RESEARCH ARTICLE

Variants of Interleukin-16 Associated with Gastric Cancer Risk

Tao Zhang*, Hui Wang

Abstract

**Aim:** We conducted a case-control matched study to investigate the role of IL-16 gene polymorphisms, rs4072111, rs1131445, rs4778889 and rs11556218, in the risk of gastric cancer in a Chinese population, also performing subgroup analysis by subsites. **Methods:** To test the hypothesis of involvement, we analyzed the four SNPs of IL-16 in 347 cancer patients and 368 controls. Demographic data and other information were collected using a newly designed questionnaire. Genotyping of IL-16 (rs4072111, rs1131445, rs4778889 and rs11556218) was performed in a 384-well plate format on the MassARRAY® platform. **Results:** In our study, we found the gastric cancer patients were more likely to be male and have a family history of cancer (P < 0.05). We found the rs4778889 CC and rs11556218 GG genotype was significantly associated with 1.97 and 1.84-fold increased risk of non-cardia gastric cancer, while we did not find significant association between the four IL-16 SNPs and cardia gastric cancer. **Conclusions:** In conclusion, our study indicated that IL-16 rs4778889 CC and rs11556218 GG genotypes are associated with an increased risk of non-cardia gastric cancer in a Chinese population. Our results offer insights into the influence of IL-16 on development of gastric cancer.

**Keywords:** Interleukin-16 - gastric cancer - polymorphisms - Chinese population

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Introduction

Worldwide, gastric cancer is the second leading cause of death from cancer, with an estimated one million new cases in 2008 (988 000 cases), accounting for 8% of all cancer-related death worldwide. More than 70% of all gastric cancer cases occurred in developing countries, and approximately half of all cases occur in China (IARC, 2008). Although many epidemiologic studies suggest that Helicobacter pylori (H. pylori) infection is one of the most important risk factors for gastric cancer, it is estimated almost 50% of the world’s population are infected with H. pylori, but only about 1% of them occur gastric cancer (Graham et al., 1991; Parsonnet et al., 1997). Therefore, changes in lifestyle/environmental factors and improved health care as well as genetic factors may influence the susceptibility to gastric cancer (Ghoshal et al., 2007; Ghoshal et al., 2008).

The interleukin (IL) represent a diverse constellation of cytokines which regulate the function of immune system in human. They are produced predominantly by T cells, monocytes, macrophages, and endothelial cells. They have multiple functions including facilitating communication between immune cells, controlling genes, regulating transcription factors, and governing the inflammation, differentiation, proliferation, and secretion of antibodies (Salazar-Onfray et al., 2007), and the single nucleotide polymorphisms of genes encoding ILs and their receptor may alter cytokine function and dysregulate its expression, as well as cause defects in cytokine cascades (Yuzhalin, 2011). Consequently, individual genetic differences caused by SNPs may be closely related to these disruptions and eventually play a role in gastric carcinogenesis. IL-16 is considered a proinflammatory cytokine and located on chromosome 15q26.3 in humans. IL-16 is precursor protein consisting of 631 amino acids, which is cleaved by caspase-3 to form the active C-terminal domain containing 121 amino acids (Baier et al., 1997; Drwinga et al., 1993; Zhang et al., 1998), and can promote the secretion of tumor-associated inflammatory cytokines by monocytes, such as IL-1b, IL-6 and IL-15 (Mathy et al., 2000), and play an important role in the carcinogenesis of human cancers (Schneider et al., 2000; Chung and Chang, 2003; Kai et al., 2005; Shanmugham et al., 2006). Recent experimental and epidemiological studies have demonstrated that IL-16 could be a candidate susceptibility gene in gliomas and prostate cancer (Liebrich et al., 2007; Thomas et al., 2008). Higher serum levels of IL-16 have also been associated with advanced stages of cancer and a worse patient outcome depending on the type of tumor.

Most of the studies on IL-16 gene polymorphisms were focused on the inflammatory related diseases (Gu et al., 2008; Mahindra et al., 2012; Huang et al., 2013; Milke et al., 2013), and few of them on the development of gastric cancer. Therefore, the role of IL-16 gene polymorphisms on the risk of gastric cancer was still unknown. We conducted a case-control matched study to investigate the role of IL-16 gene polymorphisms, rs4072111, rs1131445, rs4778889 and rs11556218, on the risk of gastric cancer in a Chinese population, and conducted subgroup analysis by subsites (cardia or non cardia gastric cancer).

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Materials and Methods

Study population and design
All the subjects were collected from the Centre Hospital of Wuhan between December 2008 and November 2011. A total of 385 patients with newly histopathologically confirmed primary gastric cancer, including cardia and non-cardia gastric cancer, were included in our study. Of 385 patients, 347 patients were willing to participate into our study, with a participation rate of 90.1%. All the cases were selected from the Centre Hospital of Wuhan. Patient who suffered from secondary or recurrent tumors were excluded from our study. A total of 426 controls were selected from the same hospital during the same time period from outpatients in Surgical Department, Plastic Surgery Department and ENT Department. Finally, 368 controls agreed to participate into our study, with a participation rate of 86.4%. All patients were asked to provide 5ml blood samples for DNA extraction.

Genotyping
Blood samples, collected and stored as described above, were collected from all study participants in EDTA-coated tubes. The buffy coat was collected and total DNA was extracted using a TIANamp blood DNA kit (Tiangen Biotech, Beijing, China). We selected potential functional SNPs of interested XPF from Database of single nucleotide polymorphisms (SNPs) of NCBI (http://www.ncbi.nlm.nih.gov/) and SNPinfo (http://snpinfo.niehs.nih.gov/) with the following criteria: (1) the minor allele frequency ≥10% of the Chinese population; (2) influencing the microRNA binding sites activity.

Genotyping of IL16 (rs4072111, rs1131445, rs4778889 and rs11556218) was performed in a 384-well plate format on the MassARRAY® platform (Sequenom®, San Diego, CA, USA), which combines polymerase chain reaction (PCR) and matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry technologies. PCR single base extension (SBE) primers (Table 1) were designed using Sequenom® Assay Design, Version 3.1 software (Sequenom®), according to the manufacturer’s instructions. Each PCR reaction mix comprised 50ng genomic DNA, 200 μM dNTP, 2.5 U Taq DNA polymerase (Promega, Madison, WI, USA) and 200 μM primers, in a total volume of 20 μl. The cycling programme involved preliminary denaturation at 94°C for 2 min, followed by 35 cycles of denaturation at 94°C for 30 s, annealing at 64°C for 30 s, and extension at 72°C for 1 min. PCR products were verified by 1.0% agarose gel electrophoresis and visualized via ethidium bromide staining and ultraviolet light. Genotyping was performed without knowledge of the case/control status of the subjects, and reproducibility was confirmed by repeat analysis of a randomly chosen subgroup of 5% of study participants.

Statistical analysis
Continuous variables were presented as mean ± SD and analysed using the independent-samples t-test. Categorical variables were presented as n (%) of subjects and analysed using the χ²-test. The Hardy–Weinberg equilibrium and between-group comparison of genotype distribution were analyzed using the χ²-test. Odds ratios (OR) and their corresponding 95% confidence intervals (CI) were used to assess the effect of each SNP on CAD risk. Multivariate logistic regression analysis was performed to calculate the OR (95% CI) after adjusting for sex, smoking status, BMI, hypertension, diabetes, TC, TG, LDL-C and HDL-C. A P-value < 0.05 was considered statistically significant. All statistical analyses were performed using SPSS® software, version 11.0 (SPSS Inc., Chicago, IL, USA) for Windows®.

Results
The demographic and clinic characteristics of the selected cases and controls were shown in Table 2. The mean ages of the 347 cases with gastric cancer and 368
The rs11556218T/G polymorphism is located in the exon 6 region of the IL-16 gene, this is a missense mutation, wherein asparagine (Asn) is substituted by lysine (Lys). Recently, several studies reported that rs11556218T/G polymorphisms were associated with risk of various diseases (Gao et al., 2009a; Azimzadeh et al., 2011; Wu et al., 2011; Batia et al., 2012). A recent study conducted in Sichuan of China reported that rs11556218T/G polymorphism was significantly associated with the susceptibility to NPC, and TG genotype was associated with a significantly higher risk of NPC as compared with the TT genotype (Gao et al., 2009a). Another study also conducted in China showed that the TG/GG genotypes of rs11556218T/G were associated with a significantly increased risk of coronary artery disease as compared with the TT genotype, with a odds ratio (95% CI) of 1.97 (1.09-3.54), and T allele of rs4778889 was associated with increased risk of non-cardia gastric cancer, while IL-16 rs4072111C>T polymorphisms were associated with risk of developing non-cardia gastric cancer, while IL-16 rs4072111C>T and rs1151445T>C polymorphisms had no association. Moreover, we did not find the four IL-16 SNPs were association with risk of cardiac gastric cancer.

**Discussion**

The IL-16 generally functions as an immunosuppressor and anti-inflammatory mediator, and has been implicated in autoimmune disease and progression of malignancies (Azimzadeh et al., 2012; Yellapa et al., 2012; Li et al., 2011; Gao et al., 2009a). Currently, there was only one study reported the association between IL-16 polymorphisms and risk of gastric cancer (Gao et al., 2009a), and this case-control study indicated that rs11556218T/G and rs4072111C/Tpolymorphisms of the IL-16 gene was significantly associated with the susceptibility to gastric cancer patients. In our case-control study, we analyzed genetic polymorphisms of IL-16 rs4072111, rs1131445, rs4778889 and rs11556218 for gastric cancer risk in a Chinese population. The main finding in our study was that IL-16 rs4778889 CC and rs11556218 GG genotypes were associated with an increased risk of developing non-cardia gastric cancer, while IL-16 rs4072111C>T and rs1131445T>C polymorphisms had no association. Moreover, we did not find the four IL-16 SNPs were association with risk of cardiac gastric cancer.
The rs4778889C/T polymorphism is located at 295 bp upstream from the start site of transcription and is associated with altered levels of gene expression (Nakayama et al., 2000). Compared with rs11556218T/G, evidences of association of rs4778889C/T polymorphism with disease are limited. Only three studies assessed the association between rs4778889C/T polymorphism and risk of disease (Gao et al., 2009a; Gao et al., 2009b; Azimzadeh et al., 2011). Azimzadeh et al. (2011) reported that IL-16 rs4778889C/T polymorphism showed significant association with 0.192 fold decreased risk of colorectal cancer. However, another two studies conducted in China reported the IL-16 rs4778889C/T polymorphism has no role in the development of gastric cancer, colorectal cancer and nasopharyngeal cancer (Gao et al., 2009a; Gao et al., 2009b). Our study reported an increased risk of gastric cancer, which was not in line with previous studies.

The inconsistency of these studies may be explained by differences in ethnicities, source of control subjects, sample size and etc. Further their confirmation of existing findings is still needed in future studies.

In the sub-analysis, we found that IL-16 rs4778889 CC and rs11556218 GG genotypes were associated with increased risk of non-cardia gastric cancer, but no association with cardia gastric cancer. This inconsistency between the non-cardia and cardia gastric cancer results could be induced by the etiology, pathology, carcinogenesis, and prognosis of cardia and non-cardia gastric cancer. This possibility is also indirectly supported by previous studies (Ni et al., 2012; Xue et al., 2012), which indicated a lack of association of Interleukin promoter polymorphisms with risk of non-cardia cancer. Caution should be taken when interpreting the significance of these findings, because the sample size of non-cardia gastric cancer cases and controls in our study are relatively same, and they may not represent the same population. Therefore, further large sample size study with a priori hypothesis for cardia and non-cardia gastric cancer risk is warranted.

In conclusion, our study indicated that IL-16 rs4778889 CC and rs11556218 GG genotypes are associated with an increased risk of non-cardia gastric cancer in a Chinese population, but no significant association was found in cardia gastric cancer. Our results should be confirmed in future large sample size study. Because the polymorphism of IL-16 can increase the risk of cancer, it could be used to explore the role of IL-10 polymorphisms in the development of gastric cancer in different clinical stages and different subsites.

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References


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