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Differential Expression of the KLK2 and KLK3 Genes in Peripheral Blood and Tissues Samples of Iranian Patients with Prostate Cancer

ABSTRACT

Background and Objectives: Prostate cancer is a highly prevalent malignancy with a high mortality rate in men. Many studies have investigated the diagnostic value of various genes involved in prostate cancer, but there is no data for Kallikrein 2 (KLK2) and Kallikrein 3 (KLK3) expression patterns among Iranian patients. Therefore, we aimed to evaluate the expression of these two genes in Iranian patients with prostate cancer.

Methods: In this case-control study, three groups consisting of healthy individuals, patients with benign prostatic hyperplasia (BPH) and patients with prostate cancer were studied. Peripheral blood samples were collected from all subjects, mRNA was extracted after cell lysis, and cDNA was synthesized. Real-time PCR was performed to assess gene expression levels relative to a reference gene (18s rRNA gene).

Results: The KLK2 gene was overexpressed in patients with prostate cancer. KLK2 expression differed significantly between the cancer patients and controls. Relative expression of the KLK3 gene in the BPH group was higher than that in the control and cancer groups. However, we observed no significant difference in the expression of KLK3 between the control and cancer subjects.

Conclusion: We demonstrate that analysis of KLK2 expression is a favorable method of diagnosing prostate cancer and discriminating normal individuals from those with BPH or prostate cancer. We also found that the KLK3 gene is highly overexpressed in individuals with BPH, which might indicate that this gene is not cancer-specific.

Keywords: Prostatic Neoplasm, Prostatic Hyperplasia, Kallikreins, Gene Expression.

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INTRODUCTION

Prostate cancer is the second leading cause of cancer death in developed countries (1, 2). It is estimated that about one out of every six men will be diagnosed with prostate cancer during his lifetime (3, 4). According to epidemiological studies, the prevalence of prostate cancer has been consistently increasing in many developed countries over the last few decades. In Iran, cancer is the third leading cause of death following cardiovascular diseases and traffic accidents (5, 6). A study in Tehran (Iran) reported that prostate cancer is the most prevalent type of cancer in men following gastric cancer. It is noteworthy to mention that the prevalence of prostate cancer is higher in Tehran than in Ardebil (Iran), Karachi (Pakistan), Izmir (Turkey) and Dubai (UAE) (7).

One of the methods for rapid detection of prostatic neoplasms is to examine the involved genes and their products. The human kallikrein genes KLK2 and KLK3 both have five coding exons and four introns and produce at least 13 and 5 types of mRNA transcripts, respectively (8, 9). These transcripts are generated because of alternative splicing or polyadenylation (8, 10, 11). KLK3 is the most popular kallikrein gene associated with prostate cancer (12). It belongs to a family of 15 kallikreins most commonly known as prostate-specific antigen (PSA), a protein produced by both normal and malignant cells of the prostate gland (13). Studies on PSA expression revealed that this molecule is not prostate-specific and is in fact produced in other tissues, such as the breast (14).

KLK2 and KLK3 are reported to show a homology degree of 80-85% (8). The expression of KLK3 is increased in benign prostatic hyperplasia (BPH) and highly differentiated prostate cancer. However, it is decreased during prostate cancer progression (15, 16). For several years, PSA has been used as a tumor marker of choice despite its low specificity. In approximately 15% of men with serum PSA levels of less than 4 ng/ml, prostate cancer is diagnosed through prostate biopsy. In addition, one out of every four individuals with a serum PSA level between 4 and 10 ng/ml is likely to be affected with cancer. The risk of developing prostatic neoplasms increases if the serum PSA level exceeds 10 ng/ml. Considering the necessity of finding appropriate prostate cancer-specific markers for improved diagnosis, this study was designed to evaluate diagnostic value of KLK2 and KLK3 genes for prostate cancer.

MATERIALS AND METHODS

The study was carried out on 48 individuals who had been referred to the urology unit of the Shahid Beheshti Hospital (Tehran, Iran). The subjects were divided into a prostate cancer group and a BPH group based on the results of biopsy and pathology tests. A control group comprising of 24 healthy individuals was also included in the study. In the prostate cancer group, patients who had been diagnosed for more than a year or had received hormone therapy, chemotherapy, radiation therapy or anti-cancer drugs were excluded from the study. In the BPH group, patients who had undergone open prostatectomy and were confirmed to be affected with BPH and not prostate cancer through histopathological analysis were excluded. A history of cancer, taking finasteride for longer than a month, taking anticancer drugs and detection of prostate cancer precursors (prostatic intraepithelial neoplasia) in prostate tissue were considered as the exclusion criteria for the BPH group. After obtaining written consent from all subjects, blood samples (2.5 ml) were taken and collected into EDTA-containing tubes and then immediately stored at 4 °C. All materials used in this study were purchased from Merck Co., Germany. RNA extraction and cDNA synthesis were performed in less than 2 hours after sampling. Before RNA extraction, lysed red blood cells (RBCs) and hemoglobin were removed from the samples. For this purpose, a lysis solution containing 10 mM Tris-HCl, sucrose, 5 mM MgCl$_2$ and 1% Triton X100 was prepared. According to the protocol, the lysis buffer was added with a 4-fold volume of the samples (10 ml). The solution was vortexed for 30-45 minutes and then centrifuged at 4000g for 20 minutes for complete lysis of RBCs. Supernatant was discarded and precipitate was washed with phosphate buffered saline. Finally, the extraction was done on the sediment (must be as transparent as possible) using a kit. Total RNA was extracted from blood using RNeasy mini kit (Qiagen, Hilden, Germany) according to the manufacturer’s instructions. Purity of the extracted RNA was evaluated using a Nanodrop spectrophotometer.
were performed to compare data. A p-value of less than or equal to 0.05 was considered significant.

RESULTS

The KLK2 was expressed in a small number of subjects. There was no significant difference between the three groups in terms of KLK2 expression. However, mean CT values of KLK2 differed significantly between the cancer and the control groups. In the case of KLK3, mean CT values did not differ significantly between the cancer and the control groups. However, there was a statistically significant difference in the mean CT value of KLK3 between the BPH group and other groups (Table 4). Relative changes in the expression of the genes were assessed using the ΔCt method. As shown in Table 5, there was no significant difference between the control and BPH groups for both KLK2 and KLK3.

Table 1- Variants of the genes under study and sequence of the primers designed by AlleleID V6 (Premier biosoft Co.)

<table>
<thead>
<tr>
<th>Gene</th>
<th>NCBI accession number</th>
<th>Primer length</th>
<th>Amount used (µl)</th>
<th>GC %</th>
<th>Tm (°C)</th>
<th>Product length(bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>KLK2</td>
<td>variant 1: NM_005551.4 (2855)</td>
<td>17</td>
<td>1</td>
<td>52.9</td>
<td>62.4</td>
<td>84</td>
</tr>
<tr>
<td>KLK2</td>
<td>variant 2: NM_001002231.2 (2892)</td>
<td>19</td>
<td>1</td>
<td>42.1</td>
<td>56.2</td>
<td></td>
</tr>
<tr>
<td>KLK2</td>
<td>variant 3: NM_00125608.1 (2695)</td>
<td>20</td>
<td>1</td>
<td>50</td>
<td>64.5</td>
<td>151</td>
</tr>
<tr>
<td>18s rRNA</td>
<td>X03205 (1869)</td>
<td>17</td>
<td>1</td>
<td>58.8</td>
<td>64.6</td>
<td>125</td>
</tr>
</tbody>
</table>

Table 2- CT of the 18s rRNA gene in the blood of subjects

<table>
<thead>
<tr>
<th>Group</th>
<th>Mean</th>
<th>Std. Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Control</td>
<td>25.6336</td>
<td>0.93006</td>
<td>24.22</td>
<td>27.23</td>
</tr>
<tr>
<td>BPH</td>
<td>25.3736</td>
<td>1.35185</td>
<td>22.20</td>
<td>28.09</td>
</tr>
<tr>
<td>Prostate cancer</td>
<td>25.5527</td>
<td>0.91593</td>
<td>24.27</td>
<td>27.42</td>
</tr>
</tbody>
</table>

P-value (ANOVA) 0.713

Table 3- The results of marker analysis and the mean CT in blood

<table>
<thead>
<tr>
<th>Blood</th>
<th>Control</th>
<th>Mean CT</th>
<th>BPH</th>
<th>Mean CT</th>
<th>Prostate cancer</th>
<th>Mean CT</th>
</tr>
</thead>
<tbody>
<tr>
<td>KLK2</td>
<td>2/24</td>
<td>33.23</td>
<td>7/24</td>
<td>31.75</td>
<td>10/24</td>
<td>30.98</td>
</tr>
<tr>
<td>KLK3</td>
<td>21/24</td>
<td>28.80</td>
<td>19/24</td>
<td>25.65</td>
<td>20/24</td>
<td>27.33</td>
</tr>
</tbody>
</table>

After performing real-time RT-PCR, the number of positive cases for expression of markers in each study group was determined (Table 3).
groups in terms of KLK2 expression. However, the ΔCt of the KLK3 gene differed significantly between the three study groups. The ΔΔCt method indicated overexpression of the KLK2 gene in the cancer group, which was 5.83-fold and 1.92-fold higher than in the control group and the BPH group, respectively (Table 6). Due to the low level of positive KLK2 expression in the study groups, we found no significant correlation between the variables and this marker. There was no significant correlation between variables of age and the Gleason score and KLK3 expression (Tables 7 and 8), but there was a significant relationship between the expression of this gene and BMI (Table 9).

DISCUSSION

PSA has been used in prostatic neoplasms screening since the mid-1980s. Diagnosis of prostate cancer is currently based on the PSA test, followed by biopsy analysis levels, which limits the applicability of the test in case of initial confirmation of abnormality. However, a number of factors can affect PSA (17, 18). As mentioned by Thomson and colleagues, the PSA test is not specific nor sensitive enough for diagnosis of prostate cancer.
cancer (19). The test has low predictive values, which can produce notable false negative results on biopsies, which in turn might bring about the need for repeated tests and biopsy. The rate of negative biopsy is 60-75% in men with PSA levels of 3-10 ng/ml (20). In approximately 15% of men whose serum PSA levels are less than 4 ng/ml, prostate cancer is diagnosed through prostate biopsy.

It has been shown that PSA is present in normal breast tissues as well as in breast, colon, uterus, liver, kidney, adrenal and parotid tumor tissues (21). Therefore, increased level of PSA cannot be always attributed to prostate and prostate diseases. Based on the results of Ogawa et al., positive expression of PSA in peripheral blood is not correlated with age, preoperative serum PSA level and clinicopathological staging (22). Results of the studies on the association of PSA mRNA expression with prostate cancer have been controversial. In a study by Zhang et al., PSA expression in blood differed significantly between BPH patients, prostate cancer patients and those with metastatic prostatic neoplasms (23). In the present study, expression of the KLK3 gene (ΔCT of KLK3) differed significantly between the three study groups. In a study by Ylikoski et al., although tumor grade was not correlated with PSA mRNA levels, there was a significant difference in PSA mRNA levels between the BPH group and prostate cancer patients, which suggests the suitability of the marker for discriminating BPH cases from patients with prostate cancer (24). Straub et al. demonstrated that preoperative PSA mRNA levels are significantly correlated with cancer stage (25). Inconsistent with this finding, two studies observed no correlation between preoperative PSA mRNA levels and cancer stage (26). Zambon et al. found no difference in the PSA mRNA level between individuals with different Gleason scores (27). In the present study, expression of blood samples of patients with prostate cancer (P = 0.852). The KLK2 gene codes for hK2, a serine protease that plays a direct role in the progression and metatasis of prostate cancer and may be a promising marker for diagnosis and discrimination of normal, BPH and cancer individuals. However, our results showed that the gene is expressed only in 26.5% of the subjects. Moreover, we only noted a significant difference in the expression of this gene between the controls and cancer patients. Few studies have investigated expression of this gene among individuals with prostatic neoplasms. In 2006, Juliana and colleagues evaluated KLK2 and KLK3 expression in peripheral blood samples and prostate cancer tissue samples. They concluded that the KLK2 is a better marker for prostate cancer and its expression is related to cancer progression. Our results show that the expression of KLK2 in peripheral blood is very low and not detectable in all individuals. Similarly, Juliana et al. detected the expression of this gene only in 14% of individuals with BPH and in 46.48% of patients with prostate cancer (28).

CONCLUSION
We demonstrate that analysis of KLK2 expression is a favorable method of diagnosing prostate cancer and discriminating normal individuals from those with BPH or prostate cancer. The KLK3 gene is highly overexpressed in individuals with BPH, which might indicate that this gene is not cancer-specific.

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CONFLICT OF INTEREST
The authors declare that there is no conflict of interest.

REFERENCES