

LncRNA LUCAT1 promotes growth, migration, and invasion of oral squamous cell carcinoma by upregulating PCNA

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Abstract. – **OBJECTIVE:** Recent studies have revealed the important role of long noncoding RNAs (lncRNAs) in the progression of tumor genesis. This study aims to identify the role of lncRNA LUCAT1 functions in the progression of OSCC (oral squamous cell carcinoma). **DESIGN:** Long noncoding RNA, LUCAT1, Oral squamous cell carcinoma, PCNA.

PATIENTS AND METHODS: Relationship between expression of lncRNA LUCAT1 in OSCC tissues and 50 paired tissue samples was detected by quantitative Real-time polymerase chain reaction (qRT-PCR). Morphological function of LUCAT1 in OSCC cells was identified by performing transwell assay, wound healing assay and proliferation assay in vitro. The underlying mechanism was explored by qRT-PCR and Western blot.

RESULTS: LUCAT1 expression was remarkably downregulated in OSCC tissues when compared with that in adjacent normal samples. Moreover, proliferation, invasion and migration of OSCC cells were inhibited after knockdown of LUCAT1 in vitro. Knockdown of LUCAT1 downregulated PCNA in OSCC cells at mRNA and protein level in vitro. Besides, PCNA expression in OSCC cells was positively correlated with the expression of LUCAT1.

CONCLUSIONS: Knockdown of LUCAT1 could inhibit migration, invasion and proliferation capacities of OSCC cells through downregulating PCNA, which may offer a new therapeutic intervention for OSCC patients.

Introduction

Oral cancer is the sixth most prevalent cancer in the world, and it ranks the third most common in developing countries¹. Oral squamous cell carcinoma (OSCC) is the main subtype of oral cancer, contributing to 3% of the newly diagnosed clinical cancer cases². Although the rapid development of diagnosis and treatment methods for OSCC has been achieved², the overall 5-year survival rate of OSCC patients still remains lower than 50%. Therefore, it is essential and urgent to find out novel molecular markers to improve the treatment efficacy of OSCC. Long non-coding RNA (lncRNA) is a cluster of non-coding RNA transcripts with over 200 nucleotides (nt) in length and it lacks the ability of encoding proteins. Evidence shows that lncRNAs act as vital regulators in many biological behaviors, including carcinogenesis, apoptosis, proliferation and metastasis in cancer. For example, lncRNA OR3A4 is upregulated in breast cancer, which may

be a novel prognostic marker and therapeutic target³. Activated by H3K27, lncRNA CCAT1 promotes cell proliferation and migration in esophageal squamous cell carcinoma through regulating SPRY4 and HOXB13⁴. lncRNA MALAT1 stimulates the cell migration and invasion in hepatocellular carcinoma by sponging miR-204 to upregulate SIRT1⁵. By suppressing p53 signal pathway, lncRNA ROR facilitates cell proliferation, invasion and chemoresistance in nasopharyngeal carcinoma⁶. Moreover, knockdown of lncRNA CRNDE-h is reported to be associated with poor prognosis of colorectal cancer, which might be used as a novel serum-based biomarker for diagnosis of colorectal cancer⁷. However, the potential influence of lncRNA LUCAT1 on the development of OSCC remains unexplored. In the present study, it is revealed that the expression level of lncRNA LUCAT1 was remarkably upregulated in OSCC samples. Moreover, functional experiments revealed that knockdown of LUCAT1 depressed cell proliferation, invasion and migration capacities of OSCC cells. Furthermore, we discovered that lncRNA LUCAT1 mediated the progression of OSCC by promoting PCNA.

Patients and Methods

Tissue Specimens

Paired OSCC tissues and adjacent non-tumorous tissues (≥ 5 cm away from the tumor site) were sequentially resected from 50 OSCC patients during July 2015 and December 2017 in the Second Affiliated Hospital of Jiamusi University in Heilongjiang Province. The Ethics Committee of Affiliated Stomatological Hospital of Jiamusi University in Heilongjiang Province approved this study protocol. All participants provided written informed consent.

OSCC Cells and Cell Transfection

Human OSCC cell lines Tca8113, TSCCA, CAL-27, C3-9 and normal cervical epithelium cell line NHOK-1 were provided by Chinese Academy of Science (Shanghai, China). Cells were cultured in Roswell Park Memorial Institute-1640 (RPMI-1640; Hyclone, South Logan, UT, USA) containing 10% fetal bovine serum (FBS; Invitrogen Life Technologies, Carlsbad, CA, USA), and 1% penicillin in 5% CO₂ incubator at 37°C. Lentivirus expressing short-hairpin RNA (shRNA) directed against LUCAT1 were provided by GenePharma (Shanghai, China). cDNA encoding LUCAT1 was amplified and inserted into pcDNA3.1 (Invitrogen, Carlsbad, CA, USA). Next, we transfected the synthesized

pcDNA3.1 into OSCC cells with Lipofectamine 2000 (Invitrogen, Carlsbad, CA, USA). Transfection efficacy was verified by qRT-PCR.

RNA Extraction and qRT-PCR

Total RNA from tissues and cells were extracted using TRIzol reagent (Invitrogen, Carlsbad, CA, USA). The total RNA was reversely transcribed to cDNA through reverse transcription Kit (TaKaRa Biotechnology Co., Dalian, China). Thermocycling conditions as follows: 95°C for 2 min, followed by 40 cycles at 95°C for 5 s, and 60°C for 30 s. Primers used for qRT-PCR were as follows: LUCAT1 forward 5'-CCTATCCCGTCTCTAAGA-3' and reverse 5'-ACTTCTGCTAAACGTGCG-3', glyceraldehyde 3-phosphate dehydrogenase (GAPDH), forward 5'-CCAAATCAGATGGGCAATGCTG-3' and reverse 5'-ATGGCATGGACTGTTCATTCA-3'. The thermal cycle was as follows: 95°C for 30 s, followed by 40 cycles at 95°C for 5 s and 60°C for 35 s. 2^{-ΔΔCt} method was utilized for calculating relative expression.

Western Blot

Total proteins were collected from cells via immunoprecipitation assay (RIPA) buffer (Beyotime, Shanghai, China) and then quantified by bicinchoninic acid (BCA) protein quantification kit (Pierce, Rockford, IL, USA). The target proteins were separated by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE). Membranes were incubated with primary antibodies after loading on the polyvinylidene difluoride (PVDF) membrane (Millipore, Billerica, MA, USA). Then rabbit anti-GAPDH and rabbit anti-PCNA were used for incubation. Pierce electrochemiluminescence (ECL) was utilized for visualizing Western blotting substrate immunoreactive bands (Santa Cruz Biotechnology, Santa Cruz, CA, USA).

Cell Proliferation Assay

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

Wound Healing Assay

Cells seeded into 6-well plates were cultured in RPMI-1640 medium overnight. After scratch-

ing with a plastic tip, cells were cultured in serum-free RPMI-1640. Wound closure was detected at the appointed time points. Each assay was independently repeated for three times.

Transwell Assay

Twenty-four hours after transfection, 2×10^5 cells in 100 μ L of serum-free RPMI-1640 were applied in the top side of an 8- μ m Transwell chamber (Corning, Corning, NY, USA) pre-coated with 50 μ g Matrigel (BD Biosciences, Franklin Lakes, NJ, USA). RPMI-1640 containing 20% fetal bovine serum (FBS) was added to the bottom chamber. After 24 h, cells were fixed in methanol for 30 min and stained by hematoxylin for 20 min. An inverted microscope ($\times 20$) was utilized for counting migrated and invaded cells in three random fields.

Statistical Analysis

Statistical analysis was conducted by Statistical Product and Service Solutions (SPSS) 18.0 (SPSS Inc., Chicago, IL, USA). Chi-square test and Student *t*-test were performed to analyze categorical data or measurement data, respectively. Kaplan-Meier curve was introduced for survival analysis. Data were presented by mean (Standard Deviation). It was considered statistically significant when $p < 0.05$.

Results

Expression Level of LUCAT1 in OSCC Tissues and Cells of OSCC

First, qRT-PCR was conducted for detecting LUCAT1 expression in 50-paired OSCC tissues.

LUCAT1 was significantly upregulated in tumor tissues than that in adjacent tissues (Figure 1A). When compared with the expression in normal human oral keratinocyte NHOK, LUCAT1 level was significantly higher in OSCC cells (Figure 1B).

Knockdown of LUCAT1 Repressed Cell Proliferation In Vitro

According to LUCAT1 expression in cancer cells, we chose SCC-9 cells for establishing the LUCAT1 knockdown model. The LUCAT1 shRNA virus (LUCAT1) and the empty vector were synthesized, and their transfection efficiency in SCC-9 cells was determined by qRT-PCR (Figure 2A). Furthermore, CCK-8 assay showed that proliferation of OSCC cells was inhibited after LUCAT1 knockdown (Figure 2B).

Knockdown of LUCAT1 Repressed Cell Migration and Invasion In Vitro

Wound healing assay revealed that knockdown of LUCAT1 inhibited OSCC cell migration (Figure 3A). Furthermore, transwell assay showed that invasion of SCC cells was inhibited after LUCAT1 knockdown (Figure 3B).

Knockdown of LUCAT1 Promoted OSCC Tumorigenesis In Vivo

QRT-PCR results further demonstrated that the mRNA expression of PCNA was downregulated in OSCC cells transfected with LUCAT1 shRNA (Figure 4A). Western blot analysis obtained the same trend at the protein level (Figure 4B). To explore the interaction between LUCAT1 and PCNA, the expression level of PCNA was detected in OSCC tissues. PCNA expression was marked

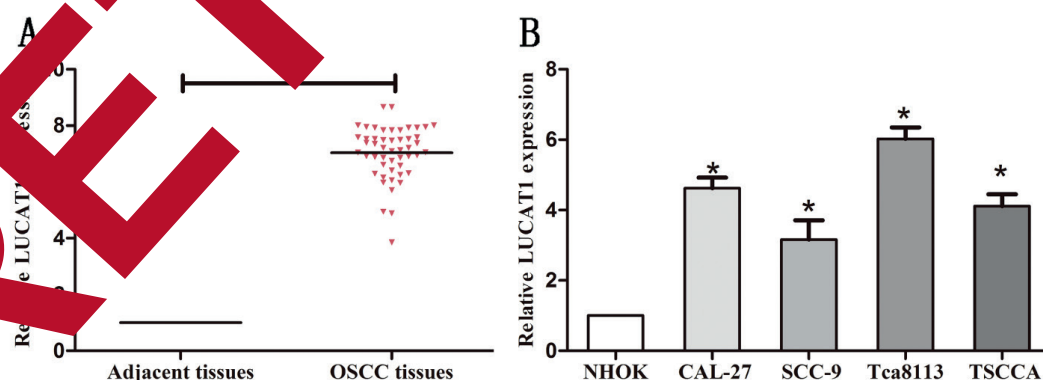


Figure 1. Expression levels of LUCAT1 were increased in OSCC tissues and cell lines. **A**, LUCAT1 expression was significantly increased in the OSCC tissues compared with adjacent tissues. **B**, Expression levels of LUCAT1 relative to GAPDH were determined in the human OSCC cell lines and normal human oral keratinocyte (NHOK) by qRT-PCR. Data are presented as the mean $\pm$ standard error of the mean. * $p < 0.05$.

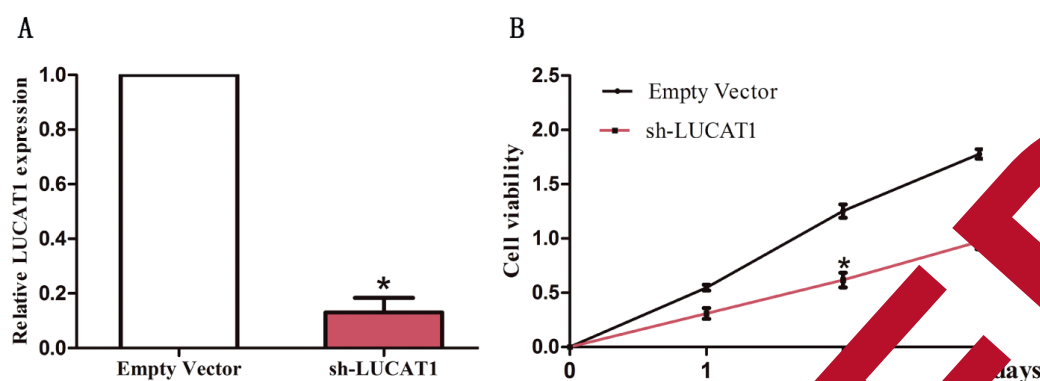


Figure 2. Knockdown of LUCAT1 inhibited OSCC cell proliferation. **A**, LUCAT1 expression in OSCC cells transfected with empty vector or LUCAT1 lentivirus (sh-LUCAT1) was detected by qRT-PCR. GAPDH was used as internal control. **B**, CCK8 assay showed that knockdown of LUCAT1 significantly repressed cell proliferation in SCC-9 OSCC cells. The results represent the average of three independent experiments (mean $\pm$ standard error of the mean). * $p < 0.05$.

edly upregulated in OSCC tissues when compared with that in adjacent tissues (Figure 4C). The results of linear correlation analysis showed that in OSCC tissues, the expression of PCNA was positively correlated to LUCAT1 expression (Figure 4D).

Discussion

Evidence demonstrated that lncRNAs participate in diverse biological behaviors in the progression of OSCC, including cell growth, metastasis and invasion. For instance, lncRNA HOTAIR facilitates cell invasion and metastasis in OSCC by indirectly recruiting EZH2 and depressing E-cadherin¹⁰. By modulating SF1 and suppressing expression level of miR-184, lncRNA

UCA1 accelerates cell proliferation and chematin-resistance in oral squamous cell carcinoma⁹. LncRNA MALAT1, which may be an important prognostic biomarker and therapeutic target in OSCC, promotes the progression of OSCC by inducing epithelial-mesenchymal transition¹⁰. LncRNA FTH1P3 enhances the development of OSCC by modulating the expression of fizzled 5¹¹. In addition, lncRNAAC132217.4 promotes cell metastasis in OSCC by regulating IGF2 expression, which is further modulated by KLF8¹². Lung cancer associated transcript 1 (LUCAT1) was firstly found in the airway epithelium of cigarette smokers, which is a cluster of transcripts located on chromosome 5¹³. Recently, lncRNA LUCAT1 is widely studied for its important role in the progression of tumorigenesis. For instance, through inhibiting

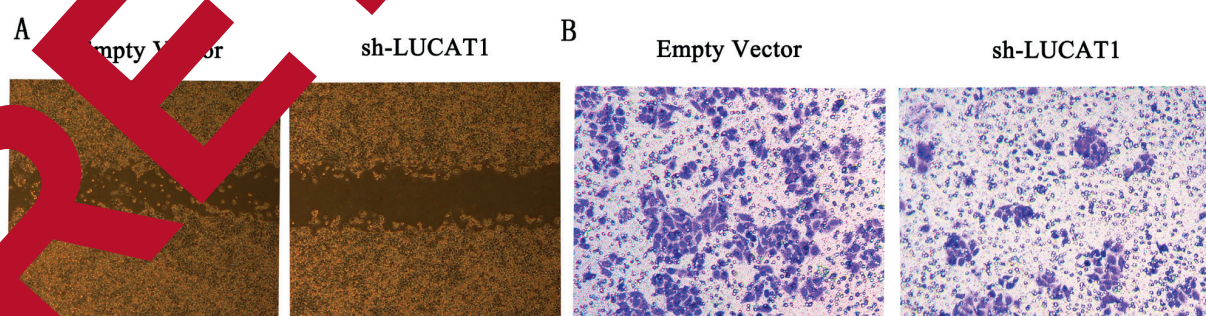


Figure 3. Knockdown of LUCAT1 repressed OSCC cell migration and invasion. **A**, Wound healing assay showed that the migrated length of cells in LUCAT1 lentivirus group was significantly decreased compared with empty control group in SCC-9 OSCC cells. **B**, Transwell assay showed that knockdown of LUCAT1 significantly repressed cell invasion in SCC-9 OSCC cells. The results represent the average of three independent experiments (mean $\pm$ standard error of the mean). * $p < 0.05$.

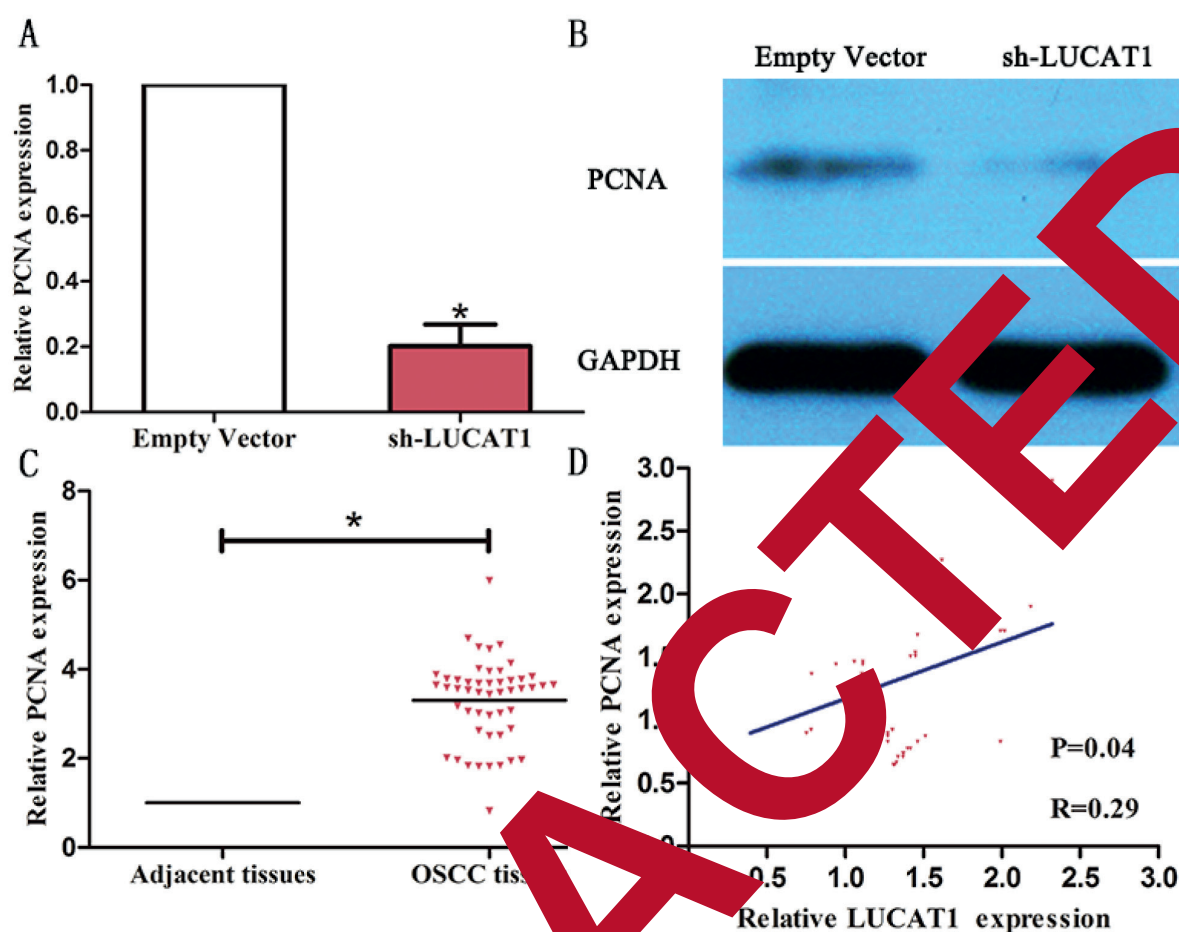


Figure 4. Interaction between PCNA and LUCAT1 in OSCC. **A**, The RNA expression level of PCNA in LUCAT1 cells was significantly decreased compared with control cells (Empty Vector) in SCC-9 cells. **B**, Protein expression of PCNA was decreased after knockdown of LUCAT1 in SCC-9 cells. **C**, PCNA was significantly upregulated in OSCC tissues compared with adjacent tissues. **D**, The linear correlation between the expression level of PCNA and LUCAT1 in OSCC tissues. The results represent the average of three independent experiments and are presented as the mean $\pm$ standard error of the mean. * $p < 0.05$.

the expressions of p21 and p57. LncRNA LUCAT1 knockdown promotes cell proliferation in human non-small lung cancer¹⁴. Through regulating the stability of Dicer1 and depressing the expressions of tumor suppressors, lncRNA LUCAT1 promotes the tumorigenesis of esophageal squamous cell carcinoma formation and tumor metastasis¹⁵. After knockdown of lncRNA LUCAT1, cell viability and invasion are suppressed¹⁶. lncRNA LUCAT1 enhances malignancy of ovarian cancer and promotes its progression through regulating miR-612/FOXO13 pathway¹⁷. Moreover, the expression of lncRNA LUCAT1 is negatively correlated to the prognosis of clear cell renal cell carcinoma and positively related to malignancy of the tumor¹⁸. In the present study, LUCAT1 was found to be upregulated in both OSCC tissues

and cells. Furthermore, LUCAT1 knockdown inhibited the abilities of cell growth, migration and invasion. These data indicated that LUCAT1 functioned as an oncogene and promoted the tumorigenesis of OSCC. Proliferating cell nuclear antigen (PCNA) is found in cancer cells and proliferating cells. Numerous researches have confirmed that PCNA is directly correlated to the prognosis, tumor stage and tumor differentiation. For instance, the positive expression rate of PCNA was 73% in breast cancer, indicating the important clinical significance in evaluating the prognosis of breast cancer¹⁹. The expression level of PCNA is significantly higher in colorectal cancer, especially in those with liver metastasis. This may help to evaluate liver metastasis in patients with colorectal cancer²⁰. Overexpression of PCNA relieves the repression of miR-363-3p on cell proliferation

and colony formation in lung adenocarcinoma²¹. In addition, upregulation of PCNA is closely related to poor prognosis of patients with osteosarcoma, which may be a potential biomarker²². In our study, PCNA was downregulated after LUCAT1 knockdown *in vitro*. PCNA was remarkably upregulated in OSCC samples when compared with that in adjacent tissues. A positive correlation was discovered between PCNA and LUCAT1 expression in OSCC tissues. The above results revealed that LUCAT1 mediated OSCC progression *via* PCNA.

Conclusions

Our research suggests a new biomarker in the development of OSCC. lncRNA LUCAT1 promotes OSCC carcinogenesis *via* regulating PCNA and it may serve as a promising marker for OSCC in the future.

Conflict of Interests

The Authors declare that they have no conflict of interest.

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