PORTLAND PRESS

Research Article

Specific expression of lncRNA RP13-650J16.1 and TCONS_00023979 in prostate cancer

Xiaochen Zhou[1],*, Qiong Chen[2],*, Haolin Wang[3],*, Cheng Zhang[1], Bin Fu[1] and Gongxian Wang[1]

[1]Department of Urology, The First Affiliated Hospital of Nanchang University, Nanchang 330006, Jiangxi, China; [2]Department of Urology, Changzheng Hospital, Second Military Medical University, Shanghai 200003, China; [3]Department of Urology, Yichun People's Hospital, Yichun 336000, Jiangxi, China

Correspondence: Gongxian Wang (wanggx-mr@126.com)

OPEN ACCESS

The aim of the present study was to explore the expression profile and the potential regulatory mechanism of two long non-coding RNAs (lncRNAs) (RP13-650J16.1 and TCONS_00023979) in prostate cancer (PCa). Expression profile of lncRNAs in PCa and para-cancerous tissues were investgated by the high-throughput gene chip technology. Specific siRNA of RP13-650J16.1 or TCONS_00023979 was transfected into DU145 cells. Then, the relative expression of RP13-650J16.1, receptor-associated coactivator 3 (RAC3), promyelocytic leukemia (PML), and TCONS_00023979 was detected by quantitative real-time PCR and Western blotting. MTT assay was used to detect the proliferation of DU145 cells. The migration ability of DU145 cells was measured by Transwell chambers. Single cell proliferation and clonogenic ability were detected by plate clone formation assay. RP13-650J16.1 and RAC3 expression was up-regulated, and TCONS_00023979 and PML expression was down-regulated in PCa tissues. Silencing RP13-650J16.1 could decrease RAC3 expression, and knockout of TCONS_00023979 also reduced PML expression. Moreover, the ability of proliferation, migration, and colony formation of DU145 cells was decreased after transfected with si-RP13-650J16.1, while these abilities were increased after transfected with si-TCONS_00023979. Collectively, our findings demonstrated that RP13-650J16.1 might be an oncogene and TCONS_00023979 might be an antioncogene in PCa.

Introduction

Prostate cancer (PCa) is the most common malignant cancer in Western developed countries. The latest cancer statistics from the American Cancer Society estimates that the incidence of PCa is the first highest amongst all men's malignancies in the United States in 2016, with the death rate at the second place [1]. Relatively, the incidence and mortality of PCa are lower in China. However, with the ageing of the population, and changes in diet and lifestyle, PCa is becoming a serious urinary malignancy affecting the health of Chinese males [2]. Data show that China's PCa has 60,300 new cases and 26,600 deaths in 2015 [2].

It has appeared a lot of studies about PCa, but the pathogenesis of PCa has not yet been fully elucidated. With the further development of research and biotechnology, especially the emergence of high-throughput sequencing technology, a large number of non-coding RNAs (ncRNAs) were found, and these ncRNAs are an important part of the complex regulatory network in the body [3,4]. ncRNA includes short non-coding RNA (sncRNA) and long non-coding RNA (lncRNA). lncRNA, a class of RNA with a length greater than 200 nts, does not encode proteins, but regulates the expression levels of genes at various levels in the form of RNA [5]. Studies found that many lncRNA expression levels have time or space specificity, that is, there are differences in the expression levels are different at different stages of cell differentiation and development or in different tissue cell types [6,7]. Therefore, lncRNAs may be related to the differentiation of cells and the growth and development of individuals. Moreover, increasing evidence

* These authors contributed equally to this work

1

reveals that lncRNAs have been involved in various levels of cellular physiological activity from chromatin structure change, transcriptional regulation, post-transcriptional regulation, and signal communication between nuclei and inside and outside the nucleus [8-10]. For example, lncRNA-CYTOR could involve colorectal cancer progression by interacting with NCL and Sam68 [11]; lncRNA-NEAT1 could accelerate lung adenocarcinoma deterioration by reducing *miR-193a-3p* [12].

At present, lncRNA which has been found to be specifically associated with PCa includes PCA3, PCGEM1, PCAT family, and MALAT-1 [13-15]. This suggests that lncRNAs play a pivotal regulatory role in the pathogenesis of PCa. Up to now, thousands of lncRNAs have been discovered, and new lncRNAs have been constantly discovered and explored, but their regulation mechanisms of biological information have not yet been thoroughly interpreted [16].

In the study, we compared the lncRNA expression profiles between PCa tissues and paracancerous tissues by using the high-throughput gene chip technology, then selected RP13-650J16.1 and TCONS_00023979 as the research objects according to a series of screening conditions (the chip results, adjacent coding genes information analysis) and previous reports of the involvement of receptor-associated coactivator 3 (RAC3) and promyelocytic leukemia (PML) in PCa [17-21]. We explored their potential regulatory mechanism in PCa, aiming to find new key lncRNAs associated with PCa. This will be helpful for providing a new theoretical basis in the prevention and treatment of PCa.

Materials and methods
Materials
Six prostate gland tissues from six PCa patients were cryopreserved immediately after radical prostatectomy performed by author's group in the Department of Urology, the First Affiliated Hospital of Nanchang University. Paracancerous tissues were used as negative control. PCa cell lines (DU145) were purchased from the ATCC cell bank of the United States. The study protocol was approved by the Medical Ethics Committee of the First Affiliated Hospital of Nanchang University, and each participant was informed consent.

Detection of lncRNA expression profile
According to the manufacturer's protocol, total RNA was extracted from PCa tissues and paracancerous tissues by using TRIzol (Thermo Fisher Scientific, U.S.A.), then reverse transcription was performed by Reverse Transcription Kit (Thermo Fisher Scientific), and hybridized with lncRNA chip (LncRNA + mRNA Human Gene Expression Microarray V3.0, 4×180K; CapitalBio, Beijing, China). The chip was scanned using a chip scanner (Agilent, U.S.A.). Agilent Feature Extraction (V10.7) software and Agilent GeneSpring software was used to analyze the data.

Cell culture
Human PCa cell line DU145 was cultured in RPMI 1640 medium (Thermo Fisher Scientific) containing 10% fetal bovine serum (FBS, Gibco, U.S.A.) and 1% penicillin-streptomycin (Thermo Fisher Scientific) with 5% CO_2 at 37°C.

Cell transfection
The siRNA sequence was designed by Ribobio (Guangzhou, China). DU145 cells were cultured in three culture dishes (60 mm, 1×10^6 cells per dish) overnight to 60–70% confluency, then transfected with siRNA expression vector using Lipofectamine 2000 (Thermo Fisher Scientific) according to manufacturer's instructions.

Quantitative real-time PCR
The method for extracting total RNA was same as section 2.2. PCR amplification was carried out using cDNA as template. β-actin was used as internal control. The relative expression of RP13-650J16.1, RAC3, PML), and TCONS_00023979 was determined by $2^{-\Delta\Delta CT}$ method. The primers sequence was as follows:

RP13-650J16.1–F: 5′-TGCAAAAAGACGATGTGGTGG-3′
RP13-650J16.1–R: 5′-CTGAGAGATGATGGGCACAGG-3′
RAC3–F: 5′-TGGACGGGAAACCAGTCAAC-3′
RAC3–R: 5′-GACGTCAGTTTGGGGGGTAGG-3′
PML–F: 5′-TGGAGTCTGAGGAGGGGAA-3′
PML–R: 5′-ATCACCACAACGCGTTCCTC-3′
TCONS_00023979–F: 5′-TGAGCTCACAACTCCAACAAGG-3′
TCONS_00023979–R: 5′-CAGGATTGCCCACTCCTCAGTC-3′
β-actin–F: 5′-CATGTACGTTGCTATCCAGGC-3′
β-actin–R: 5′-CTCCTTAATGTCACGCACGAT-3′

Western blotting

The proteins from cells were extracted using RIPA Lysis Buffer (10 µl PMSF [100 mM] was added to 1ml RIPA Lysis Buffer). Two hundred microliters of RIPA Lysis Buffer was added to each culture dish and lysed on ice for 30 min. Then, the sample was centrifuged at 4°C for 10 min (16,000 g). The supernatant was stored at −20°C. The protein concentration of each sample was measured by BCA Protein Quantitative Kit (Invitrogen, U.S.A.) following to the manufacturer's recommendations. The proteins were separated by SDS/PAGE and transferred to nitrocellulose membrane (Thermo Fisher Scientific). The membranes were blocked in 5% skim milk for 1–2 h, then incubated with anti-RAC3 antibody, anti-BCL-2 antibody, anti-PML antibody, and anti-β-actin antibody (all at 1:1000 dilutions; Abcam, U.K.) overnight at 4°C. Finally, the membranes were incubated with secondary antibodies at room temperature for 1–2 h, and developed by ECI (Thermo Fisher Scientific).

Plate clone formation assay

The logarithmic phase cells were digested with 0.05% trypsin (1 ml). After centrifuged, the cell concentration was adjusted to 1×10^3 cells/ml. Two hundred microliters of cell suspensions were seeded into three culture dishes (60 mm, 200 cells per dish) and added complete medium to 10 ml. After cultured at 37°C and 5% CO_2 for 2–3 weeks, cells were washed with PBS for two-times. Then, cells were fixed in 5 ml methanol for 15 min, and dyed with Giemsa stain for 20 min. After that, washed away the stain and dried naturally. A transparent film with grids was placed under a culture dish and counted by naked eye or under a low power microscope.

MTT assay

This experiment was used to detect the influence of the interference of lncRNA expression on the proliferation of DU145 cells. Two hundred microliters of suspensions (1×10^4 cells/ml) were seeded into 96-well plates (five wells per plate, a total of five plates) and cultured at 37°C and 5% CO_2. On the second day, one plate was taken and added 5 mg/ml MTT solution (20 µl per well). After incubation at 37°C for 4 h, the supernatant was removed and 150 µl of dimethyl sulfoxide (DMSO, 1%) was added to each well, and then shook 10 min. Finally, the absorbance of each well was measured by a microplate reader (wavelength 492 nm), and the average value of five holes was calculated. The above operation was repeated at the following 5 days.

Transwell migration assay

The migration ability of DU145 cells was measured by Transwell chambers (Corning, U.S.A.). Fifty milligram per liter of Matrigel (Qcbio S&T, Shanghai, China) was coated in the upper chamber of Transwell and solidified at room temperature. Then, each well was added with serum free 1640 medium and cultured at 37°C. After 30 min of incubation, cells were digested with 0.05% trypsin and centrifuged at 1200 r/min for 3 min (removed supernatant). Five hundred microliters of medium containing 10% FBS was added into the lower layer of each hole in 24-well plates, and then put into Transwell. Two hundred microliters of cell suspensions (1×10^5 cells/ml) were seeded into Transwell chamber, and each group was repeated three samples. After incubated at 37°C and 5% CO_2 for 48 h, the cells on the upper surface of Transwell were removed by cotton swabs, then Transwell was put into 95% alcohol for 5 min, and stained with crystal violet for 5 min. After that, Transwell was taken out and dried. Cells were counted under a microscope (200×) in ten random fields.

Statistical analysis

SPSS 19.0 statistical software was used to analyze the data. All data were expressed in the form of mean ± S.D. Test of normality and homogeneity of variance were analyzed by Kolmogorov–Smimov method and Levene method, respectively. If data had normal distribution and homogeneity of variance, paired t test and independent-sample t test was used to analyze the comparison between two groups, otherwise Wilcoxon signed rank sum test was used. $P<0.05$ was considered statistically significant.

Results

lncRNA screening

lncRNA expression profile was compared between PCa tissues and paracancerous tissues. The selection standard of differential expression is: absolute fold change ≥1.5, $P≤0.05$. The results showed that the expression levels of 2176 lncRNAs were changed in PCa tissues compared with those in paracancerous tissues, 688 lncRNAs were up-regulated and 1488 lncRNAs were down-regulated (unpublished data). Moreover, the expression levels of 2610 miRNAs were

Table 1 Gene chip screening results

lncRNA name	lncRNA ID	Expression trend	Adjacent gene
RP11-539E19.2	ENST00000419889.1	Down	*PRKG1*
RP11-40C11.2	ENST00000435271.1	Down	
RP11-96B5.3	ENST00000343087.4	Down	
RP1-142L7.5	ENST00000588689.1	Down	*LAMA4*
	ENST00000585373.1	Down	
	ENST00000425503.1	Down	
AF001548.5	ENST00000577048.1	Down	*MYH11*
AF001548.6	ENST00000574212.1	Down	
AC002465.2	ENST00000488097.1	Down	*WNT2*
–	TCONS_00023979	Down	*PML*
RP11-399O19.9	TCONS_00018268	Down	*FAS*
–	ENST00000562983.1	Down	
SLC8A1-AS1	NR_028371.1	Down	*SLC8A1*
	ENST00000413479.1	Down	
	ENST00000417875.1	Down	
	ENST00000427354.1	Down	
RP13-650J16.1	ENST00000584705.1	Up	*RAC3*
HLA-T	ENST00000448678.1	Down	*TRAF5*
	ENST00000423222.1	Down	
	ENST00000584914.1	Down	

The high-throughput gene chip technology was used to compare the lncRNA expression profile between PCa tissues and paracancerous tissues. The selection standard of differential expression was: absolute fold change $\geq$1.5, $P \leq$0.05. According to a series of screening conditions (the chip results, adjacent coding genes information analysis, and related reports of the involvement of RAC3 and PML in PCa), RP13-650J16.1 and TCONS_00023979 were selected as the research objects.

changed (689 mRNAs were up-regulated and 1921 mRNAs were down-regulated [unpublished data]). Through the pathway analysis of differentially expressed mRNA genes, it was found that the differentially expressed genes were enriched in a large number of signaling pathways. We selected the pathways closely related to cancer for further analysis. According to the possible regulation mechanism of lncRNA to adjacent genes [22,23], the lncRNAs, which is within 20 kb of these differentially expressed mRNA genes and also expressed differently between PCa and normal tissues adjacent to cancer, were identified. We finally selected nine mRNAs and 13 lncRNAs (Table 1). Then, lncRNA RP13-650J16.1 and lncRNA TCONS_00023979 were selected as research objects according to the chip results, adjacent coding genes information analysis (RAC3 and PML, respectively) and related reports of the involvement of RAC3 and PML in PCa [17-21].

The expression of RP13-650J16.1 and TCONS_00023979 in PCa

As shown in Table 1, RAC3 was the adjacent gene of RP13-650J16.1, and PML was the adjacent gene of TCONS_00023979. In this experiment, we detected their expressions in PCa. Results showed that the expressions of RP13-650J16.1 and RAC3 in PCa tissues were higher than that in paracancerous tissues (Figure 1A). Moreover, the expressions of TCONS_00023979 and PML in PCa tissues were lower than that in paracancerous tissues (Figure 1B).

The effect of RP13-650J16.1 and TCONS_00023979 on their downstream gene

To investigate the effect of RP13-650J16.1 and TCONS_00023979 on their downstream gene, DU145 cells were transfected with si-RP13-650J16.1 or si-TCONS_00023979. Results showed that si-RP13-650J16.1 could significantly reduce RAC3 expression (Figure 2A) and BCL-2 protein level (Figure 2B). Additionally, PML expression in cells transfected with si-TCONS_00023979 was markedly decreased (Figure 2C,D).

Interference efficiency of siRNA expression vector

DU145 cells were transfected with si-584705-1, si-584705-2, si-584705-3, si-584705-4, si-584705-5, si-584705-6 and their control (si-NC), or si-TCONS-1, si-TCONS-2, si-TCONS-3, si-TCONS-4 and their control (si-NC). After 48 h, cells were collected for quantitative real-time PCR (qRT-PCR) assay. As shown in Figure 3A, the expressions of
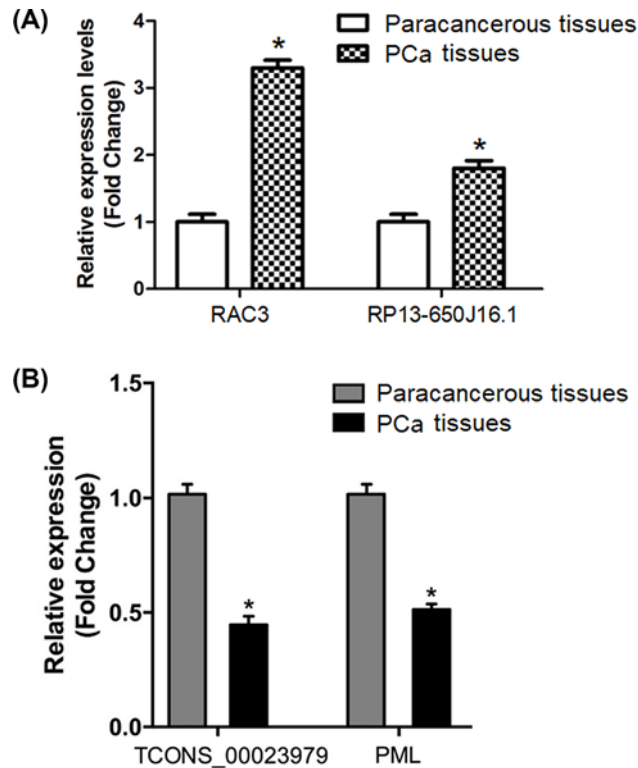
Figure 1. The expression of RP13-650J16.1 and TCONS_00023979 in PCa

(**A**) The expression of RP13-650J16.1 and and RAC3 in PCa. (**B**) The expression of TCONS_00023979 and PML in PCa. Quantitative real-time PCR was used to measure their expressions. *$P<0.05$, compared with NC.
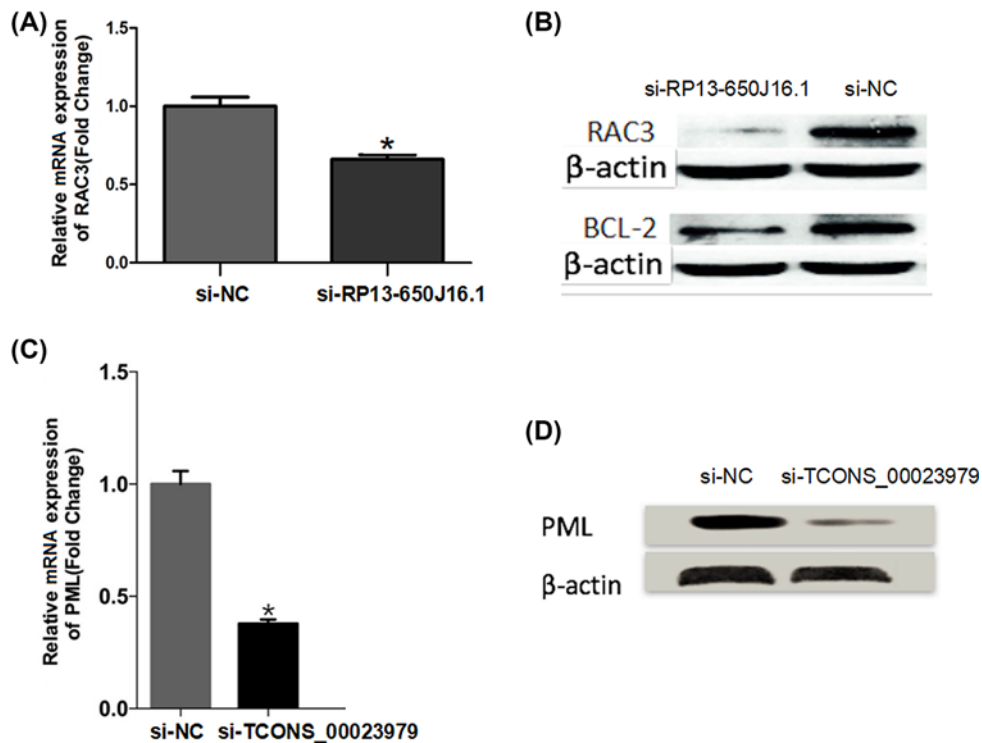

Figure 2. The effect of RP13-650J16.1 and TCONS_00023979 on their downstream gene. DU145 cells were transfected with si-RP13-650J16.1 or si-TCONS_00023979

(**A**) The mRNA expression of RAC3. (**B**) The protein expression of RAC3 and BCL-2. (**C**) The mRNA expression of PML. (**D**) The protein expression of PML.*$P<0.05$, compared with si-NC.
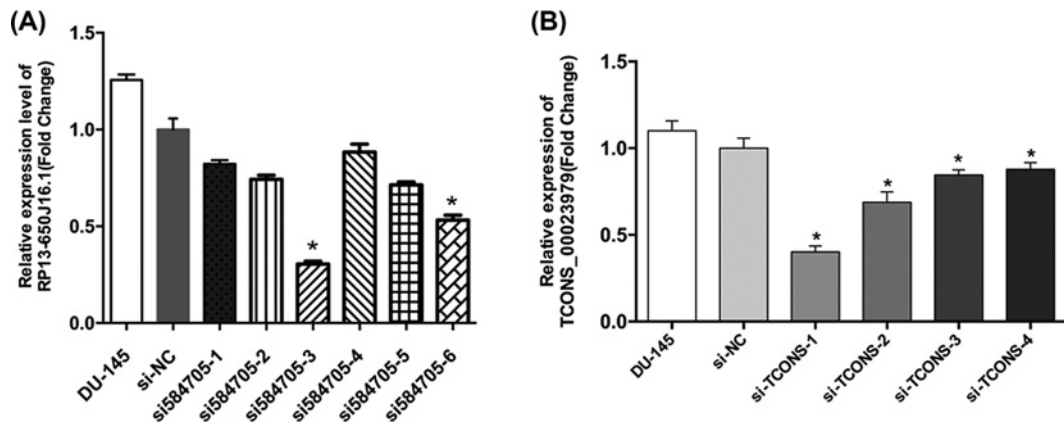
5

Figure 3. Interference efficiency of siRNA expression
DU145 cells were transfected with si-584705-1, si-584705-2, si-584705-3, si-584705-4, si-584705-5, si-584705-6 and their control (si-NC), or si-TCONS-1, si-TCONS-2, si-TCONS-3, si-TCONS-4 and their control (si-NC). After 48 h, cells were collected for qRT-PCR assay. (**A**) The expressions of RP13-650J16.1. (**B**) The expressions of TCONS_00023979. $*P < 0.05$, compared with si-NC.

RP13-650J16.1 in cells transfected with si-584705-3 and si-584705-6 were significantly decreased, and the interference efficiency of cells transfected with si-584705-3 was the best. Furthermore, TCONS_00023979 expressions in different experimental groups were all decreased, but the interference efficiency of cells transfected with si-TCONS-1 was the best (Figure 3B). Therefore, si-584705-3 and si-TCONS-1 were used in subsequent experiments.

The effects of RP13-650J16.1 and TCONS_00023979 on biological function of PCa cells

Cell proliferation

The proliferation of PCa cells transfected with siRNA was detected by MTT assay. Results showed that si-584705-3 could markedly reduce the proliferation of DU145 cells (Figure 4A), which indicated that RP13-650J16.1 might be an oncogene. The proliferation of DU145 cells was significantly enhanced after interfering with the expression of TCONS_00023979 (Figure 4B), which suggested that TCONS_00023979 might have the ability to inhibit the proliferation of PCa cells.

Colony formation

In this experiment, we detected colony forming ability of DU145 cells by plate clone formation assay, which could reflect the dependence of cell population and cell clonal proliferation. The results of plate cloning showed that the colony formation in si-584705-3 group was largely decreased (Figure 5A). Moreover, the colony formation was significantly increased in DU145 cells after TCONS_00023979 expression was inhibited (Figure 5B). These results were in accordance with MTT assay.

The migration ability of cells

The migration ability of DU145 cells was measured by Transwell migration assay. Results showed that the migration ability of DU145 cells treated with si-584705-3 was decreased (Figure 6A). Additionally, the migration ability of DU145 cells in si-TCONS-1 group was increased compared with si-NC group (Figure 6B).

Discussion

PCa is the most common malignancy in Europe and the United States [1,2], and is also becoming more prevalent in our country. At present, PCa has a very serious impact on the quality of life and life expectancy of older men [2]. In view of the high risk of PCa, numerous studies on the etiology and pathogenesis of PCa have been carried out. However, the occurrence and development of PCa is a dynamic process involving multi-molecules and stages. The pathogenesis of PCa is not clear until now.

In the past, researchers always focussed on mRNAs that could encode proteins and ignored ncRNA, especially lncRNA. Increasing evidence has demonstrated that many lncRNAs are involved in the regulation of diverse cellular processes. In addition, some lncRNAs have been shown to play an important regulatory role in the development of
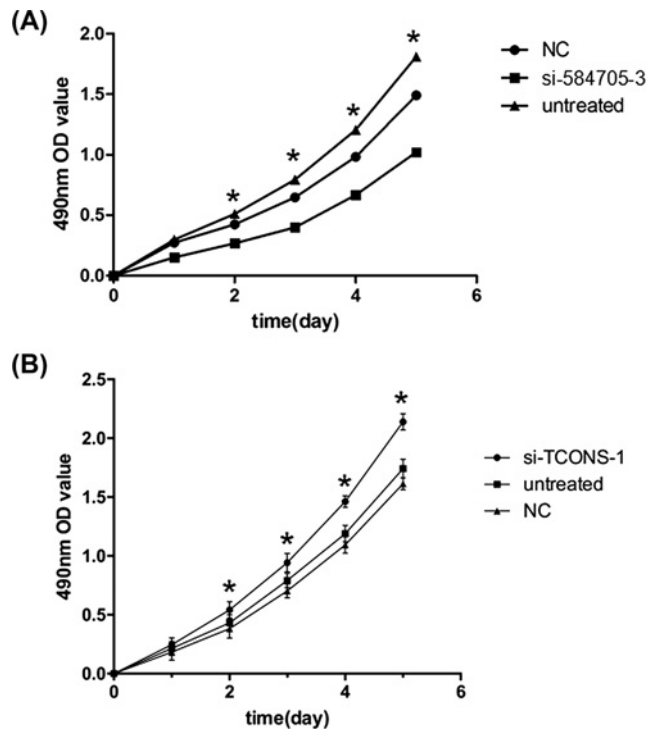
Figure 4. The proliferation of PCa cells

MTT assay was used to detect the cell proliferation. (**A**) The proliferation of DU145 cells transfected with si-584705-3. (**B**) The proliferation of DU145 cells transfected with si-TCONS-1. *$P<0.05$, compared with si-NC.
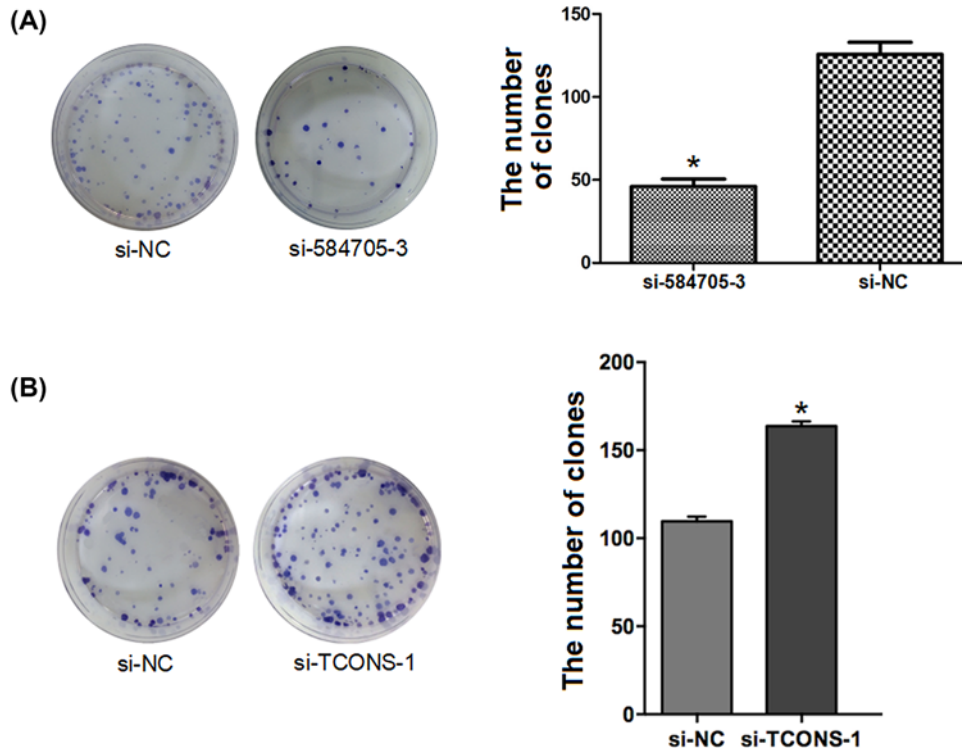

Figure 5. Colony formation

Plate clone formation assay was used to measure the colony forming ability of DU145 cells. (**A**) The effect of RP13-650J16.1 on the colony forming ability of DU145 cells. (**B**) The effect of TCONS_00023979 on the colony forming ability of DU145 cells. *$P<0.05$, compared with si-NC.
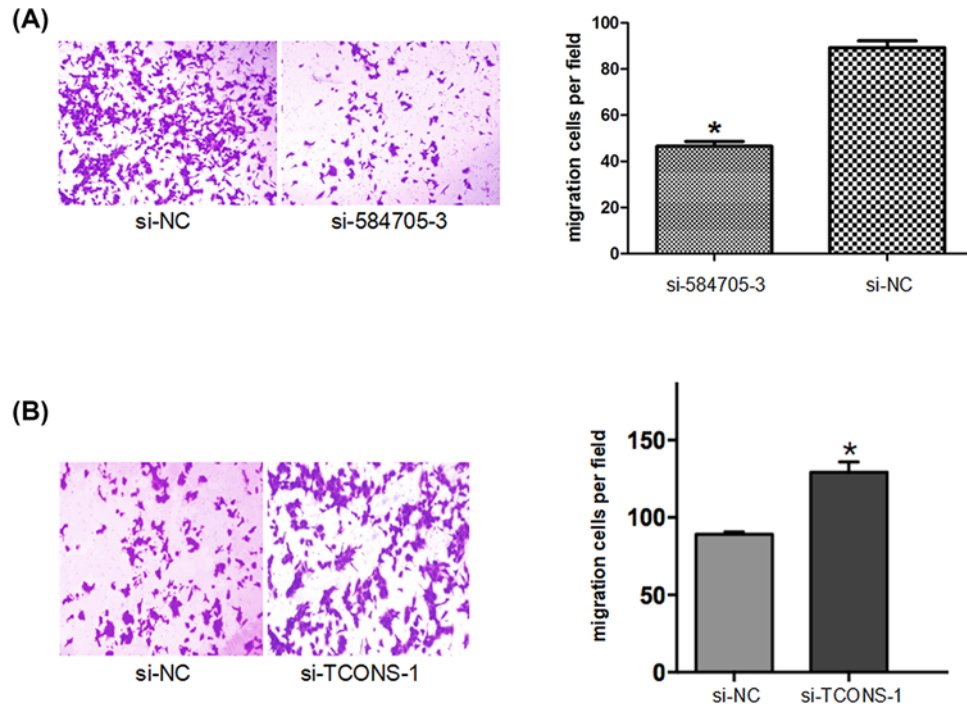
Figure 6. The migration ability of cells
The migration ability of DU145 cells was measured by Transwell migration assay. (**A**) The migration ability of DU145 cells treated with si-584705-3. (**B**) The migration ability of DU145 cells treated with si-TCONS-1. *$P<0.05$, compared with si-NC.

tumors, and even some lncRNAs can be used as markers for tumor diagnosis and prognosis [24]. Therefore, finding the abnormal expression of lncRNA in PCa and analyzing its function will help to improve the treatment of PCa. Currently, lncRNA that associated with PCa is being discovered, including PCAT-1, MALAT1, H19, and GAS5 [25-30]. Our study found 13 lncRNAs that related with PCa via using gene chip screening analysis. And according to a series of screening conditions (the distance was within 20 kb of abnormally expressed mRNA, chip results and related reports [17-21]), we chose RP13-650J16.1 and TCONS_00023979 as the research objects. Additionally, we found high expression of RP13-650J16.1 and RAC3 in PCa by gene chip screening and low expression of TCONS_00023979 and PML.

RAC3 has been found to be closely related to the development and progression of PCa, and its role in PCa has been basically understood. Zhou et al. [31] found that overexpression of RAC3 was associated with PCa proliferation, and down-regulating RAC3 could inhibit PCa proliferation and promote PCa apoptosis. PML is an antioncogene, and studies have shown that PML can inhibit PCa through a series of molecular regulation mechanisms [17-19,32]. Therefore, in order to further validate the microarray screening results, we measured the expression of RP13-650J16.1, RAC3, TCONS_00023979, and PML in 13 PCa patients' samples by qRT-PCR. It was found that the expression of RP13-650J16.1 and RAC3 was elevated, whereas the expression of TCONS_00023979 and PML was decreased, which was consistent with microarray results. Thus, we hypothesized that RP13-650J16.1 and RAC3 have coexpression relationships, and TCONS_00023979 and PML share coexpression relationships. To verify the hypothesis, we conducted siRNA interference experiments. The present study found that the silencing RP13-650J16.1 could down-regulate RAC3 expression, and knockdown of TCONS_00023979 could reduce PML expression, which indicated that RP13-650J16.1 could positively regulate RAC3, and TCONS_00023979 could positively regulate PML. Taken together, the current study suggested that RP13-650J16.1 might be an oncogene in PCa, and TCONS_00023979 might be an antioncogene.

In order to explore the role of the two lncRNAs in PCa, we investigated the effects of the two lncRNAs on cellular biological behavior by MTT assay, plate clone formation assay, and Transwell migration assay. The results showed that knockout of RP13-650J16.1 could inhibit PCa cell proliferation and migration, and silencing TCONS_00023979 could enhance the proliferation and migration of PCa cells. Thus, it indicated that the two lncRNAs were closely related to the occurrence and development of PCa.

However, due to the small number of clinical cases in the present study, a large sample study is needed to provide more reliable evidence for the follow-up. Moreover, we will explore the specific regulation mechanism of RP13-650J16.1 on RAC3, and the specific regulation mechanism of TCONS_00023979 on PML in further study, aiming to provide new therapeutic targets for the treatment and prevention of PCa.

Author contribution

X.Z. and Q.C. conceived and designed the experiments and analyzed the data. H.W. and C.Z. contributed to the quality control of data and algorithms. B.F. and G.W. wrote the manuscript. X.Z. and G.W. reviewed and edited the manuscript. All authors read and approved the final manuscript.

Funding

Competing interests

The authors declare that there are no competing interests associated with the manuscript.

Abbreviations

lncRNA, long non-coding RNA; ncRNA, non-coding RNA; PCa, prostate cancer; PML, promyelocytic leukemia; qRT-PCR, quantitative real-time PCR; RAC3, receptor-associated coactivator 3.

References

1 Siegel, R.L., Miller, K.D. and Jemal, A. (2016) Cancer statistics, 2016. *CA Cancer J. Clin.* **66**, 7–30, https://doi.org/10.3322/caac.21332

2 Chen, W. et al. (2016) Cancer statistics in China, 2015. *CA Cancer J. Clin.* **66**, 115–132, https://doi.org/10.3322/caac.21338

3 Lipovich, L., Johnson, R. and Lin, C.Y. (2010) MacroRNA underdogs in a microRNA world: evolutionary, regulatory, and biomedical significance of mammalian long non-protein-coding RNA. *Biochim. Biophys. Acta* **1799**, 597–615, https://doi.org/10.1016/j.bbagrm.2010.10.001

4 Khvorova, A. and Wolfson, A. (2012) New competition in RNA regulation. *Nat. Biotechnol.* **30**, 58–59, https://doi.org/10.1038/nbt.2092

5 Li, X. et al. (2013) Long noncoding RNAs: insights from biological features and functions to diseases. *Med. Res. Rev.* **33**, 517–553, https://doi.org/10.1002/med.21254

6 Novikova, I.V., Hennelly, S.P. and Sanbonmatsu, K.Y. (2012) Sizing up long non-coding RNAs: do lncRNAs have secondary and tertiary structure? *Bioarchitecture* **2**, 189–199, https://doi.org/10.4161/bioa.22592

7 Li, C.H. and Chen, Y. (2013) Targeting long non-coding RNAs in cancers: progress and prospects. *Int. J. Biochem. Cell Biol.* **45**, 1895–1910, https://doi.org/10.1016/j.biocel.2013.05.030

8 Fatica, A. and Bozzoni, I. (2014) Long non-coding RNAs: new players in cell differentiation and development. *Nat. Rev. Genet.* **15**, 7–21, https://doi.org/10.1038/nrg3606

9 Cech, T.R. and Steitz, J.A. (2014) The noncoding RNA revolution-trashing old rules to forge new ones. *Cell* **157**, 77–94, https://doi.org/10.1016/j.cell.2014.03.008

10 Ponting, C.P., Oliver, P.L. and Reik, W. (2009) Evolution and functions of long noncoding RNAs. *Cell* **136**, 629–641, https://doi.org/10.1016/j.cell.2009.02.006

11 Wang, X. et al. (2018) The long non-coding RNA CYTOR drives colorectal cancer progression by interacting with NCL and Sam68. *Mol. Cancer* **17**, 110, https://doi.org/10.1186/s12943-018-0860-7

12 Xiong, D.D. et al. (2018) The LncRNA NEAT1 accelerates lung adenocarcinoma deterioration and binds to Mir-193a-3p as a competitive endogenous RNA. *Cell. Physiol. Biochem.* **48**, 905–918, https://doi.org/10.1159/000491958

13 Walsh, A.L. et al. (2014) Long noncoding RNAs and prostate carcinogenesis: the missing 'linc'? *Trends Mol. Med.* **20**, 428–436, https://doi.org/10.1016/j.molmed.2014.03.005

14 Su, Y.J. et al. (2015) Circulating long noncoding RNA as a potential target for prostate cancer. *Int. J. Mol. Sci.* **16**, 13322–13338, https://doi.org/10.3390/ijms160613322

15 Salameh, A. et al. (2015) PRUNE2 is a human prostate cancer suppressor regulated by the intronic long noncoding RNA PCA3. *Proc. Natl. Acad. Sci. U.S.A.* **112**, 8403–8408, https://doi.org/10.1073/pnas.1507882112

16 Wang, K.C. and Chang, H.Y. (2011) Molecular mechanisms of long noncoding RNAs. *Mol. Cell* **43**, 904–914, https://doi.org/10.1016/j.molcel.2011.08.018

17 Buczek, M.E. et al. (2016) Cytoplasmic PML promotes TGF-β-associated epithelial-mesenchymal transition and invasion in prostate cancer. *Oncogene* **35**, 3465–3475, https://doi.org/10.1038/onc.2015.409

18 Birch, S.E. et al. (2014) Expression of E6AP and PML predicts for prostate cancer progression and cancer-specific death. *Ann. Oncol.* **25**, 2392–2397, https://doi.org/10.1093/annonc/mdu454

19 Chatterjee, A., Chatterjee, U. and Ghosh, M.K. (2013) Activation of protein kinase CK2 attenuates FOXO3a functioning in a PML-dependent manner: implications in human prostate cancer. *Cell Death Dis.* **4**, e543, https://doi.org/10.1038/cddis.2013.63

20 Tien, J.C., Zhou, S. and Xu, J. (2009) The role of SRC-1 in murine prostate cancinogenesis is nonessential due to a possible compensation of SRC-3/AIB1 overexpression. *Int. J. Biol. Sci.* **5**, 256–264, https://doi.org/10.7150/ijbs.5.256

21 Zhou, H.J. et al. (2005) SRC-3 is required for prostate cancer cell proliferation and survival. *Cancer Res.* **65**, 7976–7983, https://doi.org/10.1158/0008-5472.CAN-04-4076

22 Fatica, A. and Bozzoni, I. (2014) Long non-coding RNAs: new players in cell differentiation and development. *Nat. Rev. Genet.* **15**, 7–21, https://doi.org/10.1038/nrg3606

23 Cech, T. and Steitz, J. (2014) The noncoding RNA Revolution—trashing old rules to forge new ones. *Cell* **157**, 77–94, https://doi.org/10.1016/j.cell.2014.03.008

24 Li, D. et al. (2013) Long intergenic noncoding RNA HOTAIR is overexpressed and regulates PTEN methylation in laryngeal squamous cell carcinoma. *Am. J. Pathol.* **182**, 64–70, https://doi.org/10.1016/j.ajpath.2012.08.042

25 Kotake, Y. et al. (2011) Long non-coding RNA ANRIL is required for the PRC2 recruitment to and silencing of p15(INK4B) tumor suppressor gene. *Oncogene* **30**, 1956–1962, https://doi.org/10.1038/onc.2010.568

26 Prensner, J.R. et al. (2011) Transcriptome sequencing across a prostate cancer cohort identifies PCAT-1, an unannotated lincRNA implicated in disease progression. *Nat. Biotechnol.* **29**, 742–749, https://doi.org/10.1038/nbt.1914

27 Prensner, J.R. et al. (2013) The long noncoding RNA SChLAP1 promotes aggressive prostate cancer and antagonizes the SWI/SNF complex. *Nat. Genet.* **45**, 1392–1398, https://doi.org/10.1038/ng.2771

28 Zhu, M. et al. (2014) lncRNA H19/miR-675 axis represses prostate cancer metastasis by targeting TGFBI. *FEBS J.* **281**, 3766–3775, https://doi.org/10.1111/febs.12902

29 Pickard, M.R., Mourtadamaarabouni, M. and Williams, G.T. (2013) Long non-coding RNA GAS5 regulates apoptosis in prostate cancer cell lines. *Biochim. Biophys. Acta* **1832**, 1613–1623, https://doi.org/10.1016/j.bbadis.2013.05.005

30 Tripathi, V. et al. (2010) The nuclear-retained noncoding RNA MALAT1 regulates alternative splicing by modulating SR splicing factor phosphorylation. *Mol. Cell* **39**, 925–938, https://doi.org/10.1016/j.molcel.2010.08.011

31 Zhou, H.J. et al. (2005) SRC-3 is required for prostate cancer cell proliferation and survival. *Cancer Res.* **65**, 7976–7983, https://doi.org/10.1158/0008-5472.CAN-04-4076

32 Sahin, U., Lallemand-Breitenbach, V. and De, T.H. (2014) PML nuclear bodies: regulation, function and therapeutic perspectives. *J. Pathol.* **234**, 289–291, https://doi.org/10.1002/path.4426