OncoTargets and Therapy

Dovepress
open access to scientific and medical research

Open Access Full Text Article

ORIGINAL RESEARCH

RETRACTED ARTICLE: miR-497 inhibited proliferation, migration and invasion of thyroid papillary carcinoma cells by negatively regulating YAP1 expression

This article was published in the following Dove Press journal:
OncoTargets and Therapy

Hui Cheng[1,*]
Hui Dong[1,*]
Jianlin Feng[2]
Hongyan Tian[1]
Haixia Zhang[3]
Lina Xu[4]

[1]Department of Pathology, The People's Hospital of Shouguang, Weifang 262700, China; [2]Department of Radiology, The People's Hospital of Shouguang, Weifang 262700, China; [3]Department of Radiotherapy, The People's Hospital of Shouguang, Weifang 262700, China; [4]Department of Respiratory Medicine, The People's Hospital of Weifang, Weifang 262700, China

*These authors contributed equally to this work

Purpose: This article aimed to investigate the effect of miR-497 on thyroid papillary carcinoma.

Materials and methods: miR-497 expression was analyzed using The Cancer Genome Atlas. A total of 56 papillary thyroid carcinoma patients' tumor tissues and normal tissues were collected. Nthy-ori 3-1 and K1 cells were cultured. K1 cells were also transfected. Quantitative real-time polymerase chain reaction and Western blot were used to detect miR-497 and yes-associated protein 1 (YAP1) expression. Luciferase reporter assay was performed. MTT and Transwell assay were conducted to measure cells' proliferation, migration and invasion. Immunofluorescence detection was used to detect YAP1-positive cells.

Results: miR-497 was downregulated, while YAP1 was upregulated in thyroid papillary carcinoma tissues and K1 cells ($P<0.05$). Compared with the negative control group, the OD495 value and the migrating and invasive cell number were significantly lower in miR-497 mimics group and significantly higher in miR-497 inhibitor group ($P<0.05$). YAP1 was the target gene of miR-497. Compared with blank group, the OD495 value and the migrating and invasive cell number were significantly lower in si-YAP1 group and significantly higher in miR-497 inhibitor group ($P<0.05$), while no significant difference was found between si-YAP1+inhibitors group and blank group in these indicators.

Conclusion: miR-497 regulated the proliferation, migration and invasion of K1 cells by negatively regulating YAP1 expression.

Keywords: thyroid papillary carcinoma, miR-497, YAP1, proliferation, invasion

Introduction

About 90% of patients with thyroid malignancies are diagnosed with papillary thyroid carcinoma. It was reported that the incidence of papillary thyroid carcinoma was increased year by year over the past four decades.[1,2] In recent years, some studies also revealed that relatively higher incidence of papillary thyroid carcinoma occurred among people over 45 years of age.[3] Although the mortality caused by thyroid papillary carcinoma was relatively lower than other malignant tumors, a tremendous negative impact on quality of life and psychology was also very common in these patients.[4–6] An effective and thorough treatment method for patients with papillary thyroid carcinoma is very important. Therefore, discovery of exact therapeutic target is crucial to achieving a complete cure.

With the development of molecular biology, researches of molecular biomarkers provided an effective therapeutic target for various cancers. miRNAs, a class of small RNAs, have been reported to be involved in the progression of many cancers and

Correspondence: Lina Xu
Department of Respiratory Medicine, The People's Hospital of Weifang, No 151, Guangwen Street, Kuiwen District, Weifang 261041, China
Tel/fax +86 1 870 668 1167
Email xulina245@163.com

submit your manuscript | www.dovepress.com
Dovepress
http://dx.doi.org/10.2147/OTT.S164052

suggested to be potential biomarkers and attractive therapeutics for many cancers.[7,8] Among these numerous miRNAs, miR-497 was also found to be involved in the regulation of development of several tumors. Zhao et al[9] reported in their study that, in renal cancer cells, miR-497 was dramatically decreased and its downregulation was closely correlated with tumor stage as well as lymph node metastasis. They also found that low expression of miR-497 greatly reduced the overall survival of patients. Xu et al[10] revealed that miR-497 was obviously decreased in pancreatic cancer tissues and that upregulation of miR-497 could inhibit tumor growth in vivo. They also considered that miR-497 expression was an independent poor prognostic factor in patients with pancreatic cancer. However, the above studies did not research the underlying mechanism of miR-497 in the regulation of these cancers.

In the current study, miR-497 expression and its impact on thyroid papillary carcinoma cells proliferation, migration and invasion, as well as related mechanisms were researched. To our knowledge, literatures of miR-497 in thyroid papillary carcinoma are relatively limited. This research will provide an important theoretical basis for the targeted therapy of thyroid papillary carcinoma.

Materials and methods

The Cancer Genome Atlas (TCGA) analysis of miR-497 expression in thyroid cancer

A total of 5,898 cases of thyroid cancer clinical patients were collected through data download and screening. miR-497 relative expression was analyzed using TCGA.

Tissue samples collection

The tumor tissues and normal tissues of 56 patients with papillary thyroid carcinoma who were admitted to our hospital from February 2013 to January 2017 were collected. Patients meeting the following criteria were included in this study. Inclusion criteria: primary tumor diameter was ≤1.0 cm and histopathological types were diagnosed as thyroid papillary carcinoma. Patients with the following were excluded: a history of thyroid surgery, recurrent thyroid papillary carcinoma, a history of radiotherapy or chemotherapy in the head or neck, a history of radiation exposure and a history of radioactive iodine ablation. Patients' informed consent was obtained for tissue acquisition, and this study had been approved by our ethics committee.

Cell culture and transfection

Human normal thyroid cell line Nthy-ori 3-1 and human papillary thyroid carcinoma cell line K1 (American Type Culture Collection, Manassas, VA, USA) were cultured in 1640 medium containing 10% fetal bovine serum (FBS) at 37°C in the presence of 5% CO_2 in an incubator. At logarithmic growth phase, these cells were harvested and prepared into cell suspensions by 1640 medium (10% FBS) at a density of 1×10^5/mL. Then these cell suspensions were seeded in 24-well plates with 1 mL per well. All the 24-well plates were kept in the CO_2 incubator for an additional 72 hours of incubation.

Furthermore, K1 cells were transfected by miR-497 mimics, miR-497 inhibitors and negative expression vector. They served as the miR-497 mimics group, miR-497 inhibitors group and negative control (NC) group, respectively. To silence YAP1 gene, K1 cells were also transfected by YAP1 siRNA and these cells served as the si-YAP1 group. Moreover, si-YAP1+ inhibitor group was also set and K1 cells in this group were co-transfected with si-YAP1 and miR-497 inhibitors. In the research, K1 cells without any treatment were used as the blank group. All transfection operations were performed in strict accordance with the Lipofectamine 2000 (Thermo Fisher Scientific, Waltham, MA, USA) instruction manual. Cells of all the above groups were inoculated into 24-well plates at a density of 1×10^5/mL to carry out incubation for different time periods (24, 48, 72 and 96 hours).

Quantitative real-time polymerase chain reaction (qRT-PCR)

After incubation for 72 hours, all cells were collected and total RNA was extracted using Trizol (Thermo Fisher Scientific). In addition, total RNA of the tumor tissues and normal tissues was also extracted. All extraction operations were performed according to the manufacturer's instructions. A total of 3 μg RNA was subjected to reverse transcription reaction to obtain cDNA template by using reverse transcription polymerase chain reaction system (TaKaRa, Shiga, Japan). qRT-PCR for miR-497 and yes-associated protein 1 (YAP1) was conducted using SYBR premix real-time PCR Reagent (TaKaRa). Primer sequences were as follows: miR-497, forward primer: 5′-GTGCAGGGTCCGAGGT-3′, reverse primer: 5′-TAGCCTGCAGCACACTGTGGT-3′; U6, forward primer: 5′-GCTTCGGCAGCACATATACT AAAAT-3′, reverse primer: 5′-CGCTTCACGAAT TTGCGTGTCAT-3′; YAP1, forward primer: 5′-AGAAC AATGACGACCAATAGCTC-3′, reverse primer: 5′-GCT GCTCATGCTTAGTCCAC-3′; GAPDH, forward primer: 5′-GTCGATGGCTAGTCGTAGCATCGAT-3′, reverse primer: 5′-TGCTAGCTGGCATGCCCGATCGATC-3′. The PCR amplification reaction was performed in a 25 μL system, including 2 μL of reverse transcription product,

and 1 μL primer was included in the reaction system. This amplification reaction consisted of three steps: degeneration step (95°C, 10 seconds), followed by reannealing step (60°C, 20 seconds) and extension step (72°C, 34 seconds). The three-step reaction was cycled for 35 times.

Luciferase reporter assay

The binding sites of YAP1 and miR-497 were determined by TargetScan, and according to the forecast result, mutant sequences and wild-type sequences of the binding sites were designed separately. These sequences were cloned and ligated into Promega vectors, respectively. Co-transfection of K1 cells was performed by using mutant sequences and miR-497 mimics, or mutant sequences and miR-497 negative expression vector, or wild-type sequences and miR-497 mimics, or wild-type sequences and miR-497 negative expression vector. These co-transfected K1 cells were named as MT+mimics group, MT+NC group, WT+mimics group and WT+NC group, respectively. Luciferase kit (Beijing Yuanpinghao Biotechnology Co., Ltd., Beijing, China) was used to measure the fluorescence intensity at 48 hours after transfection.

MTT assay

In vitro proliferation was measured by MTT assay. Cells of each group were cultured for 24, 48, 72 and 96 hours in 24-well plates, respectively. Then a total of 20 μL (5 mg/mL) MTT solution was added into each well for additional 4 hours of incubation at 37°C. After the liquid in each well was removed, 150 μL of dimethyl sulfoxide was added. These plates were shaken for 10 minutes to promote the dissolution of crystals. At last, the absorbance value (OD495 value) of each well was measured at 495 nm by enzyme-linked immunosorbent assay. Each experiment was repeated for three times.

Transwell assay

After incubation for 48 hours, cells of each group were harvested and made into single cell suspension at a density of 5×10^3/mL by using serum-free medium. Transwell assay was performed to measure cell migration and invasion ability. For invasion ability test, 100 μL of the single cell suspensions was added into the upper chambers of a six-well Matrigel-coated chamber. Then 500 μL of 1640 medium containing 10% FBS was added to the bottom chamber. The six-well Matrigel-coated chamber was incubated at 37°C in 5% CO_2 for 24 hours. Cells on the upper chambers were scraped and cells on the bottom chamber were fixed with 10% formaldehyde before they were stained with crystal violet (5%). Five fields were randomly selected under the microscope to count the number of cells that passed through the membrane. For migration test, all operations were consistent with the invasion test, except that the six-well chamber was without Matrigel.

Western blot analysis

Cells of each group were cultured for 48 hours and then harvested to extract total proteins by using RIPA lysis buffer. After the proteins were separated through sodium dodecyl sulfate-polyacrylamide gel electrophoresis, they were transferred on to the polyvinylidene difluoride membrane to carry out blocking using skimmed milk powder (5%). YAP1 rabbit anti-human monoclonal antibody (1:1,000; Santa Cruz Biotechnology Inc., Dallas, TX, USA) was then added and incubated for 12 hours at 4°C, followed by washing with TBST for three times. Horseradish peroxidase-labeled goat anti-rabbit antibody (1:5,000; Cwbio Tech, Shanghai, China) was used as the secondary antibody. After incubation for 1 hour at room temperature, the membrane was also washed by TBST for three times. Finally, chemiluminescence was performed and data were analyzed. In this study, GAPDH was used as the internal reference.

Immunofluorescence detection

Cells of each group, which were incubated for 48 hours in 24-well plates, were fixed with 2.5% glutaraldehyde for 15 minutes after the upper residual liquid was removed. Then they were incubated with 0.25% Triton X-100 for 15 minutes at room temperature, followed by blocking with 4% goat serum for 30 minutes at room temperature. YAP1 antibody (1:100) was added and incubated for 12 hours at 4°C. After washing with PBS for three times, rhodamine-labeled fluorescent secondary antibody (1:200) was added and incubated in a 37°C incubator for 40 minutes. 4′,6-Diamidino-2-phenylindole was added to stain for 5 minutes. At last, the cells were observed under a fluorescence microscope and the number of positive cells was counted. Cells that exhibited blue immunofluorescence were YAP1-positive cells.

Statistical analysis

All data were processed using SPSS 18.0 statistical software and expressed as mean±SD. Student's *t*-test was adopted for analysis and $P<0.05$ was considered statistically significant difference.

Ethics

This study was conducted after obtaining the ethical committee approval of The People's Hospital of Weifang and written informed consent from the patients.

Results

Low expression of miR-497 in thyroid cancer according to TCGA

It was reported that thyroid papillary carcinoma was the most common type of thyroid cancer.[11] In this research, TCGA analysis was used to study the expression of miR-497 in thyroid cancer. The result showed that there was low expression of miR-497 in thyroid cancer (Figure 1). Based on this result, we conducted further research on the expression of miR-497 as well as its related mechanisms in thyroid papillary carcinoma tissues and K1 cells.

Downregulation of miR-497 in thyroid papillary carcinoma tissues and K1 cells

Expression of miR-497 in the tumor tissues and thyroid tissues of patients with thyroid papillary carcinoma, as well as in Nthy-ori 3-1 cells and K1 cells was examined through qRT-PCR detection. The results revealed that the relative expression level of miR-497 in tumor tissues was significantly lower than that in normal tissues ($P<0.05$; Figure 2A). We also observed a prominent increase in the relative expression level of miR-497 in K1 cells than that in Nthy-ori 3-1 cells ($P<0.05$; Figure 2B).

miR-497 was closely related to the clinical features of thyroid papillary carcinoma patients

We noted that miR-497 was closely related to the clinical features of thyroid papillary carcinoma patients, including the clinical stage and lymph node metastasis. For patients with stage II, their miR-497 relative expression was obviously lower than that of patients with stage I ($P<0.05$). Patients with stage III were with significantly lower miR-497 relative expression when compared with patients with stage I and stage II ($P<0.05$; Figure 3A). In addition, we also found th[illegible] lative expression of miR-497 in patients witho[illegible] lymph nod[illegible] metastasis was significantly higher than that in [illegible]tients with l[illegible]mph node metastases ($P<0.05$; Figure 3[illegible]). miR-49[illegible]as clo[illegible]y related to the clinical features of th[illegible]oid papi[illegible]ary car[illegible]ma patients.

miR-497 regulated K1 cells proliferation, migration and invasion

The results of qRT-PCR showed that compared with NC group, the relative expression of miR-497 in miR-497 mimics group was dramatically increased ($P<0.05$), while significantly decreased miR-497 relative expression was found in the miR-497 inhibitor group ($P<0.05$; Figure 4A).

The proliferation ability of miR-497 in K1 cells was determined by MTT assay. At 24 hours, there was no significant

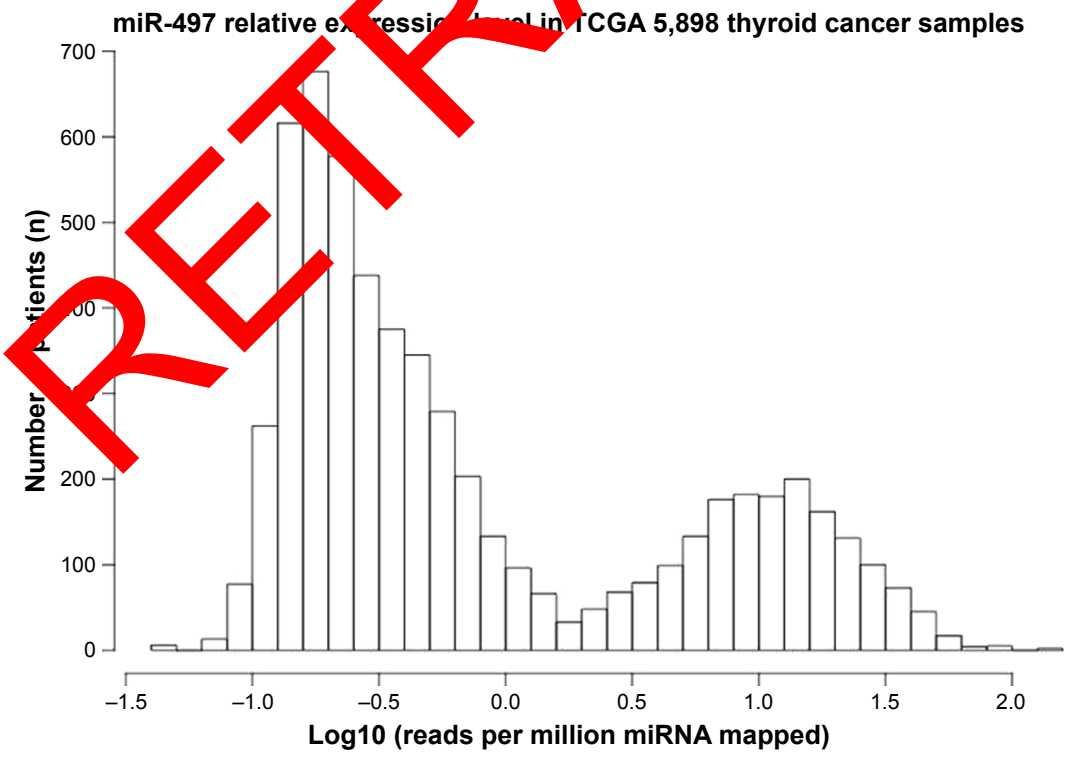

Figure 1 TCGA analysis of miR-497 expression in thyroid cancer.
Abbreviation: TCGA, The Cancer Genome Atlas.

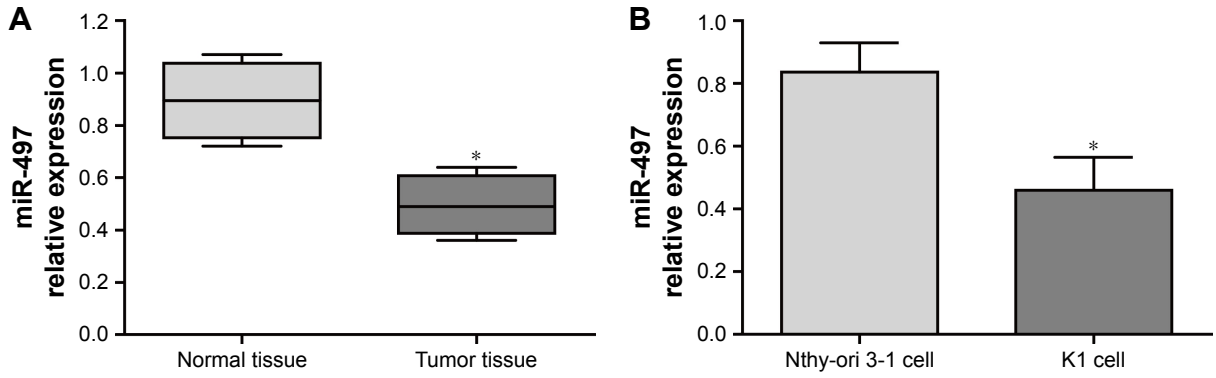

Figure 2 Relative expression of miR-497 in tumor tissues and cells by qRT-PCR.
Notes: (**A**) Relative expression of miR-497 in papillary thyroid carcinoma tumor tissues and thyroid normal tissues by qRT-PCR; (**B**) Relative expression of miR-497 in Nthy-ori 3-1 cells and K1 cells by qRT-PCR. *$P<0.05$ when compared with miR-497 expression in normal tissue and Nthy-ori 3-1 cell, respectively.

difference in OD495 values among NC group, miR-497 mimics group and miR-497 inhibitors group. However, at 48, 72 and 96 hours, compared with NC group, the OD495 values of miR-497 mimics group were significantly lower at these three time points ($P<0.05$), whereas they were markedly higher in the miR-497 inhibitor group ($P<0.05$; Figure 4B). In addition, the results of Transwell assay of cell migration and invasion showed that the number of migrating (160±13) or invasive (87±8) cells in miR-497 mimics group was significantly lower than that in NC group (242±[illegible] 156±9, respectively; $P<0.05$). However, compared with NC group, significantly higher migrating (374±36) and invasive (231±13) cells were found in miR-497 inhibitors group ($P<0.05$; Figure 4C and D).

YAP1 was upregulated in thyroid papillary carcinoma tissues and K1 cells

YAP1 expression in thyroid papillary carcinoma tumor tissues and K1 cells was measured. The results indicated that YAP1 mRNA and protein relative expression were dramatically increased in tumor tissues than that in normal tissues ($P<0.05$; Figure 5A and B). Furthermore, we also observed that compared with Nthy-ori 3-1 cells, significantly higher YAP1 mRNA and protein relative expression were found in K1 cells ($P<0.05$; Figure 5C and D). YAP1 was upregulated in thyroid papillary carcinoma tissues and K1 cells.

YAP1 was negatively regulated by miR-497

According to qRT-PCR and Western blot results, relative expression of YAP1 was significantly lower in miR-497 mimics group and markedly higher in miR-497 inhibitor group when compared with NC group ($P<0.05$; Figure 6A and B). Furthermore, immunofluorescence assay was performed and cells that exhibited blue immunofluorescence were YAP1-positive cells. We noted that, compared with NC group, YAP1-positive cells proportion was obviously decreased in

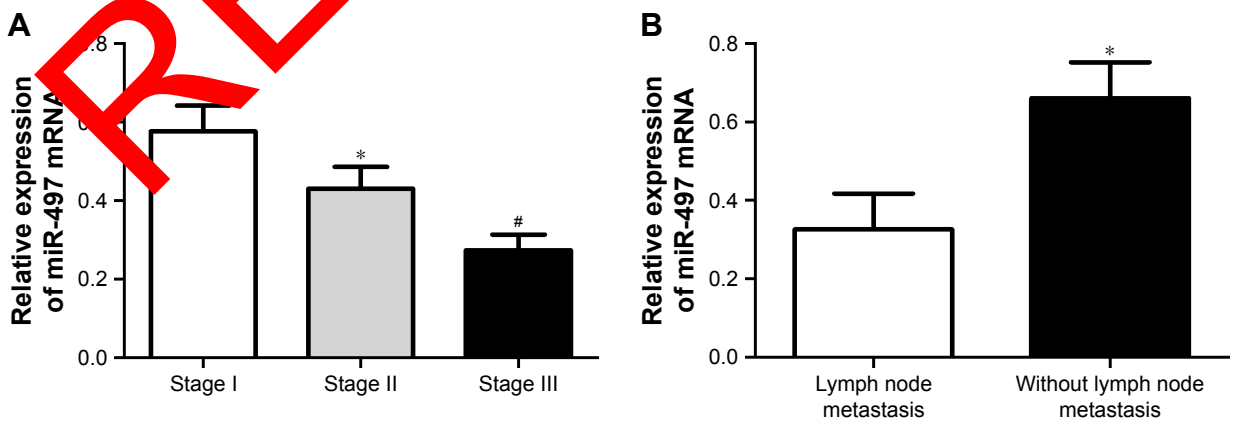

Figure 3 miR-497 was closely related to the clinical features of thyroid papillary carcinoma patients.
Notes: (**A**) qRT-PCR detection of relative expression of miR-497 in patients with different clinical stages; (**B**) qRT-PCR detection of relative expression of miR-497 in patients with or without lymph node metastases. *$P<0.05$ when compared to patients with stage I or patients with lymph node metastasis. #$P<0.05$ when compared to patients with stage I or stage II.

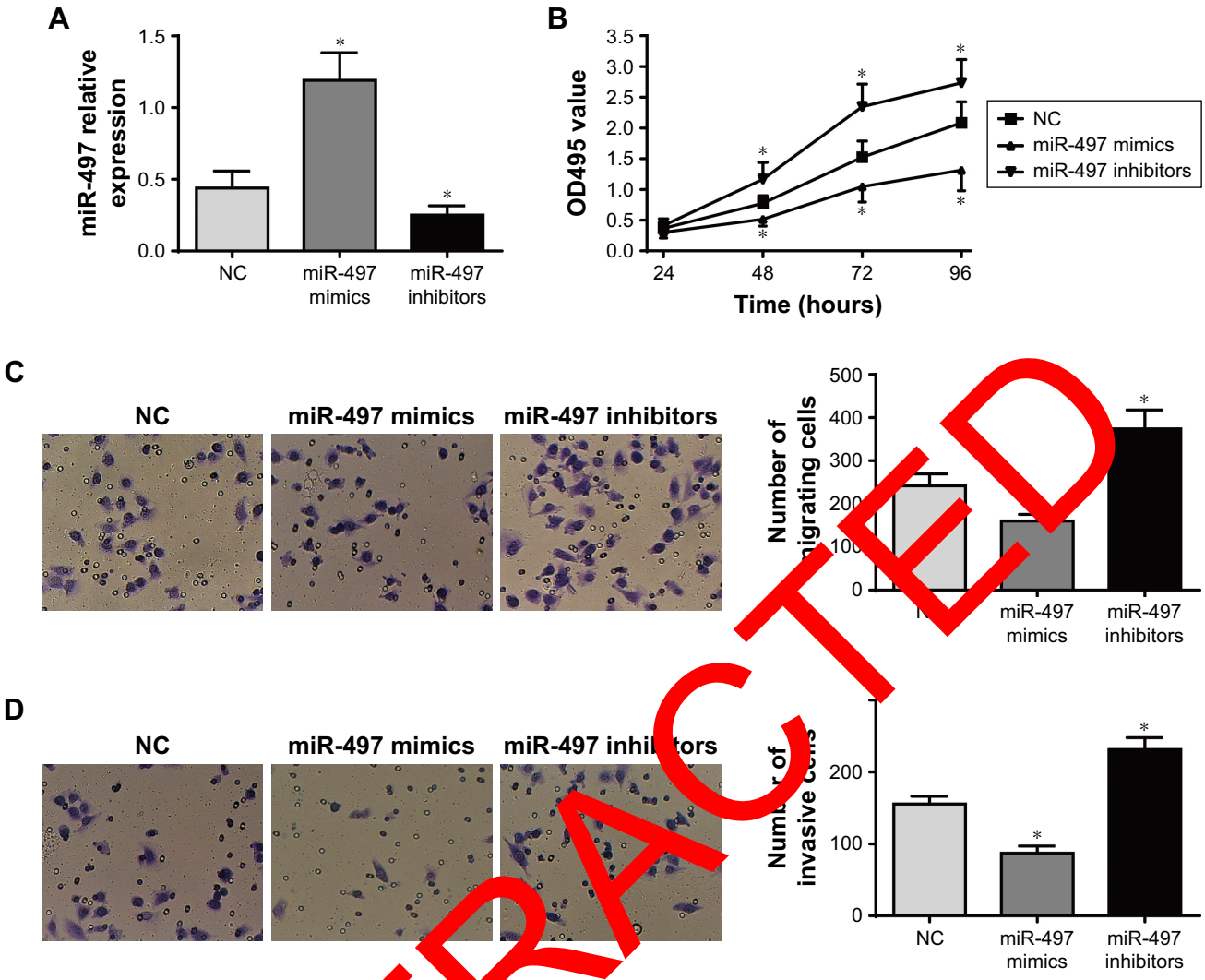

Figure 4 Effects of miR-497 expression on K1 cell proliferation, migration and invasion.
Notes: (**A**) Relative expression of miR-497 in each group by qRT-PCR detection. (**B**) Proliferation in each group determined by MTT assay. (**C**) Migration in each group determined by Transwell assay. (**D**) Invasion of each group determined by Transwell assay. *$P<0.05$ when compared with negative control (NC) group.

miR-497 mimics group and predominently increased in miR-497 inhibitor group ($P<0.05$; Figure 5C).

Based on these above results, we speculated that miR-497 might affect YAP1 expression. Further, TargetScan predicted that the binding site for YAP1 and miR-497 was 3′-untranslated region (Figure 6D). Then luciferase reporter assay was performed to validate this prediction. The results showed that no significant difference was found in luciferase activity between MT+mimics group and MT+NC group. However, luciferase activity of WT+mimics group was significantly lower than that of WT+NC group ($P<0.05$; Figure 6E). These results indicated that YAP1 was the target gene of miR-497.

miR-497 inhibited K1 cells proliferation, migration and invasion by negatively regulating YAP1 expression

We further investigated the mechanism of miR-497 affecting the proliferation, migration and invasion of K1 cells. Compared to the blank group, the relative expression of YAP1 was significantly decreased in si-YAP1 group and significantly increased in miR-497 inhibitor group ($P<0.05$). However, the relative expression of YAP1 in si-YAP1+inhibitors group was not significantly different from blank group ($P>0.05$; Figure 7A and B). This result further indicated that miR-497 negatively regulated YAP1 expression.

MTT assay was also conducted to assess the proliferation in each group. No significant difference was found in

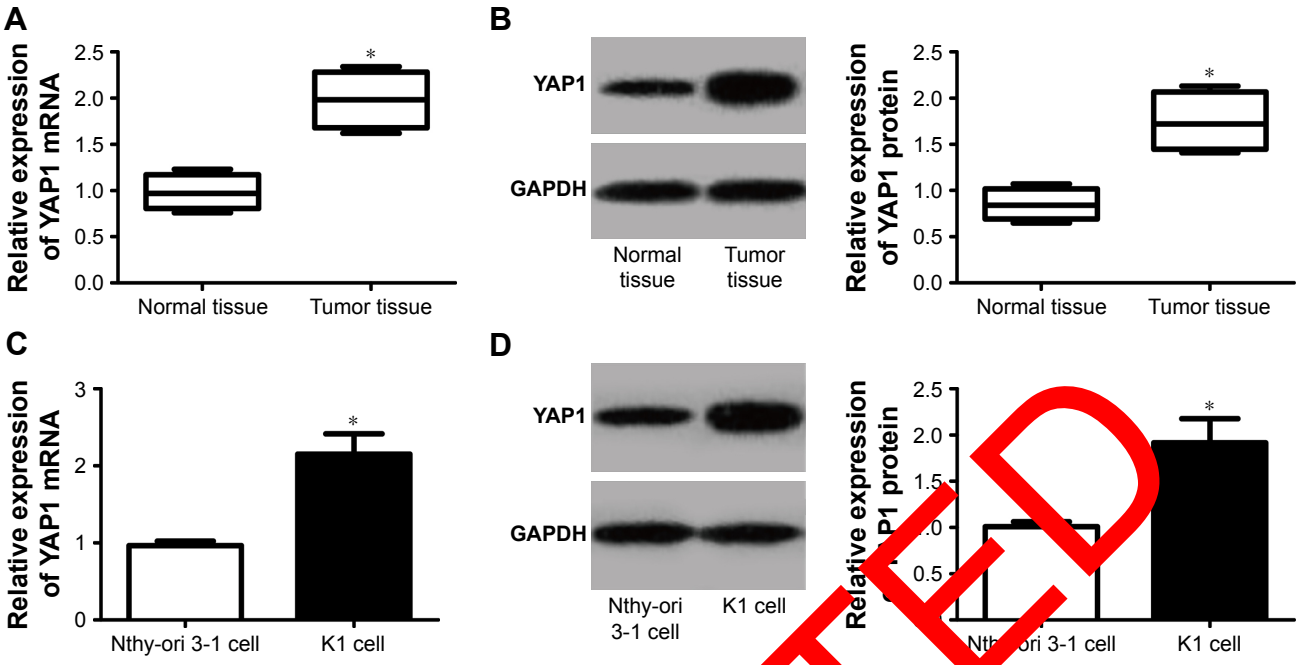

Figure 5 YAP1 was upregulated in thyroid papillary carcinoma tissues and K1 cells.
Notes: (**A**) qRT-PCR detection of YAP1 mRNA expression in normal tissues and tumor tissues. (**B**) Western blot detection of YAP1 protein expression in normal tissues and tumor tissues. (**C**) qRT-PCR detection of YAP1 mRNA expression in Nthy-ori 3-1 cells and K1 cells. (**D**) Western blot detection of YAP1 protein expression in Nthy-ori 3-1 cells and K1 cells. *$P<0.05$.

OD495 value among the four groups at 24 hours. At 48, 72 and 96 hours, compared with blank group, the OD495 value was significantly lower in si-YAP1 group and significantly higher in miR-497 inhibitor group ($P<0.05$), but no significant difference was found between si-YAP1+inhibitors group and blank group ($P>0.05$; Figure 7C). Matrigel, Transwell assay of cell migration and invasion results showed that, compared with blank group, the number of migrating or invasive cells was significantly decreased in si-YAP1 group and significantly increased in miR-497 inhibitor group ($P<0.05$). However, there was no statistically significant difference in the number of migrating or invasive cells between si-YAP1 inhibitors group and blank group ($P>0.05$; Figure 7D and E). All these results indicated that miR-497 regulated the proliferation, migration and invasion of K1 cells by negatively regulating YAP1 expression.

Discussion

In this study, we researched miR-497 expression in thyroid cancer by TCGA and found that the expression of miR-497 was low. Our further study also revealed that miR-497 was dramatically downregulated in thyroid papillary carcinoma tissues and K1 cells. miR-497 was closely related to the clinical stages and lymph node metastases. This research finally revealed that YAP1 was the target gene of miR-497. miR-497 could inhibit K1 cells proliferation, migration and invasion through negatively regulating YAP1. miR-497 was found to be involved in various human cancers and it was considered as a tumor suppressor because of its anticancer effect.[12] In the survey of global miRNA profiles of primary breast cancer, miR-497 was found to be disorganized for the first indication.[13] Subsequently, several studies confirmed the fact that miR-497 was downregulated in breast cancer.[14,15] In addition, many other researches also demonstrated downregulation of miR-497 in several other types of solid cancers such as hepatocellular carcinoma,[16] non-small-cell lung cancer,[17] cervical cancer,[18] gastric cancer,[19] colorectal cancer[20] and ovarian cancer.[21] All these studies confirmed the tumor suppressor effect of miR-497. Our result was highly consistent with the previous findings that miR-497 was obviously downregulated in thyroid papillary carcinoma. In addition, we also observed that upregulation of miR-497 significantly inhibited K1 cells proliferation, migration and invasion, dramatic increase in the proliferation, migration and invasion of K1 cells was found when miR-497 expression was inhibited. In previous studies, researchers reported that tumor (including pancreatic cancer, nasopharyngeal carcinoma, as well as bladder cancer) proliferation, migration and invasion were obviously suppressed, while apoptosis was significantly promoted when miR-497 expression was

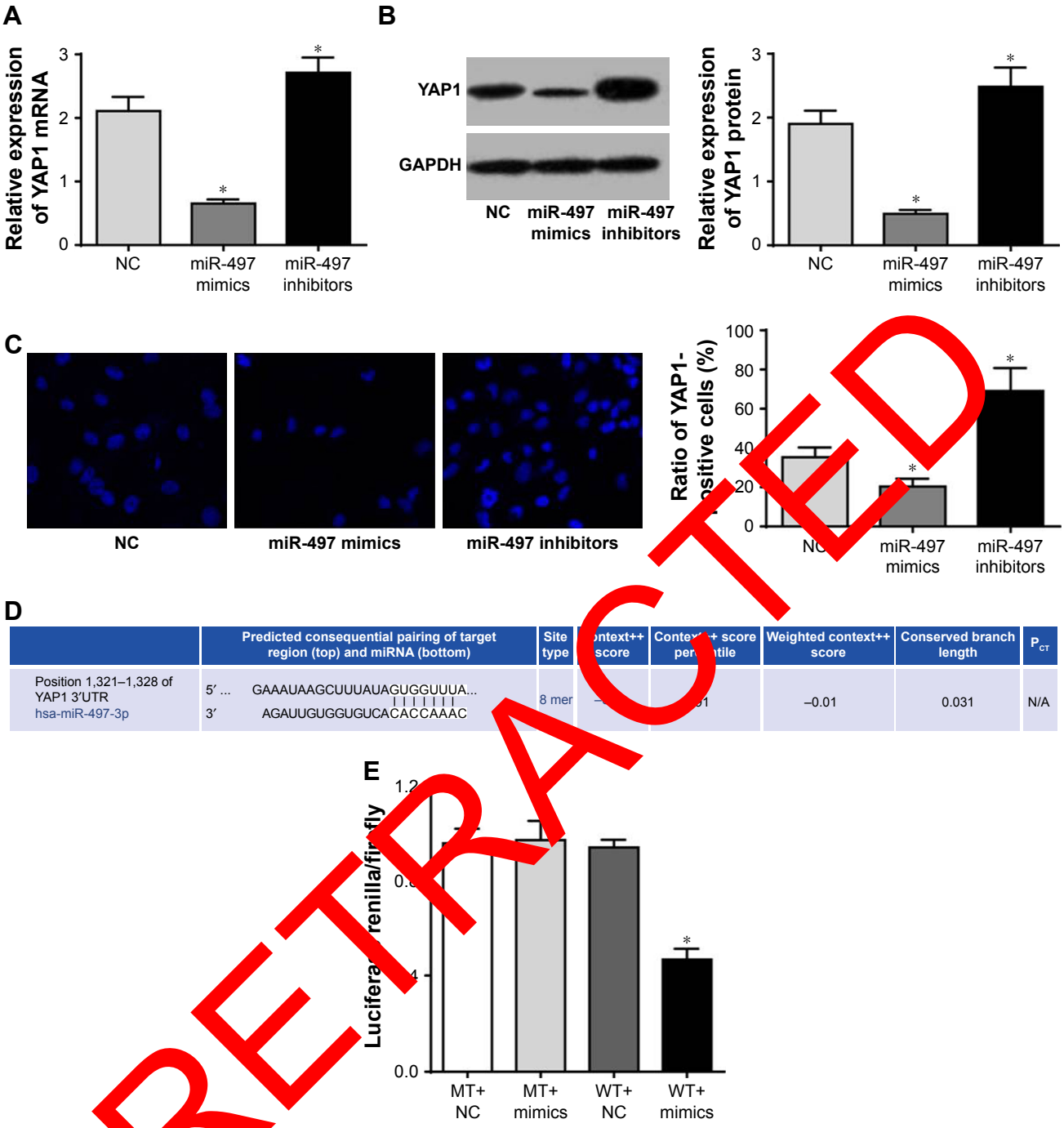

Figure 6 YAP1 was negatively regulated by miR-497.
Notes: (**A**) qRT-PCR detection of YAP1 mRNA expression in each group; (**B**) Western blot to detect YAP1 protein expression in each group; (**C**) immunofluorescence detection of YAP1-positive cells proportion in each group; (**D**) TargetScan prediction of the binding site for YAP1 and miR-497; (**E**) dual luciferase reporter gene activity assay. *$P<0.05$ when compared with NC group or WT+NC group.
Abbreviations: MT, mutant type; NC, negative control; WT, wild type.

increased by pre-miR-497 transfection.[10,12,22] However, studies also revealed that after miR-497 expression was inhibited, tumor (such as breast cancer) growth and colony formation ability were promoted.[23] Our research further confirmed these viewpoints.

In this study, luciferase reporter assay was performed to confirm the relationship between miR-497 and YAP1 to further study the mechanism of action of miR-497 in thyroid papillary carcinoma. As a result, YAP1 was demonstrated to be a target gene of miR-497 and its expression could be decreased by miR-497. Further research also indicated that miR-497 inhibited K1 cells proliferation, migration and invasion through negatively regulating the expression of YAP1. High expression of YAP1 was associated with the

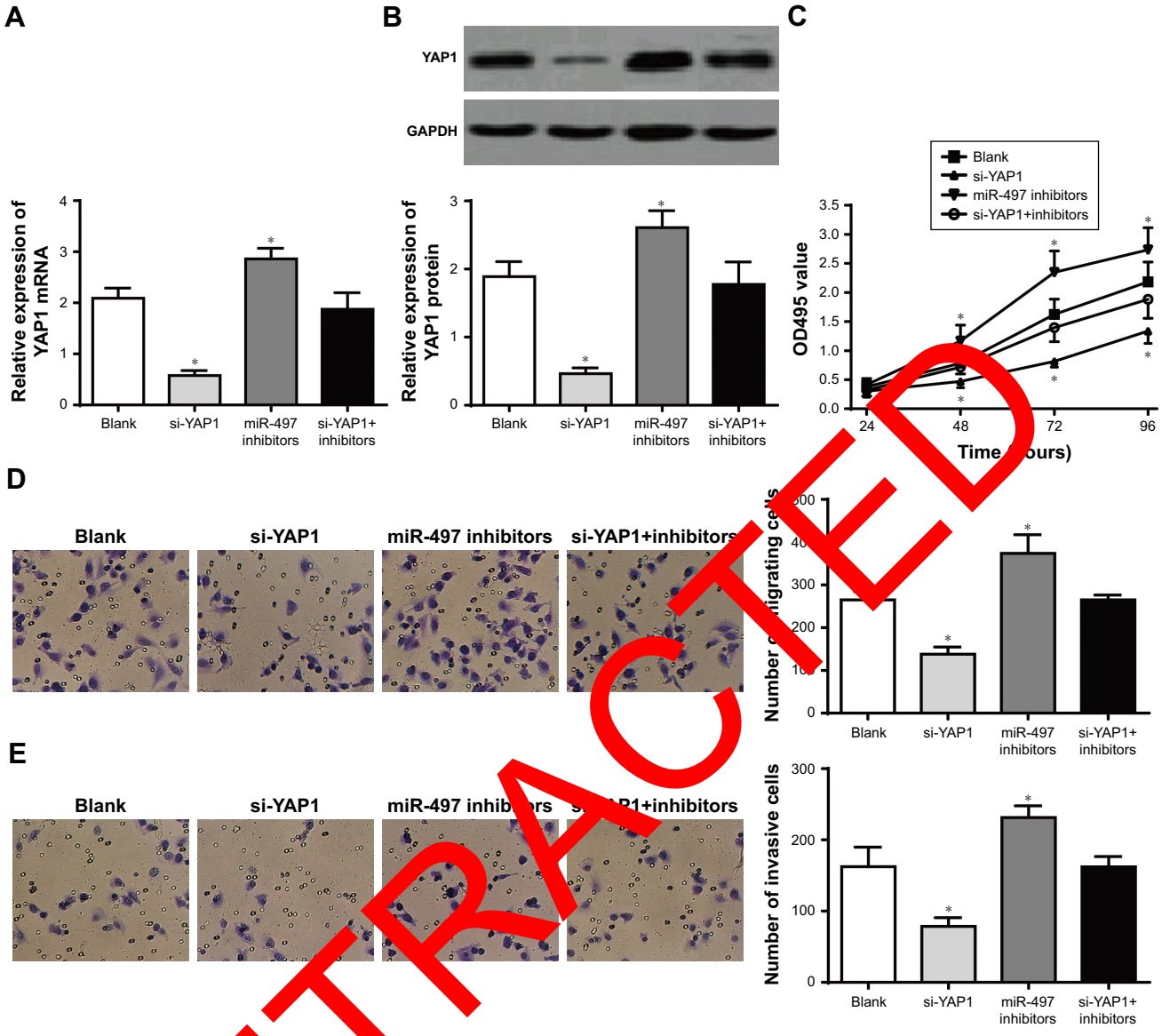

Figure 7 miR-497 inhibited the proliferation, migration and invasion of K1 cells by negatively regulating YAP1 expression.
Notes: (**A**) qRT-PCR detection of YAP1 mRNA expression in each group; (**B**) Western blot detection of YAP1 protein expression in each group; (**C**) MTT assay detection of the proliferation of cells in each group; (**D**) transwell assay detection of migration of cells in each group; (**E**) transwell assay detection of invasion of cells in each group. *$P<0.05$ when compared with blank group.

occurrence and development of a variety of cancers.[24,25] It is a terminal effect of Hippo/YAP signaling.[26] It was reported that YAP1 could promote the proliferation of liver cancer, and significantly higher expression of YAP1 was found in liver cancer tissues as well as in liver cancer cells.[27,28] A recent research also suggested that YAP1 promoted human hepatocellular carcinoma development and progression was through upregulating Jagged1 and activating the Notch pathway.[29] Moreover, several researches also revealed the target relationship between YAP1 and miR-497. Huang et al[30] suggested in their study that in non-small-cell lung cancer, miR-497 could inhibit non-small-cell lung cancer cells proliferation. They thought that the relevant mechanism might be the inhibitory effect of miR-497 on the expression of YAP1. miR-497 could inhibit the proliferation of hepatocellular carcinoma and promote the apoptosis of these cells.[31] Our conclusion in this study further verified the above findings.

This study also had some limitations. We only studied the effect of miR-497 on K1 cells. Due to the limitations of laboratory conditions, we could only obtain K1 cells. Further studies about the effect of miR-497 on other papillary thyroid cancer cell lines are also required. This will be the focus of our future research. In addition, the relationship between miR-497 expression and patients' survival should also be explored. However, we could not study this because of the

limitations of laboratory conditions. In our future research, we will work on this issue seriously.

In short, this research demonstrated that miR-497 was downregulated in thyroid papillary carcinoma, and upregulation of miR-497 could inhibit the proliferation, migration and invasion of thyroid papillary carcinoma cells. The underlying mechanism might be that miR-497 regulated the proliferation, migration and invasion of K1 cells by negatively regulating YAP1 expression. In this study, we initially studied the impact of miR-497 as well as the relevant mechanism on thyroid papillary carcinoma, which was of significant importance for the treatment of thyroid papillary carcinoma clinically.

Disclosure

The authors report no conflicts of interest in this work.

References

1. Oda H, Miyauchi A, Ito Y. Incidences of unfavorable events in the management of low-risk papillary microcarcinoma of the thyroid by active surveillance versus immediate surgery. *Thyroid*. 2016;26(1):150–155.
2. Davies L, Welch HG. Current thyroid cancer trends in the United States. *JAMA Otolaryngol Head Neck Surg*. 2014;140(4):317–322.
3. Nechiforboilă A. Distinct morphological features predictive for aggressiveness of papillary thyroid microcarcinoma: a study of 72 cases 80 tumor foci. *Acta Medica Marisiensis*. 2016;62(1):51–55.
4. Miyauchi A, Ito Y, Oda H. Insights into the management of papillary microcarcinoma of the thyroid. *Thyroid*. 2018;28(1):23–31.
5. Moritani S. Impact of lymph node metastases with recurrent laryngeal nerve invasion on patients with papillary thyroid carcinoma. *Thyroid*. 2015;25(1):107–111.
6. Grogan RH, Kaplan SP, Cao H, et al. A study of recurrence and death from papillary thyroid cancer with 27 years of median follow-up. *Surgery*. 2013;154(6):1436–1447.
7. Tang XY, Zheng W, Ding M, et al. miR-125b as a tumor suppressor in chondrosarcoma cells by the sensitization to doxorubicin through direct targeting the ErbB2-mediated glucose metabolism. *Drug Des Devel Ther*. 2016;10(571):571–583.
8. Sun JJ, Chen GY, Xie T. MicroRNA-361-5p inhibits cancer cell growth by targeting CXCR hepatocellular carcinoma. *Cell Physiol Biochem*. 2016;3 77–78
9. Zhao X, Zha , Xu W Hou J, D Down-regulation of miR-497 is associated with poor prognosis in renal cancer. *Int J Clin Exp Pathol*. 2015;8(1): –764
10. Xu J, Wang T, Z, et al. MiR-497 downregulation contributes to the malignancy of pancreatic cancer and associates with a poor prognosis. *Oncotarget*. 2014;5(:6983–6993.
11. Basnet A, Pandita A, Fullmer J, Sivapiragasam A. Squamous cell carcinoma of the thyroid as a result of anaplastic transformation from BRAF-positive papillary thyroid cancer. *Case Rep Oncol Med*. Epub October 12, 2017.
12. Wang S, Mo Y, Midorikawa K, et al. The potent tumor suppressor miR-497 inhibits cancer phenotypes in nasopharyngeal carcinoma by targeting ANLN and HSPA4L. *Oncotarget*. 2015;6(34):35893–35907.
13. Davoren PA, Mcneill RE, Lowery AJ, Kerin MJ, Miller N. Identification of suitable endogenous control genes for microRNA gene expression analysis in human breast cancer. *BMC Mol Biol*. 2008;9(1):76.
14. Tahiri A, Leivonen SK, Lüders T, et al. Deregulation of cancer-related miRNAs is a common event in both benign and malignant human breast tumors. *Carcinogenesis*. 2014;35(1):76–85.
15. Chang YY, Kuo WH, Hung JH, et al. Deregulated microRNAs in triple-negative breast cancer revealed by deep sequencing. *Mol Cancer*. 2015;14(1):36.
16. Xie Y, Wei RR, Huang GL, et al. Checkpoint kinase 1 is negatively regulated by miR-497 in hepatocellular carcinoma. *Med Oncol*. 2014;31(3):844.
17. Zhao WY, Wang Y, An ZJ, et al. Downregulation of miR-497 promotes tumor growth and angiogenesis by targeting HDGF in non-small cell lung cancer. *Biochem Biophys Res Commun*. 2013;435(3):466–471.
18. Luo M, Shen D, Zhou X, Chen X, Wa W. M RNA-497 is a potential prognostic marker in human cervical cancer and functions as a tumor suppressor by targeting the insulin-like growth fac 1 receptor. *Surgery*. 2013;153(6):836–847.
19. Siddiqui FM, Banerjee C, Zu er SM, et al. M hanical thrombectomy versus intrasinus thrombolysis for cerebral ven us thrombosis: a non-randomized com rison. *Interv Neuroradiol*. 2014;20(3):336–344.
20. Jiang Y, Meng Q J, Shen H, S, Yo eng J. MiR-497 promotes metastasis of tal cancer cells through NRDP1 inhibition. *Tumour Biol*. 2015; (10):7 –7647.
21. Xu S, Fu GB, Tao Z, e MiR-497 decreases cisplatin resistance in ov cancer cells by targeting mTOR/P70S6K1. *Oncotarget*. 2015; 8):26457–26471.
22. M, Shi D, Y L, et al. Circulating miR-497 and miR-663b in sma are potential novel biomarkers for bladder cancer. *Sci Rep*. 20 5:10437.
23. Wei Sun X, et al. MicroRNA-497 induces cell apoptosis by negatively regulating Bcl-2 protein expression at the posttranscription el in human breast cancer. *Int J Clin Exp Pathol*. 2015;8(7):7729–7739.
24. Sun D, Li X, He Y, et al. YAP1 enhances cell proliferation, migration, and invasion of gastric cancer in vitro and in vivo. *Oncotarget*. 2016;7(49):81062–81076.
25. Xiao L, Zhou H, Li X P, et al. MicroRNA-138 acts as a tumor suppressor in non small cell lung cancer via targeting YAP1. *Oncotarget*. 2016;7(26):40038–40046.
26. von Gise A, Lin Z, Schlegelmilch K, et al. YAP1, the nuclear target of Hippo signaling, stimulates heart growth through cardiomyocyte proliferation but not hypertrophy. *Proc Natl Acad Sci U S A*. 2012;109(7):2394–2399.
27. Yu W, Qiao Y, Tang X, et al. Tumor suppressor long non-coding RNA, MT1DP is negatively regulated by YAP and Runx2 to inhibit FoxA1 in liver cancer cells. *Cell Signal*. 2014;26(12):2961–2968.
28. Tu K, Yang W, Li C, et al. Fbxw7 is an independent prognostic marker and induces apoptosis and growth arrest by regulating YAP abundance in hepatocellular carcinoma. *Mol Cancer*. 2014;13(1):110.
29. Tschaharganeh DF, Chen X, Latzko P, et al. Yes-associated protein up-regulates Jagged-1 and activates the Notch pathway in human hepatocellular carcinoma. *Gastroenterology*. 2013;144(7):1530–1542.
30. Huang C, Ma R, Yue J, et al. MiR-497 suppresses YAP1 and inhibits tumor growth in non-small cell lung cancer. *Cell Physiol Biochem*. 2015;37(1):342–352.
31. Zhang L, Yu Z, Xian Y, Lin X. microRNA-497 inhibits cell proliferation and induces apoptosis by targeting YAP1 in human hepatocellular carcinoma. *FEBS Open Bio*. 2016;6(2):155–164.