

Long non-coding RNA OR3A4 promotes metastasis of ovarian cancer *via* inhibiting KLF6

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Abstract. – **OBJECTIVE:** Recently, long non-coding RNAs (lncRNAs) have attracted much attention for their roles in tumor progression. The aim of this study was to investigate the exact role of lncRNA OR3A4 in the development of ovarian cancer (OC), and to explore the possible underlying mechanism.

PATIENTS AND METHODS: OR3A4 expression in OC tissue samples was detected by Real-time quantitative polymerase chain reaction (qRT-PCR). Moreover, wound healing assay and transwell assay were performed to explore the effect of OR3A4 on the metastasis of OC. Furthermore, the underlying mechanism was explored by RT-qPCR and Western blot assay.

RESULTS: The expression level of OR3A4 in OC samples was significantly higher than that of adjacent tissues. Moreover, cell migration and invasion were significantly reduced after OR3A4 knockdown *in vitro*. Moreover, the mRNA and protein expressions of transcription factor 6 (KLF6) were remarkably increased after knockdown of OR3A4. Furthermore, the expression level of KLF6 was negatively correlated with the expression of OR3A4 in OC tissues.

CONCLUSION: Our results showed that OR3A4 could enhance cell metastasis and invasion *via* suppressing KLF6. Moreover, OR3A4 might be a potential therapeutic target for OC.

Key Words:

Long non-coding RNA, OR3A4, Ovarian cancer (OC), KLF6

Introduction

Ovarian cancer (OC) is one of the most common malignancies in women worldwide. It is reported that approximately 22,280 patients are newly diagnosed of OC in US. Meanwhile, al-

most 15.5% are estimated to die of OC in the same year. Due to the available tests, OC is often diagnosed at advanced stage, making it one of the leading causes of cancer-related death in females. The main interventions for OC include surgery, chemotherapy and radiotherapy. However, most patients develop resistance to chemotherapy or relapse after surgery. Furthermore, the prognosis of patients with OC is still dismal, with 5-year survival rate only 30%^{1,2}. Thus, the severe situation highlights the urgency of early detection and new therapeutic treatment for OC patients. Researches have indicated that long non-coding RNAs (lncRNAs) are closely involved in a variety of cellular activities. For example, lncRNA MSTO2P facilitates the proliferation and colony formation of gastric cancer cells indirectly by regulating the expression of miR-335³. LncRNA SNHG7 promotes epithelial-to-mesenchymal transition and tumor proliferation in osteosarcoma by regulation of miR-34a⁴. LncRNA PCAT-1 plays an important role in the tumorigenesis of hepatocellular carcinoma *via* modulating TP53-miR-215-PCAT-1-CRKL axis⁵. Zhang et al⁶ has indicated that up-regulation of lncRNA FENDRR inhibits the proliferation and malignancy of non-small cell lung cancer by serving as a sponge of miR-761. In addition, lncRNA RUNX1-IT1 inhibits the migration and proliferation of colorectal cancer, acting as a tumor suppressor⁷. However, the exact role of lncRNA OR3A4 in the progression of OC, as well as the underlying molecular mechanism has not been fully elucidated. In this study, we found that OR3A4 was highly expressed in OC tissues. Moreover, OR3A4 significantly promoted the migration and invasion of OC cells *in vitro*. Moreover, our further experiments explored the underlying mechanism of how OR3A4 functioned in OC development.

Patients and Methods

Cell Lines and Clinical Samples

A total of 52 OC tissues were collected from patients who received surgery at Xinhua Hospital Affiliated to Dalian University between June 2015 and July 2018. No radiotherapy or chemotherapy was performed for any patients before the operation. All fresh tissues were stored at -80°C for subsequent use. This study was approved by the Ethics Committee of Xinhua Hospital Affiliated to Dalian University. Signed written informed consents were obtained from all participants before the study and operation.

Cell Culture

Three human OC cell lines (A2780, SKOV3 and OVCAR-3) and one normal ovarian cell line (ISOE80) were cultured in Dulbecco's modified Eagle's medium (DMEM) (Gibco, Rockville, MD, USA) containing 10% fetal bovine serum (FBS; Life Technologies, Gaithersburg, MD, USA) and penicillin. Besides, all cells were maintained in an incubator with 5% CO_2 at 37°C .

Cell Transfection

After synthesis, cDNA oligonucleotides targeting OR3A4 (OR3A4/shRNA) were cloned into pGPH1/Neo vector (GenePharma, Shanghai, China). 293T cells were used for packaging OR3A4 shRNA and empty vector, which were then transfected into OC cells. 48 h after cell transfection, the expression level of OR3A4 in cells was detected using Real-time quantitative polymerase chain reaction (qRT-PCR).

RNA Extraction and RT-qPCR

Total RNA was extracted according to the instructions of TRIzol reagent (Invitrogen, Carlsbad, CA, USA). Subsequently, extracted total RNA was reverse transcribed to complementary deoxyribonucleic acids (cDNAs) in strict accordance with the instructions of the RT-PCR Kit (TaKaRa Biotechnology Co., Ltd., Dalian, China). Primers used in this study are as follows: OR3A4, forward 5'-GATCCCTCTCTAAGAA-3' and reverse 5'-ATCTGCAAAAACGTGCTG-3'; glyceraldehyde phosphate dehydrogenase (GAPDH), forward 5'-CCAAATCAGATGGGGCAATGCT-3' and reverse 5'-TGATGGCATGGACTGTGCTCA-3'. Thermal cycle was as follows: 30 s at 95°C , 5 s for 40 cycles at 95°C , and 35 s at 60°C .

Western Blot Analysis

Total proteins were extracted from cells via radioimmunoprecipitation assay (RIPA) buffer. After that, the concentration of extracted protein was quantified by the ninhydrinic acid method (Beyotime, Shanghai, China). Target protein samples were separated by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and transferred onto polyvinylidene difluoride (PVDF) membrane (Millipore, Billerica, MA, USA). Next, the membranes were incubated with primary antibodies of rabbit anti-OR3A4 (Cell Signaling Technology, Danvers, MA, USA) and rabbit anti-KLH (Muppel-like factor) (Cell Signaling Technology, Danvers, MA, USA). On the next day, the membranes were incubated with corresponding secondary antibodies. Chemiluminescent film was applied for assessment of protein expression with Image J software (NIH, Bethesda, MD, USA).

Wound Healing Assay

Cells were seeded into 6-well plates and cultured in DMEM medium overnight. After scratching with a plastic tip, the cells were cultured in serum-free DMEM medium. Wound closure was observed 48 h later. Each assay was independently repeated in triplicate.

Transwell Assay

5×10^4 cells in 200 μL serum-free DMEM were seeded into the upper chamber of an 8- μm pore size insert (Millipore, Billerica, MA, USA) coated with or without 50 μg Matrigel (BD Biosciences, Franklin Lakes, NJ, USA). Meanwhile, the lower chamber was added with DMEM and FBS. 48 h later, after wiped by cotton swab, the top surface of the chamber was immersed with precooling methanol for 10 min. Then the cells were stained with crystal violet for 30 min. Three fields randomly selected for each sample, and the number of migrated and invaded cells was counted.

Statistical Analysis

Statistical Product and Service Solutions (SPSS) 20.0 (IBM, Armonk, NY, USA) was used for all statistical analysis. Data were presented as mean \pm SD (Standard Deviation). Student's *t*-test was utilized to compare the difference between two groups. $p < 0.05$ was considered statistically significant.

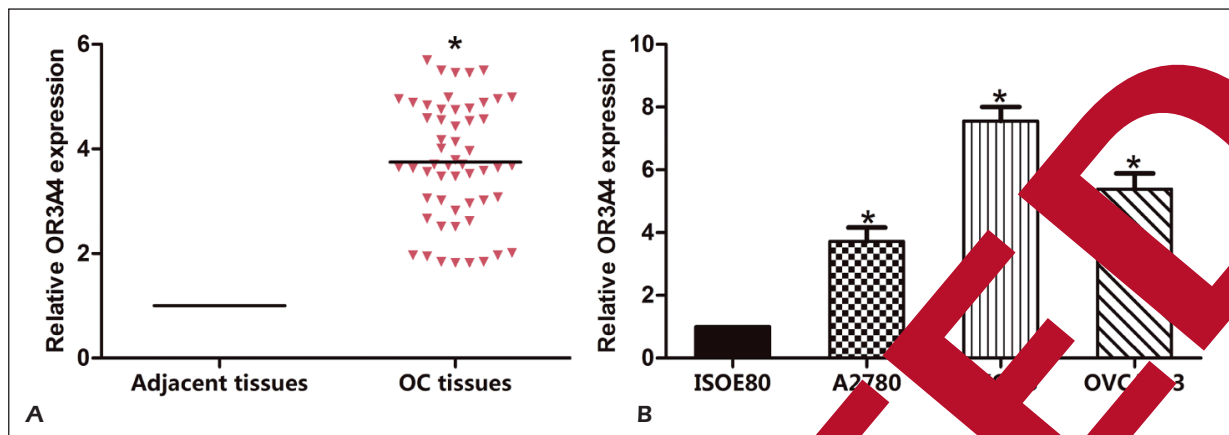


Figure 1. Expression level of OR3A4 was significantly increased in OC tissues and cell lines. **A**, OR3A4 expression was significantly increased in OC tissues when compared with adjacent tissues. **B**, Expression level of OR3A4 relative to GAPDH were determined in human OC cell lines and ISOE80 by RT-qPCR. Data were presented as mean \pm standard error of the mean. * $p < 0.05$.

Results

Expression of OR3A4 in OC Tissues and Cells

First, RT-qPCR was conducted to detect OR3A4 expression in 52 OC patients' tissues and 3 OC cell lines. Results demonstrated that OR3A4 expression was significantly up-regulated in OC tissue samples (Figure 1A). Besides, the expression of OR3A4 in OC cells was significantly higher than that of ISOE80 cells (Figure 1B).

Knockdown of OR3A4 Inhibits OC Cell Migration and Invasion

In our study, SKOV3 cells were chosen for knockdown of OR3A4. After transfection, RT-qPCR was utilized to verify the expression of OR3A4 (Figure 2A). Results of wound healing assay revealed that after OR3A4 knockdown, the migration ability of SKOV3 cells was significantly repressed (Figure 2B). Meanwhile, Transwell assay also in-

dicated that after OR3A4 knockdown in OC cells, the number of migrated cells was remarkably decreased (Figure 3A and 3B). Furthermore, the invasion of OC cells was remarkably decreased after OR3A4 knockdown (Figure 3C and 3D).

Interaction between KLF6 and OR3A4 in OC

RT-qPCR results showed that compared with empty vector group, the expression level of KLF6 in OC cells of OR3A4/shRNA group was significantly higher (Figure 4A). Western blot assay found that after OR3A4 knockdown, the protein expression of KLF6 was significantly upregulated (Figure 4B). Our results further illustrated that KLF6 expression in OC tissues was significantly lower when compared with that of adjacent tissues (Figure 4C). Subsequent correlation analysis demonstrated that the expression level of KLF6 was negatively correlated with OR3A4 expression in OC tissues (Figure 4D).

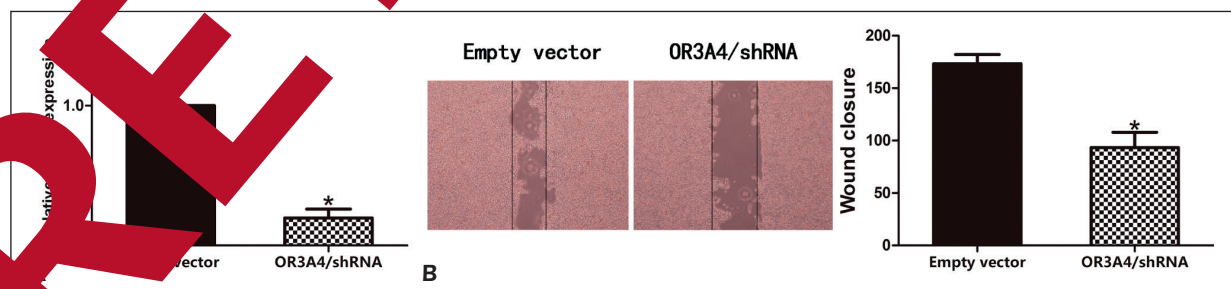


Figure 2. Wound healing assay showed that knockdown of OR3A4 inhibited OC cell migration. **A**, OR3A4 expression in SKOV3 cells transfected with OR3A4/shRNA and empty vector was detected by RT-qPCR, respectively. GAPDH was used as an internal control. **B**, Wound-healing assay showed that knockdown of OR3A4 significantly repressed the migration of OC cells. The results represented the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$.

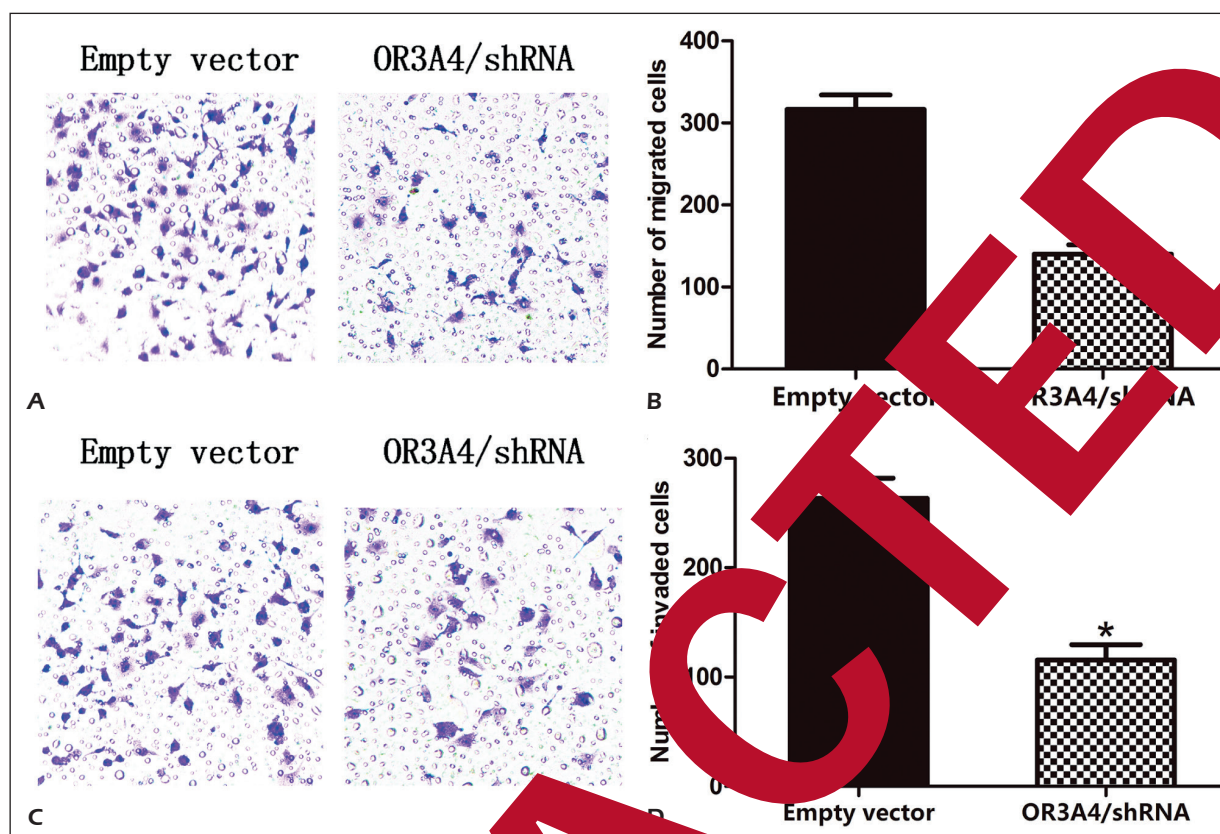


Figure 3. Transwell assay showed that knockdown of OR3A4 in OC cells significantly inhibited cell migration and invasion. **A**, Representative pictures of migrated cells in OR3A4/shRNA group and empty vector group. **B**, The number of migrated cells was significantly decreased after knockdown of OR3A4 in OC cells. **C**, Representative pictures of invaded cells in OR3A4/shRNA group and empty vector group. **D**, Transwell assay showed that number of invaded cells was significantly decreased after knockdown of OR3A4 in OC cells. The results represent the average of three independent experiments (mean \pm standard error of the mean). * $p < 0.05$.

Discussion

Evidence indicates that lncRNAs are an important regulator in the progression of OC, which can be used as a potential biomarker and therapeutic target for OC. For instance, silencing of lncRNA MNX1-AS1 suppresses the proliferation and migration of OC cells, which may be a potential target for OC. LncRNA BACE1-AS inhibits the proliferation and invasion of OC stem cells, functioning as a novel target for OC treatment⁹. LncRNA HOXA1 facilitates the proliferation and migration of serous OC, which is associated with the prognosis of patients¹⁰. Through regulation of epithelial-mesenchymal transition, downregulation of lncRNA SFY-1 enhances the metastasis of OC¹¹. In addition, lncRNA ElnRNA1, as an oncogene in the proliferation of epithelial OC cells, is significantly upregulated by estrogen¹². Olfactory receptor family 3 subfamily A member 4 (OR3A4) (Accession Number: NR_024128.1) is a novel lncRNA that

has been widely explored recently. It is abnormally expressed in several cancers, which is related to cancer progression. For instance, upregulation of OR3A4 facilitates the proliferation and metastasis of breast cancers *via* epithelial-mesenchymal transition¹³. OR3A4 promotes the proliferation and tumorigenesis of gastric cancer, serving as a potential therapeutic strategy¹⁴. In this study, we found that OR3A4 was significantly upregulated in OC tissues and cells. Besides, after OR3A4 knockdown, the migration and invasion of OC cells were found remarkably inhibited. All above results indicated that OR3A4 promoted tumorigenesis of OC and might act as an oncogene. KLF6 (Krüppel-like factor 6) functions as a tumor suppressor in a diverse of tumors by regulating various biological processes. For example, through attenuating the activity of MMP-9 and the expression level of mesenchymal markers, overexpression of KLF6 inhibits the migration and invasion of oral cancer cells¹⁵. KLF6-E2F1 axis is activated in aggressive clear cell renal

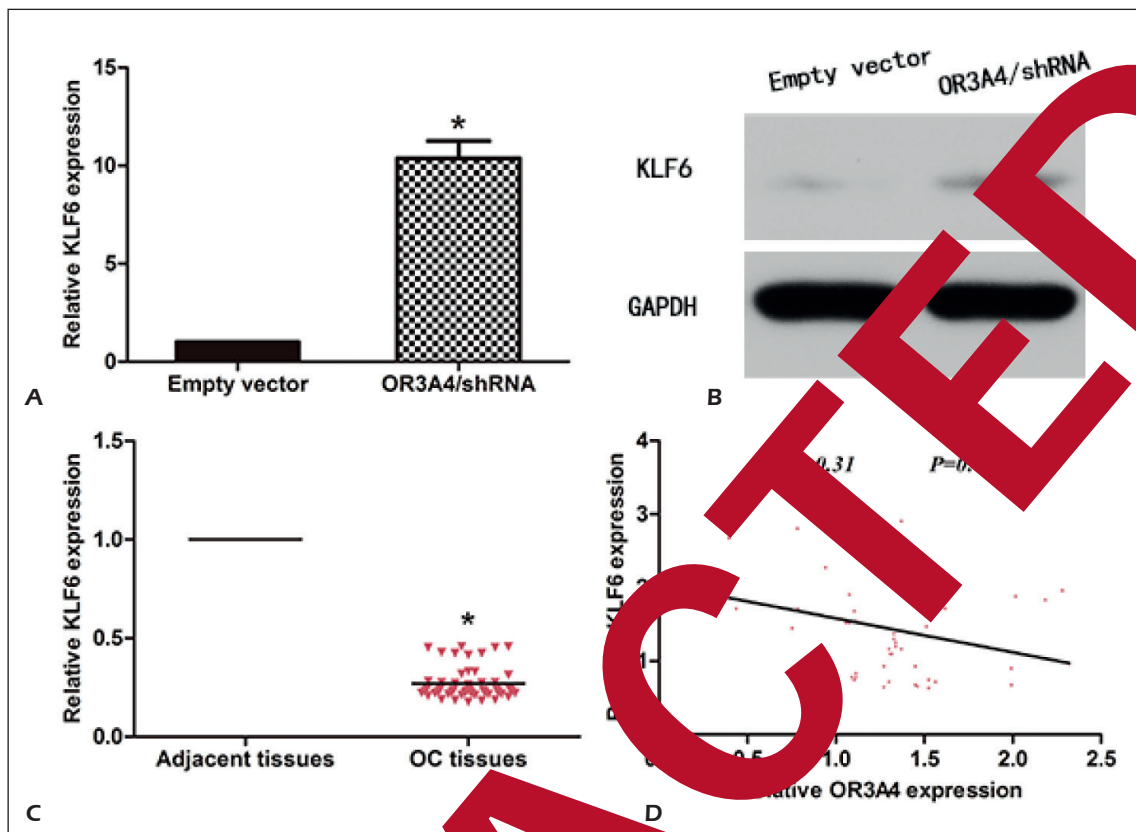


Figure 4. Interaction between OR3A4 and KLF6. **A**, qPCR results showed that KLF6 expression in OR3A4/shRNA group was significantly higher than empty vector group. **B**, Western blot assay revealed that protein expression of KLF6 in OR3A4/shRNA group was remarkably increased when compared with empty vector group. **C**, KLF6 was significantly downregulated in OC tissues when compared with adjacent tissues. **D**, Negative correlation between the expression level of KLF6 and OR3A4 in OC tissues. The results represented the mean of three independent experiments. Data were presented as mean \pm standard error of the mean. * $p < 0.05$.

cell carcinoma. Meanwhile, KLF6 functions as a tumor suppressor via transcriptional repression of E2F1¹⁶. KLF6 is downregulated in glioblastomas, which is related to poor prognosis of patients through targeting KLF6. Moreover, by targeting KLF6, overexpression of miR-619 promotes growth, proliferation and migration of epithelial OC¹⁸. Furthermore, KLF6 expression could be upregulated after knockdown of OR3A4. Moreover, KLF6 expression in OC tissues was negatively correlated with OR3A4 expression. All the above results suggested that OR3A4 might promote tumorigenesis of OC through targeting KLF6.

Conclusions

We showed that OR3A4 could enhance OC cell migration and invasion through targeting KLF6. These findings suggested that OR3A4 might contribute to therapy for OC as a candidate target.

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Conflict of Interests

The authors declare that they have no conflict of interest.

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