Association between IL-8 genetic polymorphisms and the risk of ovarian cancer in a Chinese population.

Yuchong Hu$^{1,2}$, Jingkun Lu$^3$, Aiming Wang$^{1,4,*}$

$^1$Southern Medical University, Guangzhou, PR China
$^2$Department of Obstetrics and Gynaecology, Inner Mongolia Autonomous Region People’s Hospital, Hohhot, PR China
$^3$School of Basic Medical Sciences, Inner Mongolia Medical College, Hohhot, PR China
$^4$The PLA Navy General Hospital, Beijing, PR China

Abstract

Objective: To perform a 1:1 matched case-control study to evaluate the role of IL-8 rs4073, rs1126647 and rs2227306 polymorphisms in the development of ovarian cancer in a population of China.

Methods: A total of 280 patients with ovarian cancer and 280 healthy controls were recruited. Genotyping of IL-8 rs4073, rs1126647 and rs2227306 were run in a 384-well plate format on the sequenom MassARRAY platform.

Results: Patients with ovarian cancer were more likely to have higher BMI (OR=1.12, 95% CI=1.06-1.17), a long term use of hormone replacement therapy (OR=3.58, 95% CI=1.28-10.01) and a habit of alcohol drinking (OR=1.47, 95% CI=1.01-2.14). Moreover, those carrying the AT (OR=1.50, 95% CI=1.05-2.16) and TT (OR=2.26, 95% CI=1.18-4.35) genotypes were associated with a higher risk of ovarian cancer when compared with those with the AA genotype. The AT+TT genotype was correlated with higher risk of ovarian cancer in comparison to the AA genotype (OR=1.58, 95% CI=1.12-2.24). A linkage disequilibrium was found between rs4073 and rs1126647 ($D'=0.572$, $r^2=0.12$). A total of four common haplotypes (frequency>0.03) were selected into analysis, and the A-C-T haplotype showed a reduced risk of ovarian cancer, with the OR (95% CI) of 0.74 (0.56-0.99).

Conclusions: Our results support direct association of IL-8 rs4073 polymorphism and A-C-T haplotype with the risk of ovarian cancer, suggesting that the IL-8 may be a new biomarker for the susceptibility to ovarian cancer.

Keywords: Ovarian cancer, IL-8, Polymorphism, Haplotypes.

Introduction

Ovarian cancer is common malignant tumor with high mortality in females worldwide, and it is a serious threat to women’s health [1,2]. The high mortality of this cancer is mainly due to the majority of the patients present with advanced stages at the time of diagnosis [3,4]. The etiology of ovarian cancer has been widely investigated and reported, but its pathogenesis is not fully clear. Many environment, dietary and lifestyle factors play an important role in the development of ovarian cancer, such as the choice not to or inability to bear children, higher body mass index and receiving long-term of estrogen replacement therapy and ovulation inducing drugs [3]. However, the incidence of ovarian cancer varies greatly across different populations even when they are exposure to the same environment, dietary and lifestyle factors, indicating that genetic factors play an important role in the induction of ovarian cancer.

Interleukin (IL-8) is a pro-inflammatory chemokine known for its angiogenetic activity, which is involved in regulating both inflammatory and immune processes [5-7]. IL-8 is also responsible for tumor-associated angiogenesis in several malignant tumors [5,8].

Previous studies have shown that IL-8-251A/T (rs4073), +1633C/T (rs1126647) and +781C/T (rs2227306) and genetic polymorphisms were correlated with the susceptibility of malignant tumors. Few study reported the association of IL-8 polymorphism with risk of ovarian cancer in a population of Germany [9].

Therefore, we performed a 1:1 matched case-control study to evaluate the role of IL-8 rs4073, rs1126647 and rs2227306 polymorphisms in the development of ovarian cancer in a Chinese population.
Materials and Methods

Subjects
A total of 280 patients with ovarian cancer were recruited in our study between May 2014 and May 2016, and all the patients were recruited from the Department of Obstetrics and Gynaecology at the Inner Mongolia Autonomous Region People’s Hospital and Southern Medical University. All the patients with ovarian cancer were newly diagnosed within one month and confirmed by histopathology. Patients with a history of other malignant tumors, recurrent or metastasis ovarian cancer were excluded from this study.

Simultaneously, a total of 280 healthy controls which were frequency-matched to the cases by age (within 5 y old) were recruited into our study. All the healthy controls were selected from the outpatient clinics and physical examination center of the Inner Mongolia Autonomous Region People’s Hospital and Southern Medical University.

The demographic and clinical characteristics were collected from medical records and questionnaires. All the patients and controls were interviewed face-to-face by trained graduate students. Ever smoking included current and former smoking, and it was defined as those who smoked at least 20 cigarettes within one week and lasted for 6 months. The others were defined as never smoking. Ever drinking included current and former drinking and it was defined as those who drank at least 50 ml white wine, 250 ml beer or 250 ml wine within one month and lasted for 6 months. The others were grouped into never drinking. Study subjects agreed to participate into our study and signed a consent form prior to enrolment. Our research was approved by the Research Ethics Committee of the Inner Mongolia Autonomous Region People’s Hospital and Southern Medical University.

SNP genotyping
Each patient was asked to provide a 3 mL peripheral venous blood sample. DNA samples were isolated from peripheral venous blood of patients and controls by a TIANamp Blood DNA Kit (Tiangen, Beijing, China) using standard procedures. Primers for Polymerase Chain Reaction (PCR) amplification were designed by Sequenom Assay Design 3.1 software. Genotyping of IL-8 rs4073, rs1126647 and rs2227306 were run in a 384-well plate format on the sequenom MassARRAY platform (Sequenom, San Diego, USA). PCR amplification was carried out with an initial denaturation at 94°C for 2 min; 45 cycles of 95°C for 30 s; 56°C for 30 s and 72°C for 60 s; then a final extension of 72°C for 5 min. The PCR products were desalted, dispensed to a SpectroCHIP and analyzed with MALDI-TOF MS.

Statistics
The differences in the demographic and clinical characteristics and genotype frequencies were compared by Chi-square ($\chi^2$) test and student t-test. The Hardy-Weinberg Equilibrium (HWE) of IL-8 rs4073, rs1126647 and rs2227306 was evaluated by Chi-square with one degree of freedom.

The association of IL-8 rs4073, rs1126647 and rs2227306 with the risk of ovarian cancer was evaluated by binary multivariate logistic regression, and the results were displayed by Odds Ratio (OR) and 95% confident intervals (95% CI). The linkage disequilibrium and haplotype analyses of IL-8 rs4073, rs1126647 and rs2227306 were analyzed using SHEsis software.

The analyses were performed by IBM SPSS Statistics for Windows, Version 21.0. (IBM Corp, Armonk, NY, USA), and all the statistical tests were two-sided and $P<0.05$ was set as a statistical significance.

Results
By $\chi^2$ or t-tests, we observed significant differences between patients with ovarian cancer and controls in terms of age at diagnosis ($t=0.46, P=0.02$), use of hormone replacement therapy ($\chi^2=7.66, P=0.01$) and BMI ($t=0.46, P=0.02$) (Table 1).

Table 1. Demographic and clinical data of included patients with ovarian cancer and controls.

<table>
<thead>
<tr>
<th>Category</th>
<th>Patients N=280</th>
<th>%</th>
<th>Controls N=280</th>
<th>%</th>
<th>$\chi^2$ or t tests</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age at diagnosis, years</td>
<td>51.60 ± 7.09</td>
<td>51.34 ± 6.24</td>
<td>0.46</td>
<td>0.02</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Education</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Less than middle school</td>
<td>55</td>
<td>19.64</td>
<td>58</td>
<td>20.71</td>
<td>0.75</td>
<td></td>
</tr>
<tr>
<td>Middle school or above</td>
<td>225</td>
<td>80.36</td>
<td>222</td>
<td>79.29</td>
<td>0.1</td>
<td></td>
</tr>
<tr>
<td>Smoking</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>241</td>
<td>86.07</td>
<td>240</td>
<td>85.71</td>
<td>0.46</td>
<td></td>
</tr>
<tr>
<td>Ever</td>
<td>39</td>
<td>13.93</td>
<td>39</td>
<td>13.93</td>
<td>0.02</td>
<td></td>
</tr>
<tr>
<td>Drinking</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>187</td>
<td>66.79</td>
<td>208</td>
<td>74.29</td>
<td>0.46</td>
<td></td>
</tr>
</tbody>
</table>
The AA, AT and TT genotype distributions of IL-8 rs4073 revealed significant difference between patients with ovarian cancer and controls ($\chi^2=8.35$, $P=0.02$) (Table 2). However, the genotype distribution of IL-8 rs1126647 and rs2227306 did not show significant differences between the two study groups. Moreover, the genotype frequencies of IL-8 rs4073, rs1126647 and rs2227306 confirms to the HWE in controls.

By binary logistic regression analysis, we found that patients with ovarian cancer were more likely to have higher BMI (OR=1.12, 95% CI=1.06-1.17), a long term use of hormone replacement therapy (OR=3.58, 95% CI=1.28-10.01) and a habit of alcohol drinking (OR=1.47, 95% CI=1.01-2.14). Moreover, those carrying the AT (OR=1.50, 95% CI=1.05-2.16) and TT (OR=2.26, 95% CI=1.18-4.35) genotypes were associated with a higher risk of ovarian cancer when compared with those with the AA genotype (Table 3). Moreover, the AT+TT genotype was correlated with higher risk of ovarian cancer in comparison to the AA genotype (OR=1.58, 95% CI=1.12-2.24). No significant association was found between rs1126647 and rs2227306 polymorphisms and risk of ovarian cancer.

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A linkage disequilibrium was found between rs4073 and rs1126647 (D'=0.57, r²=0.12) (Table 4). A total of four common haplotypes (frequency>0.03) were selected into analysis, and the A-C-T haplotype showed a reduced risk of ovarian cancer, with the OR (95% CI) of 0.74 (0.56-0.99) (Table 5). The other three haplotypes were not correlated with the development of ovarian cancer.

**Table 4. Linkage disequilibrium tests for IL-8 rs4073, rs1126647 and rs2227306.**

<table>
<thead>
<tr>
<th></th>
<th>rs1126647</th>
<th>rs2227306</th>
</tr>
</thead>
<tbody>
<tr>
<td>D'</td>
<td>0.572</td>
<td>0.003</td>
</tr>
<tr>
<td>rs4073</td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs1126647</td>
<td>0.09</td>
<td></td>
</tr>
<tr>
<td>r²</td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs4073</td>
<td>0.12</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>rs1126647</td>
<td></td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

**Table 5. Haplotype analysis of rs4073-rs1126647-rs2227306.**

<table>
<thead>
<tr>
<th></th>
<th>Cases N=560</th>
<th>%</th>
<th>Controls N=560</th>
<th>%</th>
<th>P value</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A-C-T</td>
<td>214</td>
<td>38.21</td>
<td>236</td>
<td>42.14</td>
<td>0.15</td>
<td>0.84 (0.66-1.07)</td>
</tr>
<tr>
<td>T-C-C</td>
<td>120</td>
<td></td>
<td>21.43</td>
<td>89</td>
<td>0.17</td>
<td>1.43 (0.90-1.94)</td>
</tr>
<tr>
<td>T-C-T</td>
<td>72</td>
<td></td>
<td>12.86</td>
<td>50</td>
<td>0.25</td>
<td>1.50 (0.92-2.20)</td>
</tr>
</tbody>
</table>

Global χ²=12.68, P=0.013.

**Discussion**

It is widely accepted that ovarian cancer is a multifactorial disease, and pathogenesis of ovarian cancer can be facilitated by a single dominant mutation altering expression of susceptibility genes. In the present study, we found that the AT and TT genotypes of IL-8 rs4073 increased the risk of ovarian cancer when compared with the AA genotype, and the A-C-T haplotype was associated with a reduced risk of ovarian cancer.

In agreement with our findings, previous studies reported a significant association between IL-8 rs4073 gene polymorphism and several kinds of human cancer, such as prostate cancer, thyroid cancer, oral squamous cell carcinoma, colorectal cancer and breast cancer as well as gastric cancer [10-15]. Chen et al. performed a study with 439 prostate cancer patients and 524 controls, and they did not find an association between rs4073 and risk of prostate cancer [10]. Kiliç et al. conducted a study consisting of 101 patients with thyroid cancer and 109 healthy controls, and they reported that the TT genotype of IL-8 rs4073 may contribute to the risk of thyroid cancer.
carcinomas [11]. Liu et al. performed a study with 270 patients with oral squamous cell carcinoma and 350 healthy control subjects in a Taiwanese population, and they suggested that IL-8 gene polymorphisms was associated with risk of oral squamous cell carcinoma in smokers [12]. Mustapha et al. done a study in Malaysians, and they observed that IL-8 rs4073 was significantly related to the colorectal cancer susceptibility and can be considered as a high-risk variant for colorectal cancer [13]. Some studies reported contrary results [16,17]. Burada et al. did not find the association between IL-8 rs4073 and colorectal cancer risk, but no significant correlation was observed between them.

However, only one study reported the association between IL-8 polymorphisms and risk of ovarian cancer. Koensgen et al. performed a study with 268 patients with ovarian cancer and 426 matched controls in a population of German, and they investigated the association of four SNPs of IL-8 gene with the risk of ovarian cancer [9]. They found that the TT genotype of IL-8 rs2227306 was correlated with an increased frequency of ovarian cancer, but the IL-8 rs4073 did not show a significant association [9]. In contrast with previous results, we found that the IL-8 rs4073 T allele contributed to increased risk of ovarian cancer.

Moreover, we firstly reported linkage disequilibrium between rs4073 and rs1126647, and the A-C-T haplotype showed a reduced risk of ovarian cancer. It could be hypothesis that mutation linked to the IL-8 haplotypes could alter the activity and expression of IL-8, and consequently affect the susceptibility to ovarian cancer.

Two limitations should be mentioned in this study. First, as a case-control study design, the selection bias is unavoidable. Second, as the low incidence of ovarian cancer, the sample size of patients with ovarian cancer was not large, potential restricting its statistical power to distinguish difference between study groups.

Conclusions

In conclusion, our results support direct association of IL-8 rs4073 polymorphism and A-C-T haplotype with the risk of ovarian cancer, suggesting that the IL-8 may be a new biomarker for the susceptibility to ovarian cancer. Further researches with larger studies in different ethnic groups into the function of IL-8 polymorphisms and its potential biological mechanisms association are needed.

Acknowledgement

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Declaration of Conflicting Interest

The authors declare no conflict of interest in preparing this article.

References


*Correspondence to
Aiming Wang
Southern Medical University
Guangzhou
PR China