# Early diagnostic role of PSA combined miR-155 detection in prostate cancer

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Abstract. – OBJECTIVE: As a kind of malignant tumor in the male genitourinary system, prostate cancer exhibits significantly increased occurrence. Prostate-specific antigen (PSA) expression can be seen in the prostate cancer, prostatitis, and other diseases, therefore, lack of diagnostic specificity. The miR-155 expression is abnormally increased in the tumors. Therefore, this study aims to explore the clinical significance of PSA combined miR-155 detection in the early diagnosis of prostate cancer.

PATIENTS AND METHODS: A total of 86 patients diagnosed with prostate cancer were enrolled in this study. PSA and miR-155 gene expression in tumor tissue were detected by using Real-time PCR. The serum levels of PSA were measured by using enzyme-linked immunosorbent assay (ELISA). The correlation of PSA and miR-155 expression with age, body mass index (BMI), tumor volume, tumor-node-metastasis (TNM) stage, lymph node metastasis (LNM), and other clinicopathological features were analyzed, respectively.

**RESULTS:** Serum PSA expression and PSA gene in tumor tissue were significantly higher compared to that in adjacent tissues (p<0.05). PSA gene and protein increased significantly with the clinical stage of TNM and decreased following the increase of grade (p<0.05). The miR-155 level was significantly elevated in the tumor tissue compared with para-carcinoma tissue (p<0.05). PSA and miR-155 expressions were positively correlated with TNM stage, tumor volume, and LNM, and negatively correlated with grade (p<0.05).

CONCLUSIONS: PSA and miR-155 were closely related to the clinicopathological features of prostate cancer. Combined detection is helpful for the early diagnosis of prostate cancer.

Key Words:

Prostate cancer, PSA, miR-155, TNM stage, Gene detection.

### Introduction

Prostate cancer is a type of malignant tumor with high morbidity in the male genitourinary system around the world<sup>1,2</sup>. In recent years, following the era of population aging, and the diet and lifestyle changes, the incidence of prostate cancer patients increased year by year with younger trends<sup>3,4</sup>. In developing countries, the early screening rate of prostate cancer is low, leading to patients advanced when diagnosed and can't receive radical surgery. Therefore, the survival and treatment effects were poor<sup>5,6</sup>. Due to lifestyle and eating habits, the incidence of prostate cancer in developed countries is also at a high level<sup>7</sup>. As the prostate cancer itself has the characteristics of concealing, most patients are at an advanced stage, so the treatment is very complicated<sup>8</sup>. The pathogenesis of prostate cancer is complex, and its metastasis and invasion mechanisms are affected by many factors. Therefore, early diagnosis of prostate cancer is the key to improve the prognosis of patients<sup>9</sup>.

Prostate-specific antigen (PSA) is a single-stranded polypeptide belonging to the serine protease family with tissue-specific and chymotrypsin-like functions<sup>10,11</sup>. PSA can decompose the main collagen in semen, therefore playing the role of semen dilution<sup>12</sup>. PSA can be synthesized in both normal and cancerous epithelial cells<sup>13</sup>. PSA has tissue specificity that only exists in human prostate acinar and ductal epithelial cell cytoplasm instead of other cells. However, it is not tumor-specific, thus can be elevated by prostatitis, benign prostatic hyperplasia, and prostate cancer<sup>14,15</sup>. MicroRNA exists in a variety of forms with a wide range of mechanisms. They participate in the regulation of growth and development,

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so as to enhance the ability to adapt the environment<sup>16</sup>. It is showed that miR-155 is overexpressed in prostate cancer, breast cancer, and other tumors<sup>17,18</sup>. Therefore, this study aims to explore the clinical significance of PSA combined miR-155 in the early diagnosis of prostate cancer.

### **Patients and Methods**

### **General Information**

A total of 86 patients with prostate cancer who were diagnosed by histopathological examination from January 2015 to December 2016 were enrolled in the Affiliated Nanhua Hospital, University of South China (Hengyang, China). All patients were treated by surgery with mean age at  $55.1 \pm 6.6$  (45-77) years old. The inclusion criteria were listed as the followings<sup>5</sup>: primary prostate cancer confirmed by the pathology, without surgery, chemotherapy, radiotherapy or other treatment. The exclusion criteria were listed as the followings5: recurrent prostate cancer, treated by surgery, radiotherapy, or chemotherapy previously, combined with other diseases, such as infectious diseases, malignant tumors, severe liver and kidney disease, pulmonary fibrosis, bone metabolic diseases, secondary renal hypertension, systemic immune diseases, and malignant tumor complications. The tumor tissue was collected during the operation for the pathological diagnosis, classification, and staging. The tumor tissues and adjacent tissues were collected intraoperatively and stored at -80°C. Another 40 patients with benign prostatic hyperplasia at the same period were selected as control with mean age at 53.1  $\pm$  5.4 (41-70) years old. This study was approved by the Academy of Medical Ethics Committee. All the enrolled subjects had signed the informed consent.

#### Clinical Data Collection

The clinical data were collected, including name, age, family history, family history of prostate cancer, body mass index (BMI), tumor size, tumor type, tumor grade, clinical stage, tumor metastasis, pathological stage.

# Main Reagents and Instruments

TRIzol reagents were purchased from Invitrogen/Life Technologies (Carlsbad, CA, USA). PSA enzyme-linked immunosorbent assay (ELISA) kit was purchased from R&D Systems (Minneapolis, MN, USA). RNA extraction kit and reverse transcription kit were purchased from Axygen (Tewksbury, MA, USA). Labsystem Version 1.3.1

Microplate reader was purchased from Bio-Rad Laboratories (Hercules, CA, USA). ABI 7700 Fast Fluorescence Quantitative PCR was derived from ABI (Foster City, CA, USA). DNA amplifier was provided by PE Gene Applied Biosystems (Foster City, CA, USA). Other common reagents were purchased from Sangon Biotech. Co. Ltd. (Shanghai, China).

# Specimen Collection

Tumor tissue and adjacent tissue (within 5 cm from tumor tissue) were collected intraoperatively and stored at -80°C. A total of 5 ml peripheral venous blood was extracted before operation using heparin sodium anticoagulant blood collection tube and centrifuged at 2000 r/min for 10 min. The supernatant was stored at -20°C.

#### Real-time PCR

Total RNA was extracted from tumor tissue and adjacent tissue, and reverse transcribed to complementary DNA (cDNA). The primers were designed by Primer 6.0 and synthesized by Invitrogen/Life Technologies (Carlsbad, CA, USA). PSA, forward, 5'-CATGGTATGATGGACC-3' reverse. 5'-TTCGAAGTCGCACAGCAGCT-3'; miR-155, 5'-CGATGGTATATGGACC-3', re-5'-TTCGAGCCGATACAGCAGCT-3'; verse. GAPDH, forward, 5'-ACCAGGTATCTGCTG-GTT-3'; reverse, 5'- TAACCATGATGTCAGC-GTGGTT-3'. Real-time PCR was performed at 55°C for 1 min, followed by 35 cycles of 55°C for 1 min, 92°C for 30 s, and 58°C for 45 s. Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) was selected as internal reference. The relative expression of mRNA was calculated by 2-\(^2\text{LC}\)t method.

# **ELISA**

The expression of human epidermal growth factor receptor 2 (HER2) in the serum was detected by ELISA. The supernatant was collected by centrifuging peripheral blood collected from each group according to the ELISA kit (R&D Systems, Minneapolis, MN, USA). The optical density (OD) of each well was measured by the microplate reader to establish the standard curve. The corresponding sample concentration was calculated.

### Statistical Analysis

All data analyses were performed on SPSS 22.0 software (SPSS Inc., Armonk, NY, USA). All data were presented as mean ± standard deviation and compared by Student's *t*-test or one-way ANOVA. Tukey's post-hoc test was used for com-

Table I. Clinical information.

	Cases	%
Age (year)		
< 60	38	44.19
> 60	48	55.81
BMI (kg/m <sup>2</sup> )		
≤23	36	41.86
> 23	50	58.14
Family history of prostate cancer (%)		
With	42	48.83
Without	44	51.17
Tumor size		
T1 (< 2 cm)	23	26.74
T2 (2-5 cm)	17	19.76
T3 (> 5 cm)	18	20.93
T4 (neoplasm invasiveness)	28	32.57
Histological grade		
Well	33	38.37
Moderate	25	29.07
Poor	28	32.56
TNM stage		
I-II	32	37.21
III-IV	54	62.79
LNM		
Without	34	39.53
With	52	60.47

paring measurement data between groups. Correlation analysis was performed using Pearson. p<0.05 was depicted as statistically significant.

# Results

### Clinicopathological Characteristics

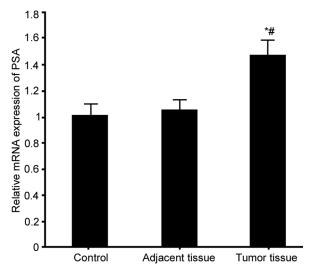
The clinicopathological features of prostate cancer patients were listed in Table I.

# PSA Gene Expression in Prostate Cancer Patients

Real-time PCR was used to detect the expression of PSA gene in tumor tissues of patients with prostate cancer. The results showed that the expression of PSA gene in prostate cancer tissues was significantly higher than that in the adjacent tissues and the control group (p<0.05, Figure 1).

# Serum Levels of PSA in Prostate Cancer Patients

The level of PSA in the serum of patients with prostate cancer was detected by ELISA. The results demonstrated that the expression of PSA protein in the serum of patients with prostate cancer was significantly higher compared to that of normal control group (p<0.05, Figure 2).



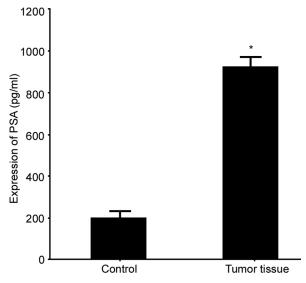
**Figure 1.** PSA gene expression in prostate cancer patients.  $^*p$ <0.05, compared with control,  $^#p$ <0.05, compared with adjacent tissue.

# Analysis of mir-155 Expression in Patients with Prostate Cancer

Real-time PCR was adopted to analyze the expression of miR-155 in tumor tissues of patients with prostate cancer. The expression of miR-155 was significantly higher in prostate cancer tissues compared to that in adjacent tissues and controls (p<0.05) (Figure 3).

# PSA Gene and Protein Expressions in Prostate Cancer Patients with Different TNM Stages

The expression of PSA gene and protein in tumor tissue and serum of prostate cancer patients



**Figure 2.** Serum PSA expression in prostate cancer patients. \**p*<0.05, compared with control.

**Table II.** Correlation analysis of PSA and miR-155 with clinicopathological features.

	TNM stage	Tumor size	LNM	Histological grade
PSA	0.639*	0.521*	0.652*	-0.611*
miR-155	0.725*	0.421*	0.512	-0.361*

\*p<0.05.

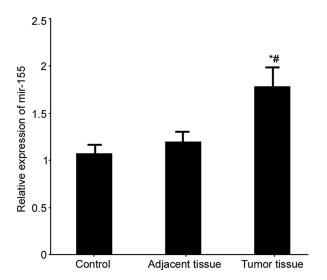
with different TNM stages were detected by Real-time PCR and ELISA. The results exhibited that the expression of PSA gene and protein in tumor tissue and serum increased following TNM upstage (p<0.05, Figure 4).

# MiR-155 Expression in Prostate Cancer Patients with Different TNM Stages

Real-time PCR was selected to test the expression of miR-155 in tumor tissue and serum of prostate cancer patients with different TNM stages. The results revealed that the expression of miR-155 in tumor tissue and serum of prostate cancer patients were enhanced following with the increase of TNM staging (p<0.05, Figure 5).

# Correlation Analysis of PSA and miR-155 with Clinicopathological Features

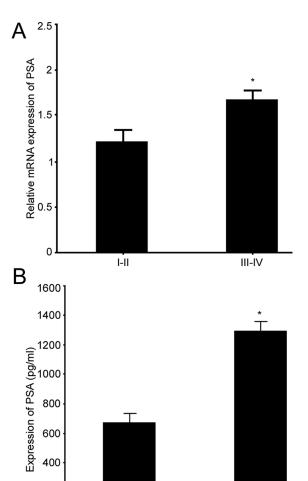
PSA expression was positively correlated with TNM stage, tumor volume, and LNM, while negatively correlated with tissue grade (p<0.05). The expression of miR-155 was positively correlated with TNM stage, tumor volume, and LNM, whereas negatively correlated with histological grade (p<0.05, Table II).



**Figure 3.** MiR-155 expression in prostate cancer patients. \*p<0.05, compared with control, \*p<0.05, compared with adjacent tissue.

### Discussion

Prostate cancer is a malignant epithelial tumor that occurs in the prostate. It has become the most common cancer in male skin cancer and accounts for the second as the cancer death factor in male<sup>19</sup>. However, since prostate cancer is lack of evident symptom in the early stage, it is difficult to make the diagnosis<sup>20</sup>. Serum PSA is a specific marker



**Figure 4.** PSA gene and protein expressions in prostate cancer patients with different TNM stages. A, PSA gene expression. B, PSA protein expression. p < 0.05, compared with stage I-II.

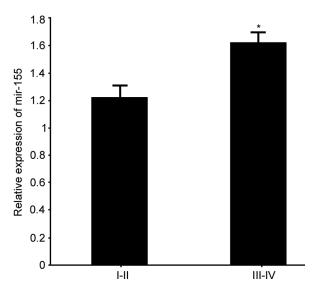
III-IV

1-11

200

of prostate tissue. PSA is a serine protease and glycoprotein secreted by prostate epithelial cells that is secreted directly into the prostate ductal system<sup>21,22</sup>. The normal function of PSA is to help semen clot hydrolysis and liquefaction, so as to regulate the male fertility<sup>23</sup>. There is a blood-epithelial barrier around the normal prostate duct system, which prevents the PSA from entering the blood directly from the prostate epithelium, thereby maintaining a low concentration of PSA in the blood<sup>24</sup>. Prostate cancer destroys the blood-epithelial barrier and increases the secretion of PSA, resulting in PSA directly entering the blood. The higher degree of malignancy, the greater damage on the normal and higher serum PSA<sup>25</sup>. PSA rises in most of the prostate tissue with clinical significance. It is also one of the most important indicators for the early detection. Although PSA is the most commonly used method for the detection of prostate cancer, PSA-positive results also appear in benign prostatic hyperplasia and prostatitis. Moreover, it is still lack of specificity for the early diagnosis of prostate cancer<sup>26</sup>.

MiRNAs are abnormal in the development of tumor and involved in the regulation of tumor<sup>27</sup>. The specific expression of miRNA in peripheral blood can reflect the occurrence, progression, and severity of the disease. MiRNA has the characteristics of stability that cannot be degraded by RNase easily. In addition, it can be repeated the freezing and thawing for long-term storage. Moreover, it is stable in the plasma and serum, so that miRNA can be used as a disease serological molecular marker<sup>28,29</sup>. It was shown that miR-155 overexpressed in prostate cancer, breast cancer, and other tumors<sup>17,18</sup>. Therefore, this study explored the role of combined PSA and mir-155 in the early diagnosis of prostate cancer. We tested PSA gene and protein, and miR-155 expressions in patients with prostate cancer to analyze their correlations with clinicopathological features. TNM staging analysis exhibited that the expressions of PSA and miR-155 increased following TNM upstaging, suggesting that PSA and miR-155 were associated with the pathological features of prostate cancer. Further analysis revealed that PSA and miR-155 expressions were not related to age, BMI, family history, pathological type; positively correlated with clinical TNM stage, tumor size, and LNM; and negatively correlated with tissue grade, indicating that PSA and miR-155 detection can be used as a molecular target for the diagnosis and prognosis of prostate cancer. These results demonstrated that



**Figure 5.** MiR-155 expression in prostate cancer patients with different TNM stages. \*p<0.05, compared with stage I-II.

the combination of PSA and miR-155 are early diagnostic indicators of prostate cancer. Further in-depth investigations are needed to discuss their mechanism in prostate cancer.

### Conclusions

PSA and miR-155 are closely related to the clinicopathological features of prostate cancer. Combined detection is helpful to the early diagnosis of prostate cancer. Therefore, this study provides a new theoretical basis for the early diagnosis of prostate cancer.

### Acknowledgments

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#### **Conflict of Interest**

The Authors declare that they have no conflict of interest.

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