

LINC00052 inhibits tumor growth, invasion and metastasis by repressing STAT3 in cervical carcinoma

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Abstract. – **OBJECTIVE:** The vital role of long noncoding RNAs (lncRNAs) in tumor progression has been identified in numerous studies. In this research, the biological function of lncRNA LINC00052 during the development of cervical cancer was mainly explored.

PATIENTS AND METHODS: LINC00052 expression was detected by quantitative Real-time polymerase chain reaction (qRT-PCR) in cervical cancer tissue samples and cell lines. Moreover, the correlation between LINC00052 expression level and disease-free survival rate of cervical cancer patients was analyzed. *In vitro* function of LINC00052 in cervical cancer cells were evaluated by proliferation assay, cell cycle analysis assay and transwell assay. In addition, qRT-PCR and Western blot were utilized to explore the underlying mechanism of LINC00052 inhibiting the progression of cervical cancer.

RESULTS: LINC00052 expression level was lower in cervical cancer samples than that in adjacent tissues, which was correlated with disease-free survival time. Moreover, cell proliferation, migration and invasion were inhibited through overexpression of LINC00052 *in vitro*. The mRNA and protein expression of signal transducers and activators of transcription 3 (STAT3) was downregulated after overexpression of LINC00052 in cervical cancer cells. The STAT3 expression level was negatively correlated with the expression of LINC00052 in cervical cancer tissues.

CONCLUSION: LINC00052 could repress migration, invasion and metastasis of cervical cancer cell via repressing STAT3. LINC00052 might be a novel tumor suppressor in cervical cancer.

Keywords:

long noncoding RNA, LINC00052, STAT3, Cervical cancer

Introduction

Cervical cancer is the fourth most common gynecologic malignancy globally, which is also the most prevalent cancer among Chinese women. There were 528,000 newly diagnosed cases and approximately 266,000 death cases of cervical cancer in 2012¹. In developing countries, the morbidity accounts for 10% of cervical cancer cases, resulting in more than 25,000 female deaths annually^{2,3}. Conventional therapeutic strategies for cervical cancer include surgery, radiotherapy and chemotherapy. Though the cure rate of cervical cancer reaches 90% in early stage, the prognosis of metastatic cervical cancer is very poor. Therefore, it is urgent to clarify the underlying molecular mechanism and develop a new treatment strategy for cervical cancer. Long non-coding RNAs (lncRNAs) are one subtype of non-coding RNAs, which are longer than 200 nucleotides in length. Recently, lncRNAs are widely explored in a variety of biological behaviors. Moreover, evidence proved that lncRNAs serve as an important regulator in the progression of malignant tumors. For example, lncRNA CCAT2 promotes proliferation and metastasis of intrahepatic cholangiocarcinoma, which predicts a poor prognosis of these patients⁴. lncRNA OR3A4 is upregulated in breast cancer and may be a potential therapeutic target and prognostic marker⁵. Interacted with miR-124, lncRNA XIST functions as an oncogene, which promotes cell growth, migration and invasion in bladder cancer⁶. lncRNA SNHG7 promotes cell proliferation and cycle progression in cervical cancer through miR-503/Cyclin D1 pathway⁷. In addition, lncRNA 91H exerts oncogenic properties by up-regulating expression of H19/IGF2, which increases aggres-

sive phenotype of breast cancer cells⁸. However, the clinical role and biological mechanisms of lncRNA LINC00052 in the development of cervical cancer remain unexplored. In this study, we found out that the expression of LINC00052 was downregulated in cervical cancer. Moreover, LINC00052 inhibited the proliferation, migration and invasion of cervical cancer cells *in vitro*. Furthermore, we explored the underlying mechanism of LINC00052 in mediating the development of cervical cancer.

Patients and Methods

Cell Lines and Clinical Samples

Cervical cancer tissues and adjacent normal tissues were harvested from 60 cervical cancer patients undergoing surgery at Affiliated Hospital of Guilin Medical University. Tissues samples were immediately preserved at -80°C . Before operation, written informed consent was achieved. This study conformed as the Ethics Committee of Affiliated Hospital of Guilin Medical University required. Human cervical cancer cell lines SiHa, HeLa, C4-1 and C33a and normal cervical epithelium cell line HEC-1A were offered by Chinese Academy of Science (Shanghai, China). Cells were cultured in Corning Well Park Memorial Institute-1640 (RPMI-1640) (HyClone, South Logan, UT, USA) consisted of 10% fetal bovine serum (FBS) (Rockville, MD, USA) and 1% penicillin/streptomycin. Cells were maintained in an incubator with 5% CO_2 at 37°C .

Cell Transfection

Lentiviral virus transducing LINC00052 was compounded and inserted into the pLenti6-EGFP-F2A-Puro vector (Addgene, Boston, MA, USA). Empty vector and the LINC00052 lentiviruses (LINC00052) were packaged in 293T cells.

RNA Extraction and Quantitative Real-time Polymerase Chain Reaction (qRT-PCR)

Total RNA was extracted using TRIzol reagent (Invitrogen, Carlsbad, CA, USA) and reverse-transcribed into complementary deoxyribose nucleic acid (cDNAs) using the reverse Transcription Kit (Takara Biotechnology Co., Ltd., Dalian, China). Following the primers using for qRT-PCR: LINC00052, forward 5'-CCTATCCCTTTCTCTA-3' and reverse 5'-ACTTCTGCAAAAAC-3'; MTA1, forward 5'-GCTCTAGAAGTGG-3' and reverse 5'-GCTCTAGACAAGA-3' and reverse 5'-GATC-3' and reverse 5'-GGCA-3'.

5'-GCTCTAGACAAGA-3' and reverse 5'-GATC-3' and reverse 5'-GGCA-3'. Thermal cycle was as follows: 30 s at 95°C , 5 s at 95°C , 35 s at 60°C , for a total of 40 cycles.

Western Blot Analysis

Reagent radioimmunoprecipitation (RIPA) (Beyotime, Shanghai, China) was utilized to extract protein from cells. Bicinchoninic acid (BCA) protein assay (TaKaRa, Dalian, China) was chosen for quantifying protein concentrations. Target proteins were separated by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE). Next, they were incubated with primary antibodies after loading on the polyvinylidene difluoride (PVDF) membranes (Millipore, Billerica, MA, USA). Cell Signaling Technology (CST, Danvers, MA, USA) provided rabbit anti- β -tubulin and rabbit anti-STAT3 (signal transducers and activators of transcription 3), as well as goat anti-rabbit secondary antibody. Chemiluminescent film was applied for assessment of protein expression with Image J software (NIH, Bethesda, MD, USA).

Cell Proliferation Assay

Cervical cancer cells were seeded in the 96-well plate (1×10^3 cells/well). After that, we added cell-counting kit-8 (CCK-8) (10 μL) (Dojindo, Kumamoto, Japan) into these wells at the appointed time points. Microplate reader was used for measuring absorbance at 450 nm (Bio-Rad, Hercules, CA, USA).

Wound Healing Assay

Cells seeded into 6-well plates were cultured in RPMI-1640 medium overnight. After scratched with a plastic tip, cells were cultured in serum-free RPMI-1640. Wound closure was viewed at the appointed time points. Each assay was independently repeated in triplicate.

Transwell Assay

5×10^4 cells in 200 μL serum-free RPMI-1640 were applied on the top side of the transwell chamber (8 μm in pore size, Millipore, Billerica, MA, USA) pre-coated with 50 μg Matrigel (BD Biosciences, Franklin Lakes, NJ, USA). The bottom chamber was added with RPMI-1640 containing 10% fetal bovine serum (FBS). 48 h later, after wiped by cotton swab, the top surface of chambers was immersed for 10 min with precooling

methanol and stained in crystal violet for 30 min. Invasive cells were counted in three randomly selected fields per well (magnification 40×).

Statistical Analysis

Statistical analysis was conducted through Statistical Product and Service Solutions (SPSS) 18.0 (SPSS Inc., Chicago, IL, USA). Chi-square test, Student *t*-test and Kaplan-Meier method were utilized. Data were presented as mean ± SD (Standard Deviation). *p*<0.05 was considered of statistically significance.

Results

LINC00052 Expression Level in Cervical Cancer Tissues and Cells

First, qRT-PCR was conducted for detecting LINC00052 expression in 60 paired cervical

cancer tissues and 4 cervical cancer cell lines. As a result, LINC00052 was significantly downregulated in tumor tissue samples (Figure 1A). The overall survival of cervical cancer patients after surgery was analyzed through Kaplan-Meier method. A total of 60 cervical cancer patients were divided into high-LINC00052 and low-LINC00052 groups based on the median expression level of LINC00052. Kaplan-Meier analysis showed that cervical cancer patients with the high LINC00052 level had a better disease-free survival (Figure 1B). LINC00052 level was significantly upregulated in cervical cancer cells than the normal cervical epithelium cell line NC104 (Figure 1C). In our study, we chose C-33a cervical cancer cell line for the overexpression of LINC00052. QRT-PCR was utilized for detecting the transfection efficacy (Figure 1D).

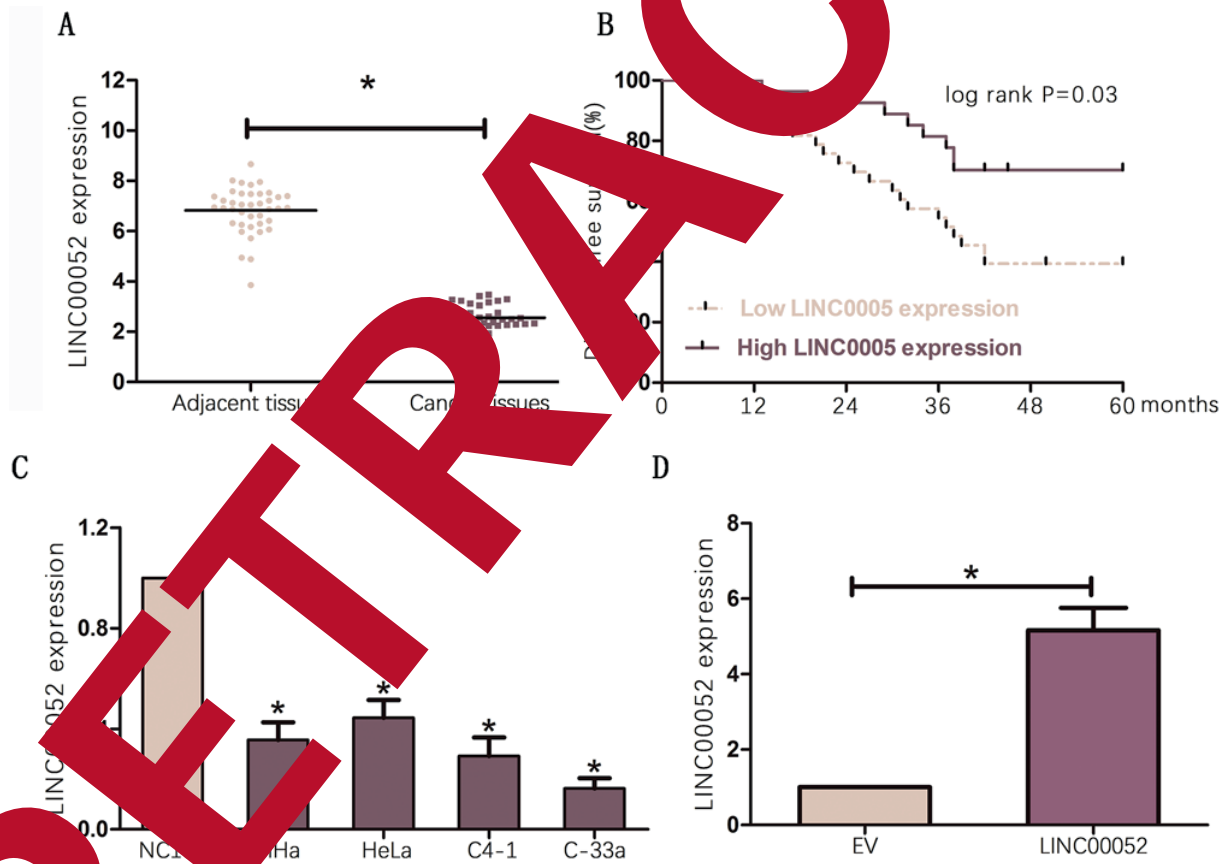


Figure 1. Expression level of LINC00052 was downregulated in cervical cancer tissues and cell lines and associated with better disease-free survival of cervical cancer patients. **A**, LINC00052 expression was significantly downregulated in the cervical cancer tissues compared with adjacent tissues. **B**, High level of LINC00052 was associated with better disease-free survival of cervical cancer patients. **C**, Expression level of LINC00052 relative to β-actin was determined in the human cervical cancer cell lines and normal cervical epithelium cell line NC104 by qRT-PCR. **D**, LINC00052 expression in cervical cancer cells transfected with LINC00052 lentiviruses (LINC00052) and the empty vector (EV) was detected by qRT-PCR. β-actin was used as an internal control. Data are presented as the mean ± standard error of the mean. **p*<0.05.

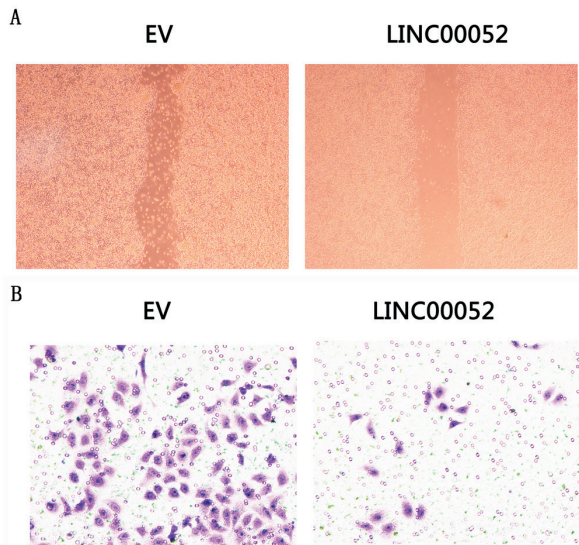


Figure 2. Overexpression of LINC00052 promoted cervical cancer cell migration and invasion. **A**, Wound healing assay showed that overexpression of LINC00052 significantly repressed cell migration in cervical cancer cells. **B**, Transwell assay showed that number of invaded cells significantly decreased *via* overexpression of LINC00052 in cervical cancer cells. 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.

Overexpression of LINC00052 Inhibited Cell Migration and Invasion in Cervical Cancer Cells

Results of wound healing assay revealed that the wound closure of cells significantly increased after overexpression of LINC00052 in C-33a cells (Figure 2A). Transwell assay also revealed that the invasive ability of cells was markedly repressed through overexpression of LINC00052 in C-33a cells (Figure 2B).

Overexpression of LINC00052 Inhibited Cell Growth in Cervical Cancer Cells

CCK-8 assay was conducted to detect cell growth ability. The results revealed that after LINC00052 was overexpressed in C-33a cells, the cell growth ability was significantly repressed (Figure 3).

Overexpression of LINC00052 Inhibited the Interaction between STAT3 and LINC00052 in Cervical Cancer

Q-PCR results showed that compared with the control group in empty vector (EV) group, the expression level of STAT3 in cervical cancer cells was lower in LINC00052 lentiviruses (LINC00052) group (Figure 4A). Western blot found that overexpression of LINC00052 down-

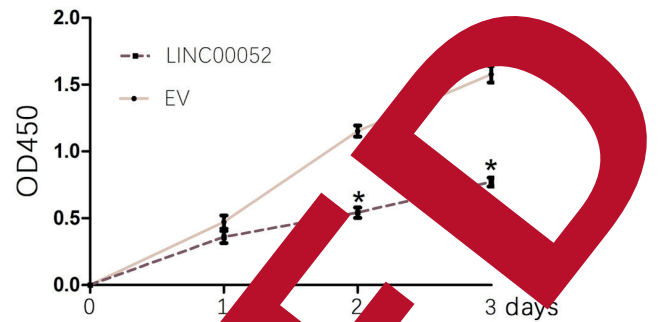


Figure 3. Overexpression of LINC00052 inhibited cervical cancer cell proliferation. CCK8 assay revealed that cell viability significantly decreased *via* overexpression of LINC00052 in cervical cancer cells. The results represent the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$, as compared with the control cells.

regulated protein level of STAT3 in cervical cancer cells (Figure 4B). We further found that STAT3 expression of cervical cancer tissues was obviously upregulated compared with that of adjacent tissues (Figure 4C). Correlation analysis demonstrated that STAT3 expression level was negatively correlated to LINC00052 expression in cervical cancer tissues (Figure 4D).

Discussion

LncRNAs have been reported to be associated with pathogenesis of many cancers. Recently, evidence proved that lncRNAs serve as a crucial part in the development of cervical cancer. For instance, by regulation of miR-21-5p, lncRNA MEG3 functions as a tumor-suppressor gene in cervical cancer to inhibit tumor growth⁹. LncRNA HOTAIR promotes the proliferation and invasion of cervical cancer cells through targeting the Notch pathway, which may be a potential treatment target¹⁰. LncRNA CCAT2 promotes cell proliferation and survival in cervical cancer¹¹. Increased expression level of lncRNA CCHE1 is associated with poor prognosis of cervical cancer, which could be a potential prognostic marker¹². In addition, overexpression of lncRNA NNT-AS1 facilitates the proliferation and invasion of cervical cancer cell *via* Wnt/beta-catenin signaling pathway¹³. Recently, lncRNA LINC00052 has been reported to participate in tumorigenesis of multiple cancers. For instance, overexpression of LINC00052 promotes the progression of breast cancer by HER3-me-

diated downstream signaling, which could be used as a potential diagnostic and therapeutic marker¹⁴. Through activating Wnt/beta-Catenin signaling pathway, lncRNA LINC00052 promotes the proliferation and metastasis of gastric cancer cells¹⁵. In addition, lncRNA LINC00052 inhibits migration and invasion of hepatocellular carcinoma cells through upregulating EPB41L3 via miR-452-5p¹⁶. Our current study demonstrated that LINC00052 was downregulated both in cervical cancer samples and cell lines. Besides, expression level of LINC00052 was closely related to the prognosis of cervical cancer. Furthermore, after LINC00052 was overexpressed, cervical cancer cell migration and invasion were

found to be suppressed. Above results indicated that LINC00052 inhibited tumorigenesis in cervical cancer as a tumor suppressor. The signal transducer and activator of transcription (STAT) transcription factors have been indicated to be widely expressed in hematological and various cell types. It has been reported that mutations, such as STAT3, are associated with various immunodeficiency syndromes and tumorigenesis^{17,18}. For example, the JAK/STAT3 pathway functions as a crucial factor in development of colorectal cancer, which may contribute to develop potential therapeutic approach. STAT3 is activated in more than 40% of breast cancers, which promotes progression of breast tumor

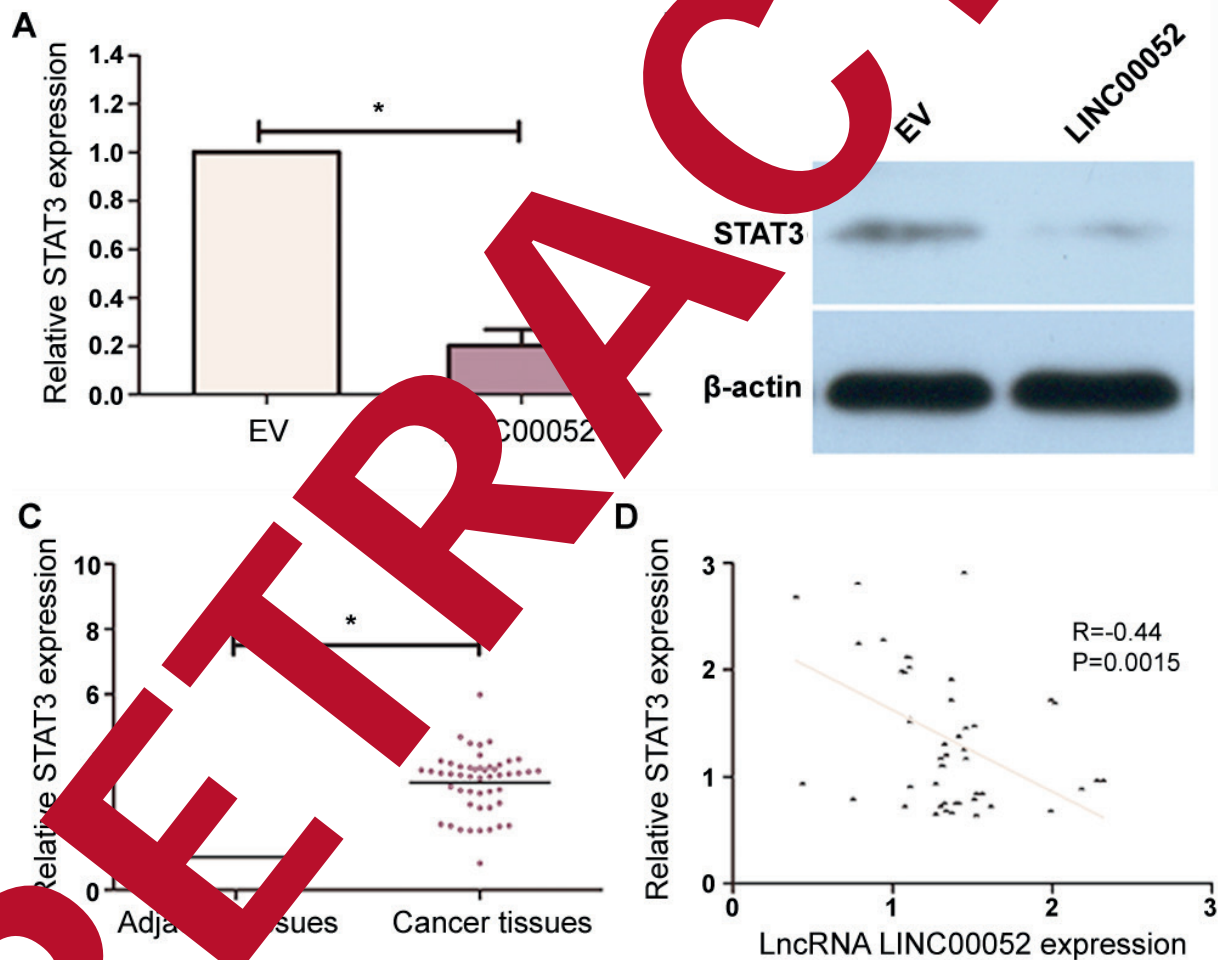


Fig 3. Correlation between LINC00052 and STAT3. **A**, QRT-PCR results showed that STAT3 expression was lower in LINC00052 lentiviruses (LINC00052) group compared with the empty vector (EV) group. **B**, Western blot assay revealed that STAT3 protein expression decreased in LINC00052 lentiviruses (LINC00052) group compared with the empty vector (EV) group. **C**, STAT3 was significantly upregulated in cervical cancer tissues compared with adjacent tissues. **D**, The linear correlation between the expression level of STAT3 and LINC00052 in cervical cancer tissues. The results represent the average of three independent experiments. Data are presented as the mean ± standard error of the mean. * $p < 0.05$.

by regulating expressions of downstream target genes²⁰. Overexpression of STAT3 promotes tumor progression and metastasis of ovarian cancer cells, highlighting a potential therapeutic target for ovarian cancer²¹. Moreover, inhibited by WP1066, the STAT3 signaling pathway depresses the growth and invasiveness of bladder cancer cells²². In the present study, mRNA and protein expressions of STAT3 were downregulated *via* overexpressing LINC00052. STAT3 expression was higher in cervical cancer tissues. Moreover, STAT3 expression in cervical cancer tissues was negatively related with LINC00052 expression. All the above results suggested that LINC00052 might repress tumorigenesis of cervical cancer *via* STAT3.

Conclusions

We identified that LINC00052 was remarkably downregulated and was correlated to disease-free survival of cervical cancer patients. Besides, LINC00052 could suppress cell growth, proliferation and invasion of cervical cancer cell by regulating STAT3. LINC00052 may serve as a therapeutic target for cervical cancer.

Conflict of Interests

The Authors declare that they have no conflicts of interests.

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