

Long noncoding RNA AK027294 acts as an oncogene in non-small cell lung cancer by up-regulating STAT3

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Abstract. – **OBJECTIVE:** Recent researches have proved that long noncoding RNAs (lncRNAs) play an important role in multiple diseases, including malignant tumors. The aim of this study was to explore the exact role of lncRNA AK027294 in the development of non-small cell lung cancer (NSCLC), and to investigate the possible underlying mechanism.

PATIENTS AND METHODS: Real Time-quantitative Polymerase Chain Reaction (RT-qPCR) was utilized to detect the AK027294 expression in NSCLC patients. Then, cell counting kit-8 (CCK-8) assay, colony formation assay, and 5-Ethynyl-2'-deoxyuridine (EdU) incorporation assay were performed, respectively. Furthermore, RT-qPCR, Western blot assay were used to explore the potential mechanism.

RESULTS: The expression level of AK027294 in NSCLC samples was significantly higher than that of adjacent tissues. Subsequent functional assays showed that the growth ability of NSCLC cells was markedly inhibited after AK027294 knock-down. In addition, after AK027294 knock-down, the expression of signal transducer and activator of transcription 3 (STAT3) was remarkably down-regulated. Furthermore, the results demonstrated that the STAT3 expression was positively correlated with the AK027294 expression in NSCLC tissues.

CONCLUSIONS: The above results indicated that AK027294 could enhance the growth ability of NSCLC by up-regulating STAT3. Our findings suggest that AK027294 may be a potential therapeutic target for NSCLC.

Key words: Long noncoding RNA, AK027294, Non-small cell lung cancer (NSCLC), STAT3.

Introduction

Lung cancer is one of the leading causes of cancer-related death globally. Meanwhile, it remains a public threat to the society¹. In 2016, approximately 224,390 cases of lung cancer were diagnosed in the

US, including men and female patients². In China, the total number of newly diagnosed lung cancer patients was 73 in 2011³. Non-small cell lung cancer (NSCLC) accounts for 85% of lung cancer cases⁴. A great advance has been achieved in exploring the molecular mechanism and therapeutic treatment. However, the 5-year survival rate of NSCLC patients remains lower than 15%⁵. Therefore, it is an urgent need to realize the underlying molecular mechanism of NSCLC and to search for novel therapeutic targets for NSCLC patients.

Long noncoding RNAs (lncRNAs) are a type of non-protein-coding RNAs with longer than 200 nucleotides in length. Numerous studies have shown that lncRNAs are a new frontier in the research of malignant diseases. For instance, the up-regulation of PVT1 promotes the proliferation, cell cycle progression and metastasis of melanoma cells⁶. Through modulating the signal transducers and activators of transcription 1-mitogen-activated protein kinase (STAT1-MAPK) signal pathway, down-regulation of lncRNA P7 facilitates the proliferation of hepatocellular carcinoma cells. Meanwhile, lncRNA P7 is associated with unfavorable prognosis⁷. By sponging miR-124-3p, lncRNA OGFRP1 has been reported to participate in the proliferation of NSCLC cells⁸. In addition, lncRNA AF147447 represses the proliferation and invasion of gastric cancer infected with *Helicobacter pylori* through regulating miR-34c expression and targeting MUC2⁹. However, the exact function of lncRNA AK027294 in NSCLC, as well as the potential molecular mechanism, have not been elucidated so far.

Patients and Methods

Tissue Samples

A total of 50 paired NSCLC tissues and adjacent tissues were obtained from NSCLC patients who underwent surgery at Shanghai Pulmonary Hospital. No radiotherapy or chemotherapy was

performed before surgery. All fresh tissues collected from the surgery were stored immediately at -80°C for subsequent use. This study was approved by the Review Board of Shanghai Pulmonary Hospital.

Cell Culture

Human NSCLC cell lines (A549, SPCA1, and H358) and normal human bronchial epithelial cell line (16HBE) were obtained from American Type Culture Collection (ATCC; Manassas, VA, USA). Cells were cultured in Dulbecco's Modified Eagle Medium (DMEM; Gibco, Rockville, MD, USA) consisting of 10% fetal bovine serum (FBS; Invitrogen Life Technologies, Carlsbad, USA) and penicillin. Besides, all cells were maintained in a 5% CO_2 , 37°C incubator.

Cell Transfection

The cDNA oligonucleotides specifically targeting AK027294 (sh-AK027294) was synthesized by GenePharma (Shanghai, China), and was inserted into shRNA expression vector pGPH1/Neo. Subsequently, sh-AK027294 was transfected into NSCLC cells according to the instructions. 48 h later, Real Time-quantitative Polymerase Chain Reaction (RT-qPCR) was used to verify the transfection efficiency.

Cell Counting Kit-8 (CCK-8) Assay

24, 48, and 72 hours after transfection, the growth ability of cells in 6-well plates was assessed following the instructions of CCK8 assay (Dojindo Laboratories, Shanghai, China) respectively. Absorbance at 490 nm was detected by a spectrophotometer (Thermo Scientific, Waltham, MA, USA).

Colony Formation Assay

H358 cells were first seeded into 6-well plate, followed by culture for 10 days. Then, the formed colonies were fixed with 10% formaldehyde for 30 min and stained with 0.5% crystal violet for 5 min. Image-Pro Plus 6.0 (Silver Springs, MD, USA) was used for data analysis.

5-Ethynyl-2'-Deoxyuridine (EdU)

Incorporation Assay

According to the manufacturer's instructions, EdU (Molecular Biology, Mannheim, Germany) was utilized to monitor the proliferation of transfected cells. Zeiss Axiophot Photomicroscope (Carl Zeiss Jena, Oberkochen, Germany) was used to capture representative images.

RNA Extraction and RT-qPCR

TRIzol reagent (Invitrogen, Carlsbad, CA, USA) was utilized to extract the total RNA in NSCLC cells. The extracted total RNA was reverse transcribed to complementary deoxyribonucleic acids (cDNAs) through reverse Transcription Kit (TaKaRa Biotechnology Co., Ltd., Dalian, China). Primers used in this study were as follows: AK027294 primers forward: 5'-ATGAGTCCCTATTGGAG-3'; reverse: 5'-TAAGCAGTCTGACTAAT-3'; GAPDH primers forward: 5'-CAGGTCAGATGCGGCAATGCTGG-3'; reverse: 5'-TGATGTCATGACTGTGGTATTCA-3'. The reaction cycle was as follows: 30 min at 42°C , 5 sec for a total of 40 cycles at 95°C , 30 sec at 55°C , 30 sec at 60°C .

Statistical Analysis

Statistical Product and Service Solutions (SPSS) 17.0 (SPSS, Chicago, IL, USA) was used for all statistical analyses. The Student *t*-test was performed to compare the difference between the two groups. Experimental data were presented as mean \pm standard deviation. $p < 0.05$ was considered statistically significant.

Results

Expression Level of AK027294 in NSCLC Tissues and Cells

Firstly, the AK027294 expression in 50 NSCLC tissues and 3 cell lines was detected via RT-qPCR. The results showed that AK027294 in NSCLC tissue samples was significantly up-regulated (Figure 1A). The AK027294 expression level in NSCLC cells was significantly higher than that of 16HBE cells (Figure 1B).

Silence of AK027294 Suppressed the Proliferation of NSCLC Cells

In this study, the H358 NSCLC cells were chosen for the silence of AK027294. Subsequently, the AK027294 expression in cells was detected by RT-qPCR (Figure 2A). The results of CCK8 assay showed that silence of AK027294 significantly inhibited the growth ability of NSCLC cells (Figure 2B). Meanwhile, colony formation assay revealed that the number of formed colonies was remarkably decreased after AK027294 silence in NSCLC cells (Figure 3A). Moreover, EdU incorporation assay indicated that the percentage of EdU positive cells was remarkably reduced after silencing AK027294 in H358 cells (Figure 3B).

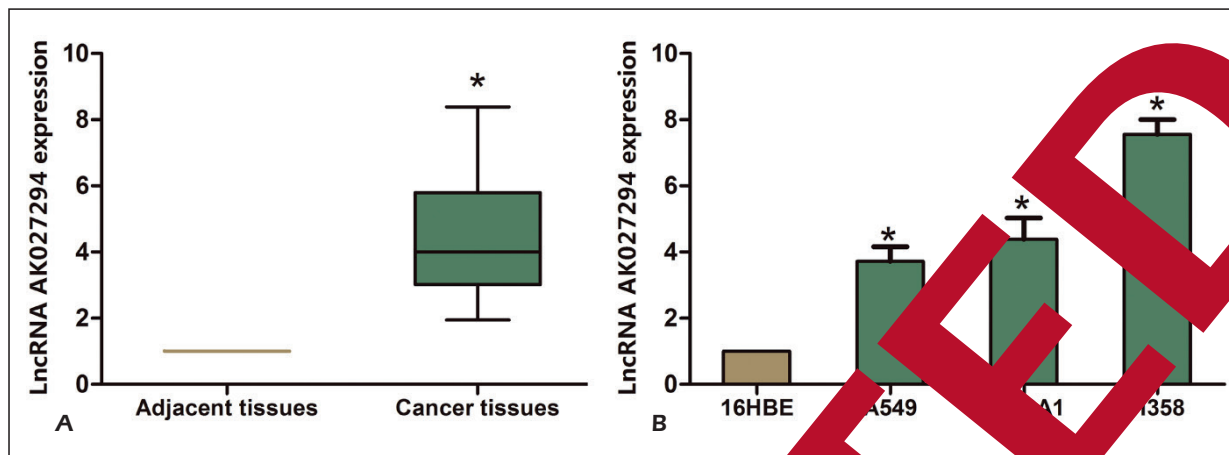


Figure 1. Expression levels of AK027294 were significantly increased in NSCLC tissues and cell lines. **A**, AK027294 expression was significantly increased in NSCLC tissues when compared with adjacent tissues. **B**, Expression levels of AK027294 relative to GAPDH in human NSCLC cell lines and 16HBE (normal human bronchial epithelial cell line) were determined by RT-qPCR. Data were presented as mean \pm standard error of the mean.

Interaction Between STAT3 and AK027294 in NSCLC

RT-qPCR results showed that the expression level of STAT3 in NSCLC cells of sh-AK027294 group was remarkably lower than that of control group (Figure 4A). Besides, we found that the expression of STAT3 in NSCLC cells was significantly increased when compared with 16HBE cells (Figure 4B). Furthermore, the results showed that the STAT3 expression in NSCLC tissues was remarkably higher than that in adjacent tissues (Figure 4C). Furthermore, the correlation analysis demonstrated that the STAT3 expression was positively correlated with the AK027294 expression in NSCLC tissues (Figure 4D).

Discussion

lncRNAs are important regulators in lung cancer occurrence and progression. For example, lncRNA HEIH facilitates the metastasis and proliferation of NSCLC cells, which may help to identify a novel therapeutic intervention¹⁰. LncRNA LINC01091 functions as an oncogene in NSCLC, which promotes tumor progression through regulating miR-488/HEY2 signal network¹¹. By sponging miR-27b-3p, lncRNA KCNQ1OT1 promotes the proliferation and invasion of NSCLC progression through up-regulating the expression of HSP90AA1¹². In addition, overexpression of lncRNA-p21 suppresses the apoptosis of NSCLC

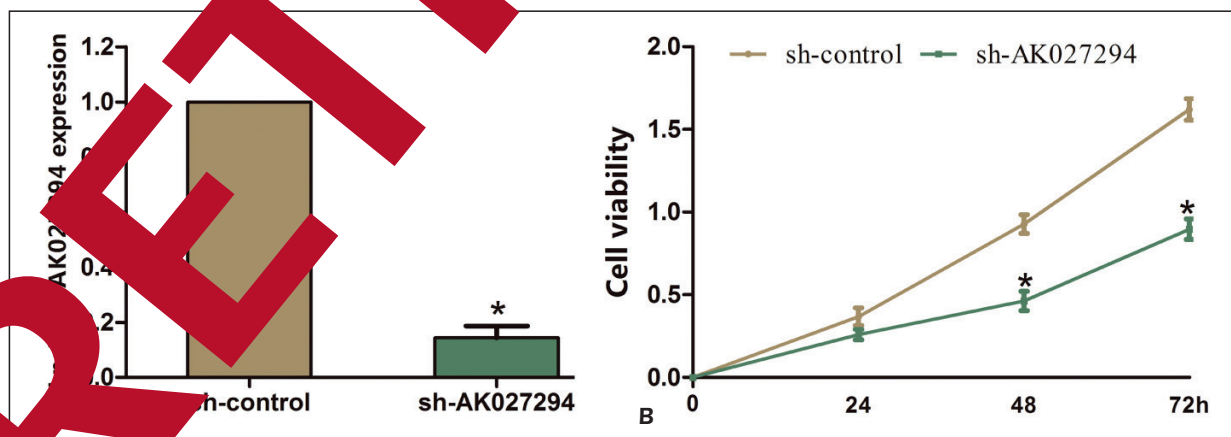


Figure 2. Silence of AK027294 repressed NSCLC cell proliferation. **A**, AK027294 expression in NSCLC cells transfected with sh-AK027294 and control vector was detected by RT-qPCR. GAPDH was used as an internal control. **B**, CCK8 assay showed that silence of AK027294 significantly repressed the proliferation of NSCLC cells. The results represented the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$, as compared with control cells.

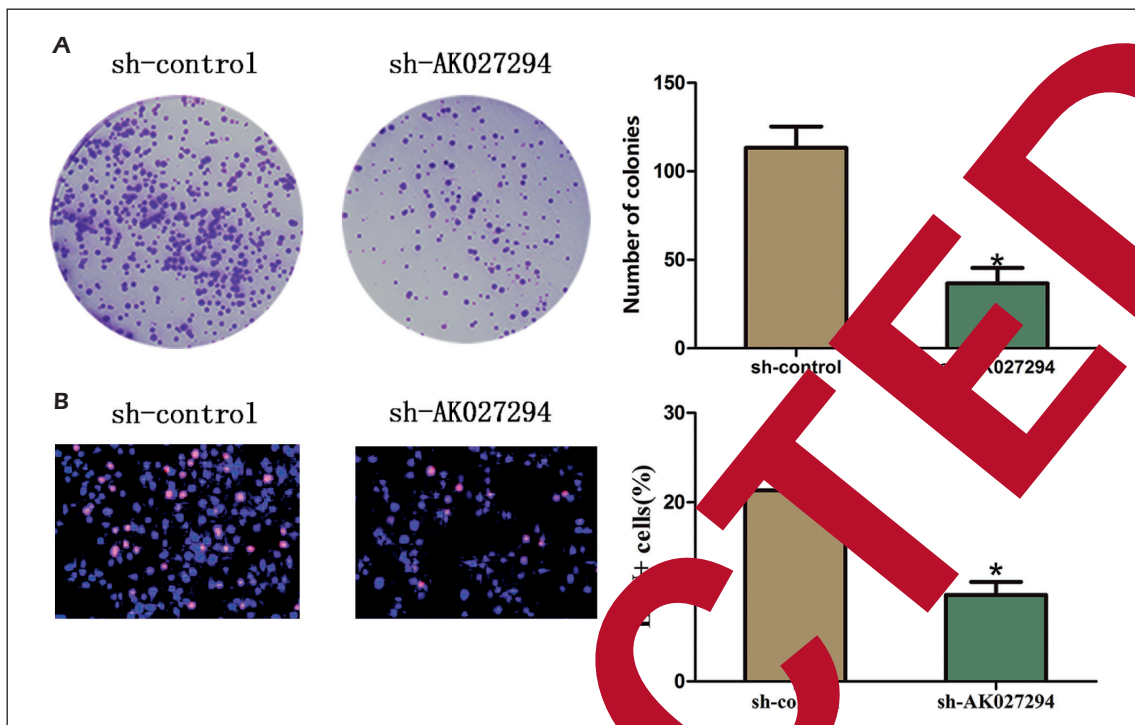


Figure 3. Silence of AK027294 inhibited NSCLC cell proliferation. Colony formation assay showed that the number of colonies was significantly decreased after silencing AK027294 in NSCLC cells. EdU incorporation assay showed that the number of EdU positive cells was significantly decreased after silencing AK027294 in NSCLC cells. The results represented the average of three independent experiments (mean \pm standard deviation). * $p < 0.05$, as compared with control cells.

cells by directly down-regulating the expression level of PUMA¹³.

LncRNA AK027294, as a novel molecular, has been found to participate in the cell cycle process. Meanwhile, it is involved in the progression of colorectal cancer, promoting cell proliferation and migration. We found that AK027294 was significantly up-regulated both in NSCLC tissues and cell lines. Besides, silence of AK027294 markedly inhibited the proliferation of NSCLC cells. The above results indicated that AK027294 promoted the tumorigenesis of NSCLC, which might act as an oncogene.

STAT3 is a member of the signal transducer and activator of transcription (STAT) factors, which has been shown to be expressed in various cell types¹⁶. For example, the STAT3 signaling pathway promotes the growth and invasiveness of bladder cancer cells *via* inhibiting WIF1 expression¹⁷. The IL-6/JAK/STAT3 pathway plays a crucial role in the progression of colorectal cancer, which may help to offer potential therapeutic approaches¹⁸. MicroRNAs can function as an oncogene in the progression of prostate tumor through impairing

ubiquitination and activating STAT3¹⁹. Moreover, miR-124 suppresses NSCLC growth and induces cell apoptosis through negatively regulating STAT3 expression²⁰. In the present work, we firstly verified the interaction between STAT3 and AK027294. The results showed that the expression level of STAT3 was significantly down-regulated after silencing AK027294. Besides, STAT3 expression was remarkably elevated in NSCLC cell lines. Furthermore, STAT3 expression in NSCLC tissues was positively correlated with AK027294 expression. All the results above suggested that AK027294 might promote the tumorigenesis of NSCLC through up-regulating STAT3.

Conclusions

We showed that AK027294 was remarkably up-regulated in NSCLC tissues. Meanwhile, it could facilitate the proliferation of NSCLC cells through up-regulating STAT3. These findings suggested that AK027294 might act as a candidate target for the treatment of NSCLC.

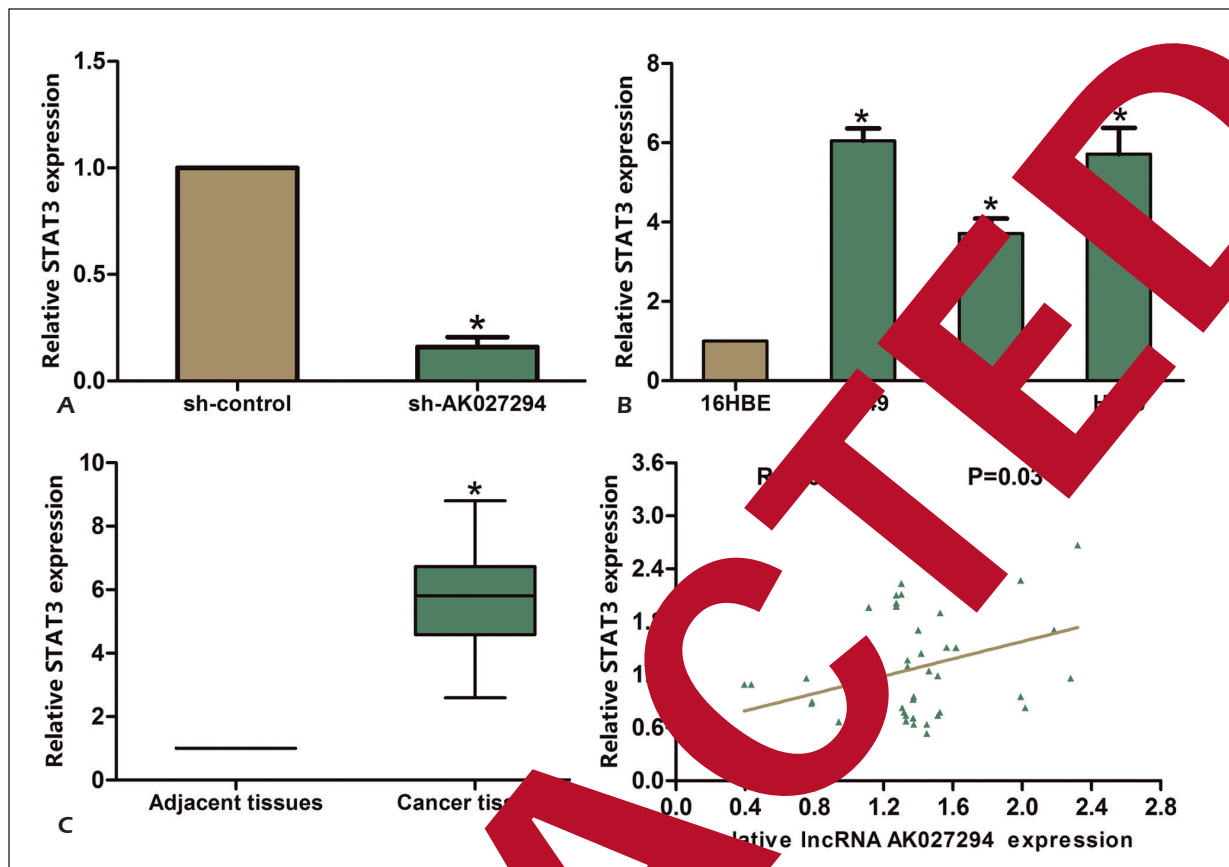


Figure 4. Interaction between AK027294 and STAT3. RT-qPCR results showed that STAT3 expression was significantly decreased in sh-AK027294 group when compared with sh-control group. **B**, Expression levels of STAT3 relative to GAPDH in human NSCLC cell lines and 16HBE (normal human bronchial epithelial cell line) were determined by RT-qPCR. **C**, STAT3 was significantly up-regulated in NSCLC tissues when compared with adjacent tissues. **D**, Linear correlation between the expression level of STAT3 and AK027294 in NSCLC tissues. The results represented the average of three independent experiments. Data were presented as mean \pm standard error of the mean. * $p < 0.05$.

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Conflict of Interests

The authors declare that they have no conflict of interest.

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