Vascular endothelial growth factor (VEGF) rs3025039 polymorphism is associated with increased risk of osteosarcoma.

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Abstract

Background: The role of vascular endothelial growth factor (VEGF) rs3025039 polymorphism on osteosarcoma risk was not fully clear. Thus, we did a case-control study to evaluate the association between VEGF rs3025039 polymorphism and osteosarcoma risk.

Method: This study included 242 patients with osteosarcoma and 253 controls. The genotyping was conducted using the matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS).

Results: The VEGF rs3025039 TT genotype was significant higher in the osteosarcoma group than in the control group (OR=2.42, 95% CI 1.00-5.85, P=0.04). The TT genotype and CT genotype was also significantly associated with osteosarcoma risk (OR=1.43, 95% CI 1.00-2.05, P=0.04). Under the allelic model, T allele of rs3025039 was significantly associated with higher osteosarcoma risk (OR=1.41, 95% CI 1.05-1.90, P=0.02). In addition, VEGF rs3025039 TT genotype was not associated with tumor location (OR=1.02, 95% CI 0.59-1.77, P=0.94) and metastasis (OR=1.76, 95% CI 0.90-3.43, P=0.10).

Conclusion: In conclusion, this study confirmed that VEGF rs3025039 polymorphism was significantly associated with higher risk of osteosarcoma.

Keywords: Vascular endothelial growth factor, Osteosarcoma, Genetic.
which contained ethylenediamine tetra-acetic acid (EDTA). Genomic DNAs were isolated using genomic DNA extraction kit (QIA amp DNA Blood Mini Kit, Qiagen, Berlin, Germany) under the manufacturer's instructions.

**Genotyping method**

The SNP genotyping was conducted using the matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF MS) (Sequenom Inc., San Diego, CA, USA). The PCR reaction was performed in a 20 μl reaction mixture containing 40-160 ng DNA template, 0.25 units Taq DNA polymerase (Sangon Biotech), 250 μM each deoxyribonucleotide triphosphate (dNTP) (Sangon Biotech), 0.5 μM forward primer, 0.5 μM reverse primer, and 1X PCR buffer with 1.2 mM MgCl₂. The SNaPshot assay (Applied Biosystems) was performed to confirm genotypes of 6 DNA samples. All genotyping procedures were carried out in a double-blind manner and the whole assays were proved to be reliable.

**Statistical analysis**

Data are presented as mean ± standard deviation (SD) or number (percentage). The chi-square test and Student’s t-test were used to compare case and control groups, as appropriate. The statistical comparison between 2 groups was conducted using the t-test or the analysis of variance (ANOVA). Genotype distribution in the control group was tested by Hardy-Weinberg equilibrium (HWE). The differences in genotype and allele distribution between the patients and the controls are represented as odds ratio (OR) and 95% confidence interval (CI). P values for all tests are 2-tailed, and <0.05 was considered as statistically significant. Statistical analysis was conducted using SPSS 18 software (SPSS Inc., Chicago, IL, USA).

**Results**

Table 1 shows the demographic and clinical characteristics of 242 patients with osteosarcoma and 253 controls. Comparisons between the osteosarcoma group and the control group demonstrated that family history of cancer was significantly higher in patients with osteosarcoma than in controls (P<0.05). No statistical differences were seen in age and gender (all P>0.05).

**Table 1. Characteristics of the cases and controls.**

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>Case (n=242)</th>
<th>Control (n=253)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at diagnosis</td>
<td>26.1 ± 16.6</td>
<td>28.1 ± 12.2</td>
<td>0.17</td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td>0.87</td>
</tr>
<tr>
<td>Male</td>
<td>118</td>
<td>122</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>124</td>
<td>131</td>
<td></td>
</tr>
<tr>
<td>Family history of cancer</td>
<td></td>
<td></td>
<td>&lt;0.01</td>
</tr>
<tr>
<td>Yes</td>
<td>198</td>
<td>142</td>
<td></td>
</tr>
</tbody>
</table>

The genotype and allele frequencies of the VEGF rs3025039 polymorphism in patients and controls are displayed in Table 2. The VEGF rs3025039 TT genotype was significantly higher in the osteosarcoma group than in the control group (OR=2.42, 95% CI 1.00-5.85, P=0.04). The TT genotype and CT genotype was also significantly associated with osteosarcoma risk (OR=1.43, 95% CI 1.00-2.05, P=0.04). Under the allelic model, T allele of rs3025039 was significantly associated with higher osteosarcoma risk (OR=1.41, 95% CI 0.59-3.43, P=0.04). Table 3 and metastasis (OR=1.76, 95% CI 0.90-3.43, P=0.10; Table 3).

**Table 2. The genotype and allele frequencies of VEGF polymorphism in the cases and controls.**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Case</th>
<th>Control</th>
<th>OR</th>
<th>95% CI</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC</td>
<td>131</td>
<td>159</td>
<td>1.00</td>
<td>Reference</td>
<td></td>
</tr>
<tr>
<td>CT</td>
<td>95</td>
<td>86</td>
<td>1.34</td>
<td>0.92-1.94</td>
<td>0.12</td>
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<tr>
<td>TT</td>
<td>16</td>
<td>8</td>
<td>2.42</td>
<td>1.00-5.85</td>
<td>0.04</td>
</tr>
<tr>
<td>TT+CT</td>
<td>111</td>
<td>94</td>
<td>1.43</td>
<td>1.00-2.05</td>
<td>0.04</td>
</tr>
<tr>
<td>C</td>
<td>357</td>
<td>404</td>
<td>1.00</td>
<td>Reference</td>
<td></td>
</tr>
<tr>
<td>T</td>
<td>127</td>
<td>102</td>
<td>1.41</td>
<td>1.05-1.90</td>
<td>0.02</td>
</tr>
</tbody>
</table>

**Table 3. Relation of VEGF polymorphism and characteristics.**

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>TT+CT (n=111)</th>
<th>CC (n=94)</th>
<th>OR</th>
<th>95% CI</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tumor location</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Extremities</td>
<td>49</td>
<td>42</td>
<td>1.00</td>
<td>Reference</td>
<td></td>
</tr>
<tr>
<td>Non-extremities</td>
<td>62</td>
<td>52</td>
<td>1.02</td>
<td>0.59-3.43</td>
<td>0.94</td>
</tr>
<tr>
<td>Metastasis</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>80</td>
<td>77</td>
<td>1.00</td>
<td>Reference</td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>31</td>
<td>17</td>
<td>1.76</td>
<td>0.90-3.43</td>
<td>0.10</td>
</tr>
</tbody>
</table>

**Discussion**

In the current study, we investigated the association between the VEGF rs3025039 polymorphism and osteosarcoma risk. The VEGF rs3025039 TT genotype was significantly higher in the osteosarcoma group than in the control group. The TT genotype and CT genotype was also significantly associated
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with osteosarcoma risk. Under the allelic model, T allele of rs3025039 was significantly associated with higher osteosarcoma risk. In addition, VEGF rs3025039 TT genotype was not associated with tumor location and metastasis.

Zhang et al. found that vascular endothelial growth factor overexpression predicted a worse prognosis for laryngeal cancer patients [9]. Zhao et al. indicated that high plasma/intratumoral VEGF-A level at baseline could predict poor treatment effect (depressed PFS and OS) of BEV-based chemotherapy in mCRC [10]. Cai et al. found that high level of VEGF is associated with poor outcomes in HCC patients treated with sorafenib [11]. Hui et al. indicated that the OS of the VEGF-positive group with ovarian cancer was significantly poorer than the VEGF-negative group [12]. Ma et al. suggested that both the VEGF +936C/T and -634G/C polymorphisms influence breast cancer susceptibility and tumor growth, instead of metastasis [13].

This study has some limitations. The selective bias was mostly controlled by the design of a hospital-based case-control study. As other case-control studies, this study raises concern about recall bias and residual confounding. The major difficulty is still the inability to separate exposures to factors prior to clinical onset from exposures to factors after clinical onset.

In conclusion, this study confirmed that VEGF rs3025039 polymorphism was significantly associated with higher risk of osteosarcoma risk.

References


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