MicroRNA-542-3p represses OTUB1 expression to inhibit migration and invasion of esophageal cancer cells

JUN SUN¹, YONG DENG², JIN SHI² and WENGANG YANG²

¹Oncology Department, Jianhu Hospital Affiliated to Nantong University, Jianhu, Jiangsu 224700; ²Thoracic Surgery Department, Sheyang People's Hospital, Sheyang, Jiangsu 224300, P.R. China

Received August 20, 2018; Accepted April 24, 2019

DOI: 10.3892/mmr.2019.10836

Abstract. Dysregulation of microRNAs (miRNAs) is involved in the pathogenesis of esophageal cancer. miRNA (miR)-542-3p is a tumor suppressor in multiple types of cancer. However, whether and how miR-542-3p contributes to the progression of esophageal cancer remains unknown, and this is the aim of the present study. In the current study, decreased expression of miR-542-3p was detected in tumor tissues compared with normal tissues from patients with esophageal cancer, and miR-542-3p expression was negatively correlated with mRNA expression levels of ovarian tumor domain-containing ubiquitin aldehyde-binding protein 1 (OTUB1) in tumor tissues from patients with esophageal cancer. In KYSE150 human esophageal squamous cell carcinoma cells, overexpression of miR-542-3p significantly decreased OTUB1 at mRNA and protein levels, whereas downregulation of miR-542-3p significantly increased OTUB1 expression. Using a dual-luciferase assay, OTUB1 was validated to be a target gene of miR-542-3p in KYSE150 cells. Functionally, miR-542-3p significantly inhibited the migration and invasion of KYSE150 cells by repression of OTUB1 expression. These results demonstrated that miR-542-3p may promote the metastasis of esophageal cancer cells, and indicated that miR-542-3p may be a treatment target for esophageal cancer.

Introduction

Esophageal cancer is the sixth most commonly diagnosed cancer and the fifth leading cause of cancer mortality globally (1). It was estimated that esophageal cancer accounted for >4% of cancer-related mortality in the USA in 2017 (2). In East Asia, the risk of incidence for esophageal cancer is almost 4-fold higher compared with North America (1). The two major types of esophageal cancer are esophageal squamous-cell carcinoma and esophageal adenocarcinoma (3). Owing to its aggressive nature and difficulty to diagnose, the overall 5-year survival rate of patients with esophageal cancer is ~20% (4,5). Therefore, there is an urgent necessity to discover the molecular mechanisms that lead to the metastasis of esophageal cancer.

MicroRNAs (miRNAs) are a class of small, non-coding, single-stranded RNAs that are ubiquitously expressed in eukaryotic cells (6). Through directly binding to the 3’ untranslated region (UTR) of target gene mRNA, miRNAs induce degradation of mRNA or inhibit mRNA translation, resulting in downregulation of target gene expression (7). Previous studies have revealed that mRNA-miRNA regulatory networks are crucial for normal biological processes, including cell differentiation, migration and apoptosis (8-10). Dysregulation of miRNA expression contributes to a number of human diseases such as cancer (11). A microarray study has demonstrated that the expression levels of several miRNAs are promising biomarkers for esophageal cancer (12). miRNA (miR)-542-3p downregulation has been reported in several cancer types (13,14); however, the potential role and molecular mechanism of miR-542-3p in esophageal cancer remains to be determined.

Ovarian tumor domain-containing ubiquitin aldehyde-binding protein 1 (OTUB1) is a hydrolase that is able to specifically remove ubiquitin from proteins to prevent protein degradation (15). By upregulating the expression of oncoproteins, OTUB1 facilitates tumor progression in several types of cancers (15-17). In esophageal cancer, OTUB1 stabilizes Snail protein to promote the metastasis of cancer cells (18); however, it is unknown how OTUB1 is regulated in esophageal cancer.

In the present study, miR-542-3p and OTUB1 mRNA expression levels were examined in normal and tumor tissues from patients with esophageal cancer. A negative correlation was observed between miR-542-3p and OTUB1 mRNA expression in tumor tissues. Western blotting and reverse transcription-quantitative PCR (RT-qPCR) data indicated that OTUB1 was negatively regulated by miR-542-3p in esophageal cancer cells. A dual-luciferase assay validated OTUB1 as a target gene for miR-542-3p. Furthermore, function assays demonstrated that miR-542-3p inhibited the migration and invasion of KYSE150 human esophageal squamous cell carcinoma cells through repression of OTUB1 expression. The data from the present study suggested a potential tumor suppressor role for miR-542-3p in esophageal cancer.

Key words: microRNA-542-3p, ovarian tumor domain-containing ubiquitin aldehyde-binding protein 1, esophageal cancer
Material and methods

Tissue collection. Tumor tissues and matched normal tissues were collected from 40 patients (mean age 56.33±7.21, male:female = 25:15) with esophageal squamous cell carcinoma or esophageal adeno carcinoma in Sheyang People's Hospital (Sheyang, China) between June 2015 and July 2017. Written consent was provided by all participants before the experiments and all procedures were approved by the Ethics Committee of Sheyang People's Hospital (IRB no. SYPH1506). Tissues were stored at -80°C upon collection.

Cell culture. Human esophageal squamous cell carcinoma line KYSE150 was purchased from American Type Culture Collection and used within 6 months. Cells were maintained in DMEM ( Sigma-Aldrich, Merck KGaA) supplemented with 10% FBS (Gibco; Thermo Fisher Scientific, Inc.) at 37°C.

Overexpression and downregulation of miR-542-3p. miR-542-3p mimic (5'-UGUGACAGAUUGAUAAUCGAAAA-3'), miR-negative control (NC) mimic (5'-AAUUUCCCGAAGCGUGUCA TT-3'), miR-542-3p inhibitor (5'-UUUCAGUUAUACUCGUGAC-3') and miR-NC inhibitor (5'-UGUGACAGCU UCGGAGAUUTT-3') were synthesized by and purchased from Shanghai GenePharma Co., Ltd. For overexpression or downregulation of miR-542-3p, miR-542-3p mimic (50 nM) or miR-542-3p inhibitor (50 nM) was mixed with Lipofectamine® 3000 (Invitrogen; Thermo Fisher Scientific, Inc.) in serum-free DMEM medium for 15 min. The mixtures were added into each well in 6-well plates and incubated for 48 h before the cells (2x10^3) were harvested for subsequent experiments.

RNA extraction and RT-qPCR. Total RNA from cell lines (1x10^5) or tissue samples (50-100 mg) was extracted using TRIzol reagent (Invitrogen; Thermo Fisher Scientific, Inc.) according to the manufacturer's protocol. For mRNA quantification, RNA was reverse-transcribed into first-stranded cDNA using PrimeScript RT Master Mix (Takara Bio, Inc.). RT-qPCR was conducted using a SYBR-Green qPCR Master Mix kit (Takara Bio, Inc.) followed by thermocycling parameters: 40 cycles of 95°C for 15 sec and 64°C for 30 sec. For miRNA thermocycling parameters:

- 40 cycles of 94°C for 15 sec, 60°C for 1 min, 72°C for 1 min followed by a final extension at 72°C for 10 min, and aqPCR run on an ABI PRISM 7900HT Real-Time PCR System (Applied Biosystems; Thermo Fisher Scientific, Inc.).
- Primer sequences were as listed: miR-542-3p forward, 5'-TGT GACAGATTGATAACT-3' and stem-loop RT primer, 5'-GTC GTATCCAGTGCAAGGCGGAGTTCTCGCCAGCTTGA TACGACCTGCGGTTCAGT-3'; U6 forward, 5'-TGT GACAGATTGATAACT-3' and reverse, 5'-GGTCTT GCAGGATGTACAGT-3'; U6 forward, 5'-GGTCTT GCAGGATGTACAGT-3' and reverse, 5'-GTTATGGAACGCTTC ACAGAT-3'; GAPDH forward, 5'-GGAGCGGATCCCTC CAAAT-3' and reverse, 5'-GGTGTTGTCATACCTTCCTC AG-3'. Expression level of miR-542-3p was normalized to U6. Expression level of OTUB1 was normalized to GAPDH.

Protein lysate preparation and western blotting. The antibodies used were as follows: OTUB1 (cat. no. A302-917A; 1:1,000; Bethyl Laboratories, Inc.); GAPDH (cat. no. G8795; 1:5,000; Sigma-Aldrich; Thermo Fisher Scientific, Inc.); Snail (cat. no. sc-393172; 1:1,000; Santa Cruz Biotechnology, Inc., CA, USA); horseradish peroxidase-conjugated secondary antibodies against rabbit (cat. no. 7074, 1:10,000; Cell Signaling Technology, Danvers, MA, USA) and mouse (cat. no. 7076, 1:10,000; Cell Signaling Technology). Protein lysates from cells (1x10^5) were prepared using RIPA lysis buffer (Roche Diagnostics GmbH) followed by determination of protein concentration by the BCA method. Then, protein samples (20 µg) were separated on an 10% SDS-PAGE gel and transferred to a PVDF membrane. The, PVDF membrane was blocked by 5% bovine serum albumin (BSA, Beijing Solarbio Science & Technology Co., Ltd.) at room temperature for 2 h. Following incubation with the primary antibody at 4°C overnight and a secondary antibody at room temperature for 2 h, the bands were visualized using ECL Western Blot Substrate (Pierce; Thermo Fisher Scientific, Inc.). Densitometric analysis was performed by ImageJ software (version 1.8.0; National Institutes of Health). GAPDH was used to normalize expression data.

Dual-luciferase reporter assay. The position 107-114 of 3'UTR of OTUB1 (5'-UUUCCCUCUCUUCUCCUGUCA CA...) mRNA containing the putative target site of miR-542-3p (3'AAGUCAUAGUAGACAGUGU) was determined by TargetScan version 7.1 (20) and amplified from the cDNA of KYSE150 cells and ligated into the pGL3-basic vector (Promega Corporation). pGL3-OTUB1-3'UTR-mutant (Mut, 5'-UUUCCCUCUCUUCUCCUGAACA...) was created by introducing two site mutations into miR-542-3p potential target sites using QuickChangeSite-Directed Mutagenesis kits (Agilent Technologies, Inc.). pGL3-OTUB1-3'UTR-WT (200 ng) or pGL3-OTUB1-3'UTR-Mut (200 ng) was co-transfected with Renilla plasmid into KYSE150 cells using Lipofectamine® 3000, followed by transfection of miR-NC mimic (10 nM) or miR-542-3p mimic (10 nM) for 48 h at 37°C. The Dual-Luciferase Reporter Assay System (Promega Corporation) was used to measure the relative luciferase activity of each well. The firefly luciferase expression was normalized to Renilla.

OTUB overexpression plasmid construction and transfection. Full-length OTUB1 cDNA was amplified by KYSE150 cells and ligated to a pcDNA3.1 vector (https://www.70dir.com/seo/report_world_youbio_cn.html, YouBio) with the restriction sites of KpnI and XhoI. For overexpression of OTUB1, pcDNA3.1-OTUB1 was mixed with Lipofectamine® 3000 (Invitrogen; Thermo Fisher Scientific, Inc.) in serum-free DMEM medium for 15 min. The mixtures were then added into each well in 6-well plates (1x10^5) and incubated for 48 h at 37°C before the cells were harvested for subsequent experiments.

Cell migration assay. A wound healing assay was used to examine the migratory ability of transfected KYSE150 cells. Briefly, 1x10^5 cells were seeded in each well of 6-well plates. Following transfection, as aforementioned, the cells were cultured in 37°C to 90-100% confluence. A wound area was made in the center of each well using a 10 µl pipette tip. The culture medium of the cells was replaced with serum-free
medium. Images were captured using an inverted microscope (Nikon Corporation) at 0 and 24 h to observe the cells (magnification, x100) that migrated into the wound area. The migrated areas were quantified using Image Pro Plus and normalized to the miR-NC mimic + pcDNA3.1 group.

Cell invasion assay. For the cell invasion assay, BD Matrigel Invasion Chambers (8-µm pore; BD Biosciences) were used. In brief, KYSE150 cells (1x10^5) transfected with miR-NC mimic + pcDNA3.1, miR-542-3p mimic + pcDNA3.1 or miR-542-3p mimic + pcDNA3.1-OTUB1 were cultured in the upper chamber in serum-free DMEM at 37˚C. Following 72 h of invasion, cells on the upper side of the filter were removed and cells that invaded to the underside of the membranes were fixed using 8% formaldehyde at room temperature for 15 min, followed by staining with crystal violet at room temperature for 30 min. The number of invaded cells (x400) was counted using a light microscope (Olympus Corporation).

Statistical analysis. Data were analyzed with GraphPad Prism 7 (GraphPad Software, Inc.) and presented as the mean ± standard error of the mean. For in vitro experiments, the statistical differences were evaluated using Student's t-test (two groups) or using ANOVA followed by Newman Keuls method (three groups). For ex vivo experiments in tumor tissues, the statistical analyses were performed using paired Student's t-test (two groups). Pearson's correlation analysis was performed to determine the correlation between miR-542-3p and OTUB1 mRNA expression levels in esophageal tumor tissues. P<0.05 was considered to indicate a statistically significant difference. All experiments were performed thrice.

Results

miR-542-3p is downregulated in esophageal tumor tissues. To investigate the role of miR-542-3p in esophageal cancer, RT-qPCR was performed to detect miR-542-3p expression levels in tumoral and adjacent normal tissues from 40 patients with esophageal cancer. The results demonstrated that the expression of miR-542-3p was significantly down-regulated in tumor tissues compared with adjacent normal tissues (Fig. 1A).
OTUB1 is a newly identified oncogene in esophageal cancer and has been reported to be regulated by miR-542-3p in colorectal cancer (13,18). In the present study, OTUB1 mRNA levels were significantly increased in tumor tissues compared with adjacent normal tissues (Fig. 1B). Western blotting revealed that the protein expression of OTUB1 was also significantly increased in tumor tissues compared adjacent normal tissues (Fig. 1C). In addition, Pearson's correlation analysis indicated that expression of miR-542-3p was significantly negatively correlated with OTUB1 mRNA expression levels in esophageal tumor tissues (Fig. 1D). These results suggested that miR-542-3p may inhibit esophageal cancer progression and act as a tumor suppressor.

Expression of OTUB1 is repressed by miR-542-3p in esophageal cancer cells. To further study the regulatory association between OTUB1 and miR-542-3p, miR-542-3p mimic was used to elevate miR-542-3p expression in KYSE150 cells. Compared with cells transfected with miR-NC mimic, transfection with miR-542-3p mimic significantly increased miR-542-3p expression in KYSE150 cells (Fig. 2A). Overexpression of miR-542-3p significantly decreased OTUB1 mRNA levels and
OTUB1 protein levels in cells (Fig. 2B and C). Conversely, transfection with miR-542-3p inhibitor significantly decreased miR-542-3p expression in KYSE150 cells and led to an increased expression of OTUB1 at mRNA and protein levels (Fig. 2D-F). These data demonstrated that miR-542-3p may negatively regulate OTUB1 in esophageal cancer cells.

OTUB1 is a target gene of miR-542-3p in esophageal cancer cells. To confirm whether miR-542-3p directly regulated OTUB1 expression, dual-luciferase reporter assay was performed in KYSE150 cells. Transfection of miR-542-3p mimic significantly reduced luciferase activity of OTUB1 3'UTR-WT compared with cells transfected with miR-NC.
miR‑542‑3p INHIBITS THE PROGRESSION OF ESOPHAGEAL CANCER

SUN et al: miR‑542‑3p INHIBITS THE PROGRESSION OF ESOPHAGEAL CANCER

miR‑542‑3p INHIBITS THE PROGRESSION OF ESOPHAGEAL CANCER

miR‑542‑3p inhibits esophageal cancer cell migration and invasion through regulation of OTUB1. To study the biological function of miR‑542‑3p in esophageal cancer cells, wound healing and cell invasion assays were performed to detect cell migratory and invasive abilities of cells transfected with the miR‑542‑3p mimic either with or without overexpression of OTUB1.

Transfection of miR‑542‑3p mimic reduced OTUB1 protein expression whereas co‑transfection of miR‑542‑3p mimic and recombinant OTUB1 reversed the downregulation of OTUB1 in KYSE150 cells (Fig. 4A). In the wound healing assays, overexpression of miR‑542‑3p significantly inhibited cell migration towards the wound areas, which indicated that the migration ability of cells was reduced (Fig. 4B and C). In addition, overexpression of OTUB1 reversed migration inhibition induced by miR‑542‑3p mimic (Fig. 4B and C). Similarly, overexpression of miR‑542‑3p significantly inhibited the invasive ability of the cells, which was reversed by overexpression of OTUB1 (Fig. 5). The results demonstrated that miR‑542‑3p may inhibit the migratory and invasive abilities of esophageal cancer cells through repression of OTUB1.

Discussion

miRNAs regulate a number of oncogenes and tumor suppressors in cells, which can lead to the initiation and progression of cancer (21,22). Several miRNAs have been identified as key regulators of esophageal cancer development and accurate predictors of clinical outcome for patients with esophageal cancer (23‑25). Decreased expression of miR‑542‑3p has been observed in certain types of cancers, including hepatocellular carcinoma, osteosarcoma, colorectal cancer and melanoma (13,26‑29). In the present study, miR‑542‑3p expression and function were investigated in esophageal cancer. RT‑qPCR revealed that miR‑542‑3p expression was decreased in tumor tissues compared with adjacent normal tissues from patients with esophageal cancer. In KYSE150 cells, overexpression of miR‑542‑3p markedly reduced cell migratory and invasive abilities. Thus, consistent with its tumor suppressor role in other cancer types, miR‑542‑3p may also function as a tumor suppressor in esophageal cancer.

OTUB1 is a cysteine protease that removes ubiquitin from modified proteins to stabilize target proteins (30). OTUB1 is involved in the regulation of several proteins that are pivotal for the progression of cancer, such as estrogen receptor, p53 and forkhead box M1 (17,30,31). Recently, OTUB1 was demonstrated to promote the metastasis of esophageal cancer by stabilizing Snail (18). miR‑542‑3p has been demonstrated to bind to 3'UTR of OTUB1 mRNA to downregulate OTUB1 in colorectal cancer cells (13).
Consistent with the previous study, an increase in OTUB1 mRNA expression was observed in tumor tissues compared with adjacent normal tissues from patients with esophageal cancer. Additionally, OTUB1 expression levels were inversely correlated with miR-542-3p expression levels in tumor tissues, and in KYSE150 cells, overexpression of miR-542-3p decreased OTUB1 expression.

Snail is a member of the Snail superfamily, which functions in cell survival and cell differentiation of cancer cells (32). Furthermore, the development and metastasis of cancer were blocked by Snail suppression (33). Recently, Snail silencing was found to inhibit cell migration of esophageal cells (34). Notably, in KYSE150 cells, overexpression of miR-542-3p decreased Snail expression.

Finally, cell migration and invasion inhibition induced by miR-542-3p overexpression was partially attenuated by co-transfection of recombinant OTUB1 in KYSE150 cells. These results demonstrated that miR-542-3p may regulate OTUB1 to inhibit cell metastasis of esophageal cancer, which were consistent with a previous study about the role of OTUB1 in esophageal cancer (18). Future studies are needed to determine whether the expression of miR-542-3p may be used as a biomarker to predict distant metastasis and overall survival of patients with esophageal cancer.

The results of the present study indicated a potential tumor suppressor role for miR-542-3p in esophageal cancer. Overexpression of miR-542-3p inhibited migration and invasion of esophageal cancer cells. Therefore, upregulation of miR-542-3p may be a potential treatment approach for patients with esophageal cancer.

Acknowledgements

Not applicable.

Funding

No funding was received.

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Authors' contributions

JuS and WY designed the study, JuS, JJS and YD acquired and interpreted the data. YD and JiS collected clinical samples. WY prepared the manuscript and supervised the study.

Ethics approval and consent to participate

The present study was approved by the Ethics Committee of Sheyang People's Hospital (Sheyang, China). All patients signed written informed consent.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

References


This work is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International (CC BY-NC-ND 4.0) License.