Abstract. Increasing evidence has demonstrated the important roles of long non-coding (lnc) RNA in non-small cell lung cancer (NSCLC). lncRNA gastric cancer-associated transcript 1 (GACAT1) has been reported to play an oncogenic role in different types of cancer; however, the function of GACAT1 in NSCLC remains unclear. The present study found that GACAT1 was overexpressed in NSCLC tissues and was associated with poor outcomes in patients with NSCLC. Functional experiments revealed that GACAT1 downregulation inhibited proliferation, induced apoptosis and cell cycle arrest of 2 NSCLC cell lines. GACAT1 was found to target microRNA(miR)-422a mechanically and negatively regulated miR-422a expression. Reduced expression of miR-422a in NSCLC tissues was inversely correlated with that of GACAT1. Furthermore, YY1 transcription factor (YY1) was identified as a downstream miR-422a target. Reduced expression of GACAT1 inactivated YY1 by sponging miR-422a in NSCLC cells. YY1 reintroduction reversed the reduced proliferation of NSCLC cells via GACAT1 knockdown. Taken together, these results revealed the novel role of the GACAT1/miR-422a pathway in the progression of NSCLC cell lines, providing a possible therapeutic strategy for NSCLC treatment.

Introduction

Lung cancer, particularly non-small cell lung cancer (NSCLC), which accounts for 85% of all cases, remains one of the highest cancer-related mortalities worldwide (1,2). Currently, surgery, in combination with chemotherapy and radiotherapy, remains the primary option for treating NSCLC (3). While most patients respond well to these treatments, recurrence and metastasis are common and considered a major challenge of survival. Currently, the five-year overall survival time of patients with NSCLC remains as low as 15% (4,5). Therefore, identifying novel therapeutic targets and characterizing the underlying molecular mechanisms of NSCLC are urgently required.

Long non-coding (Inc) RNAs are non-protein coding nucleotides, >200 nucleotides in length (6). IncRNAs play important roles in both biological and pathological processes by regulating gene expression at the translational, post-transcriptional, or epigenetic levels (7,8). Recent studies indicated that the abnormal expression of IncRNAs, which acted as either tumor suppressors or oncogenes, modulated NSCLC cell line progression (9-15). For example, lncRNA FEZF1-AS1 enhanced epithelial-mesenchymal transition of NSCLC cells by E-cadherin suppression and regulating Wnt signaling (16). lncRNA -XIST knockdown inhibited NSCLC cell line autophagy and promoted its chemosensitivity (17). In addition, a recent study showed that IncARSR promoted NSCLC progression by targeting the PTEN/Akt signaling pathway (18). IncRNA AC096655.1-002 is located on chromosome 2q12.3, which was initially found to be associated with gastric cancer and named gastric cancer-associated transcript 1 (GACAT1) (19). Decreased GACAT1 expression was identified in gastric cancer and was significantly associated with lymph node metastasis, differentiation, and TNM stages in patients with gastric cancer (20-22). GACAT1 was also reported to promote breast cancer development and progression (23). These findings revealed an important function of GACAT1 in tumorigenesis; however, the functional roles and associated mechanism of GACAT1 in NSCLC have rarely been reported.

Increasing evidence suggested that IncRNAs act as competitive endogenous (ce)RNAs to sponge cancer cell microRNA (miRNA/miR) functions (6,8,24-26). miRNAs have been characterized as small, single-stranded, non-coding RNAs without protein-coding capacity (27-29). miRNAs negatively regulate gene expression by targeting the 3'-untranslated

**Downregulation of long non-coding RNA GACAT1 suppresses proliferation and induces apoptosis of NSCLC cells by sponging microRNA-422a**

YOUQING ZHONG1*, HUI LIN2*, QI LI1, CHANG LIU1 and LEI ZHONG3

1Department of Respiratory Medicine, The First Affiliated Hospital of Hainan Medical University, Haikou, Hainan 571100; 2Department of Anesthesia, Hainan General Hospital, Haikou, Hainan 570311; 3Clinical Laboratory, Ganzhou People's Hospital of Jiangxi Province, Ganzhou, Jiangxi 341000, P.R. China

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**Correspondence to:** Dr Lei Zhong, Clinical Laboratory, Ganzhou People's Hospital of Jiangxi Province, 18 Meiguan Road, Ganzhou, Jiangxi 341000, P.R. China

E-mail: leizhongggz@163.com

*Contributed equally

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region (UTR) of mRNAs, thereby inhibiting translation and facilitating mRNA degradation (30). miRNAs have shown significant promise in cancer diagnosis and prognosis (27-29). Research into the regulation of ceRNA indicated that lncRNA may act as sponges by competitively binding to target miRNAs and blocking miRNA interactions with the target mRNAs (31,32). Therefore, establishing a lncRNA and miRNA connection could improve the understanding of the target miRNAs and blocking miRNA interactions with the lncRNA may act as sponges by competitively binding to miRNAs. Therefore, establishing a lncRNA-miRNA connection could improve the understanding of the target mRNAs (31,32). Therefore, establishing a lncRNA-miRNA connection could improve the understanding of the target mRNAs (31,32).

Recent advances in the field of ceRNA have led to the discovery of lncRNAs that can regulate the expression of miRNAs and mRNAs. This phenomenon, known as the ceRNA hypothesis, has opened new avenues for the development of targeted Therapeutic strategies. The relationship between lncRNA and miRNA has been extensively studied in various diseases, and recent findings have provided valuable insights into the potential regulatory mechanisms.
2000 (Invitrogen; Thermo Fisher Scientific, Inc.). Cells were cultured for 48 h at 37˚C with 5% CO₂. Luciferase activity was determined using the dual-luciferase reporter assay (Promega corporation) according to the manufacturer’s instructions. The activity of Renilla was also detected for normalization. The experiment was performed with three replicates. Data was obtained from three independent experiments.

Western blot analysis. Cells were collected and lysed using RIPA buffer, containing protease inhibitor, and the protein concentration was determined using a BCA kit (both from Beyotime Institute of Biotechnology). An equal amount of total protein (20 µg) was separated using a 15% SDS-PAGE and transferred onto a PVDF membrane (EMD Millipore). After blocking with 5% skimmed milk for 1 h at room temperature, the membrane was incubated with primary antibodies against YY1 (1:1,000 dilution; cat. no. ab109228) or GAPDH (1:2,000 dilution; cat. no. ab181202) (both from Abcam) overnight at 4˚C. Subsequently, the membrane was washed twice with PBS-Tween-20 and incubated with the HRP-conjugated secondary goat anti-rabbit IgG antibody (1:5,000 dilution; cat. no. ab205718; Abcam) for 1 h at room temperature. GAPDH expression level was used as the loading control. Protein signals were analyzed using an enhanced chemiluminescence substrate reagent kit (Thermo Fisher Scientific, Inc.) and a Gel Doc XR Imaging System (Bio-Rad Laboratories, Inc.).

Bioinformatics prediction. The potential binding sites between GAcAT1 and miR-422a, as well as between miR-422a and YY1, were predicted using the miRdb database (http://mirdb.org).

Cell apoptosis. NSCLC cell apoptosis was determined using an Annexin V-fluorescein isothiocyanate (FITC) Apoptosis Detection kit (BD Biosciences) according to the manufacturer’s instructions. Cells transfected with siRNA-GAcAT1 or siRNA-control were harvested and digested with 0.25% trypsin. After centrifugation at 800 x g for 5 min at 4˚C, the sediments were washed twice with PBS. Then, the cells were incubated with 5 µl FITC and 5 µl PI at room temperature for 15 min, in the dark. Cell apoptosis percentage was detected using the Beckman Coulter FC500 flow cytometer (Beckman Coulter, Inc.). Data was obtained from three independent experiments.

Determination of caspase-3 activity. The activity of caspase-3 was detected with the Caspase-3 Activity Assay kit (cat. no. 5723; Cell Signaling Technology, Inc.) according to the

Figure 1. GAcAT1 is increased in NSCLC. (A) GACAT1 expression was examined using RT-qPCR in NSCLC tissues and adjacent normal tissues and the data was analyzed using a Student’s t-test. The experiments were performed with three replicates. (B) GACAT1 expression was significantly associated with lymph node metastasis in patients with NSCLC. The experiments were performed with three replicates and the data was analyzed using a Student’s t-test. (C) Higher GACAT1 mRNA expression levels were associated with a shorter five-year overall survival time in patients with NSCLC. The data was analyzed using a log-rank test. (D) The mRNA expression levels of GACAT1 in four NSCLC cell lines, A549, H1299, H460, and SK-MES-1 and a normal cell, NHBE were detected using RT-qPCR. The experiments were performed with three replicates and the data was analyzed using one-way ANOVA. ***P<0.001; NSCLC, non-small cell lung cancer; RTq-PCR, reverse transcription-quantitative PCR; GACAT1, gastric cancer-associated transcript 1; LYN, lymph node metastasis.
manufacturer's instructions. Briefly, cells were seeded into 96-well plates, at the density of 2,000 cells per well and transfected with siRNA-control or siRNA-GAcAT1. After transfection for 48 h, cells were harvested and lysed with 50 µl lysis buffer (cat. no. 7018; Cell Signaling Technology, Inc.). A total of 25 µl lysate solution was mixed with 200 µl substrate solution B in a black plate and incubated at 37˚C for 1 h. The absorbance was detected using a fluorescence plate reader, with excitation set as 380 nm and emission set as 420-460 nm. The experiment was performed with three replicates. Data was obtained from three independent experiments.

Statistical analysis. All of the data are shown as the mean ± standard deviation. The differences between two or multiple groups were analyzed using un-paired Student's t-test or one-way ANOVA, respectively. Paired Student's t test was used for the comparing the expression level of genes in NSCLC tissues and paired adjacent normal tissues. The correlation between the expression levels of GACAT1 and miR-422 were determined using a Spearman's correlation test. Survival curves were plotted using the Kaplan-Meier method and compared with the log-rank test. P<0.05 was considered to indicate a statistically significant difference.

Results

GACAT1 is highly expressed in NSCLC tissues and cells. To investigate the potential function of GACAT1 in NSCLC, mRNA GACAT1 expression levels in NSCLC and paired adjacent normal tissues was examined using RT-qPCR. The results showed that the GACAT1 expression levels were significantly increased in NSCLC tissues compared with that in the adjacent normal tissues (Fig. 1A). In addition, GACAT1 mRNA expression level was also increased in patients with positive lymphatic metastasis (Fig. 1B). To further determine the clinical significance of GACAT1 in NSCLC, the association between GACAT1 mRNA expression level and the 5-year overall survival rate of the patients with NSCLC was determined using the Kaplan-Meier survival analysis method.
Fig. 1c indicated that patients with high GA-cAT1 mRNA expression levels had significantly shorter survival times compared with that in patients with low GA-cAT1 expression levels. This result suggested that increased GA-cAT1 mRNA expression level was significantly associated with worse prognosis in patients with NSCLC. Furthermore, GA-cAT1 mRNA expression level in 4 NSCLC cell lines was significantly higher compared with that in the NHBE cell line (Fig. 1d). Taken together, these findings revealed that GA-cAT1 was increased in NSCLC tissues and cell lines.

GACAT1 downregulation inhibits the proliferation, initiates apoptosis, and cell cycle arrest of NSCLC cells. As GA-cAT1 mRNA expression was increased in NSCLC tissues and cell lines, siRNA-GACAT1 was used to transfect both A549 and H1299 cells to silence GACAT1 expression (Fig. 2A). The CCK-8 assay showed that GACAT1 downregulation significantly repressed NSCLC cell proliferation (Fig. 2B and C). To determine whether the suppressed NSCLC cell growth with GACAT1 siRNA was associated with cell cycle arrest, flow cytometry was performed to determine cell cycle progression of both A549 and H1299 cells transfected with either siRNA-GACAT1 or siRNA-control. The results showed that knockdown of GA-cAT1 mRNA expression levels induced cell accumulation at the G1 phase and a decrease in the S phase, which suggested that the cell cycle was arrested at the G1 phase with GACAT1 knockdown (Fig. 2D). In addition, apoptosis of the NSCLC cells transfected with GACAT1 siRNA was also determined using flow cytometry. Fig. 2E showed that GACAT1 knockdown significantly increased early apoptosis of the NSCLC cells compared with that in cells transfected with siRNA-control. To further confirm the increase in apoptosis of the NSCLC cells with knockdown of GACAT1, the activity of caspase-3 was also determined. The results showed that knockdown of GACAT1 significantly increased the activity of caspase-3 in both A549 and H1299 cells (Fig. 2F). These results suggested that GACAT1 knockdown inhibited malignant NSCLC cell behavior.

GACAT1 acts as a miR-422 sponge in NSCLC cells. To understand the GACAT1 regulatory mechanism, the cell lines. miR-422a potential miRNA targets of GACAT1 were predicted using the miRDB online database. The bioinformatics analysis showed that miR-422a contained the GACAT1
complementary binding site (Fig. 3A). To confirm the binding of miR-422a and GACAT1, a luciferase reporter assay was performed by constructing luciferase vectors expressing wild-type (WT) or mutated (Mut) miR-422a binding sites in GACAT1 and co-transfected with miR-422a mimic into the A549 and H1299 overexpression was detected using RT-qPCR (Fig. 3B). The results indicated that the WT-GACAT1 luciferase activity was decreased by miR-422a overexpression, while the Mut-GACAT1 activity was not significantly affected by miR-422a mimic transfection (Fig. 3C and D). These results demonstrated the specific binding between miR-422a and GACAT1 in NSCLC cells.

Furthermore, to investigate the consequence of the miR-422a and GACAT1 interaction, the miR-422a mRNA expression level in both the A549 and H1299 cell lines, transfected with siRNA-GACAT1 or siRNA-control was detected using RT-qPCR. Fig. 3E showed that knockdown of GACAT1 significantly increased miR-422a mRNA expression level in the NSCLC cells. To support this observation, the miR-422a mRNA expression level in NSCLC and paired normal adjacent tissues was detected. Fig. 3F showed that miR-422a mRNA expression level was decreased in NSCLC tissues compared with that in the normal adjacent tissue. As miR-422a was negatively regulated by GACAT1, the correlation between the expression levels of miR-422a and GACAT1 in NSCLC tissues was also determined. The Spearman’s correlation analysis indicated that the miR-422a and GACAT1 mRNA expression levels were inversely correlated in the NSCLC tissues.
tissues (Fig. 3G). These findings revealed that miR-422a was a downstream target of GACAT1 in NSCLC cell lines.

GACAT1 regulates YY1 by suppressing miR-422a in NSCLC cells. As miR-422a mRNA expression level was decreased in NSCLC tissues and cell lines, the effects of miR-422a on NSCLC cell proliferation were determined by transfecting miR-422a mimic into both the A549 and H1299 cell lines. Cell proliferation was determined using CCK-8 assay in the NSCLC cell lines transfected with miR-422a mimic or miR-NC. Fig. 4A and B showed that miR-422a overexpression significantly inhibited A549 and H1299 cell proliferation. These results indicated the miR-422a tumor suppressive function in NSCLC. To further investigate the underlying mechanism of miR-422a in NSCLC, miR-422a targets were predicted using the miRDB database. The YY1 3’-UTR was shown to harbor the predicted binding sequence of miR-422a (Fig. 4C). It was found that, miR-422a mimic transfection reduced the mRNA and protein expression levels of YY1, in both A549 and H1299 cells (Fig. 4D and E), which is consistent with the prediction results. As miR-422a was negatively regulated by GACAT1, the effects of GACAT1 on YY1 expression were also determined. Fig. 4F and G showed that GACAT1 knockdown significantly suppressed YY1 expression, at both the mRNA and protein levels. These results demonstrated that GACAT1 sponged miR-422a and regulated YY1 expression in NSCLC cells.

YY1 overexpression reverses the suppressed NSCLC cell proliferation induced by GACAT1 knockdown. To investigate whether YY1 was critical for the function of GACAT1 in modulating the malignant NSCLC cell behaviors, the full length of YY1 cDNA was ligated into the pcDNA-vector. The overexpression of pcDNA-YY1 was confirmed using western blot analysis (Fig. 5A). To determine the involvement of YY1 in GACAT1’s function in NSCLC, YY1 expression was rescued in the A549 and H1299 cells by transfecting them with pcDNA-YY1 in combination with siGACAT1. YY1 mRNA and protein expression levels in NSCLC cells were confirmed using RT-qPCR and western blot analysis (Fig. 5B and C). The CCK-8 assay showed that knockdown of GACAT1 repressed the cell proliferation of both the A549 and H1299 cells, while YY1 reintroduction partially abrogated the GACAT1 knockdown-mediated suppression of cell proliferation (Fig. 5D and E). These data suggested that YY1 plays an important role in mediating the function of GACAT1 in NSCLC cell malignancy.

Discussion

Increasing evidence has suggested that increased or decreased expression level of IncRNA has been associated with various human diseases, particularly with different types of cancer (7,35,36). Identification of novel IncRNAs involved in NSCLC progression is a hot topic, that would benefit in the diagnosis and treatment of NSCLC. In the present study, the results showed that GACAT1 mRNA was highly expressed in NSCLC tissues and was associated with shorter overall survival times of patients with NSCLC. Patients with higher GACAT1 expression levels showed shorter overall survival times, suggesting the potential for the application of GACAT1 in the prognosis of NSCLC.
The crucial roles of GACAT1 in cancer development have attracted increasing attention since its discovery in gastric cancer. GACAT1 expression was found to be increased in gastric cancer and promoted cancer cell proliferation, invasion, and migration (22). Similarly, overexpressed GACAT1 drove breast cancer development by facilitating proliferation and cell cycle progression (23). In the present study, GACAT1 knockdown inhibited proliferation, induced apoptosis, and the cell cycle arrest of NSCLC cells, supporting its oncogenic role in different types of cancer. To solidify the function of GACAT1 in NSCLC, the effects of GACAT1 on tumor growth should be determined using in vivo studies. In addition, whether or not GACAT1 still plays a role in the progression of other subtypes of lung cancer remains a question that should also be addressed.

Research into the ceRNA regulatory network suggested that IncRNAs act as endogenous decoys for miRNAs, which in turn affected the binding of miRNAs to the mRNA targets. GACAT1 was found to target miR-875-3p and regulated breast cancer progression (23). A recent study reported that GACAT1 modulated ZBTB2 and SPI1 mRNA expression levels by sponging miR-149 in gastric cancer (22). In the present study, the potential miRNA binding sites were predicted and miR-422a was identified as a GACAT1 target. GACAT1 knockdown increased the miR-422a expression level in NSCLC cell lines. Consistently, miR-422a mRNA expression levels were reduced in NSCLC tissues and were also inversely correlated with the mRNA expression levels of GACAT1. According to previous publications, miR-422a was found to be a tumor suppressor in several types of cancer (37-39). miR-422a inhibited colorectal cancer proliferation by AKT1 and MAPK1 suppression (40). Furthermore, miR-422a upregulation attenuated breast cancer stem cell properties (41). miR-422a targeted pyruvate dehydrogenase kinase 2 in gastric cancer and inhibited metabolic reprogramming, which suggested that miR-422a could be a promising therapeutic target for anti-cancer treatment (42).

In the present study, miR-422a overexpression inhibited NSCLC cell proliferation. The mechanism study revealed that miR-422a targeted YY1 and repressed YY1 mRNA and protein expression levels in NSCLC cell lines. YY1 is a ubiquitous multifunction transcription factor, that is required for cell survival (43,44). The YY1 oncogenic function has been reviewed and gained increasing interest. Higher YY1 protein expression levels were found in patients with advanced stages of the disease and was associated with shorter survival times in patients with gastric cancer (45). A direct role of YY1 in regulating the cell cycle of cancer cells has been established in a previous study (45). In addition, YY1 was found to modulate MDM2-mediated p53 degradation and affect tumorigenesis of pancreatic cancer (46-48). In the present study, GACAT1 knockdown increased the mRNA expression levels of miR-422a and consequently reduced the mRNA and protein expression levels of YY1. YY1 reintroduction attenuated the NSCLC cell suppressed proliferation induced by knockdown of GACAT1. Further study may be necessary to identify the effects of GACAT1 on the downstream target effects of YY1 in NSCLC progression.

In conclusion, the present study demonstrated that GACAT1 mRNA expression level was increased in NSCLC tissues and cell lines and was associated with poor clinical outcomes in patients with the disease. GACAT1 knockdown inhibited NSCLC malignancy by acting as a ceRNA of miR-422a, which consequently inactivated YY1. These results suggested the GACAT1/miR-422a axis could be a novel therapeutic target for NSCLC treatment.

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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

YQZ, HL and LZ designed the study, performed the experiments and interpreted the data. QL and CL collected the tissues from the patients and performed the RT-qPCR assay. LZ wrote the manuscript. All authors approved the final version of the manuscript. All authors agreed to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

Ethics approval and consent to participate

The study was approved by the Ethics Committee of the Ganzhou People's Hospital of Jiangxi Province and conducted according to the Declaration of Helsinki.

Patient consent for publication

Not applicable.

Competing interests

These authors declare that they have no competing interests.

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