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ORIGINAL RESEARCH

Next-generation sequence detects *ARAP3* as a novel oncogene in papillary thyroid carcinoma

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Purpose: Thyroid cancer is the most frequent malignancies of the endocrine system, and it has became the fastest growing type of cancer worldwide. Much still remains unknown about the molecular mechanisms of thyroid cancer. Studies have found that some certain relationship between *ARAP3* and human cancer. However, the role of *ARAP3* in thyroid cancer has not been well explained. This study aimed to investigate the role of *ARAP3* gene in papillary thyroid carcinoma.

Methods: Whole exon sequence and whole genome sequence of primary papillary thyroid carcinoma (PTC) samples and matched adjacent normal thyroid tissue samples were performed and then bioinformatics analysis was carried out. PTC cell lines (TPC1, BCPAP, and KTC-1) with transfection of small interfering RNA were used to investigate the functions of *ARAP3* gene, including cell proliferation assay, colony formation assay, migration assay, and invasion assay.

Results: Using next-generation sequence and bioinformatics analysis, we found *ARAP3* genes may play an important role in thyroid cancer. Downregulation of *ARAP3* significantly suppressed PTC cell lines (TPC1, BCPAP, and KTC-1), cell proliferation, colony formation, migration, and invasion.

Conclusion: This study indicated that *ARAP3* genes have important biological implications and may act as a potentially drugable target in PTC.

Keywords: papillary thyroid carcinoma, next-generation sequence, *ARAP3*, oncogene

Introduction

Thyroid cancer is one of the most frequent malignancies of the endocrine system, and it has become the fastest growing type of cancer worldwide.[1,2] Recently, the number of thyroid cancer cases annually had increased by 4% globally and its incidence is predicted to become the fourth leading cancer diagnosis by 2030.[3]

Papillary thyroid carcinoma (PTC) is the most common type of thyroid malignancy, accounting for 80%–85% of all types of thyroid cancers.[4] Recent studies have found that the tumorigenesis and development of thyroid cancer predominantly are driven by genetic factors, including the activation of oncogenes and inactivation of tumor suppressor genes.[4–6] BRAF mutation, which can aberrantly activate the MAP kinase pathway, plays a fundamental role in thyroid tumorigenesis, especially in PTC.[5] Other mutations such as TERT mutation,[7] RAS mutation,[4,8] PIK3CA mutation,[9–11] PTEN mutation,[12] and TP53 mutation[13,14] also play an important role in thyroid tumorigenesis and development.

Although much progress has been made in genetic research, much still remains unknown about the molecular mechanisms of PTC. To further understand the genetic mechanism of thyroid cancer, we performed whole exon sequence of 65 primary PTC

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tissue samples and matched adjacent normal thyroid tissue samples and whole genome sequence of 10 primary PTC tissue samples and matched adjacent normal thyroid tissue samples. We then identified *ARAP3* gene may act as a novel tumor oncogene in PTC.

ARAP3 (ArfGAP with RhoGAP domain, ankyrin repeat, and PH domain 3) encodes a phosphoinositide-binding protein containing ARF-GAP, RHO-GAP, RAS-associating, and pleckstrin homology domains. *ARAP3* was first identified for its ability to bind to phosphatidylinositol (3,4,5)-triphosphate in porcine leukocytes.[15] *ARAP3*, on activation of PI3K signaling, is found to be recruited to the plasma membrane, regulating lamellipodia formation and growth factor signaling.[15,16] Song et al revealed that *ARAP3* minimally impacts hematopoietic stem cells in adult bone marrow despite its critical role in embryonic vascular development.[17] Several studies have found that *ARAP3* gene has certain relations with human cancers. Yagi et al found that *ARAP3* inhibits peritoneal dissemination of scirrhous gastric carcinoma cells by regulating cell adhesion and invasion.[18] However, whether *ARAP3* gene also plays an important role in PTC is still unknown.

Although studies have found that some certain relationship between *ARAP3* and human cancer, the role of *ARAP3* in thyroid cancer has not been well explained. In this study, by performing next-generation sequence and bioinformatics analysis, we found that *ARAP3* gene may also play an important role in thyroid cancer, which has not been reported before. This study aims to investigate the real role of *ARAP3* gene in PTC.

Materials and methods

Patients and tissue collection

Primary PTC samples and matched adjacent normal thyroid tissue samples were obtained at the time of initial surgery. Samples were snap-frozen in liquid nitrogen immediately after surgical resection and subsequently stored at a −80°C freezer. Histopathological slides were reviewed retrospectively for all cases to confirm the histological diagnosis and to ensure abundant cancer content of the tumor by two pathologists. All procedures performed in studies involving human participants were in accordance with the ethical standards of the Ethics Committee of the First Affiliated Hospital of Wenzhou Medical University. Informed consent for the scientific use of biological material was obtained from each patient.

Cell lines and cell culture

The TPC1 and BCPAP cell lines were kindly provided by Professor Mingzhao Xing of the Johns Hopkins University School of Medicine, Baltimore, MA, USA. KTC-1 cell line was kindly provided by Stem Cell Bank, Chinese Academy of Sciences. The TPC1 and BCPAP were cultured in RPMI1640 supplemented with 10% fetal bovine serum and 1× MEM nonessential amino acids +1× sodium pyruvate. The KTC-1 was cultured in RPMI1640 supplemented with 10% fetal bovine serum and 1× MEM nonessential amino acids. All cell lines were incubated at 37°C in a humidified atmosphere containing 5% CO_2.

RNA isolation and real-time reverse transcription-polymerase chain reaction

Total RNA was isolated using TRIZOL Reagent (Invitrogen) and reverse transcription (Toyobo, Osaka, Japan) was performed according to the manufacturer's instructions. Real-time PCR analysis was performed in triplicate on the ABI prism 7300 sequence detection system (Applied Biosystems, USA) using the THUNDERBIRD SYBR qPCR Mix (Toyobo) according to manufacturer's instructions. The GAPDH mRNA level was used for normalization. Primer sequences were as follows: *ARAP3*: 5′-GTGGCTGGCTAGACAAGCTC-3′ (forward) and 5′-TCCTCCCATTGAACTGCACAA-3′ (reverse); GAPDH: 5′-GGTCGGAGTCAACGGATTTG-3′ (forward); and 5′-ATGAGCCCCAGCCTTCTCCAT-3′ (reverse).

Protein extraction and Western blot analysis

Treated cells were lysed in RIPA lysis buffer (Beyotime, Shanghai, China). An equal amount of protein of about 20 μg was separated by sodium dodecyl sulfate polyacrylamide gel electrophoresis and transferred onto the polyvinylidene fluoride membrane. After blocking with 5% skimmed milk, the polyvinylidene fluoride membrane was incubated with anti-*ARAP3* antibody (Abcam, USA). After washing three times with tris-buffered saline and Tween 20, the membrane was incubated with horseradish peroxidase-linked secondary anti-goat immunoglobulin G antibody (Abcam) at room temperature for 1.5 h. GAPDH protein, detected using an anti-GAPDH antibody (Abcam), was used for control.

RNA interference

Small interfering RNA (siRNA) for *ARAP3* was purchased from Shanghai Gene Pharma (Shanghai, China) for siRNA-mediated gene knockdown, 8×10^4 (TPC1) or 2×10^5 cells (BCPAP, KTC-1) were transfected with 10 μL (TPC1) or 7.5 μL (KTC-1) or 5 μL (BCPAP) siRNA (20 μM) and 4 μL RNAiMAX (Life Technologies, Carlsbad, CA, USA) in a 6-well plate according to the manufacturer's

recommendations. Cells were harvested 48 h after transfection for subsequent protein or RNA expression analysis.

Cell proliferation assay and colony formation assay

For the proliferation assay, TPC1, KTC-1 cells (3×10^3 cells) and BCPAP cells (5×10^3 cells) were seeded in 96-well plates and then transfected with siRNA. All cells were then incubated at 37°C for consecutive 5 days. MTS (Solution Cell Proliferation Assay; Promega, Fitchburg, WI, USA) was added to the cells and, following a 2-h incubation, absorbance was measured at 490 nm using Spectramax M5 (Molecular Devices, Sunnyvale, CA, USA).

For the colony forming assay, the three transfectant cells or control cells (2×10^3 cells for TPC1 and KTC-1, 4×10^3 cells for BCPAP) were seeded in 6-well plates, incubated for 8–14 days and then fixated with 4% PFA (paraformaldehyde; Sigma, USA) for 30 min and stained with 0.01% crystal violet for 30 min. All assays were performed in triplicate.

Migration and invasion assays

To detect the changed capacity of tumor cell migration, transwell cell culture chambers were used, according to the manufacturer's instructions (Corning Costar Corp, Cambridge, MA, USA). The three transfectant cells or control cells (5×10^4 cells) were seeded in the upper chamber and the lower chamber was filled with culture medium supplemented with 10% fetal bovine serum. The cells were then incubated at 37°C in a humidified incubator in 5% CO_2 for 24 h. Cells that did not traverse the filter were wiped off. Migrating cells on the reverse side of the filter were fixated with 4% PFA (Sigma) for 30 min and stained with 0.01% crystal violet for 30 min, and photographed under light microscope.

To detect the changed capacity of tumor cell invasion, transwell cell culture chambers were used, according to the manufacturer's instructions (Corning Costar Corp). The three transfectant cells or control cells (1×10^5 cells for TPC1, 2×10^5 cells for BCPAP and KTC-1) were seeded in the upper chamber and the lower chamber was filled with culture medium supplemented with 20% fetal bovine serum. The cells were then incubated at 37°C in a humidified incubator in 5% CO_2 for 24 h. Cells that did not traverse the filter were wiped off. Cells on the reverse side of the filter were fixated with 4% PFA (Sigma) for 30 min and stained with 0.01% crystal violet for 30 min, and photographed under light microscope.

Statistical analysis

Data on normal distribution were expressed as mean ± standard deviation and were compared with *t*-test. Categorical variables were expressed as percentage and were compared with chi-square test or Fisher's exact test, as appropriate. All *P*-values were two sided, and a *P*-value of <0.05 was considered statistically significant. Statistical analysis was performed with SPSS software version 19.0 (SPSS, Chicago, IL, USA). GraphPad Prism 5 (GraphPad Software, La Jolla, CA, USA) was used for graphs.

Results

ARAP3 mutation was all found in patients without BRAF V600E mutation

We performed whole exon sequence of 65 paired PTC tissue samples and whole genome sequence of 10 paired PTC tissue samples. Among all the 75 patients (38 patients are BRAF V600E positive and 37 patients are BRAF V600E negative), *ARAP3* mutation (141052399) was found in 4 patients without BRAF V600E mutation. None was found in patients with BRAF V600E mutation. A recurrence mutation (141052399) in 4 of all the 75 patients was identified. The detailed information of *ARAP3* mutation (141052399) detected by next-generation sequence is shown in Table 1. The mutation rate was low in these four patients, with 11.76%, 13.04%, 12.5%, 11.54%, respectively.

ARAP3 downregulation suppressed TPC1, BCPAP, and KTC-1 cell proliferation and colony formation

To determine whether *ARAP3* really plays an oncogenic role in thyroid cancer, we downregulated the gene expression level of *ARAP3* by using siRNA. As shown in Figure 1, *ARAP3* mRNA expression was effectively downregulated in both RNA and protein level. Then we carried out cell proliferation assays and colony formation assays in three PTC cell lines

Table 1 The detailed information of *ARAP3* mutation detected by next-generation sequence (4/75)

Sample	CHROM	POS	Mutation rate (%)	RefNr	RefAA	ThisNr	ThisAA	Mutation type	BRAF V600E
Q1	chr5	141052399	11.76	CTC	Leu	CCC	Pro	Missense	Wild type
Q4	chr5	141052399	13.04	CTC	Leu	CCC	Pro	Missense	Wild type
Q8	chr5	141052399	12.5	CTC	Leu	CCC	Pro	Missense	Wild type
Q10	chr5	141052399	11.54	CTC	Leu	CCC	Pro	Missense	Wild type

Note: Mutation rate means the proportion of mutation bases accounts for all the bases detected by next-generation sequence.

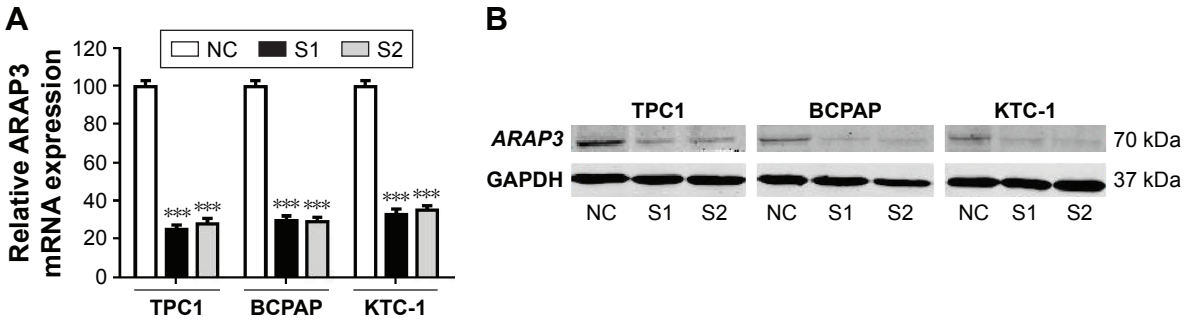

Figure 1 Knockdown of *ARAP3* gene in three papillary thyroid carcinoma cell lines (TPC1, BCPAP, and KTC-1).
Notes: *ARAP3* depletion was monitored by real-time polymerase chain reaction (**A**) and Western blotting (**B**). *ARAP3* mRNA expression was effectively downregulated in TPC1, BCPAP, and KTC-1 cells transfected with small interfering RNA compared with NC in both RNA and protein level. ***$P<0.01$ in comparison with NC using Student's *t*-test.

(TPC1, BCPAP, and KTC-1). As shown in Figure 2A, an evident inhibition of cell proliferation by downregulating *ARAP3* expression (transfection with siRNA) compared with the control (transfection with NC) was detected in three cell lines ($P<0.05$). Cell lines transfected with siRNA showed decreased proliferation capacity, starting to reach statistical significance at 3 or 4 days of cell culture. The inhibitory effect is more obvious in TPC1.

To confirm the results of cell proliferation assays, we performed colony formation assays. Cell colony formation was also significantly inhibited by *ARAP3* downregulation ($P<0.05$) (Figure 2B and C), consistent with the finding of cell proliferation assays.

ARAP3 downregulation inhibited TPC1, BCPAP, and KTC-1 migration and invasion

Next, to investigate the role of *ARAP3* in the migratory and invasive abilities of thyroid cancer cell lines (TPC1, BCPAP, and KTC-1), we carried out the migration and transwell invasion assays. The migration assays showed that it was significantly reduced in *ARAP3* downregulation groups (S1 and S2) compared with the control cells (NC) (Figure 3). All three cell lines (TPC1, BCPAP, and KTC-1) transfected with siRNA migrated much less cells than the control cells after 24 h seeding (Figure 3, $P<0.05$). It was more distinct in TPC1 and BCPAP than KTC-1. The transwell invasion assays also showed a similar result that *ARAP3* downregulation significantly inhibited invasive capacity of three thyroid cancer cell lines (TPC1, BCPAP, and KTC-1). As shown in Figure 4, an obvious decrease in the number of invading cells between cell lines transfected with siRNA and the control cells ($P<0.05$). These together indicated *ARAP3* gene as a significant oncogene involving in tumorigenesis metastasis in PTC.

Discussion

Although much progress in genetic research had been made for thyroid cancer, much still remains unknown about the molecular mechanisms of PTC. There are still more than 4% PTC cases with unknown oncogenic driver and many epigenetic alterations have not yet been well studied.[19] Using

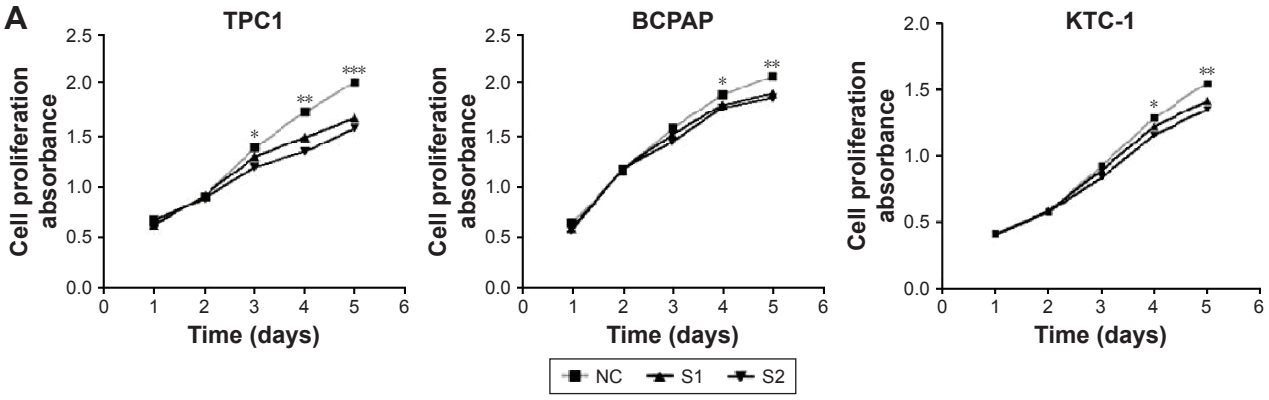

Figure 2 (*Continued*)

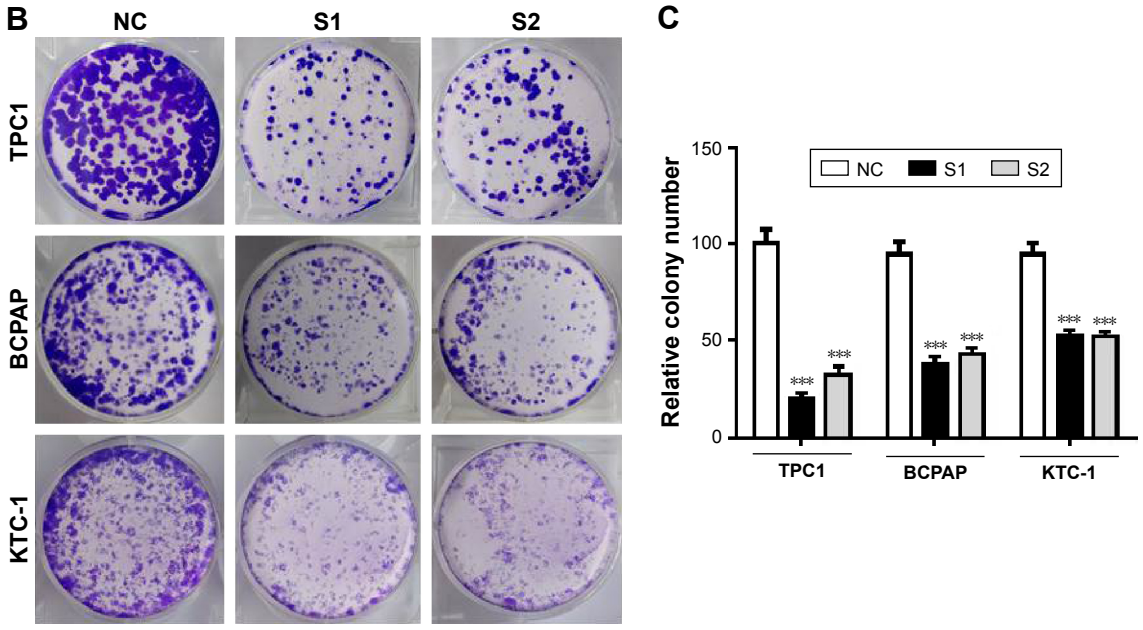

Figure 2 Downregulation of *ARAP3* suppressed papillary thyroid carcinoma cell lines (TPC1, BCPAP, and KTC-1) proliferation and colony formation.
Notes: (**A**) Cell proliferation assay. TPC1, BCPAP, and KTC-1 cells transfected with small interfering RNA or control cells (NC) were cultured in 96-well plates for the successive time (1–5 days), and cell proliferation was measured using MTS. Cell proliferation was significantly suppressed in TPC1, BCPAP, and KTC-1 cells transfected with small interfering RNA compared with NC. (**B**) Colony formation assay. TPC1, BCPAP, and KTC-1 cells transfected with small interfering RNA and NC cells were plated in 6-well plates at proper density. After 8–14 days of incubation, cells were fixated with 4% paraformaldehyde and stained with 0.01% crystal violet. (**C**) Relative quantification of the colony number. The columns represent the mean colony number from at least three independent experiments and the little vertical bars on the top of the columns represent SD. *$P<0.1$, **$P<0.05$, ***$P<0.01$ in comparison with NC using Student's *t*-test.

whole exon sequence and whole genome sequence, *ARAP3* gene was found to may be act as an important oncogenic role in PTC. Some studies have demonstrated that *ARAP3* gene was associated with human diseases such as embryonic vascular development and gastric cancer. *ARAP3* gene were previously found to inhibit peritoneal dissemination of scirrhous gastric carcinoma cells by regulating cell adhesion and invasion.[18] However, little is known about its function in human cancer especially thyroid cancer.

In this study, the aim was to investigate the potential tumorigenic role of *ARAP3* gene in thyroid cancer. Using whole exon sequence and whole genome sequence, a recurrence mutation (141052399) was found in 4 of all the 75 patients in *ARAP3* gene. Moreover, it was missense mutation and amino

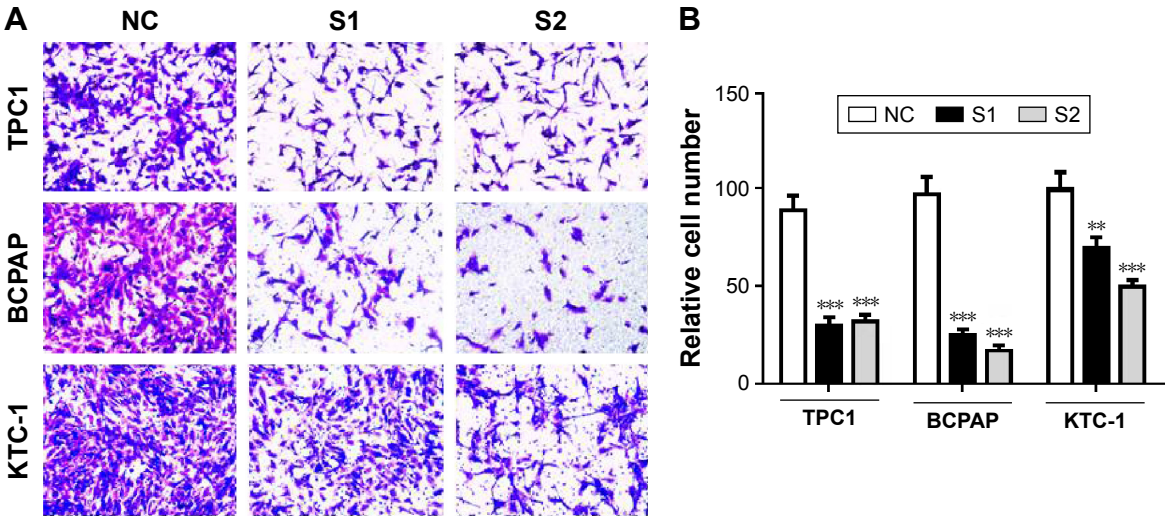

Figure 3 Downregulation of *ARAP3* suppressed papillary thyroid carcinoma cell lines (TPC1, BCPAP, and KTC-1) cell migration.
Notes: (**A**) Migration assay. Migrating cell number was much less in TPC1, BCPAP, and KTC-1 cells transfected with small interfering RNA compared with NC. (**B**) Relative quantification of migrating cell number. Columns represent the mean of migrating cell numbers from at least three independent experiments and the little vertical bars at the top of the columns represent SD. **$P<0.05$, ***$P<0.01$ in comparison with NC using Student's *t*-test.

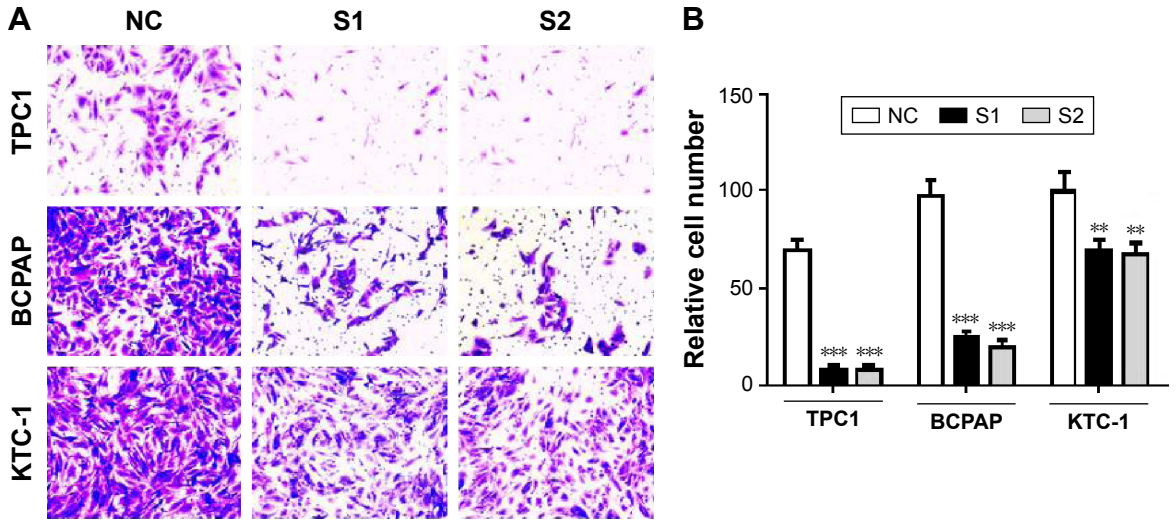

Figure 4 Downregulation of *ARAP3* inhibited papillary thyroid carcinoma cell lines (TPC1, BCPAP, and KTC-1) cell invasion.
Notes: (**A**) Invasion assay. Invading cell number was much less in TPC1, BCPAP, and KTC-1 cells transfected with small interfering RNA compared with NC. (**B**) Relative quantification of invading cell number. Columns represent the mean of invading cell numbers from at least three independent experiments and the little vertical bars at the top of the columns represent SD. $^{**}P<0.05$, $^{***}P<0.01$ in comparison with NC using Student's *t*-test.

acid was located in one of the protein domains. These findings suggest that *ARAP3* may play a critical role in thyroid cancer and prompted us to take the next step to functionally study the *ARAP3* gene in cell lines. Therefore, three thyroid cancer cell lines, TPC1, BCPAP, and KTC-1, were chosen as cellular models for PTC. Then, using cellular and molecular approaches, *ARAP3* downregulation was shown to lead to the inhibition of the ability of cell proliferation and the ability of migration and invasion, which are all well consistent with *ARAP3* being a tumorigenic role in thyroid cancer.

However, this study has some limitations. First, this study has not yet confirmed the existence of aforementioned point mutation detected by next-generation sequence. Conventional methods such as Sanger sequence were not sensitive enough to detected the mutation, because the rate of mutation bases is too low (Table 1). More sensitive methods need to be explored. Second, our study did not analysis relationship between clinicopathologic features and *ARAP3* gene mutation and expression, such as lymph node metastasis and disease-free survival. Third, the specific mechanisms involved in the tumorigenic role of *ARAP3* and whether there is epigenetic alteration in the *ARAP3* gene in thyroid cancer still remains to be investigated.

All in all, in this study, by using high-throughput sequence, bioinformatics analysis, and cellular and molecular approaches, exertion of *ARAP3* gene as a tumorigenic role in PTC was demonstrated, particularly in proliferation and tumor metastasis, which add to our understanding of the molecular pathogenesis of PTC. This study indicated that *ARAP3* gene has important biological implications and may act as a potentially drugable target in PTC.

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Disclosure

The authors report no conflicts of interest in this work.

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