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ORIGINAL RESEARCH

RETRACTED ARTICLE: Long Non-Coding RNA TRG-AS1 Promoted Proliferation and Invasion of Lung Cancer Cells Through the miR-224-5p/SMAD4 Axis

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Introduction: The aim of this study was to investigate the role and mechanism of long non-coding RNA (lncRNA) TRG-AS1 in mediating the proliferation, invasion and migration of lung cancer cells as well lung tumor growth.

Methods: Firstly, the expression levels of TRG-AS1, miR-224-5p in lung cancer tissues or cells were quantified by quantitative real-time PCR. Western blot analysis was conducted to measure the expression levels of protein SMAD4. CCK-8 assay, wound healing assay and transwell assay were conducted to evaluate cell proliferation, migration and invasion, respectively. The interaction between TRG-AS1 and miR-224-5p was predicted by bioinformatics analysis. Dual-luciferase assay and RNA pull-down assay were performed to further confirm their interaction. In addition, the interaction between miR-224-5p and SMAD4 was detected by RIP assay.

Results: The results showed that TRG-AS1 was highly upregulated and miR-224-5p was downregulated in lung cancer. A negative correlation was found between TRG-AS1 and miR-224-5p. Furthermore, upregulation of TRG-AS1 promoted cell proliferation and invasion, while overexpression of miR-224-5p attenuated the effects of TRG-AS1. The downstream protein SMAD4 played an important role. In vivo study showed that knockdown of TRG-AS1 effectively retarded tumor growth.

Discussion: Our data suggested that the TRG-AS1/miR-224-5p/SMAD4 axis may be a potential therapeutic target in lung cancer.

Keywords: lung cancer, TRG-AS1, miR-224-5p/SMAD4 axis, therapeutic target

Introduction

Lung cancer is one of the most prevalent cancers, causing more deaths than all the other types of cancer combined.[1] Globally, 12.4% of total new cancer cases are lung cancer, which has a mortality rate of 17.6%. The 5-year survival rate for lung cancer in the United States is 15.6%.[2] Besides environmental factors such as smoking, dysregulation of cancer-related genes is one major contributor to tumorigenesis of lung cancer, and extensive efforts have been made to search for new therapeutic targets in lung cancer.[3,4]

Protein-coding genes only take up 2% of the human genome and the rest genes were classified as non-coding genes.[5,6] Long non-coding RNAs (lncRNAs) are nucleotides longer than 200 nt that lack an open reading frame.[7] Recent studies have been exploring the roles of lncRNAs in cancer progression. Aberrant expression of lncRNAs may be one of the major contributors to tumorigenesis,[8] such as

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the metastasis-associated lung adenocarcinoma transcript 1 (MALAT1)[9] and HOX antisense intergenic RNA (HOTAIR).[10] HOXA distal transcript antisense RNA (HOTTIP)[11] and ANRIL[12] have been identified as important regulators of lung cancer tumorigenesis. With the development of gene therapy, such as efficient delivery of siRNAs to attenuate the expression of target lncRNAs,[13] the specific suppression of dysregulated lncRNAs has been a promising strategy in cancer treatment.[14]

This study was carried out to characterize the role and mechanism of the lncRNA T cell receptor gamma locus antisense RNA 1 (TRG-AS1) in lung cancer. It has been reported that lncRNA TRG-AS1 stimulates hepatocellular carcinoma progression by sponging miR-4500 to modulate BACH1, promoting glioblastoma cell proliferation by competitively binding with miR-877-5p to regulate the expression of SUZ12, a potent driver of oncogenicity of tongue squamous cell carcinoma through microRNA-543/Yes-associated protein 1 axis regulation. Our results showed that TRG-AS1 was highly upregulated in lung cancer samples. Up-regulation of TRG-AS1 promoted cancer cell proliferation and invasion. Furthermore, we observed that miR-224-5p was a target of TRG-AS1. MiR-224-5p is a recently identified important regulator in hepatocellular cancer,[15,16] colorectal cancer,[17] breast cancer[18] and lung cancer.[19] By suppressing miR-224-5p, TRG-AS1 exerted a cancer-promoting role by promoting the expression of SMAD4, which was a putative oncogene in lung cancer.

Materials and Methods

Human Specimen Collection

All procedures of clinical studies were approved by the Ethics Committee of Fujian Medical University Cancer Hospital & Fujian Cancer Hospital (No. 65356). Cancerous tissues and adjacent normal tissues were collected from 64 lung cancer patients admitted to the aforementioned hospital from May 2012 to September 2014. Tissue samples were snap-frozen in liquid nitrogen and stored at −80 °C before use. All patients signed the written informed consent.

Cell Culture and Oligonucleotide Transfection

Human lung cancer cells, SPC-A-1, A549, H1975, H1299, and normal human lung epithelial cells BEAS-2B were obtained from American Type Culture Collection Company (ATCC; Manassas, VA, USA). Cells were cultured in RPMI-1640 medium (Gibco, Grand Island, NY, USA) supplemented with 10% fetal bovine serum (FBS; Gibco), 100 U/mL penicillin (Gibco), and 100 U/mL streptomycin (Gibco) at a humidified incubator at 37 °C with 5% CO_2. MiR-224-5p inhibitor, miR-224-5p mimic and the siRNA against TRG-AS1 (Si-TRG-AS1), a short hairpin RNA plasmid directed against TRG-AS1 (sh-TRG-AS1), si-SMAD4 and their controls were purchased from GenePharm (China). SiRNA oligos (50 nM) were transfected into cells using lipofectamine 2000 (Invitrogen, Carlsbad, CA) And 1×10^6 cells were cultured to 60% confluence in 6-well plates with 2 mL complete medium. The siRNA sequences of TRG-AS1 and its control were:

si-TRG-AS1, sense: 5′-CCCCATGATGGTCCTCAGTT-3′; antisense: 5′-GGAAAGCAACTGCAGGTTACTC-3′;

si-*SMAD4*, sense: 5′-AGATGAATTGGATTCTTTA-3′, antisense: 5′-TAAAGAATCCAATTCATCT3′;

Control: sense: 5′-GGCCGTCACTCAATGATTCCG-3′, antisense: 5′-UUTTGGATGGCATACGCATGA-3′.

MiR-224-5p mimic sense: 5′-UAAGUCACUAGUGGUUCCGUU-3′; antisense: 5′-UUACUCAGUGAUCACCAAGGC-3′;

MiR-224-5p inhibitor: 5′-AACGGAACCACUAGUGACUUA-3′.

NC sense: 5′-UUCUCCGAACGUGUCACGUTT-3′; antisense: 5′-ACGUGACACGUUCGGAGAATT-3′.

BLAST Alignment and Quantitative RT-PCR

The NCBI's BLAST was used to search for the targets of TRG-AS1. Total RNAs were extracted using the miRNeasy Mini Kit (Invitrogen), followed by checking the RNA quantity and purity using a NanoDrop 2000 (Thermo Fisher, Wilmington, DE, USA). The cDNA was synthesized with 1 μg of RNA samples using SuperMix (TransGen, Beijing, China). SYBR green qPCR SuperMix (Applied Biosystems Life Technologies, Foster, CA, USA) and an ABI prism 7500 Sequence Detection System (Applied Biosystems Life Technologies) were used for real-time PCR. The relative expression of each gene was calculated using the $2^{-\Delta\Delta Ct}$ (Ct, cycle threshold) method. U6 and GADPH were used to normalize the expression levels of miRNA and lncRNA/target genes, respectively.

TRG-AS1: F: 5′-GGAGTCTGCTCTAAGAGCTG-3′,

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R: 5′-CAGAGCAAAGATGCTCTGC-3′;
miR-224-5p: F: 5′-GGTCC TAAGTCACTAG TGGTTCCGTT-3′,
R: 5′-CCAGTGCAGGGTCCGAGGT-3′;
SMAD4: F: 5′-AAAGGTGAAGGTGATGTTTGGGTC-3′,
R: 5′-CTGGAGCTATTCCACCTACTGATCC-3′;
U6: F: 5′-CTCGCTTCGGCAGCACA-3′,
R: 5′-AACGCTTCACGAATTTGCGT-3′;
GAPDH: F: 5′-ATGGAAATCCCATCACCATCTT-3′,
R: 5′-CGCCCCACTTGATTTTGG-3′.

Luciferase Reporter Gene Assay

The luciferase report system non-viral carrier pmirGLO plasmid (GenePharm, China) was used to prepare oligonucleotides containing the TRG-AS1 cDNA fragment with the miRNA binding sites, and the site-directed mutated TRG-AS1 counterpart. Next, 100 ng plasmids and 200 nmol/L miR-224-5p mimic or miR-NC mimic and the luciferase reporter plasmid were used to transfect cells (1 x10^5 per mL) using Attractene Transfection Reagent (Qiagen). Relative luciferase activity was quantified using a luminometer after 48 h. The luciferase activity was assessed by determining the ratio of firefly to Renilla luciferase activity with a dual-luciferase reporter system (Promega, USA).

RNA Pull-Down

For miRNA pull-down, A549 cells were transfected with biotinylated miR-224-5p (224 probe) or control probe (GenScript, Nanjing, China), and harvested in lysis buffer (20 mM Tris pH 7.5, 100 mM KCl, 5 mM $MgCl_2$, 0.5% NP-40) and 1 U/ml Recombinant RNAse inhibitor (TaKaRa). Total RNAs were pretreated with DNaseI and heated at 65 °C for 5 min, and then treated with instant ice bath. Afterwards, RNAs were incubated with streptavidin-coated magnetic beads (New England BioLabs, S1420S) at 4 °C for 2 h. After incubation, beads were washed twice with lysis buffer and total RNAs were extracted with Trizol (Invitrogen, CA, USA). The expression of TRG-AS1 was detected by RT-qPCR.

Cell Proliferation Assay

Cell proliferation rates were measured by Cell Counting Kit-8 (CCK-8; Dojindo, JPN). Briefly, cells were cultured for 24, 48, 72 or 96 h in 96-well plates and 10 μL CCK-8 reagent was added. After another 2 h, absorbance at 480 nm was measured using a microplate reader (Bio-rad, Hercules, CA, USA). Cells (1 × 10^3 cells per well) were seeded in a 6-well plate and incubated for 1 week. After washing with PBS, cells were fixed with 4% formaldehyde for 15 min and stained for 10–30 min with 2.5% Giemsa. The colonies were then counted with a diameter of over 100 μm.

Wound Healing Assay and Transwell Assay

In wound healing assay, cells were cultured to 60% confluence in 6-well plates and a sterile pipette tip was used to enforce a wound gap. After 24 h, the width was the remaining wound gap divided by the initial width of the wound gap of 0 h. Migration rate was calculated as follows: migration rate = distance (24 h)/original distance (0 h). In transwell assay, cells (5 × 10^4 per well) were planted in Matrigel coated upper chambers (8 mm, BD Biosciences) of a transwell apparatus. The lower chamber was added with DMEM medium with 600 uL 1% FBS. After incubation at 37 °C for 24 h, cells in the upper surface of the membrane were removed with a cotton tip, followed by staining of cells on the lower surface for 30 min with 0.1% crystal violet.

Western Blot Analysis

Cells were lysed by RIPA buffer (Sigma-Aldrich, St. Louis, MO) and total proteins were extracted. Protein concentrations were detected using BCA assay. Equal amount of protein samples were separated by electrophoresis and then transferred onto PVDF membrane (Millipore, Bedford, MA). After blocking, the PVDF membrane was incubated with anti-SMAD4 and anti-GADPH, followed by incubation with conjugated goat anti-rabbit IgG (Abcam). Finally, protein bands were viewed using the ECL detection kit (GenePharm, China).

Flow Cytometry

Firstly, cells (10^6 cells/mL) were re-suspended in PBS. After treatment with FITC-Annexin V and propidium iodide (Becton-Dickinson Biosciences, San Jose, CA, USA), cells were analyzed using FACScan flow cytometer (Becton-Dickinson Biosciences).

RIP Assays

RIP assays were conducted using a Magna RNA-binding protein immunoprecipitation kit (Millipore) following the manufacturer's instructions. Briefly, cell lysates were

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incubated with RIP buffer containing magnetic beads conjugated with negative IgG or anti-SMAD4 antibody. Immunoprecipitated RNAs were obtained by digestion with Proteinase K. Then, RNA samples were reversely transcribed into complementary DNA and subjected to quantitative real-time PCR analysis.

Xenograft Experiments

All animal experiments were approved by the Institutional Animal Care and Use Committee of Fujian Medical University Cancer Hospital & Fujian Cancer Hospital. The institutional guideline was followed for the welfare of the laboratory animals. Tumor-bearing nude mice (18–22 g, 6-week-old, nude 30) were purchased from the Animal Center of Fujian Hospital. Mice were placed in an animal laboratory without specific pathogens and the conditions were: temperature (23 ± 2 °C), humidity (52.56 ± 2.03%), standard photoperiod (12 h/12 h light/dark cycle), free access to food and water. Nude mice were divided into 4 groups with 5 nude mice in each group. Firstly, 1×10^7 A549 cells were transfected with lentivirus mediated sh-TRG-AS1 or sh-NC and then subcutaneously injected into BALB/c-nu mice. Before injecting the cells, cells were sorted and the dead cells were removed by trypan blue staining, and the number of living cells was determined by cell count. Cells were then mixed with Matrigel (Corning, USA) with a ratio of 1:1. Tumor growth was monitored every 3 days using caliper, and the tumor size was evaluated with the following formula: size = 0.5 × length × width × width.

Immunohistochemical Staining

Tumor tissue sections from nude mice were dried at 60 °C, dewaxed in xylene, and rehydrated by alcohol solution. After antigen retrieval, sections were blocked with goat serum (GenePharma, China) and incubated with Ki67 antibody (1:200; Wuhan, Shanghai, China) or TUNEL Apoptosis Assay Kit (Vazyme). Tumor sections were incubated in One-step polymer detection system (ZSGB-BIO, Beijing, China) for 20 min and counterstained with hematoxylin.

Statistical Analyses

Data were expressed the as means ± standard deviation (SD) using at least 3 independent experiments. One-way ANOVA or two-tailed Student's *t*-test, followed by LSD post hoc test was used for comparison between groups. The Pearson analysis was used for correlation analysis. The Kaplan–Meier method followed by Log rank test was used for survival analysis. $P < 0.05$ was considered as statistically significant.

Results

TRG-AS1 Was Upregulated in Lung Cancer

To explore the role of TRG-AS1 in lung adenocarcinoma, the expression levels of TRG-AS1 in tumor and normal tissues from 64 patients with stage I–II lung adenocarcinoma were determined using qRT-PCR analysis. As shown in Figure 1A, the expression levels of TRG-AS1 were significantly higher in tumor tissues than that in normal tissues ($p < 0.05$, n = 64). To correlate the expression of TRG-AS1 to patient survival, patients were divided into high and low expression groups according to the mean expression level of TRG-AS1 (Figure 1B). In addition, patients with high expression levels of TRG-AS1 had poor survival than that with low expression levels of TRG-AS1 ($p = 0.05$, n = 64) (Figure 1C). Furthermore, the results showed that the expression of TRG-AS1 correlated with tumor, TNM stage and N stage, but there was no relationship between the expression of TRG-AS1 and age, gender, location, and T stage (Tables 1 and 2).

Knockdown of TRG-AS1 Inhibited Proliferation, Migration and Invasion of Lung Cancer Cells

Analysis of the expression levels of TRG-AS1 in lung adenocarcinoma cell lines confirmed that upregulation of TRG1-AS1 was also found in A529, H1299, H1975 and SPC-1A-1 cells (Figure 2A). Because A549 and H1299 cells showed higher expression levels of TRG-AS1, these two cells lines were selected for subsequent experiments. Three small-interfering RNAs (siRNAs) against TRG-AS1 (si-TRG-AS1-1, si-TRG-AS1-2 and si-TRG-AS1-3) were designed to evaluate the effects of knockdown of TRG-AS1 on lung cancer cells. Si-TRG-AS1-3 was demonstrated to have the highest knockdown efficiency and was used in further knockdown studies ($p < 0.05$) (Figure 2B). It showed that knockdown of TRG-AS1 effectively reduced cell proliferation, colony formation, migration and invasion of A549 and H1299 cells ($p < 0.05$) (Figure 2C–F). These results indicated the anti-cancer role of knockdown of TRG-AS1 in vitro.

MiR-224-5p Was an Inhibitory Target for TRG-AS1

BLAST alignment indicated that TRG-AS1 had a binding site with miR-224-5p (Figure 3A). We used

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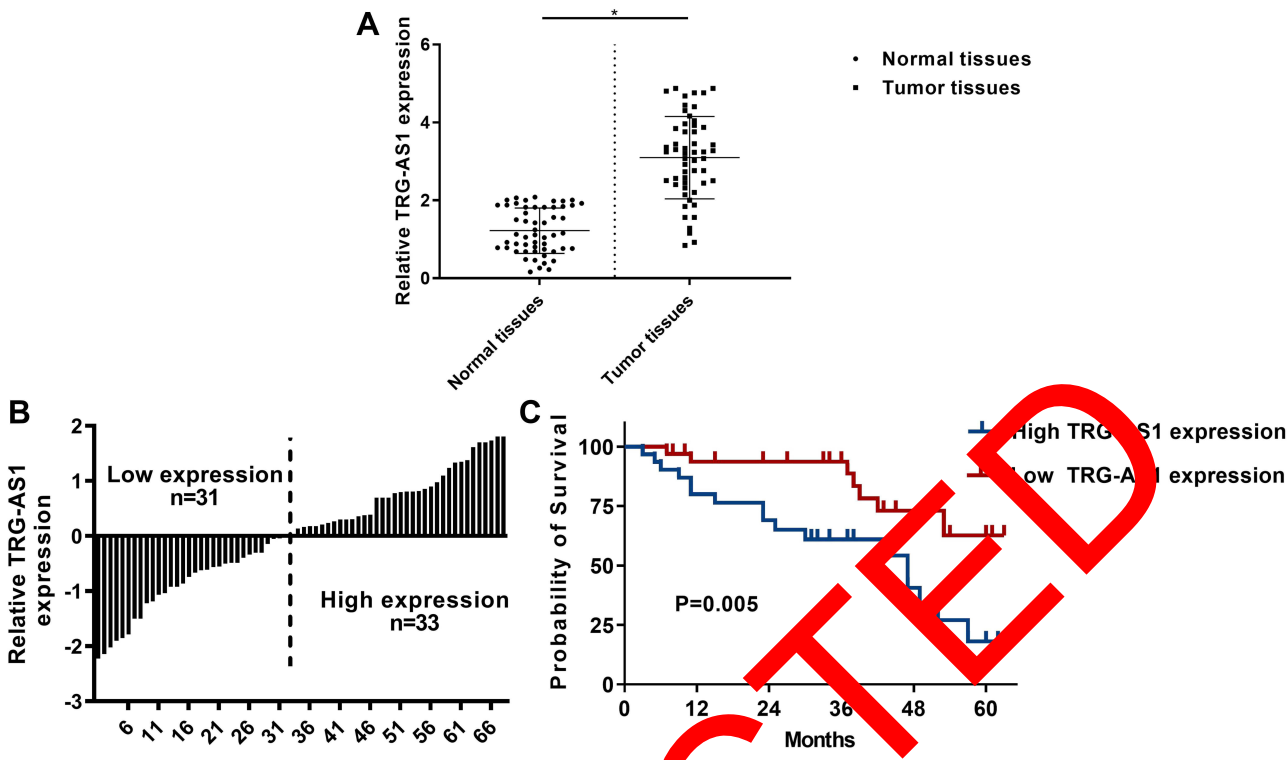

Figure 1 TRG-AS1 was upregulated in lung adenocarcinoma. (**A**) qRT-PCR analysis of TRG-AS1 expression in tumor tissues and normal tissues from 64 lung adenocarcinoma patients. (**B**) Histogram of TRG-AS1 levels in patients which was used to subgroup the patients into high TRG-AS1 expression group and low TRG-AS1 expression group. (**C**) Survival analysis of patients with high and low TRG-AS1 expression. qRT-qPCR were repeated 3 times. *$p < 0.05$.

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site-directed mutagenesis to generate a mutant TRG-AS1 sequence to abolish the binding between TRG-AS1 and miR-224-5p. Luciferase assay results showed that miR-224-5p-mimic reduced luciferase expression around TRG-AS1 ($p < 0.05$, Figure 3B). RNA pull-down assay showed that TRG-AS1 could only be precipitated by miR-224-5p probe but not the control probe, indicating that miR-224-5p interacted with TRG-AS1 ($p < 0.05$) (Figure 3C). In addition, it showed that the transfection of 224-5p-mimic/224-5p-inhibitor successfully increased or decreased the expression levels of miR-224-5p in A549 and H1229 cells ($p < 0.05$) (Figure 3D). Moreover, knockdown of TRG-AS1 elevated the expression levels of miR-224-5p, and this effect could be abolished by 224-5p-inhibitor. On the other hand, pcDNA3.1-TRG-AS1 transfection inhibited the expression of miR-224-5p, and this effect could be reversed by 224-5p-mimic ($p < 0.05$) (Figure 3D). For the effect of miR-224-5p on TRG-AS1, it was found that 224-5p inhibitor significantly promoted the expression of TRG-AS1, while 224-5p mimic played an opposite role, which could be reversed by overexpression of TRG-AS1 ($p < 0.05$) (Figure 3E).

MiR-224-5p Inhibited Proliferation, Migration and Invasion of Lung Cancer Cells

CCK-8 assay (Figure 4A), colony formation assay (Figure 4B), scratch wound (Figure 4C) and transwell assay (Figure 4D) were conducted to explore the role of TRG-AS1 or miR-224-5p in A549 and H1299 cells. The results showed that overexpression of miR-224-5p could inhibit cell proliferation ($p < 0.05$) (Figure 4A), colony formation ($p < 0.05$) (Figure 4B), migration ($p < 0.05$) (Figure 4C) and invasion ($p < 0.05$) (Figure 4D), and these effects could be abolished by overexpression of TRG-AS1 ($p < 0.05$) (Figure 4A–D). It was also shown that 224-5p inhibitor significantly promoted cell proliferation ($p < 0.05$) (Figure 4A), colony formation ($p < 0.05$) (Figure 4B), migration ($p < 0.05$) (Figure 4C) and invasion ($p < 0.05$) (Figure 4D). However, these roles could be reverse by knockdown ofTRG-AS1 ($p < 0.05$) (Figure 4A–D).

Table 1 Correlation Between TRG-AS1 Expression and Lung Adenocarcinoma Patients

Variables	Low TRG-AS1	High TRG-AS1	P value
Age (yrs)	57.2±8.6	59.1±9.0	0.270
Gender			0.468
Male Female	16 (51.6%) 15 (48.4%)	18 (54.5%) 15 (45.5%)	
Location			0.623
Left Right	14 (45.2%) 17 (54.8%)	14 (42.4%) 19 (57.6%)	
Tumor TNM stage			0.028
I II III	17 (54.8%) 12 (38.7%) 2 (6.5%)	11 (33.3%) 18 (54.5%) 4 (12.1%)	
T stage			0.060
T1 T2 T3 T4	17 (54.8%) 12 (38.7%) 2 (6.5%) 0 (0%)	13 (39.4%) 16 (48.5%) 2 (6.1%) 2 (6.1%)	
N stage			0.011
N0 N1 N2	21 (67.7%) 9 (29.0%) 1 (3.2%)	13 (39.4%) 17 (51.5%) 3 (9.1%)	

TRG-AS1 and miR-224-5p Had No Effect on the Apoptosis of Lung Cancer Cells

Since promoting cell apoptosis is one of the major approaches associated with cancer therapy, we therefore investigated whether TRG-AS1 or miR-224-5p had any effects on the pro-apoptosis of lung cancer cells. Flow cytometry was performed 72 h post transfection in A549 (Figure 5A) and H1299 (Figure 5B) cells by Annexin V-FITC/PI assay, and the results showed that there was no significant difference in the population of apoptotic cells among the transfection with si-TRG-AS1, 224-5p inhibitor and the combination of si-TRG-AS1 plus 224-5p inhibitor.

Table 2 Cox Multivariate Regression Analysis

Factors	P value	HR	95% CI
LINC00842 expression	0.015	1.538	1.050–2.274
Age	0.222	1.765	0.603–4.656
TNM stage	0.007	1.652	1.108–3.052
T stage	0.530	1.324	0.587–2.832
N stage	0.048	1.572	1.001–2.384

Abbreviations: HR, hazard ratio; CI, confidence interval.

SMAD4 Was a Downstream Target for miR-224-5p and as Regulated by the TRG-AS1/miR-224-5p Complex

RIP was performed to detect the interaction between miR-224-5p and SMAD4. It was shown that miR-224-5p could be precipitated by SMAD4 antibody but not IgG ($p < 0.01$) (Figure 6A). Moreover, compared to normal tissue, tumor tissues with elevated expression levels of TRG-AS1 had higher expression levels of SMAD4 ($p < 0.05$) (Figure 6B). In A549 and H1229 cells, knockdown of TRG-AS1 significantly inhibited the expression of SMAD4, which had the same effect with 224-5p mimic ($p < 0.05$) (Figure 6C). And the effect of 224-5p mimic could be reversed by overexpression of TRG-AS1 ($p < 0.05$) (Figure 6C). However, 224-5p inhibitor remarkably increased the expression levels of SMAD4 in A549 and H1229 cells, which played the same role with overexpression of TRG-AS1 ($p < 0.05$) (Figure 6C). And this effect could be abolished by 224-5p mimic ($p < 0.05$) (Figure 6C). Moreover, the regulation of SMAD4 to miR-224-5p was also detected and knockdown or overexpression of SMAD4 had no effect on the expression of miR-224-5p (Figure 6D).

Knockdown of TRG-AS1 Inhibited Tumor Growth

To explore the effect of knockdown of TRG-AS1 on tumor growth, tumor cells transfected with lentivirus mediated sh-TRG-AS1 or sh-control were injected into mice. Firstly, successful knockdown of TRG-AS1 in tumors was confirmed by RT-qPCR ($p < 0.05$ at 8 weeks, n = 6) (Figure 7A). Meanwhile, a relative higher expression levels of miR-224-5p was observed in sh-TRG-AS1 tumors ($p < 0.05$ at 8 weeks, n = 6) (Figure 7B). In additional, tumor volume of Lv-sh-TRG-AS1 group was much lower than that of the control group ($p < 0.05$ at 8 weeks, n = 6) (Figure 7C). Moreover, tumor transfected with Lv-sh-TRG-AS1 was associated with low expression levels of Ki67 as revealed by immunohistochemistry ($p < 0.05$ at 8 weeks, n = 6) (Figure 7D), suggesting the potential role of knockdown of TRG-AS1 in inhibiting tumor cell proliferation and metastasis abilities. Finally, the expression levels of SMAD4 in sh-TRG-AS1 or sh-control tumors were analyzed, and the results showed that SMAD4 was downregulated in sh-TRG-AS1 tumor ($p <$

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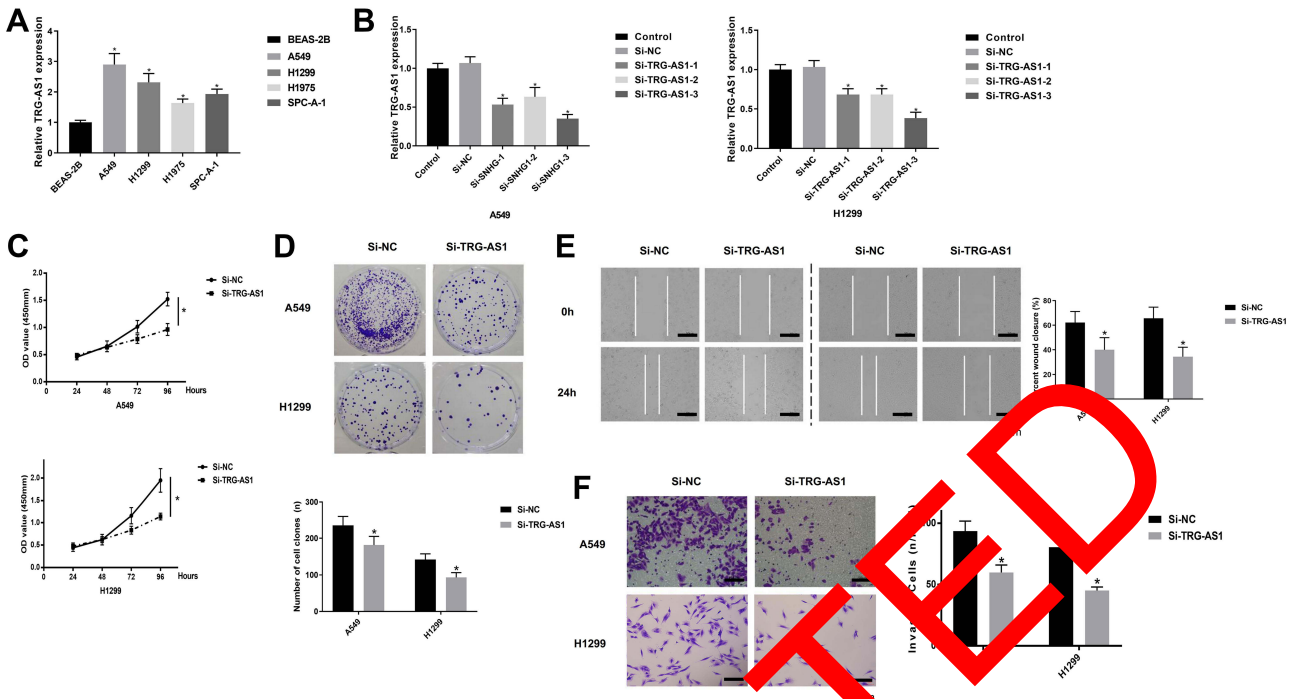

Figure 2 Knockdown of TRG-AS1 inhibited lung cancer cell proliferation, migration and invasion. (**A**) Comparison of TRG-AS1 expression levels in BEAS-2B, A549, H1299 H1975 and SPC-A-1 cells. (**B**) Efficacy of siRNAs for TRG-AS1 knockdown in A549 and H1299 cells. CCK-8 (**C**), colony formation (**D**), scratch wound assay (**E**) and transwell assay (**F**) for analysis of the effects of TRG-AS1 knockdown on cell proliferation, migration and invasion, respectively. All experiments were repeated 3 times. *p < 0.05.

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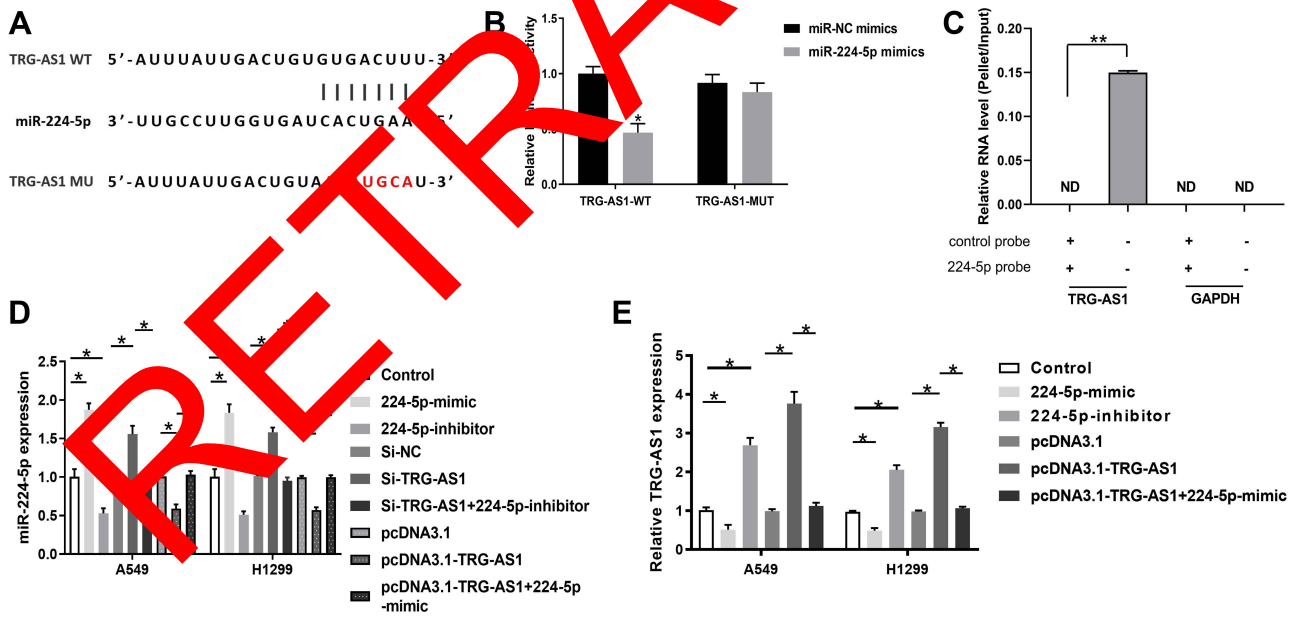

Figure 3 MiR-224-5p was the inhibitory target for TRG-AS1. (**A**) BLAST alignment analysis of the binding target of TRG-AS1, which identified a binding site between TRG-AS1 and miR-224-5p. Site-directed mutagenesis generated a mutated form of TRG-AS1 without binding sites to miR-224-5p. (**B**) Luciferase assay of the interaction between TRG-AS1 and miR-224-5p. *p < 0.05. (**C**) RNA pull-down exhibited an interaction between miR-224-5p and TRG-AS1. **p < 0.05. (**D**) The expression of miR-224-5p in A549 and H1229 was detected using RT-qPCR. PcDNA3.1-TRG-AS1 transfection significantly inhibited miR-224-5p expression, but si-TRG-AS1 promoted miR-224-5p expression. *p < 0.05. (**E**) Analysis of relative TRG-AS1 levels in A549 and H1299 cells transfected with 224-5p-mimic or 224-5p-inhibitor in comparison of the levels of the untransfected cells (control). All experiments were repeated 3 times. *p < 0.05.

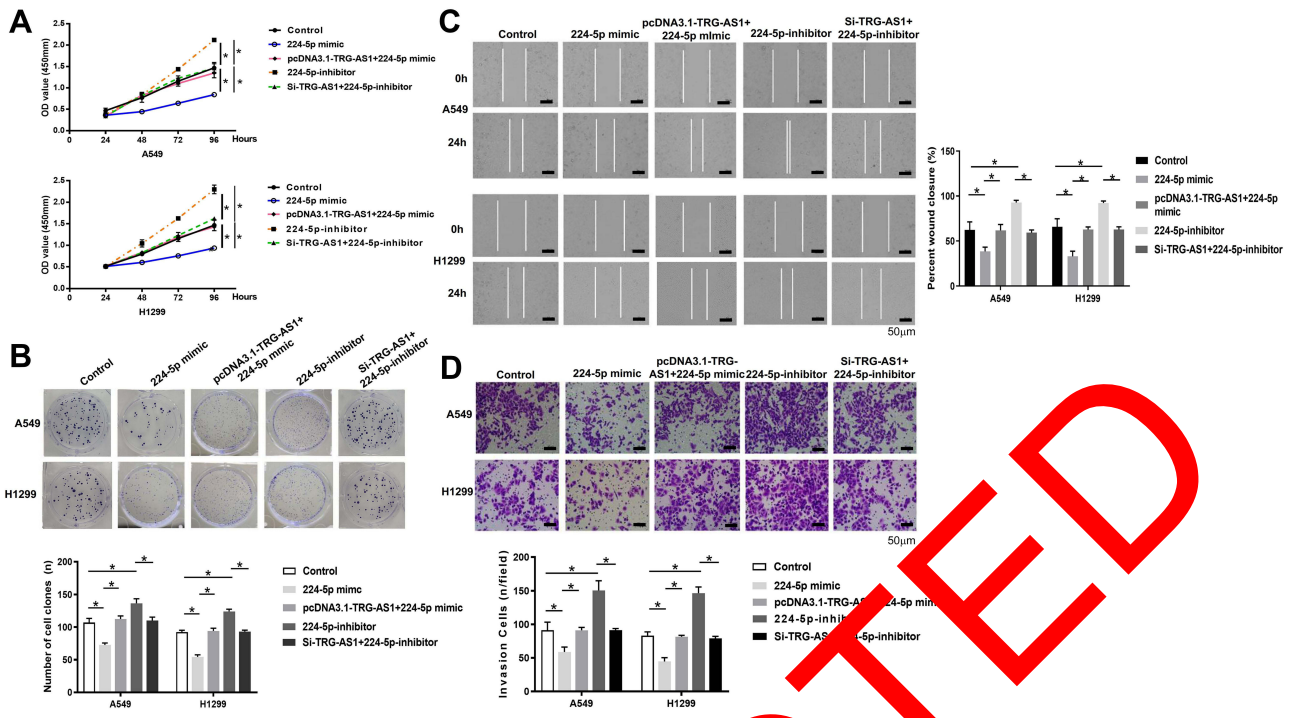

Figure 4 MiR-224-5p regulated lung cancer cell proliferation, migration and invasion. CCK-8 (**A**), colony formation (**B**), scratch wound (**C**) and transwell assay (**D**) of A549 and H1299 cells transfected with 224-5p mimic, 224-5p mimic plus pcDNA3.1-TRG-AS1, 224-5p inhibitor or 224-5p inhibitor plus si-TRG-AS1. All experiments were repeated 3 times. *$p < 0.05$.

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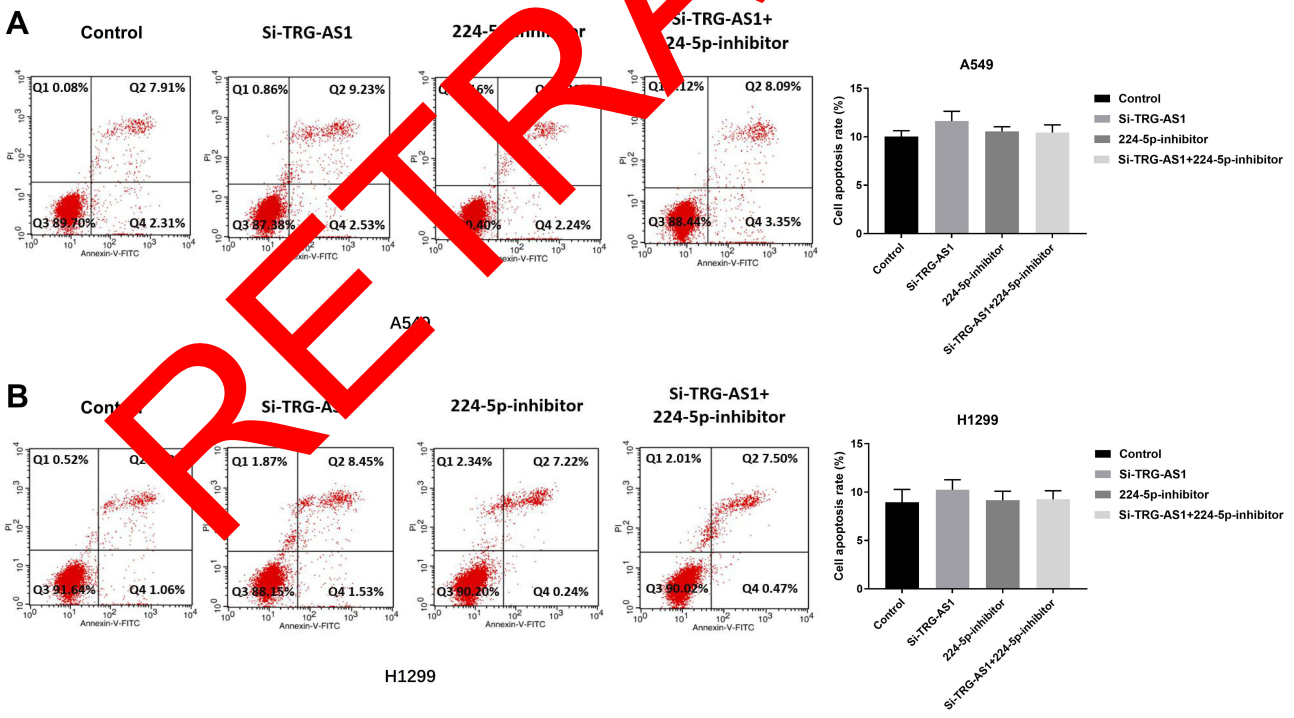

Figure 5 TRG-AS1 and miR-224-5p had no effect on the apoptosis of cells. Flow cytometry analysis of cell apoptosis of A549 cells (**A**) and H1299 cells (**B**). No effect was observed in apoptotic cell ratio of the cells transfected with si-TRG-AS1or 224-5p inhibitor compared with control. All experiments were repeated 3 times.

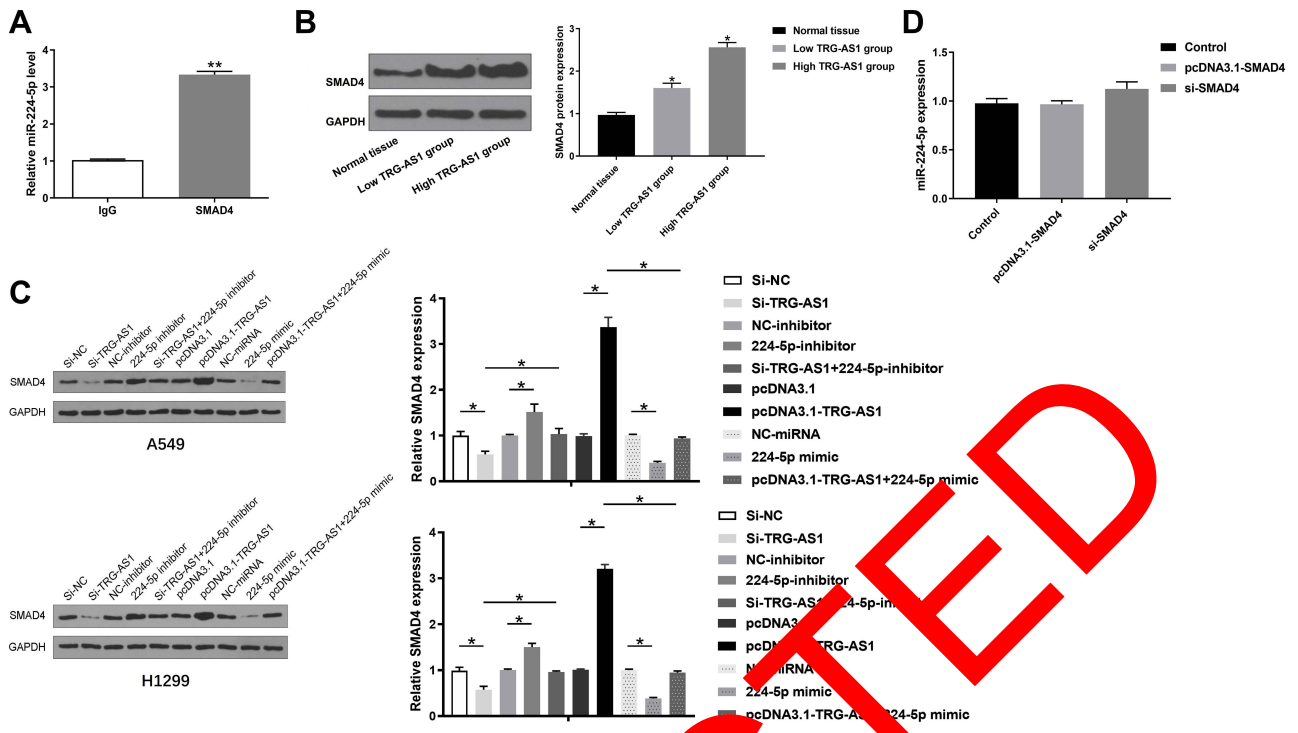

Figure 6 Overexpression of TRG-AS1 promoted the expression levels of SMAD4. (**A**) [illegible]P was used to detect the interaction between TRG-AS1 and miR-224-5p. (**B**) The expression of SMAD4 in normal tissue, low TRG-AS1 level tissue and high TRG-AS1 [illegible]vel tissue. (**C**) T[illegible] expression of SMAD4 in A549 and H1229 was evaluated by Western blots. (**D**) The effect of SMAD4 overexpression or silence on the expression [illegible]miR-224-5p. Al[illegible]xperiments were repeated 3 times. *$p < 0.05$; **$p < 0.01$.

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0.05 at 8 weeks, n = 6) (Figure 7E). Moreover, imm[illegible]no-histochemistry assay also showed that the expres[illegible]on levels of SMAD4 were significantly lowe[illegible] L[illegible]sh-TRG-AS1 tumor than that in Lv-sh-control t[illegible]mor (p [illegible]0.05 at weeks, n = 6) (Figure 7F). These res[illegible]ts i[illegible]dicated [illegible]at knockdown of TRG-AS1 mig[illegible] prevent [illegible]mor growth in vivo.

Discussion

Previous studies d[illegible]onstr[illegible]ed that TRG-AS1 was significantly upregul[illegible]ted in [illegible]r cance[illegible] tissues compared to that in normal tissues. Patient[illegible] high expression levels of TRG-A[illegible]1 had p[illegible]or prognosis than that with low expression leve[illegible] TRG-AS, which is consistent with the observation t[illegible] upregulation of specific lncRNAs, such as MALAT1,[9] HOTAIR,[10] HOTTIP[11] and ANRIL,[12] was linked to adenocarcinoma, giving the potentiality for applying TRG-AS1 as a biomarker for lung cancer diagnosis and therapy. These lncRNAs have been shown to enhance tumorigenesis by promoting cell proliferation, migration, invasion as well as inhibiting apoptosis.[20] Our results also showed that upregulation of TRG-AS1 might serve as a potential diagnostic marker of lung cancer, which would require further validation in lung cancer patients with different stages. We observed that the expression levels of TRG-AS1 were elevated in lung adenocarcinoma cell lines. With the knockdown of TRG-AS1, the proliferation, invasion and migration abilities of lung cancer cells were reduced substantially, confirming the indispensable role of TRG-AS1 in the aggressive progression of lung cancer.

Extensive studies have found that miRNAs may function as oncogenes or tumor suppressors in different cellular processes during tumor formation.[21] In the present study, we found that TRG-AS1 interacted with miR-224-5p and thus suppressively regulated miR-224-5p. On the other hand, miR-224-5p also inhibited the expression of TRG-AS1, indicating an inhibitory post-transcriptional regulation of miR-224-5p to TRG-AS1. MiR-224 has been reported to be upregulated in several solid tumors including hepatocellular carcinoma[15,16] colorectal cancer,[17] breast cancer[18] and lung cancer.[19] Previous studies showed that miR-224 was involved in the pathogenesis of lung cancer through direct targeting of CASP3 and CASP7. Several pathways are involved in the signaling of miR-224-5p. One of the recently reported pathways that have been established for NSCLC was the NF-κB/p65 signaling pathway.[19] In this study, we found that miR-224-5p was a suppressive regulator in lung

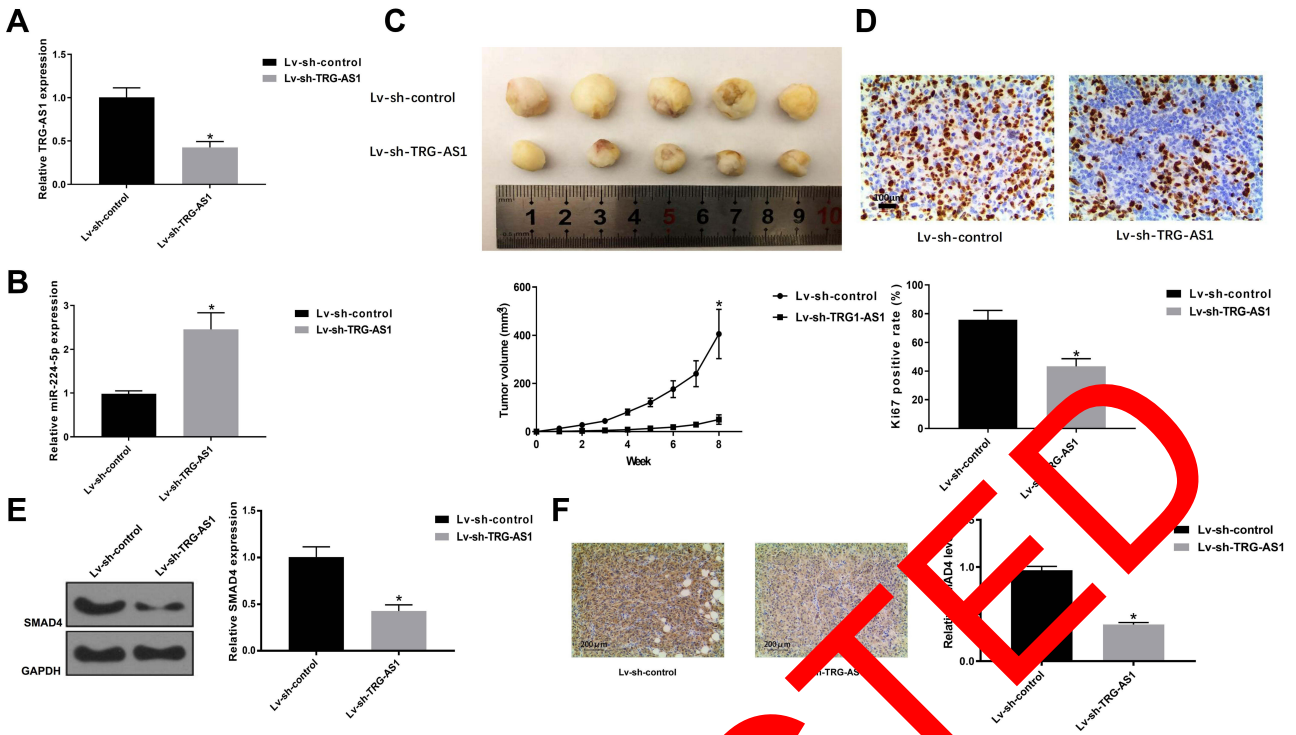

Figure 7 Knockdown of TRG-AS1 inhibited tumor growth in vivo. (**A**) The expression of TRG-AS1 in mice tumor tissues infected with Lv-sh-control or Lv-sh-TRG-AS1 was detected by RT-qPCR. (**B**) The expression of miR-224-5p in mice tumor tissues infected with Lv-sh-control or Lv-sh-TRG-AS1 was detected by RT-qPCR. (**C**) Tumor volume of Lv-sh-control or Lv-sh-TRG-AS1 mice tumor was measured. (**D**) Ki-67 immunohistochemistry (**B**), Western blots analysis of SMAD4 expression (**E**) and SMAD4 immunohistochemistry (**F**) in mice of Lv-sh-control group or Lv-sh-TRG-AS1 group. All experiments were repeated 3 times. *$p < 0.05$.

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cancer cell proliferation, invasion and migration and could abolish the effects of TRG-AS1, suggesting the promoted role of TRG-AS1 in lung cancer cell biological behavior might be achieved via targeting miR-224-5p.

One of the major factors associated with cancer therapy is apoptosis. We sought to evaluate whether TRG-AS1 and miR-224-5p exerted any pro-apoptosis effects on lung cancer cells. Our results did not show any effect of TRG-AS1 and miR-224-5p on apoptosis. This is contrary to what has been observed in other lncRNAs. However, we did not observe any impacts of TRG-AS1 or miR-224-5p on cell apoptosis, indicating that the regulation of TRG-AS1 or miR-224-5p on lung cancer cell behaviors was not through cell apoptosis.

SMAD4 is a putative oncogene in lung cancer.[22] Previous studies have also confirmed that SMAD4 is a downstream target of miR-224-5p,[23,24] and there was an interaction between miR-224-5p and SMAD4 in tumor.[23,25] Our study suggested that TRG-AS1 might mediate lung cancer development by regulating the miR-224-5p/SMAD4 axis. Firstly, we verified that miR-224-5p could interact with SMAD4. Furthermore, we also found that the expression levels of SMAD4 were elevated along with the increasing of the expression levels of TRG-AS1 in lung cancer tissues and could be suppressed by si-TRG-AS1 and 224-5p mimic in lung cancer cells. Also, we explored the roles of TRG-AS1 in tumor growth, the expression of Ki67 and SMAD4 in vivo. We found that lung tumors infected with sh-TRG-AS1 significantly inhibited tumor growth including reduced tumor volume and the expression levels of Ki67. Moreover, the expression levels of miR-224-5p and its downstream target SMAD4 were elevated in sh-TRG-AS1 infection tumor, indicating the significance of knockdown of TRG-AS1 in prohibiting lung cancer progression.

Conclusion

In summary, our study is the first to characterize the cancerogenic role of TRG-AS1 in lung cancer and demonstrate that knockdown of TRG-AS1 was a potential approach for prohibiting lung cancer progression in vitro. However, further investigations are needed to develop TRG-AS1 as a therapeutic target for lung cancer in clinic.

Data Sharing Statement

The analyzed data sets generated during the study are available from the corresponding author on reasonable request.

Ethics Approval and Consent to Participate

The present study was approved by the Ethics Committee of Fujian Medical University Cancer Hospital & Fujian Cancer Hospital. The research has been carried out in accordance with the World Medical Association Declaration of Helsinki. All patients provided written informed consent prior to their inclusion within the study.

Consent for Publication

All authors have read and approved the final manuscript.

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Disclosure

The authors report no conflicts of interest in this work.

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