RESEARCH ARTICLE

Lack of Association of Common Polymorphisms in MUC1 Gene with *H. pylori* Infection and Non-cardia Gastric Cancer Risk in a Chinese Population

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Abstract

Several lines of evidence support the notion that MUC1 is often aberrantly expressed in gastric cancer, and it is a ligand for Helicobacter pylori. Genetic variation in MUC1 gene may confer susceptibility to *H. pylori* infection and gastric cancer. We assessed the association of common polymorphisms in MUC1 gene with *H. pylori* infection and non-cardia gastric cancer using an LD-based tag SNP approach in north-western Chinese Han population. A total of four SNPs were successfully genotyped among 288 patients with non-cardia gastric cancer and 281 age- and sex-matched controls. None of the tested SNPs was associated with *H. pylori* infection. SNP rs9426886 was associated with a decreased risk of non-cardia gastric cancer, but lost significance after adjustment for multiple testing. Overall, our data indicated that common genetic variations in MUC1 gene might not make a major contribution to the risk of *H. pylori* infection and non-cardia gastric cancer in our studied population.

Keywords: Non-cardia gastric cancer - MUC1 - *H. pylori* infection - polymorphism - risk

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Introduction

Gastric cancer, the second most common cause of cancer-related death in the world, is characterized as a multifactorial disease that results from individual genetic predisposition and exposure to environmental factors (Brenner et al., 2009). According to anatomic site, gastric cancer can be classified as cardia and non-cardia subtypes. In non-cardia gastric cancer, Helicobacter pylori (*H. pylori*) infection is an established etiological factor (Peek and Blaser, 2002). However, nearly half of the world’s population is infected with *H. pylori*, but only a very small proportion of those infected eventually develop non-cardia gastric cancer (Peek and Blaser, 2002), suggesting that genetic factors of host may play an important role in gastric carcinogenesis.

Upon infection, *H. pylori* primarily resides within the mucus layer, adhering to mucins, high molecular weight glycoproteins and major components of the protective layer across the upper mucous surfaces (Peek and Blaser, 2002; Lindén et al., 2008). Some works have documented the role of MUC1 in the *H. pylori* infection and gastric cancer risk. Thus, MUC1 is often aberrantly expressed in stomach cancer, and it is a ligand for *H. pylori* (Ng et al., 2008). Susceptibility to *H. pylori* infection and gastric cancer appears to be associated with MUC1 allele length (Costa et al., 2008; Vinall et al., 2002). Recently, a functional single nucleotide polymorphism (SNP) rs4072037 in MUC1 gene has been associated with risk of gastric cancer (Xu et al., 2009; Jia et al., 2010; Zhang et al., 2011) with controversial results (Abnet et al., 2010; He et al., 2013). Because gastric cancer has potential genetic heterogeneity among different populations, the current study was conducted to investigate whether common polymorphisms in MUC1 gene were associated with *H. pylori* infection, and with non-cardia gastric cancer risk in north-western Chinese Han population.

Materials and Methods

Subjects

This case control study was carried out in Baotou, Inner Mongolian Autonomous Region, north-western China. Patients were consecutively recruited between June 2008 and December 2010 at the cancer hospital of Baotou. All patients with histopathologically confirmed incident non-cardia gastric cancer were enrolled. The exclusion criteria of cases included having previous cancer, any metastasized cancer (carcinomas were not originally from stomach) and having previous radiotherapy or chemotherapy. The controls, frequency-matched to the cases on age (± 5 years) and sex, were cancer-free individuals randomly selected from a community health examination program in Baotou during the same period.

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Genomic DNA was isolated by standard proteinase K digestion and phenol-chloroform extraction from the blood sample. Among all subjects, SNP rs4072037 was genotyped by sequence-specific primers-polymerase chain reaction (PCR-SSPs) as described elsewhere (Xu et al., 2009), but with a little modification. Briefly, the forward primer was 5'-CTATGGGCACAGAGAAGGAG-3' (primer 1), the reverse SSPs 5'-AGCTTGCATGCCAGAACCT-3' (primer 2) and 5'-AGCTTGCATGCCAGAACCT-3' (primer 3) were used in combination with the consensus forward primer. The primer 1 and 2 led to the allele G, while the primer 1 and 3 led to the allele A. PCRs were conducted in 25 µl volumes containing 60 ng genomic DNA, 200 µM dNTPs, 0.2 µM each upstream and downstream primer, 1xPCR buffer, and 1 U Taq DNA polymerase. The primers and reagents were purchased from Takara Inc., Japan. The PCR protocol was 95°C for 1 min, 5 cycles with 95°C for 40 sec, 70°C for 45 sec, 72°C for 30 sec, then followed by 21 cycles of 95°C for 40 sec, 63°C for 50 sec, 72°C for 30 sec, and then 8 cycles of 95°C for 50 sec, 55°C for 60 sec, 72°C for 90 sec. The PCR product size was 233 bp. More than 10% of the samples were randomly selected for the repeated assays by different persons, and the results were 100% consistent. Genotyping of other four SNPs were performed at Chinese national human genome center, Beijing, using TagMan method (Applied Biosystems, Foster City, CA, USA). SNP rs3738808 was excluded because of genotyping failure. The genotyping rates of other three SNPs were all above 90% and failed genotypes were not repeated. For quality control purpose, genotyping was performed with blinding to the subjects’ case and control status. In addition, six negative experimental controls (water) and six positive experimental controls with known genotype were included in each reaction plate.

### Statistical analysis

The student’s t- and χ² test were used to evaluate differences in the distributions of age and sex between cases and controls, respectively. Hardy-Weinberg equilibrium was tested by a goodness-of-fit χ² test. Haplotypes were constructed based on the LD blocks derived from the Haplovie 4.0 program. Unconditional logistic regression was used to calculate odds ratios (ORs) and 95% confidence intervals (CIs) adjusted for age and sex for non-cardia gastric cancer risk and H. pylori infection in association with genotypes and haplotypes. Statistical significance was assessed by empirical p values derived from the Westfall & Young permutation (n=10,000) to account for type I errors of multiple testing (Westfall and Young, 1993). All statistical analyses were conducted by SPSS software version 16.0 (SPSS Inc., Chicago, IL, USA).

### Results

There were 281 controls and 288 cases in the study. The demographic of subjects are summarized in Table 1. There were no significant differences between the two groups with respect to the age and gender distribution. The infection rate of H. pylori among controls was 43.6%. All studied SNPs followed Hardy-Weinberg equilibrium in controls. None of the four SNPs analyzed...
Table 3. Association Between Studied SNPs and Non-cardia Gastric Cancer

<table>
<thead>
<tr>
<th>SNPs</th>
<th>Genotype</th>
<th>Controls</th>
<th>Cases</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs4072037</td>
<td>AA</td>
<td>177 (63.0)</td>
<td>179 (62.6)</td>
<td>Reference</td>
</tr>
<tr>
<td></td>
<td>AG</td>
<td>92 (32.7)</td>
<td>92 (33.2)</td>
<td>1.022 (0.717-1.456)</td>
</tr>
<tr>
<td></td>
<td>GG</td>
<td>12 (4.3)</td>
<td>12 (4.2)</td>
<td>0.990 (0.433-2.265)</td>
</tr>
<tr>
<td>rs2990245</td>
<td>TT</td>
<td>192 (69.8)</td>
<td>222 (77.6)</td>
<td>Reference</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>77 (28.0)</td>
<td>61 (21.4)</td>
<td>0.689 (0.467-1.017)</td>
</tr>
<tr>
<td>rs9628662</td>
<td>GG</td>
<td>169 (61.2)</td>
<td>184 (65.2)</td>
<td>Reference</td>
</tr>
<tr>
<td></td>
<td>GT</td>
<td>90 (32.6)</td>
<td>88 (31.3)</td>
<td>0.900 (0.627-1.291)</td>
</tr>
<tr>
<td>rs4926886</td>
<td>TT</td>
<td>157 (67.7)</td>
<td>214 (75.4)</td>
<td>Reference</td>
</tr>
<tr>
<td></td>
<td>AT</td>
<td>65 (28.0)</td>
<td>66 (23.2)</td>
<td>0.747 (0.500-1.122)</td>
</tr>
<tr>
<td></td>
<td>AA</td>
<td>10 (4.3)</td>
<td>4 (1.4)</td>
<td>0.290 (0.089-0.942)</td>
</tr>
</tbody>
</table>

*Sum of column did not add up to total study subjects because of missing data; *a Adjusted for age and sex; *The permutation p value >0.05

demonstrated a significant association with *H. pylori* infection (Table 2). Minor allele homozygote of rs9426886 was associated with a decreased risk of non-cardia gastric cancer when compared with its major allele homozygote, but was not significant after adjustment for multiple testing. No significant association was detected between other three SNPs and non-cardia gastric cancer risk (Table 3).

Based on the LD data in our study, four SNPs formed one main block and two singletons. rs2990245 and rs9628662 were in one block, but neither the status of *H. pylori* infection nor the risk of non-cardia gastric cancer was significantly associated with any haplotypes in our population (data not shown).

Discussion

To our best knowledge, this is the first comprehensive study to investigate the association of common polymorphisms in MUC1 gene with *H. pylori* infection and non-cardia gastric cancer risk by tagSNP approach in Chinese population. None of the four studied SNPs showed a statistically significant association with the status of *H. pylori* infection and the overall risk of non-cardia gastric cancer in our studied population.

Gastric cancer includes non-cardia gastric and cardia gastric carcinoma. Two subtypes might have different clinical, epidemiological, etiological, and molecular features (Kim et al., 2005; Correa, 2004). So we restricted our samples to patients with non-cardia gastric cancer to supply relatively more homogeneous samples and improve the power of association study.

One population-based case-control study has been conducted to investigate the association between polymorphisms in MUC1 gene and *H. pylori* infection as well as gastric cancer risk by a comprehensive LD-based tagSNP approach in Polish population (Jia et al., 2010). The results indicated that common polymorphisms were not associated with *H. pylori* infection, which was in agreement with ours. On the contrary, the study showed all tested tagSNPs were significantly associated with an increased risk of gastric cancer. The inconsistency of two studies may be due to the different ethnic population with genetic heterogeneity. Further studies are needed to clarify the possible mechanisms.

SNP rs4072037, located at the 5’ end of exon 2 in **MUC1** gene, controls the alternative splicing of **MUC1** (Xu et al., 2009). In our study, the frequencies of AA, AG, and GG genotypes in controls were 62.7, 32.4, and 4.9%, respectively, which was similar to the data from other studies in Chinese population (Xu et al., 2009; Zhang et al., 2011) and those from HapMap Chinese data. And our results indicated that SNP rs4072037 was not significantly associated with non-cardia gastric cancer. To date, several reports about the relationship between rs4072037 and gastric cancer have been published. Xu et al reported that the AA genotype of SNP rs4072037 was significantly associated with an increased risk of gastric cancer based on 138 cases and 241 controls from north-eastern Chinese (Xu et al., 2009). But their controls consisted of 131 patients with superficial gastritis and 110 patients with atrophic gastritis. And atrophic gastritis is the well-established precursor lesion of gastric cancer. Moreover, their study did not provide information for association between rs4072037 and non-cardia gastric cancer. Furthermore, the same group failed to identify that rs4072037 was associated with the risk of gastric cancer in another study (He et al., 2013). Zhang et al found that SNP rs4072037 was significantly associated with both non-cardia gastric cancer and cardia gastric cancer in eastern Chinese population using a relatively larger sample size (Zhang et al., 2011). One possible explanation for the discrepancy between their study and ours is that the modulation of gastric cancer risk might depend not only on a single gene/single SNP, but also on a joint effect of multiple polymorphisms within different genes, or on close interaction between polymorphisms and environmental factors (Jiang et al., 2010). Of course, we could not exclude that the inconsistent might be result from our small sample size. More interestingly, on the basis of Chinese population, Anbet et al performed a GWAS in 1625 cases with gastric cancer and 2100 controls and identified that SNP rs4072037 was significantly associated with gastric cancer risk in the initial scanning phase. However, the observed association was not supported in the second phase, as well as in the combined data (Anbet et al., 2010). Moreover, one study reported that SNP 4072037 was not associated with the risk of chronic atrophic gastritis (Frank et al., 2012), the important precursor lesion of gastric cancer. Three studies mentioned above suggested that our results might not be by chance.

Several limitations in our study needed to be addressed. First of all, we recruited cases from one hospital and selected controls from communities, which might not be representative of the general population and resulted in potential selection bias. Secondly, because the data of *H. pylori* infection was not available among cases, it is difficult for us to adjust the potential confounding bias from *H. pylori* infection. However, it is difficult to measure *H. pylori* infection in gastric cancer patients because the loss of *H. pylori* from the stomach and reduced immune response occurs during gastric carcinogenesis (Karnes et
al., 1991; Farinati et al., 1993). Thus, a prospective study should be further conducted for concomitant analysis of the genetic susceptibility and exposure to H. pylori. Finally, our sample size was in general small, so we cannot exclude the possibility that we failed to detect a smaller genetic effect of MUC1 polymorphisms.

In conclusion, our results indicated that common polymorphisms in MUC1 gene were not associated with H. pylori infection and non-cardia gastric cancer risk in our studied population. Additional studies are required to reveal the real relationship between genetic variations of MUC1 gene and gastric cancer risk.

Acknowledgements

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References


