

Long noncoding RNA CASC15 is upregulated in non-small cell lung cancer and facilitates cell proliferation and metastasis *via* targeting miR-130b-3p

D.-J. YU, M. ZHONG, W.-L. WANG

Department of Respiratory, China-Japan Union Hospital of Jilin University, Changchun, China

Abstract. – **OBJECTIVE:** Recent researches have discovered a class of long noncoding RNAs (lncRNAs), which are dysregulated in various tumors and linked to carcinogenesis. This study aims to uncover the molecular functions of lncRNA CASC15 in non-small cell lung cancer (NSCLC) tumorigenesis.

PATIENTS AND METHODS: Real Time-quantitative Polymerase Chain Reaction (RT-qPCR) was performed to detect CASC15 expression in 55 NSCLC samples and four NSCLC cell lines. Besides, the function of CASC15 was detected through proliferation assay, transwell assay, and wound healing assay in NSCLC cells. Furthermore, the interaction between CASC15 and miR-130b-3p in NSCLC was studied by performing dual-luciferase reporter assay. In addition, tumor formation and metastasis were performed *in vivo*.

RESULTS: CASC15 expression was remarkably upregulated in NSCLC samples compared with that in adjacent samples. Proliferation, invasion, and migration in NSCLC were inhibited *via* knockdown of CASC15 *in vitro*. Moreover, RT-qPCR results revealed that miR-130b-3p was upregulated *via* knockdown of CASC15 *in vitro*. In addition, miR-130b-3p was a direct target of CASC15 in NSCLC. Tumor formation and metastasis were inhibited after CASC15 was knocked down *in vivo*.

CONCLUSIONS: Our study indicates that CASC15 could promote metastasis and proliferation of NSCLC through sponging miR-130b-3p *in vitro* and *in vivo*, which may offer a new therapeutic intervention for NSCLC patients.

Keywords:

long noncoding RNA, CASC15, NSCLC, MiR-130b-3p.

Introduction

Lung cancer is one of the most common and life-threatening cancers in the world, which is the leading cause of cancer-related deaths among

men and women (26% and 23%, respectively)^{1,2}. It has been reported that 234,000 new cases are diagnosed with lung cancer in America in 2018, which has contributed to 154,000 deaths in the same year³. As the most common type of lung cancer, non-small cell lung cancer (NSCLC) accounts for approximately 85% of all lung cancer cases³. The primary feature of NSCLC is the migration and invasion of neoplasms which lead to the late diagnosis of lung cancer patients⁴. Moreover, most of NSCLC cases are diagnosed at advanced stages without the opportunity to take radical surgery. Thus, it's important to understand the molecular mechanism of metastasis and progression of NSCLC.

Long noncoding RNAs (lncRNAs), as one subgroup of non-coding RNAs, have been reported to participate in many cellular processes of tumorigenesis. For instance, the lncRNA-CCHE1 expression is positively related to the malignancy of colorectal carcinoma *via* regulation of ERK/COX-2 pathway⁵. LncRNA HCCL5 activated by ZEB1 accelerates cell viability, cell migration, epithelial-mesenchymal transition, and malignancy of hepatocellular carcinoma⁶. LncRNA linc-PINT functions as a tumor suppressor in gastric cancer *via* the interaction with miR-21 and is associated with a poor survival of GC patients⁷. LncRNA SNHG1 could inhibit the differentiation of Treg cells and suppress the immune escape of breast cancer⁸.

In this study, we firstly found out that the expression level of CASC15 was remarkably upregulated in NSCLC samples. Moreover, further experiments revealed that CASC15 promoted cell proliferation, invasion, and migration of NSCLC *in vitro* and *in vivo*. Furthermore, we discovered that CASC15 played its function in NSCLC by sponging miR-130b-3p.

Patients and Methods

Clinical Samples

Human tissues were obtained from 55 NSCLC patients who underwent surgery during China-Japan Union Hospital of Jilin University. All tissues were kept at -80°C . The written informed consent was obtained by all the participants in this study before the operation. This investigation was approved by the Ethics Committee of China-Japan Union Hospital of Jilin University.

Cell Culture

The NSCLC cell lines (SPCA1, H1299, PC-9, and H358) were obtained from the Chinese Type Culture Collection, Chinese Academy of Sciences (Shanghai, China). The normal human bronchial epithelial cell line (16HBE) was obtained from the American Type Culture Collection (ATCC; Manassas, VA, USA). The Dulbecco's Modified Eagle's Medium (DMEM; Hyclone, South Logan, UT, USA) and 10% fetal bovine serum (FBS; Gibco, Invitrogen, Carlsbad, CA, USA) were used to incubate the cells in an incubator containing 5% CO_2 at 37°C .

Cell Transfection

For transfection, lentivirus expressing short-hairpin RNA (shRNA) targeting CAS15 was compounded and then cloned into pLenti-EF1a-EGFP-F2A-Puro vector (Bioseed, Inc., San Diego, CA, USA). CAS15 shRNA (CAS15/shRNA) and scramble vector were transfected in 293T cells and then for transfection in 59 NSCLC cells. The entire transfection process was performed by polybrene-mediated transfection (Invitrogen, Carlsbad, CA, USA).

RNA Extraction and Real-time Quantitative Polymerase Chain Reaction (RT-qPCR)

Total RNA was extracted from cultured NSCLC cells and patient tumor tissues by using RNeasy spin columns (Qiagen, Crawley, UK) and then reverse-transcribed to complementary deoxyribose nucleic acids (cDNAs) using the PrimeScript RT-PCR kit (TaKaRa, Otsu, Shiga, Japan). Real-time PCR was performed using a FastStart Universal SYBR Green Master kit (Roche, Basel, Switzerland). Expression data were normalized by β -actin levels. The relative expression was calculated by performing the $2^{-\Delta\Delta\text{CT}}$ method. The primers used were: CAS15, forward 5'-CACACGCATGGAAAACCCAG-3'

and reverse 5'-GAGGACCTGAGCTGTAAGCC-3'; β -actin, forward 5'-GATGGAAATCGTCAGAGGCT-3' and reverse 5'-TGGCACTTAGTTGGAAATGC-3'. The thermal cycle was as follows: 30 sec at 95°C , 5 sec for 40 cycles at 95°C , 35 sec at 60°C .

Cell Proliferation Assay

Following the protocol (Dojindo Molecular Technologies, Inc., Kumamoto, Japan), cell proliferation of these treated cells in 96-well plates was monitored by cell counting kit-8 (CCK-8) assay every 24 h. Spectrophotometer (Thermo Scientific, Waltham, MA, USA) was utilized to measure the absorbance at 450 nm.

Wound Healing Assay

1.0×10^4 cells were seeded into a 6-well plate. Three parallel lines were made on the back of each well. After reaching about 90% confluency, cells were scratched with a pipette tip and cultured in a medium. Cells were photographed under a light microscope after 48 h. Each assay was independently repeated in triplicate.

Transwell Assay

A 0.4 μm pore size insert was provided by Corning (Corning, NY, USA). 4×10^4 cells in 150 μL serum-free DMEM were transformed to the top chamber of the insert coated with 50 μg Matrigel (BD, Bedford, MA, USA). The bottom chamber was filled with DMEM and FBS. 48 h later, the top surface of chambers was immersed for 10 min with precooling methanol and was stained in crystal violet for 30 min.

Dual-Luciferase Reporter Assay

DIANA LncBASE Predicted v.2 was used to predict the potential target of microRNAs and fragment sequences containing CAS15 reaction sites. For the luciferase assay, the 3'-UTR of CAS15 was cloned into the pGL3 vector (Promega, Madison, WI, USA), which was identified as wild-type (WT) 3'-UTR. Quick-change site-directed mutagenesis kit (Stratagene, La Jolla, CA, USA) was used for site-directed mutagenesis of the miR-130b-3p binding site in CAS15 3'-UTR, which was named as mutant (MUT) 3'-UTR. Cells were transfected with WT-3'-UTR or MUT-3'-UTR and negative control or miR-130b-3p for 48 h. Then, the luciferase assay was conducted on the dual luciferase reporter assay system (Promega, Madison, WI, USA).

Tumor Formation and Metastasis Assay

Transfected H1299 cells ($6 \times 10^5/\text{mL}$) were re-placed into NOD/SCID mice (6 weeks old) subcutaneously. Tumor diameters were detected every 5 days after inoculation. Tumor volume was calculated as the formula (volume = length \times width² \times 1/2). Tumors were extracted after 4 weeks. Transfected H1299 cells ($6 \times 10^5/\text{mL}$) were injected into the tail vein of NOD/SCID mice (6 weeks old). The mice were sacrificed, and the lungs were extracted after 4 weeks. Then, the number of metastatic nodules in the lung was counted.

Statistical Analysis

GraphPad Prism 5.0 (La Jolla, CA, USA) was utilized to conduct the statistical analysis. The two-tailed Student's *t*-test was performed to analyze the significance. When $p < 0.05$, the data were considered statistically significant.

Results

Expression Level of CASC15 in Tissues and Cells of NSCLC

RT-qPCR was conducted for detecting CASC15 expression in 55 patients' tissues and four NSCLC cell lines. CASC15 was significantly upregulated in tumor tissue samples that in adjacent tissues (Figure 1A). In addition, CASC15 level was significantly higher in NSCLC cells than that in 16HBE (Figure 1B).

Knockdown of CASC15 Repressed Cell Growth, Migration and Invasion in NSCLC Cells

According to CASC15 expression in NSCLC cells, we chose H1299 NSCLC cells for knockdown of CASC15. The CASC15 (CASC15/shRNA) and the scramble vector (NC) were synthesized and transduced into H1299 cells. Then, the CASC15 expression was determined by RT-qPCR (Figure 2A). Results of CCK-8 assay suggested that the cell growth ability of NSCLC cells was inhibited after CASC15 was knocked down (Figure 2B). The results of wound healing assay showed that the migrated length of NSCLC cells was inhibited by knockdown of CASC15 (Figure 2C). In addition, the results of the transwell assay showed that the number of invaded NSCLC cells was reduced after CASC15 was knocked down (Figure 2D).

Knockdown of CASC15 Inhibited NSCLC Tumorigenesis Via Sponging miR-130b-3p

Using the online software LncBASE Predicted v.2 to predict the target microRNAs of CASC15. miR-130b-3p was one of those predicted microRNAs, which was reported to suppress tumorigenesis in many tumors. The binding area of CASC15 by miR-130b-3p was shown in Figure 3A. Moreover, miR-130b-3p was upregulated in CASC15/shRNA group compared with NC group (Figure 3B). Furthermore, the results of luciferase assay showed that luciferase activity was significantly reduced through co-transfection of CASC15-WT

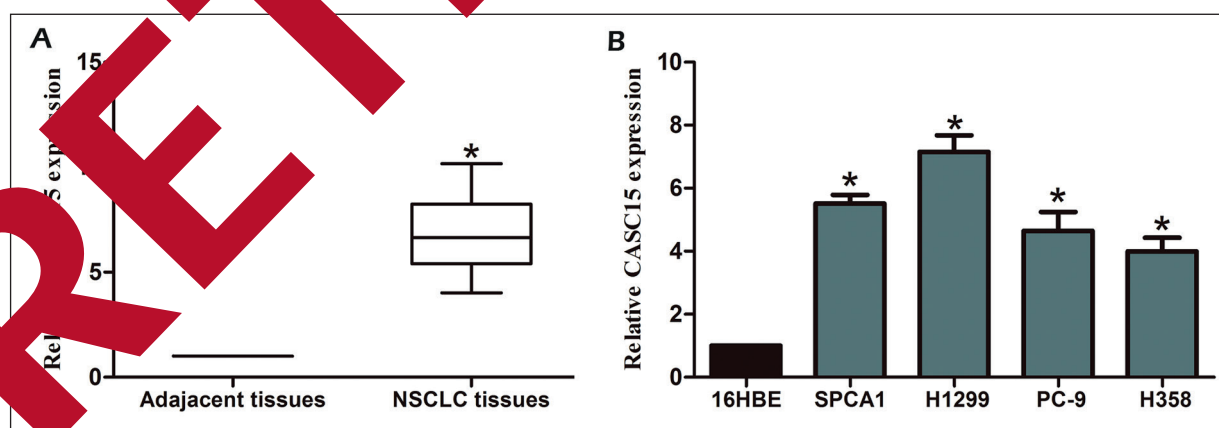


Figure 1. Expression levels of CASC15 were upregulated in NSCLC tissues and cell lines. **A**, CASC15 expression was significantly upregulated in the NSCLC tissues compared with adjacent tissues. **B**, Expression levels of CASC15 relative to β -actin were determined in the human NSCLC cell lines and normal human bronchial epithelial cell (16HBE) by RT-qPCR. Data are presented as the mean \pm standard error of the mean. * $p < 0.05$.

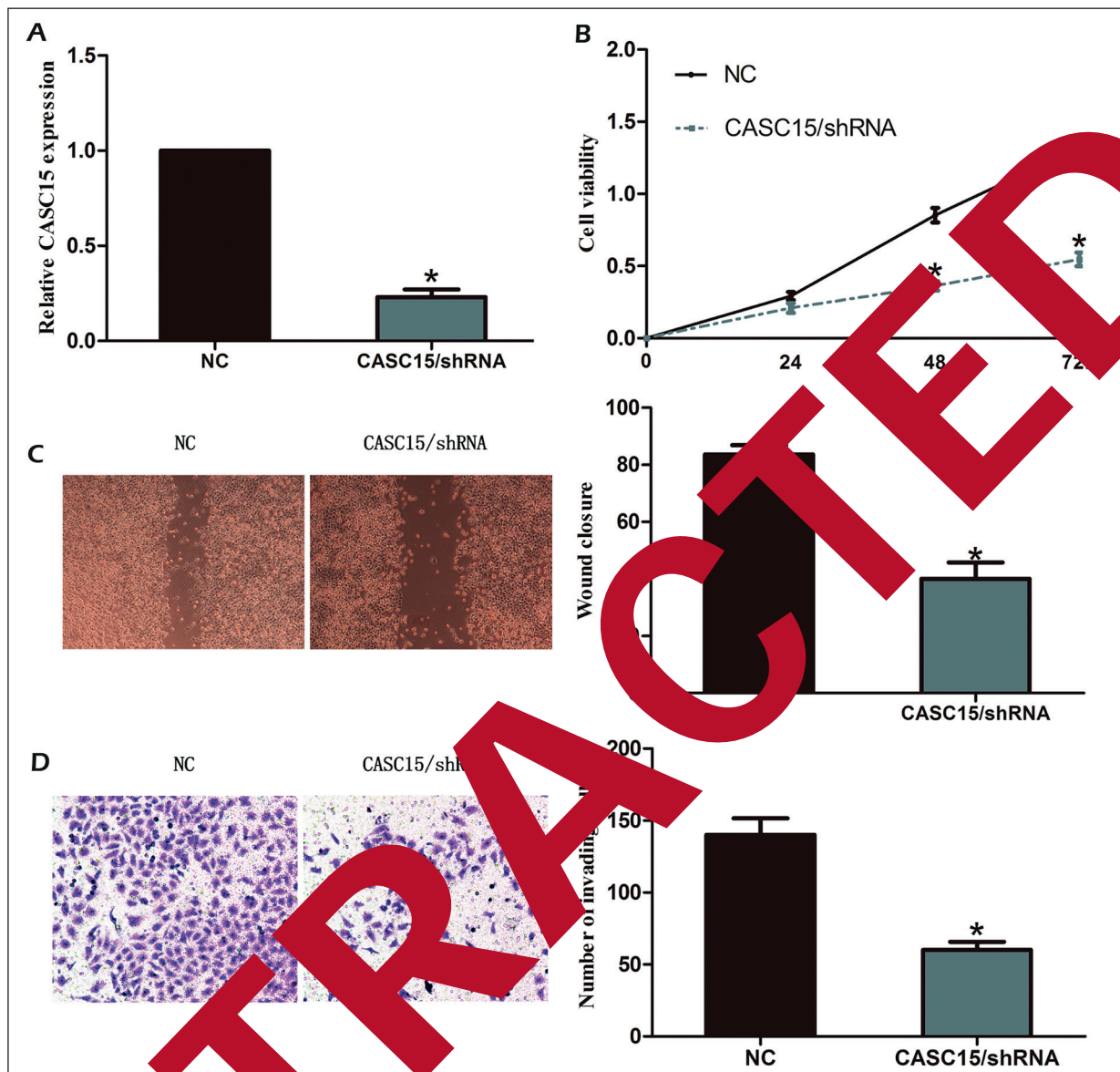


Figure 2. Knockdown of CASC15 inhibited H1299 NSCLC cell proliferation, migration, and invasion. **A**, CASC15 expression in NSCLC cells transduced with empty vector (NC) or CASC15 shRNA (CASC15/shRNA) was detected by RT-qPCR. β -actin was used as an internal control. **B**, CCK8 assay showed that knockdown of CASC15 significantly repressed cell proliferation in H1299 NSCLC cells. **C**, Wound healing assay showed that the migrated length of cells in CASC15/shRNA group was significantly decreased compared with NC group in H1299 NSCLC cells (magnification: 10 \times). **D**, Transwell assay showed that number of invaded H1299 NSCLC cells was decreased in CASC15/shRNA group compared with NC group (magnification: 40 \times). The results represent the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$.

and miR-130b-3p, while no significant changes in luciferase activity were observed through co-transfection of CASC15-MUT and miR-130b-3p (Figure 3C).

Knockdown of CASC15 Inhibited Tumor Formation and Metastasis In Vivo

The ability of CASC15 in tumor formation and metastasis was detected *in vivo*. The tumor size

in CASC15/shRNA group was smaller compared with NC group (Figure 4A). The number of metastatic nodules in the lung of the CASC15/shRNA group was significantly reduced compared with NC group (Figure 4B). Moreover, the expression level of CASC15 and miR-130b-3p in dissected tumor tissues was detected by RT-qPCR. The results showed that CASC15 was lower-expressed in CASC15/shRNA group compared with NC

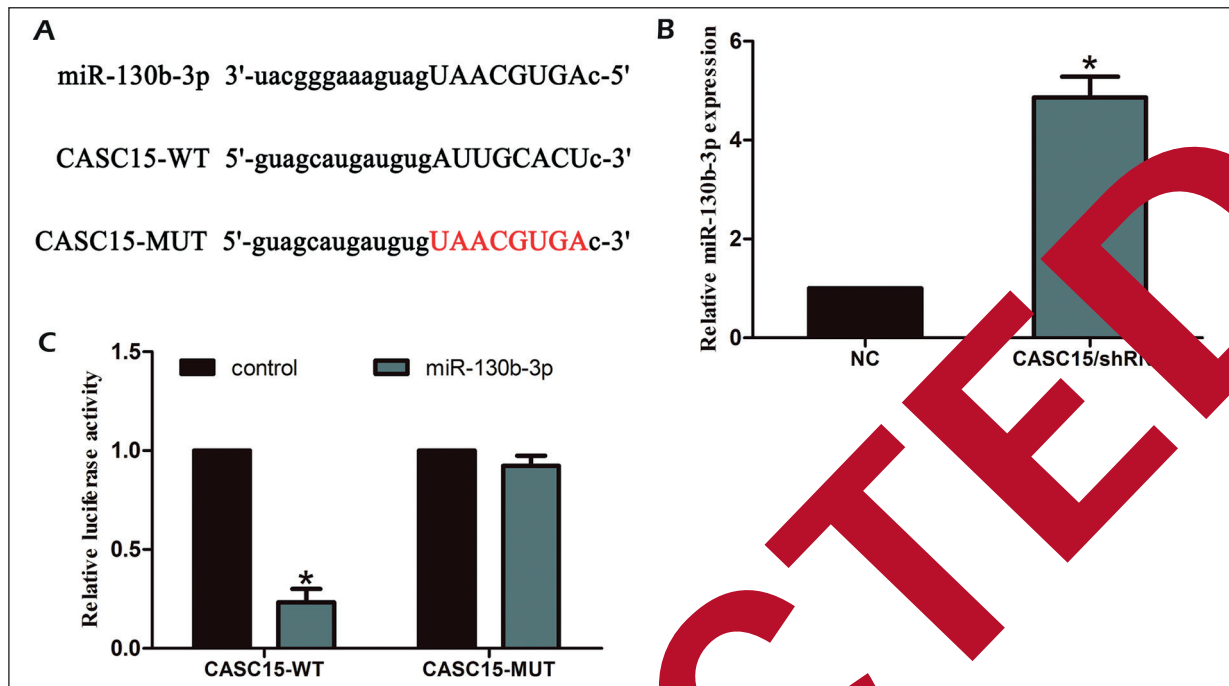


Figure 3. Interaction between miR-130b-3p and CASC15 in NSCLC. **A**, The binding sites of miR-130b-3p on CASC15. **B**, The miR-130b-3p expression was increased in CASC15/shRNA group compared with NC group. **C**, Co-transfection of miR-130b-3p and CASC15-WT strongly decreased the luciferase activity, while co-transfection of miR-130b-3p and CASC15-MUT did not change the luciferase activity either. The results represent the average of three independent experiments. Data are presented as the mean \pm standard error of the mean. * $P < 0.05$.

group (Figure 4C), while miR-130b-3p was higher-expressed in CASC15/shRNA group compared with NC group (Figure 4D).

Discussion

Evidence has proved that lncRNAs participates in the regulation of NSCLC development. For example, by sponging to miR-124-3p, lncRNA OGEF1 has been reported to take part in cell proliferation in NSCLC. LncRNA HEIH accelerates cell metastasis and proliferation of NSCLC *in vitro*. LncRNA PRNCR1 promotes the tumor progression of NSCLC through PRNCR1-miR-481-3p-EY2 network¹¹. By sponging miR-27b-3p, lncRNA KCNQ1OT1 facilitates cell proliferation and invasion in the progression of NSCLC through upregulating HSP90AA1¹².

Cancer susceptibility candidate 15(CASC15), located on chromosome 6p22.3, is firstly discovered in silico. Some researches have indicated that CASC15 plays an important role in tumorigenesis in several cancers. For example, CASC15 enhances cell metastasis and hepatocarcinogen-

esis in hepatocellular carcinoma, which is also correlated with poor prognosis of the patients¹³. CASC15 is also reported to promote cell proliferation in gastric cancer and is a risk factor for gastric cancer patients' prognosis¹⁴. In addition, by regulating the expression of SOX4, CASC15 is found to participate in RUNX1-rearranged acute leukemia¹⁵. Our study showed that the expression of CASC15 was upregulated in both NSCLC tissues and cells. Furthermore, after CASC15 was knocked down, the cell growth ability, migrated and invaded ability were suppressed in NSCLC. These results indicated that CASC15 functioned as an oncogene and promoted the tumorigenesis of NSCLC.

Then, bioinformatics analysis was used to predict the potential target microRNAs of CASC15. MiR-130b-3p, as one of those predicted RNAs, takes part in regulating numerous biological processes of cancers. For example, miR-130b-3p inhibits cell growth and promotes cell apoptosis *via* regulating CYLD in gastric cancer¹⁶. MiR-130b-3p is aberrantly expressed in prostate cancer and inhibits prostate cancer metastasis *via* targeting MMP2^{17,18}. Moreover, miR-130b-3p

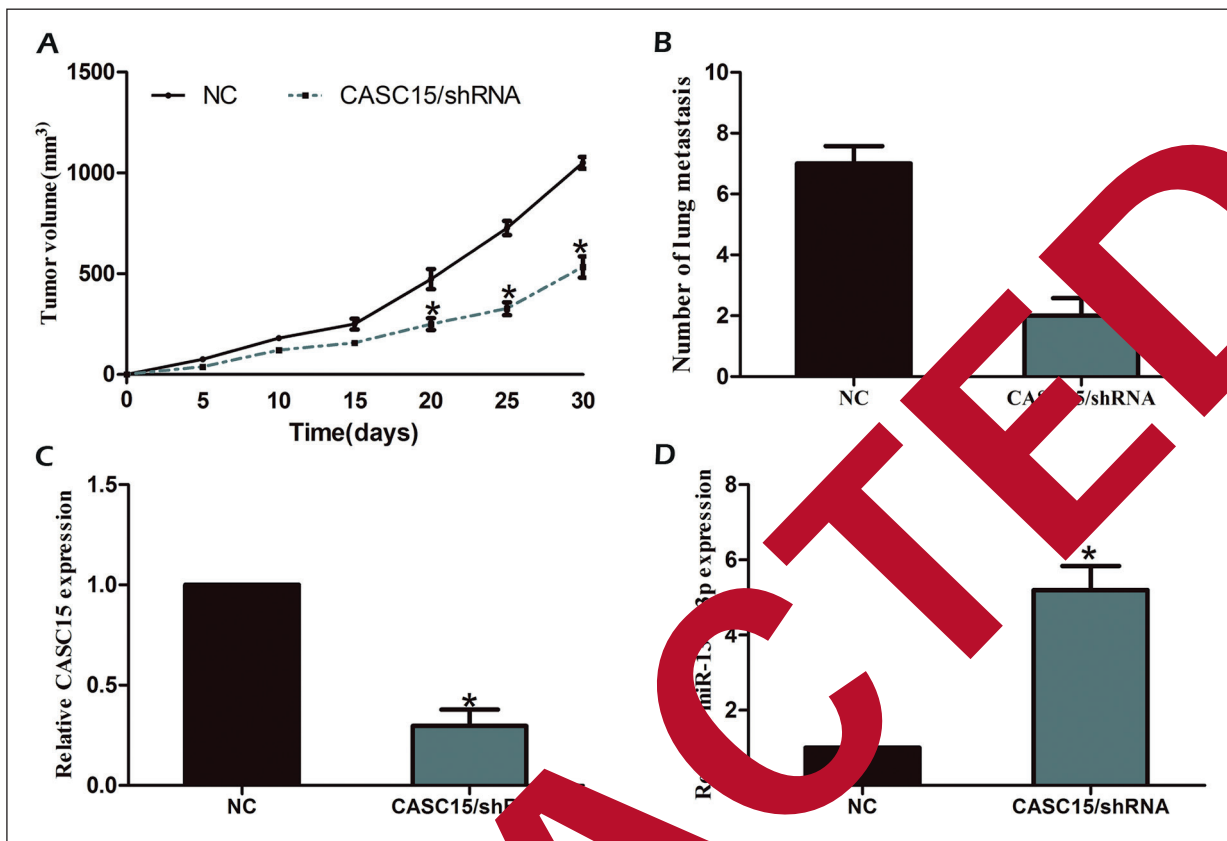


Figure 4. Knockdown of CASC15 inhibited tumor formation and metastasis of NSCLC *in vivo*. **A**, The tumor size in CASC15/shRNA group was smaller compared with NC group. **B**, The number of metastatic nodules in the lung from the CASC15/shRNA group was significantly reduced compared to NC group. **C**, CASC15 of those dissected tumors was lower-expressed in CASC15/shRNA group compared with NC group. **D**, miR-130b-3p of those dissected tumors was higher-expressed in CASC15/shRNA group compared with NC group. The results represent the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$, as compared with the control cells.

is downregulated in breast cancer and inhibits cell invasion and migration *in vitro*. In our study, the interaction between miR-130b-3p and CASC15 was further explored. MiR-130b-3p was downregulated after CASC15 was knocked down *in vitro*. What's more, the luciferase assay results showed that miR-130b-3p could be directly targeted by CASC15. Moreover, a negative correlation was discovered between miR-130b-3p and CASC15 expression in NSCLC tissues. The results above revealed that CASC15 could regulate miR-130b-3p expression and its function in NSCLC *via* sponging miR-130b-3p.

To further verify the function of CASC15 in NSCLC *in vivo*, tumor formation and metastasis assay were conducted. Results of the tumor formation assay revealed that knockdown of CASC15 could inhibit tumor formation in nude mice. Results of tumor metastasis assay revealed

that knockdown of CASC15 could significantly suppress tumor metastasis in nude mice. Through the detection of CASC15 and miR-130b-3p expression in those extracted tumors, we found that CASC15 was downregulated and miR-130b-3p was upregulated in nude mice treated with CASC15/shRNA.

Conclusions

LncRNA CASC15 is a new biomarker in the progression of NSCLC and could enhance NSCLC cell proliferation, migration, and invasion through sponging miR-130b-3p.

Conflict of Interest

The Authors declare that they have no conflict of interests.

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