were obtained from patients undergoing surgery at Tianjin Hospital. The protocol was approved by the Ethics Committee of Tianjin Hospital. All patients gave informed consent.

Human chondrosarcoma cell lines JJ012 (Grade II) and SW1353 (Grade II) were purchased from ATCC (Manassas, VA, USA), and OUMS-27 (Grade III) was purchased from JCRB (Tokyo, Japan). All cells were cultured in DMEM medium with 10% fetal bovine serum (FBS; Invitrogen) at 37°C in a 5% CO_2 atmosphere in an incubator. Normal chondrocyte cell line C-28/I2 was maintained in F12/DMEM medium supplemented with 10% FBS at 37°C in a 5% CO_2 atmosphere.

Quantitative RT-PCR

Total RNA was isolated from cells using TRIzol reagent (Sigma-Aldrich). The preparation of cDNA and qRT-PCR of miR-497 was performed using MicroRNA First-Strand Synthesis and miRNA Quantitation kits (Takara, Dalian, China). Expression of Cdc25A was detected using a CellAmp Direct RNA Prep kit for qPCR and a Protein Analysis kit (Takara, Dalian, China) according to the manufacturer's instructions. The reaction was as follows: 10 min at 95°C, then 40 cycles of 1 min at 95°C, 2 min at 63°C, and 1 min at 72°C, and then a final annealing step at 72°C for 10 min. All primers were synthesized by Takara as follows: Cdc25A: 5′-GTG AAGGCGCTATTTGGCG-3′ (forward) and 5′-GGTCCA TAGTGACGGTCAGGT-3′ (reverse); GAPDH: 5′-ACC ACAGTCCATGCCATCAC-3′ (forward) and 5′-ACCAC AGTCCATGCCATCAC-3′ (reverse). U6 was used as the internal control to normalize the relative expression of miR-497, and Ct values of GAPDH were used to normalize the relative expression of Cdc25A. All PCRs were performed in triplicate. Relative expression levels were presented using the $2^{-\Delta\Delta CT}$ method.

Western Blotting

Cell lysates were prepared for total protein isolation. Equal amounts of proteins were separated using SDS-PAGE gels (Invitrogen), followed by electrophoretic transfer to PVDF membrane. Antibodies [rabbit anti-Cdc25A, p21 1:1,000 and cyclin D1 1:200 dilution (Abcam); mouse anti-p53 1:1,000 dilution (Abcam); mouse anti-β-actin 1:3,000 dilution (ABclonal)] were incubated with blots overnight at 4°C. Then, secondary antibodies were reacted with blots for 1 h at room temperature, followed by enhanced chemiluminescence (ECL; Amersham Pharmacia, NJ, USA). The bands were measured using Image Quant software.

Cell Transfection

Transfection with 100 nM miR-497 mimic, antagomir, and negative control miRNA (RiboBio, Guangzhou China) or 1 μg CDc25A plasmid (NM_001789) (Origene, Rockville, MD, USA) was performed using Lipofectamine 2000 (Invitrogen) according to the manufacturer's instructions. Cells grown to approximately 80% confluence were transfected twice in 48 h, followed by subsequent experiments. The transfection efficacy was assessed by RT-PCR or Western blotting. Cotransfection of CDc25A plasmid and miR-497 mimic was performed using Lipofectamine 2000.

Cell Proliferation Assay

Cell proliferation was measured using the Cell Counting Kit (CCK-8/WST-8) (Bioroot, Shanghai, China) according to the manufacturer's instructions. After transfection, cells were seeded into 96-well plates (5×10^3 cells/ml) for 12, 24, 48, and 72 h, then 10 μl CCK-8 solution was added to each well for 4 h at 37°C. Absorbance at 450 nm was measured using an ELISA plate reader (Bio-tek, Winooski, VT, USA).

Cell Apoptosis Assay

Cell apoptosis was assessed by flow cytometric analysis using an Annexin V-fluorescein isothiocyanate kit (Immunotech, Marseille, France). Briefly, cells were seeded in serum-free DMEM medium for 16 h

after transfection, followed by harvesting with ice-cold PBS. Then cells were resuspended with binding buffer containing 10 mM HEPES (pH 7.4), 150 mM NaCl, 4% BSA, 1 mM $MgCl_2$, and 5 mM $CaCl_2$. A 250-µl aliquot of cell suspension (5×10^6 cells) was incubated with 0.5 µg/ml annexin V-fluorescein isothiocyanate and 0.6 µg/ml propidium iodide (PI) for 15 min in the dark at room temperature. The stained cells were analyzed immediately using FACS CaliburTM (Becton Dickinson).

Dual-Luciferase Reporter Assay

The fragment containing the 3′-UTR of Cdc25A mRNA was cloned into the pGL3 luciferase promoter vector (Promega, Madison, WI, USA) using the PCR method. A QuikChange Lightning Site-Directed Mutagenesis Kit (Stratagene) was used to introduce site-directed mutagenes is in the miR-497 binding site of Cdc25A mRNA. Cells were plated (1×10^5 cells/well) in 96-well plates and cotransfected with 200 ng plasmid DNA and 100 nM miR-497 mimic using Lipofectamine 2000. After 36 h, reporter assays were carried out with the Dual Luciferase Assay (Promega). pRL-TK vector (Promega) was employed as the internal control. Relative luciferase activity was expressed as luciferase activity/Renilla activity. All experiments were performed at least three times.

Statistical Analysis

The data are expressed as mean ± SEM. GraphPad Prism 5 (La Jolla, CA, USA) was used to measure the differences between groups by one-way ANOVA. All experiments were performed at least three times. A value of $p < 0.05$ was considered to be statistically significant.

RESULTS

miR-497 Is Aberrantly Regulated in Human Chondrosarcoma Samples and Cells

To determine whether miR-497 plays a regulatory role in human chondrosarcoma, we first evaluated the expression levels of miR-497 in chondrosarcoma tissue of patients using real-time quantitative PCR. Analysis showed that miR-497 was aberrantly downregulated in chondrosarcoma tissue samples compared with normal adjacent tissues (Fig. 1A). Furthermore, we investigated the expression of miR-497 in the human chondrosarcoma cell lines JJ012 (Grade II), SW1353 (Grade II), and OUMS-27 (Grade III). As seen in Figure 1B, the expression level of miR-497 in all investigated chondrosarcoma cells was low compared to the normal chondrocyte cell line C-28/I2. These data suggested that miR-497 might represent a potential tumor suppressor in human chondrosarcoma.

miR-497 Decreases the Proliferation and Induces the Apoptosis of Human Chondrosarcoma Cells

To further elucidate the possible role of low miR-497 expression in the progression of human chondrosarcoma, we employed miR-497 mimic and antagomir to investigate their effect on human chondrosarcoma cell lines JJ012 and OUMS-27. The efficiency of overexpression and silencing of miR-497 was confirmed by RT-PCR as shown in Figure 2A. The expression of miR-497 was significantly increased by miR-497 mimic but decreased by specific antagomir to extremely low levels compared with the control. No significant change in miR-497 expression was observed in the negative control miRNA group.

The proliferation and apoptosis of JJ012 and OUMS-27 cells were then determined by CCK-8 assay and flow

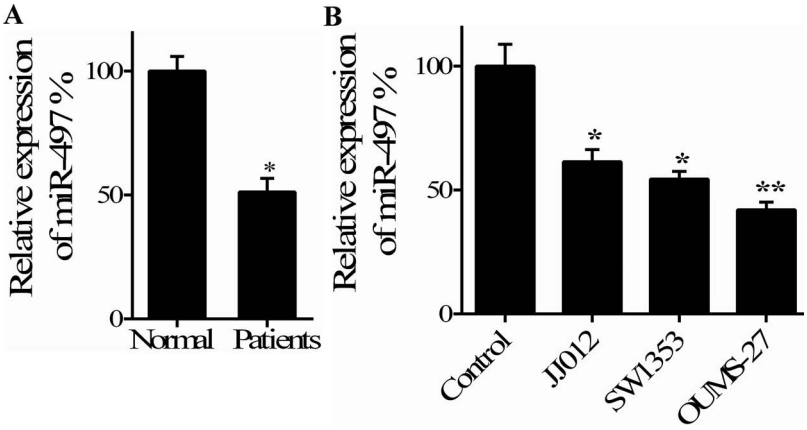

Figure 1. The expression of miR-497 in human chondrosarcoma tissue and cells. (A) RT-PCR was applied to test the expression of miR-497 in normal adjacent tissues (Normal) and human chondrosarcoma tissue (*$p < 0.05$ vs. Normal). (B) The levels of miR-497 in human chondrosarcoma cell lines JJ012 (Grade II), SW1353 (Grade II), and OUMS-27 (Grade III) as well as the normal chondrocyte cell line C-28/I2 (control) were examined using RT-PCR. **$p < 0.01$, *$p < 0.05$ versus control.

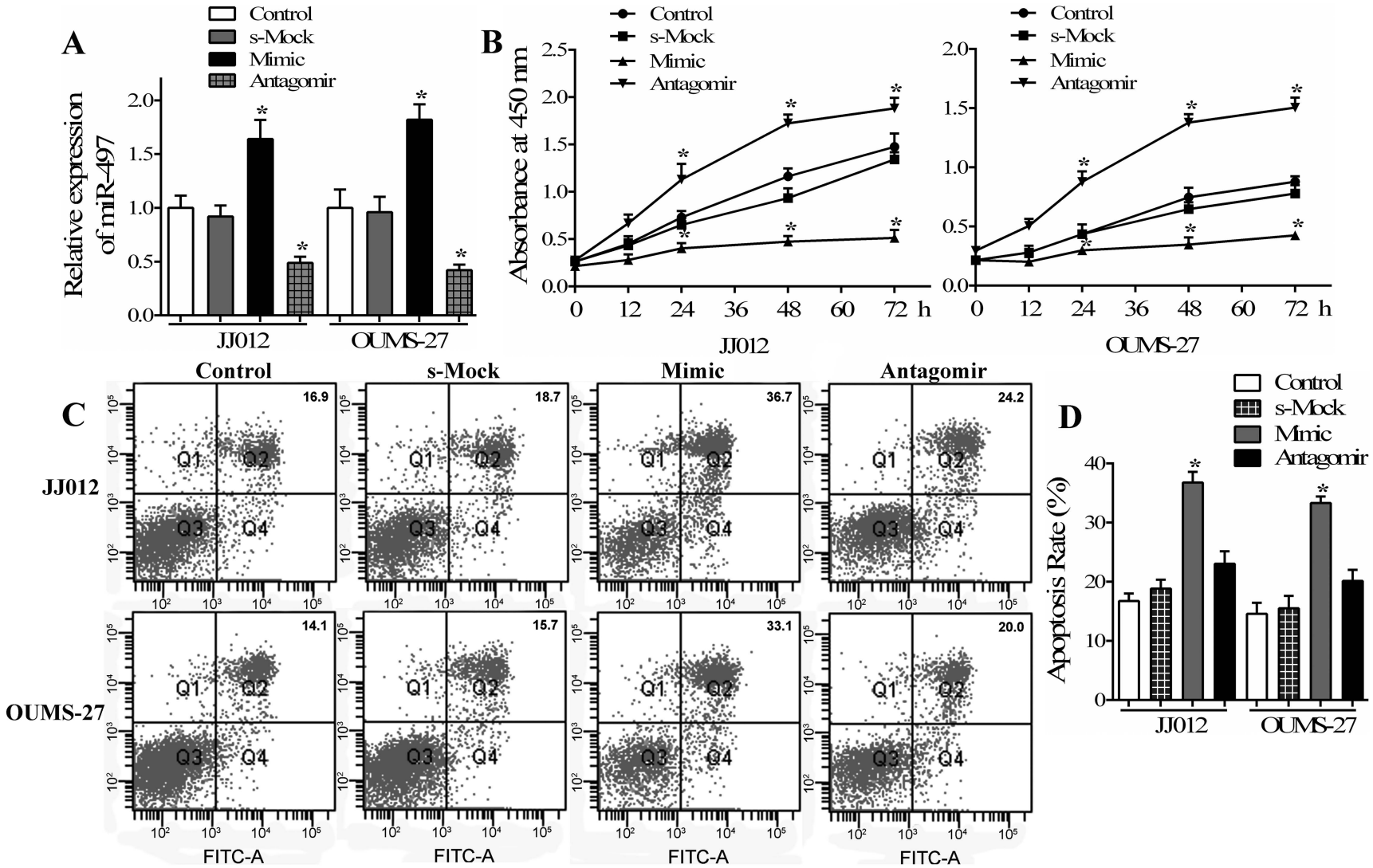

Figure 2. Effects of miR-497 on chondrosarcoma cell proliferation and apoptosis. JJ012 and OUMS-27 cells were cultured in medium (control), followed by transfection with miR-497 mimic, antagomir, or nontargeting control miRNA (s-Mock). (A) The expression levels of miR-497 were determined after 48 h by RT-PCR. (B) Proliferation of cells was tested by CCK-8 assays at 12, 24, 48, and 72 h of culture. (C) Cell apoptosis was investigated using flow cytometric analysis, and the apoptosis rate was quantified in (D). $*p < 0.05$ versus control.

cytometric analysis, respectively. Results showed that the proliferation capacity of JJ012 and OUMS-27 cells was significantly decreased by miR-497 overexpression but increased by miR-497 repression compared with the control (Fig. 2B). In contrast, the apoptosis of both JJ012 and OUMS-27 cells was remarkably enhanced by miR-497 mimic but inhibited by miR-497 antagomir (Fig. 2C and D), indicating that miR-497 plays a negative role in the regulation of cell proliferation and migration during chondrosarcoma tumorigenesis.

The Expression of Cdc25A Is Regulated Directly by miR-497

To explore the potential roles of miR-497 in chondrosarcoma, we searched the potential targets of miR-497 using miRNA databases (TargetScan and miRDB). Bioinformatics analysis indicated that Cdc25A might be a potential target for miR-497 with a possible binding site of miR-497 in its 3′-UTR. We then determined the expression of Cdc25A in JJ012 and OUMS-27 cells transfected by miR-497 mimic or antagomir using RT-PCR and Western blotting. Overexpression of miR-497 significantly downregulated the protein level of Cdc25A while miR-497 silencing restored the expression of Cdc25A protein in both JJ012 and OUMS-27 cells (Fig. 3A). However, the mRNA expression of Cdc25A was affected by neither miR-497 mimic nor antagomir, suggesting that Cdc25A expression is regulated by miR-497 at the posttranscriptional level in chondrosarcoma cells.

Further, we performed luciferase reporter analysis to validate Cdc25A as a miR-497 target. The 3′-UTR region of Cdc25A containing the predicted binding site of miR-497, and the mutant site was cloned into the pGL3 luciferase promoter vector (Fig. 3B). The luciferase activities of Cdc25A-3′UTR-wt reporter in JJ012 and OUMS-27 cells were strongly suppressed by miR-497 mimic transfection, but no inhibitory effects of miR-497 mimic on the activities of the mutant reporter were observed in either cell type (Fig. 3C), suggesting the specificity of this sequence. Taken together, these data indicate that Cdc25A is a direct target of miR-497 in chondrosarcoma cells.

miR-497 Modulates the Growth of Chondrosarcoma Cells by Targeting Cdc25A

Cdc25A is an important regulator of cell cycle progression. To evaluate the role of Cdc25A in miR-497-modulated chondrosarcoma cell growth, we transfected a Cdc25A plasmid into JJ012 and OUMS-27 cells. The mRNA and protein levels of Cdc25A were significantly increased in both cells by Cdc25A plasmid expression (Fig. 4A). The upregulation of Cdc25A expression restored the inhibitory effect of miR-497 on the growth rate of JJ012 and OUMS-27 cells (Fig. 4B). The apoptosis of cells induced by miR-497 mimic was also repressed by Cdc25A overexpression (Fig. 4C). This suggests that miR-497 regulates the proliferation and apoptosis of chondrosarcoma cells by suppressing Cdc25A expression.

Previous studies have shown that Cdc25A plays an induced oncogenic role in the cell cycle by competing for cyclin-cdks with p21. We further investigated the expression profile of other cell cycle regulatory proteins in chondrosarcoma cells that have been reported to be associated with the regulatory role of Cdc25A. As shown in Figure 4D, the expression of p21, a cell cycle inhibitor, was significantly downregulated in JJ012 and OUMS-27 cells compared to the normal chondrocyte cell line C-28/I2. In contrast, Cdc25A and cyclin D1 were expressed at low levels in normal chondrocyte cells, but were aberrantly upregulated in both JJ012 and OUMS-27 cells. The above results indicate that miR-497 dysregulation-mediated upregulation of Cdc25A contributes to chondrosarcoma cell cycle progression, in which the cell cycle inhibitor p21 is involved. However, the involvement of p21 seems to be independent of p53, a tumor suppressor, as no significant difference in the expression level of p53 was found in JJ012 or OUMS-27 cells compared with chondrocyte C-28/I2 cells.

DISCUSSION

Dysregulation of miRNAs has been reported in various cancers and has been proven to contribute to the progression of cancers (16). As a tumor suppressor, aberrant expression of miR-497 has also been found in several cancers (13,14). A recent miRNA array analysis indicated that miR-497 is downregulated in human chondrosarcoma, suggesting the tumor-suppressor function of miR-497 in chondrosarcoma (11). However, the explicit role of miR-497 in chondrosarcoma is still not well defined. Our study provides a novel understanding of miR-497 in regulating the cell growth and metastasis of chondrosarcoma cells. miR-497 was observed to be significantly downregulated in chondrosarcoma tissue samples. Furthermore, the expression of miR-497 was decreased in cultured chondrosarcoma cell lines compared with the normal chondrocyte cells, implying that miR-497 might represent a tumor suppressor and a potential therapeutic target in human chondrosarcoma.

Cdc25A is a highly conserved phosphatase that belongs to the Cdc25 family of proteins. Previous studies have shown that Cdc25A dephosphorylates and activates cyclin-dependent kinase (CDK) complexes, contributing to cell cycle progression (17). Wan et al. reported that Cdc25A is directly targeted by miR-21 in colon cancer cells to regulate cell cycle progression and tumorigenesis following stress (8). In non-small cell lung cancer, CDC25A expression is negatively regulated by miR-184 at the posttranscriptional level and is involved in

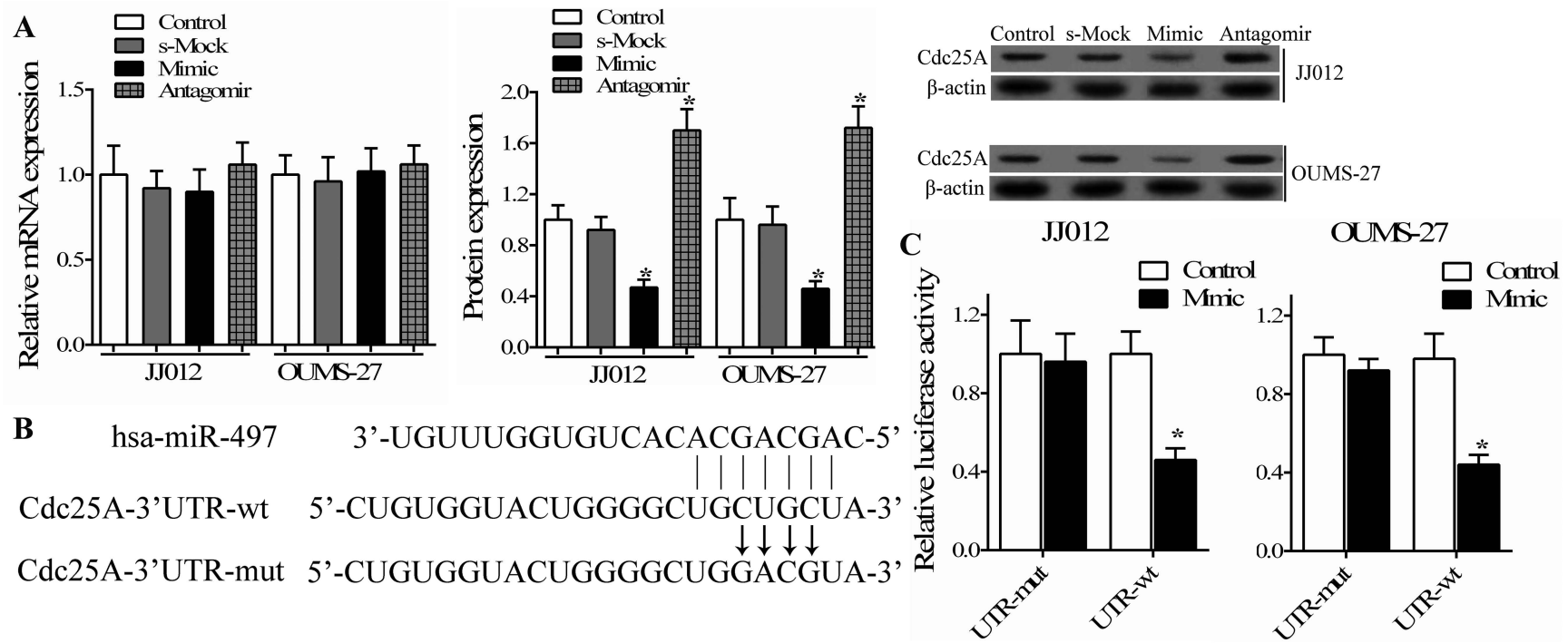

Figure 3. miR-497 targets the 3′-UTR of Cdc25A. (A) The mRNA and protein expression of Cdc25A were detected by qRT-PCR and Western blot in JJ012 and OUMS-27 cells transfected with miR-497 mimic and antagomir. (B) Predicted miR-497 target sequences in the 3′-UTR of Cdc25A. (C) Luciferase assay of cells transfected with Cdc25A-3′UTR-wt (UTR-wt) and Cdc25A-3′UTR-mut (UTR-mut) *$p<0.05$ versus control.

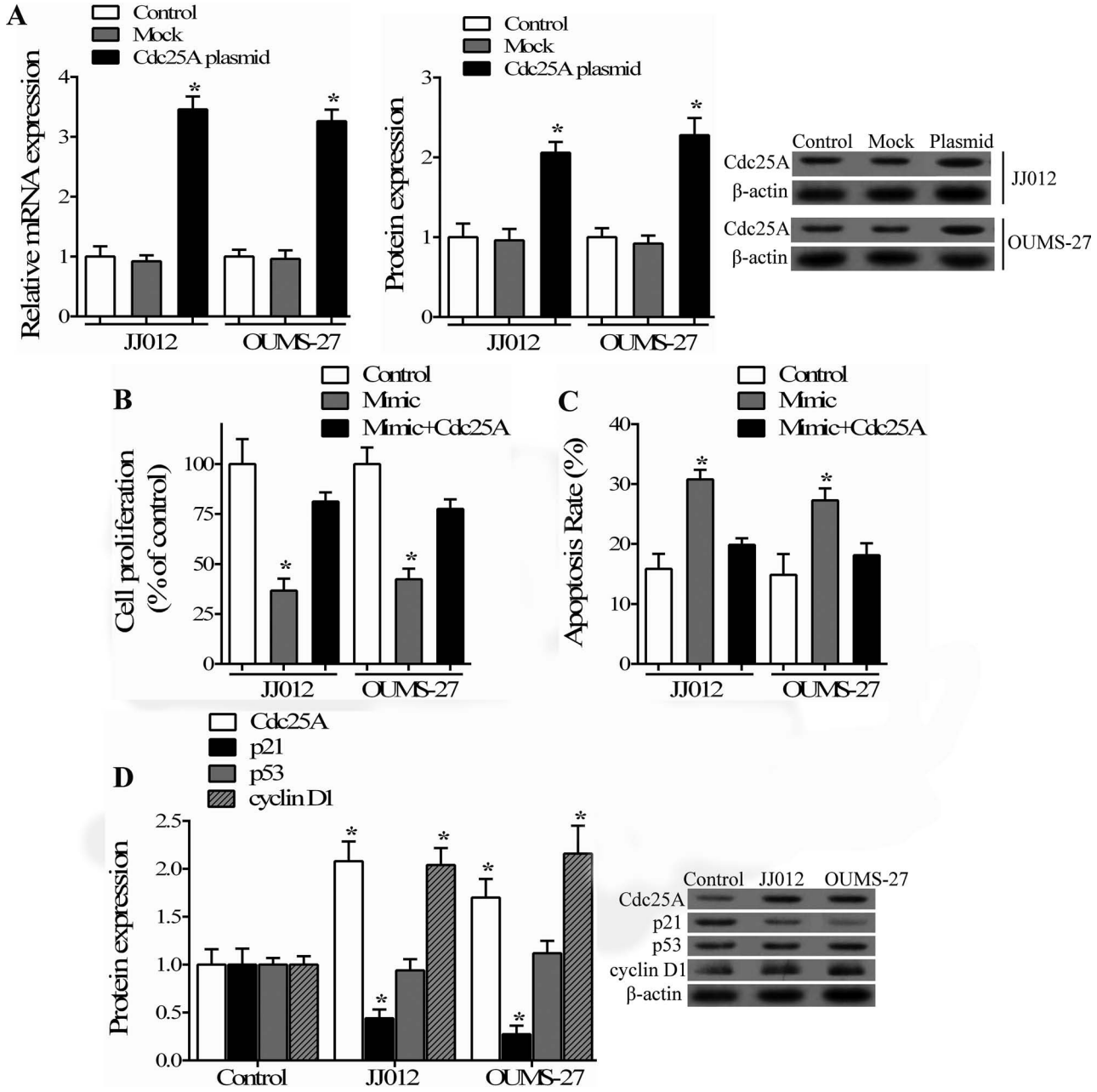

Figure 4. miR-497 modulates cell cycle progression by targeting Cdc25A. (A) The mRNA and protein levels of Cdc25A were measured by qRT-PCR and Western blot in JJ012 and OUMS-27 cells transfected with specific Cdc25A plasmid or control plasmid (Mock). The proliferation (B) and apoptosis (C) of cells were investigated in JJ012 and OUMS-27 cells after transfection by miR-497 mimic and Cdc25A plasmid. (D) Western blotting was used to measure the levels of Cdc25A, p21, p53, and cyclin D1 in the normal chondrocyte cell line C-28/I2 (Control) as well as JJ012 and OUMS-27 cells. *$p < 0.05$ versus control.

the modulation of cell proliferation and invasiveness (18). By searching the miRNA databases and performing luciferase reporter analysis, we found that Cdc25A is a direct target of miR-497 with the binding site on its 3′-UTR of mRNA. Further study showed that the protein level of Cdc25A is significantly downregulated by miR-497 overexpression but restored by miR-497 silencing in chondrosarcoma cells, while the mRNA expression of Cdc25A is not affected by miR-497, suggesting that miR-497 regulates the expression of Cdc25A at the posttranscriptional level in chondrosarcoma cells.

Cell motility is the basic pathology involved in the progression of human cancers. Deregulation of chondrosarcoma cell proliferation, invasion, and apoptosis

contributes to chondrosarcoma tumorigenesis. Increasing evidence suggests that dysregulation of miRNAs plays a crucial role in chondrosarcoma tumorigenesis (9,11). Moreover, Horng et al. reported that upregulation of miR-141 induced by paeonol inhibits the migration and invasion of human chondrosarcoma through the PKCδ and c-Src pathways to suppress chondrosarcoma metastasis (19). In human chondrosarcoma cells SW1353, miR-518b was proven to be upregulated by gallic acid to induce cell apoptosis and inhibit cell migration (20). In the present study, our results show that the proliferation capacity of cultured chondrosarcoma cells is significantly decreased by miR-497 overexpression but increased by miR-497 repression. In contrast, the apoptosis of cells was remarkably enhanced by miR-497 mimic but inhibited by miR-497 antagomir, indicating the negative role of miR-497 in chondrosarcoma tumorigenesis.

Notably, we found that the upregulation of Cdc25A expression stimulated by specific plasmid restored the inhibitory effect of miR-497 on the growth rate of chondrosarcoma cells, but repressed apoptosis induced by miR-497. This suggests that Cdc25A plays an important role in cell cycle progression and tumorigenesis of chondrosarcoma as an activator of CDK complexes and that the regulation of miR-497 to chondrosarcoma tumorigenesis is associated with Cdc25A expression.

p21 is a negative regulator of cell cycle progression by inhibiting the activity of CDK. This inhibitory role of p21 has been proven to be associated with the direct interaction between p21 and cyclin–CDK complexes (21,22). This interaction occurs through the cyclin-binding motif 1 (Cy1) on p21, a conserved region near the N terminus, or the cyclin-binding motif 2 (Cy2) near the C terminus (23). Interestingly, there is a similar cyclin-binding motif near the N terminus of Cdc25A. Furthermore, competitive antagonism between Cdc25A and p21, an activator and an inhibitor of cyclin–CDK complexes, has been reported (24). In this report, we observed that the expression of p21 was significantly downregulated in chondrosarcoma cells compared to normal chondrocyte cells. In contrast, Cdc25A and cyclin D1 were expressed at low levels in normal chondrocyte cells, but aberrantly upregulated in chondrosarcoma cells. This indicates that miR-497 dysregulation-mediated upregulation of Cdc25A contributes to chondrosarcoma cell cycle progression, in which the cell cycle inhibitor p21 is involved.

Additionally, although p21 has been proven to be transcriptionally induced by p53, the involvement of p21 in Cdc25A-mediated regulation of the chondrosarcoma cell cycle seems to take place via a p53-independent pathway, as no significant difference in the expression of p53 was found in chondrosarcoma cells compared with normal chondrocyte cells. This might be associated with the mutation of p53. As a tumor suppressor, mutation in the gene and alteration in the function of p53 is the most common mechanism of pathogenesis in many cancers, and p53 mutation is also found in human chondrosarcoma (25,26). Our observation is consistent with previous studies in which p21 was reported to regulate G_1–S transition and inhibit cell proliferation in a p53-independent manner in gastric cancer (27,28). It will be important in our next study to further investigate the interaction of Cdc25A, p21, and p53 in chondrosarcoma.

In summary, we have demonstrated that miR-497 represents a potential tumor suppressor in human chondrosarcoma, by regulating the growth and metastasis of chondrosarcoma cells by targeting Cdc25A. This may provide a novel therapeutic target for chondrosarcoma.

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