Susceptibility to Gastric Cardia Adenocarcinoma and Genetic Polymorphisms in Methyleneetetrahydrofolate Reductase in an At-Risk Chinese Population

Xiaoping Miao, Deyin Xing, Wen Tan, Jun Qi, Wenfu Lu, and Dongxin Lin

Department of Etiology and Carcinogenesis, Cancer Institute, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100021, People’s Republic of China

Abstract
Methylenetetrahydrofolate reductase (MTHFR) plays a central role in converting folate to methyl donor for DNA methylation, an epigenetic modification known to be dysregulated in carcinogenesis. Our previous study revealed that MTHFR polymorphisms contribute to a great risk of esophageal cancer in a Chinese population. This case-control study was to examine the association between MTHFR polymorphisms and gastric cardia adenocarcinoma (GCA), which is also prevalent in high-risk areas of esophageal cancer. The study subjects were 217 patients with GCA and 468 population controls matched on sex and age. The MTHFR C677T and A1298C genotypes were detected by a PCR-based RFLP assay. It was found that subjects with the MTHFR C677T variant genotype had a 2-fold increased risk of GCA (odds ratio, 2.04; 95% confidence interval, 1.28–3.26). Moreover, a significantly elevated risk was also seen among the MTHFR 677CT heterozygotes (odds ratio, 1.56; 95% confidence interval, 1.03–2.36). The MTHFR A1298C polymorphism had no effect on risk of GCA. These findings are generally consistent with our initial observation for esophageal cancer and suggest that the MTHFR genotype may be a determinant of GCA among this at-risk Chinese population.

Introduction
Epidemiological studies have shown an association between low consumption of vegetables and fruits and increased risk of cancers including gastroesophageal cancer (1–3). Folate is one of the important constituents of vegetables and fruits that may provide protection against cancer. An important function of folate is to provide methyl groups required for intracellular methylation reactions and de novo deoxyribonucleoside synthesis. Therefore, folate deficiency is thought to be carcinogenic through disruption of DNA methylation, synthesis, and repair (4, 5). However, to serve as a mediator of methylation, folate requires metabolism catalyzed by several enzymes. Thus, it is likely that not only folate deficiency but also functional polymorphisms in genes associated with impaired folate metabolism may contribute to cancer risk.

MTHFR plays a central role in biotransformation of folate to form S-adenosylmethionine, the universal methyl donor in cells (6). Two single nucleotide polymorphisms in the MTHFR gene, 677C→T and 1298A→C, have been identified, and the variant genotypes are associated with a significant reduction of enzyme activity (7, 8). Individuals with the MTHFR variant genotypes have elevated plasma homocysteine levels compared with the wild-type genotype, indicating a decline in remethylation of homocysteine to methionine (9, 10). It has been shown that genomic DNA methylation is diminished in subjects with the MTHFR 677TT genotype, particularly when folate intake is inadequate (11, 12). DNA hypomethylation has been linked to the activation of oncogenes and chromosome instability (13, 14), which are common events in carcinogenesis.

GCA is a common cancer in China as well as in the rest of the world. In China, this cancer is more prevalent in areas of high-risk of esophageal cancer. For example, in Linxian, a well-known high-risk area for esophageal cancer, one-third of the gastroesophageal cancers occurred in the gastric cardia (15). GCA differs from gastric cancer at other sites in epidemiological characteristics, etiology, pathogenesis, and clinical behavior (16) but may share common risk factors with esophageal cancer for carcinogenesis. Epidemiological studies have identified some environmental risk factors for esophageal cancer and GCA, which include nutritional deficiency, especially low consumption of vegetables and fruits, a major source of folate (1–3, 17–19). Because folate deficiency is linked to carcinogenesis, we hypothesized that the MTHFR polymorphisms, which disrupt folate metabolism, may play a role in developing gastroesophageal cancer. Recently, we have shown a strong association between MTHFR C677T and A1298C polymorphisms and increased risk of esophageal cancer in a high-risk population in China (20). This report described a case-control study that aimed to test the hypothesis in GCA in the same population.

Materials and Methods
Study Subjects. This case-control study consisted of 217 patients with GCA and 468 population controls. All subjects were...
Table 1  Select characteristics and smoking status in patients with GCA and controls

<table>
<thead>
<tr>
<th>Variable</th>
<th>Cases (n = 217)</th>
<th>Controls (n = 468)</th>
<th>P*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, n (%)</td>
<td>0.68</td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤55 years</td>
<td>79 (36.4)</td>
<td>178 (38.0)</td>
<td></td>
</tr>
<tr>
<td>&gt;55 years</td>
<td>138 (63.6)</td>
<td>290 (62.0)</td>
<td></td>
</tr>
<tr>
<td>Sex, n (%)</td>
<td>0.25</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>178 (82.0)</td>
<td>366 (78.2)</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>39 (18.0)</td>
<td>102 (21.8)</td>
<td></td>
</tr>
<tr>
<td>Smoking status, n (%)</td>
<td>0.81</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>92 (42.4)</td>
<td>203 (43.4)</td>
<td></td>
</tr>
<tr>
<td>Ever</td>
<td>125 (57.6)</td>
<td>265 (56.6)</td>
<td></td>
</tr>
</tbody>
</table>

*Two-sided χ² test.

Table 2  Genotype frequencies of MTHFR 677 and 1298 polymorphisms among cases with GCA and controls and their contributions to the risk of GCA

<table>
<thead>
<tr>
<th>MTHFR 677</th>
<th>Cases (n = 217)</th>
<th>Controls (n = 468)</th>
<th>OR (95% CI)*</th>
</tr>
</thead>
<tbody>
<tr>
<td>C677T</td>
<td>n (%)</td>
<td>n (%)</td>
<td></td>
</tr>
<tr>
<td>CC</td>
<td>47 (21.7)</td>
<td>151 (32.3)</td>
<td>1.19 (0.81–1.74)</td>
</tr>
<tr>
<td>CT</td>
<td>107 (49.3)</td>
<td>217 (46.4)</td>
<td>1.56 (1.03–2.36)</td>
</tr>
<tr>
<td>TT</td>
<td>63 (29.0)</td>
<td>100 (21.3)</td>
<td>2.04 (1.28–3.26)</td>
</tr>
<tr>
<td>T allele frequency</td>
<td>0.54</td>
<td>0.44</td>
<td></td>
</tr>
<tr>
<td>A1298C</td>
<td>n (%)</td>
<td>n (%)</td>
<td></td>
</tr>
<tr>
<td>AA</td>
<td>150 (69.1)</td>
<td>324 (69.2)</td>
<td>1.19 (0.81–1.74)</td>
</tr>
<tr>
<td>AC</td>
<td>64 (29.5)</td>
<td>139 (29.7)</td>
<td>1.19 (0.81–1.74)</td>
</tr>
<tr>
<td>CC</td>
<td>3 (1.4)</td>
<td>5 (1.1)</td>
<td>2.41 (0.51–11.37)</td>
</tr>
<tr>
<td>C allele frequency</td>
<td>0.16</td>
<td>0.16</td>
<td></td>
</tr>
</tbody>
</table>

* ORs and 95% CIs were calculated in a logistic regression model with MTHFR 677CC or 1298AA as the reference group and adjusted for sex, age, smoking status, and relevant polymorphism.

Results

The relevant characteristics of the study subjects are shown in Table 1. The distributions of age and gender among cases and controls were not statistically different. The median age was 56.5 years (range, 41–72 years) for the case group and 54.1 years (range, 45–76 years) for the control group. Eighty-two percent of cases and 78.2% of controls were male. The distribution of smokers was not significantly different between cases (57.6%) and controls (56.6%). No familial GCA was reported among cases with GCA and controls and their contributions to the risk of GCA.

The 1298AA wild-type homozygotes produce five fragments of 56, 31, 30, 28, and 18 bp; 1298AC heterozygotes produce six fragments of 84, 56, 31, 28, and 18 bp; and 1298CC homozygous variants produce four fragments of 84, 31, 28, and 18 bp. To ensure quality control, genotyping was performed with blinded to case/control status, and a 15% random sample of cases and controls was genotyped twice by different persons, and the reproducibility was 100%.

Statistical Analysis.  Pearson’s χ² test was used to examine differences in demographic variables, smoking, and distributions of genotypes between cases and controls. The association between the MTHFR polymorphisms and risk of GCA was estimated using ORs and their 95% CIs, which were calculated by unconditional logistic regression and adjusted for age, sex, and smoking status. Tests for interaction between the MTHFR 677 and 1298 polymorphisms were performed by using the likelihood ratio test. All analyses were performed with Statistical Analysis System software (version 6.12; SAS Institute, Cary, NC).

Genotyping results (Table 2) show that the allele frequency for MTHFR 677T was 0.54 among GCA patients compared with 0.44 among controls. The observed frequencies of three MTHFR C677T genotypes among controls (CC, 32.3%; CT, 46.4%; and TT, 21.3%) were not different from those expected from the Hardy-Weinberg equilibrium (P = 0.65). However, they were significantly different from those among cases (CC, 21.7%; CT, 49.3%; and TT, 29.0%; χ² = 9.7; P = 0.008). Subjects who carried the MTHFR 677TT genotype were at a 2-fold increased risk for developing GCA (adjusted OR, 2.04; 95% CI, 1.28–3.26) compared with subjects who carried the MTHFR 677CC genotype. Furthermore, a significantly elevated risk of GCA was also observed among subjects carrying...
the MTHFR 677CT genotype (adjusted OR, 1.56; 95% CI, 1.03–2.36).

The allele frequencies for MTHFR 1298C were 0.16 in both GCA patients and controls. The distribution among AA, AC, and CC (1.1%) was also in accordance with the Hardy-Weinberg equilibrium (P = 0.17) and was not significantly different from that among cases (AA, 69.1%; AC, 29.5%; and CC, 1.4%). Although the adjusted ORs of GCA for the MTHFR 1298AC and 1298CC genotypes were 1.19 (95% CI, 0.81–1.74) and 2.41 (95% CI, 0.51–11.37) compared with the 1298AA genotype, none of them reached statistical significance (Table 2). In the stratification analysis, sex, age, and smoking status had no effect on the risk of GCA related to the two polymorphisms in the MTHFR gene, whereas adjustment for the MTHFR 677 polymorphism had great effect on the OR for the 1298CC genotype (OR increased from 1.30 to 2.41).

Results of the analysis of the combined effect of the MTHFR 677 genotypes and 1298 genotypes on risk of GCA are shown in Table 3. No subject in our study was homozygous for the mutant alleles at both sites (677TT/1298CC). Although the existence of the 677CT/1298CC or 677TT/1298AC variants was rare, cases appeared more likely to carry both of these variant genotypes than their corresponding controls. Among subjects carrying both MTHFR 677CT and 1298AA genotypes, the OR was 2.47 (95% CI, 1.33–4.60); however, the OR was 13.46 (95% CI, 1.19–infinity) among individuals who carried both 677CT and 1298CC genotypes. Similarly, the OR for individuals carrying the 677TT/1298AC genotype was 11.03 (95% CI, 1.37–88.89) compared with 2.80 (95% CI, 1.50–5.24) for those carrying 677TT/1298AA genotype. However, a homogeneity test showed that none of these differences was statistically significant, probably due to the very small number of both variant alleles in analysis.

Discussion

We have shown in our previous study that the MTHFR 677 and 1298 polymorphisms were strong genetic risk factors for esophageal cancer in a high-risk Chinese population (20). Starting with the hypothesis that GCA may share common etiological factors with esophageal cancer in this population, we examined the hypothesis that GCA may share common etiological factors with esophageal cancer in this population, we examined the hypothesis that GCA may share common etiological factors with esophageal cancer in this population. After this paper had been submitted for publication, Stolzenberg-Solomon et al. (23) reported a similar result in a cohort study in Linxian, China, a high-risk area for esophageal squamous cell carcinoma and GCA. They showed that individuals with the MTHFR 677TT genotype had significantly higher risk for these two cancers (relative risk, 1.45; 95% CI, 1.02–2.05). In addition, they showed that an increased risk of esophageal cancer was also related to a polymorphism in MTRR, a gene encoding for methionine synthase reductase, for which folate and vitamin B12 are cofactors. These findings further support our observations in the present study and previous one (20).

Although selection bias and/or systematic error might occur in a case-control study due to inappropriate selection of subjects and the presence of other confounding factors, the results in this study, which had a relatively large number of subjects, solid and reproducible genotyping techniques, and significantly increased ORs with small Ps, are unlikely to be due to selection bias. The fact that allele and genotype frequencies among our controls in this independent study are consistent with those in our previous study (20) and those reported in the Chinese population by other investigators (21, 24) further supports the randomness of our control selection. In addition, the observed risk effect of the variant MTHFR 677 genotypes was not influenced by other potential predictors of GCA risk such as age, sex, and smoking. Thus, it is unlikely that subject selection or unknown confounding factors could have biased our results in this study.

Because folate deficiency is associated with cancer, and folate requires metabolism for its functions, an impact on cancer risk by impaired folate metabolism resulting from polymorphisms of MTHFR is biologically plausible. MTHFR plays a central role in folate metabolism, and low MTHFR activity may prevent the shunting of methyl groups from de novo dTMP synthesis, a rate-limiting step for DNA synthesis, to methyla-

<p>| Table 3: Risk of GCA associated with the MTHFR C677T genotypes by A1298C genotypes |
|---------------------------------|-------------------|-------------------|-------------------|</p>
<table>
<thead>
<tr>
<th>MTHFR 677 MTHFR 1298 Cases (%)</th>
<th>Controls (%)</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC AA</td>
<td>17 (7.8)</td>
<td>78 (16.7)</td>
</tr>
<tr>
<td>CC AC</td>
<td>28 (12.9)</td>
<td>68 (14.5)</td>
</tr>
<tr>
<td>CC CC</td>
<td>2 (0.9)</td>
<td>5 (1.1)</td>
</tr>
<tr>
<td>CT AA</td>
<td>73 (33.5)</td>
<td>148 (31.6)</td>
</tr>
<tr>
<td>CT AC</td>
<td>33 (15.2)</td>
<td>69 (14.8)</td>
</tr>
<tr>
<td>CT CC</td>
<td>1 (0.5)</td>
<td>0 (0.0)</td>
</tr>
<tr>
<td>TT AA</td>
<td>60 (27.8)</td>
<td>98 (20.9)</td>
</tr>
<tr>
<td>TT AC</td>
<td>3 (1.4)</td>
<td>2 (0.4)</td>
</tr>
<tr>
<td>TT CC</td>
<td>0 (0.0)</td>
<td>0 (0.0)</td>
</tr>
</tbody>
</table>

* ORs and 95% CIs were calculated in a logistic regression model with both MTHFR677CC and 1298AA as the reference group and adjusted for sex, age, and smoking status.

**Test of significance and the 95% CI were based on the exact conditional distribution.

P = 0.19.

P = 0.008.

A1298C polymorphism with risk of GCA and joint effect between A1298C and C677T polymorphisms, which is consistent with that reported by Shen et al. (21) for GCA but is not in agreement with our previous observation for esophageal cancer (20). Possible explanation for this difference between GCA and esophageal cancer could be that the esophageal tissue may be more susceptible than gastric cardia to carcinogenesis due to MTHFR polymorphisms because reduction of MTHFR functional activity caused by the 1298A→C mutation is significantly less than that caused by the 677C→T mutation (10). After this paper had been submitted for publication, Stolzenberg-Solomon et al. (23) reported a similar result in a cohort study in Linxian, China, a high-risk area for esophageal squamous cell carcinoma and GCA. They showed that individuals with the MTHFR 677TT genotype had significantly higher risk for these two cancers (relative risk, 1.45; 95% CI, 1.02–2.05). In addition, they showed that an increased risk of esophageal cancer was also related to a polymorphism in MTRR, a gene encoding for methionine synthase reductase, for which folate and vitamin B12 are cofactors. These findings further support our observations in the present study and previous one (20).

Although selection bias and/or systematic error might occur in a case-control study due to inappropriate selection of subjects and the presence of other confounding factors, the results in this study, which had a relatively large number of subjects, solid and reproducible genotyping techniques, and significantly increased ORs with small Ps, are unlikely to be due to selection bias. The fact that allele and genotype frequencies among our controls in this independent study are consistent with those in our previous study (20) and those reported in the Chinese population by other investigators (21, 24) further supports the randomness of our control selection. In addition, the observed risk effect of the variant MTHFR 677 genotypes was not influenced by other potential predictors of GCA risk such as age, sex, and smoking. Thus, it is unlikely that subject selection or unknown confounding factors could have biased our results in this study.

Because folate deficiency is associated with cancer, and folate requires metabolism for its functions, an impact on cancer risk by impaired folate metabolism resulting from polymorphisms of MTHFR is biologically plausible. MTHFR plays a central role in folate metabolism, and low MTHFR activity may prevent the shunting of methyl groups from de novo dTMP synthesis, a rate-limiting step for DNA synthesis, to methyla-

Downloaded from cebp.aacrjournals.org on November 6, 2017. © 2002 American Association for Cancer Research.
tion pathways (6). Although these two pathways are both important in protecting against carcinogenesis, different mechanisms might exist to influence susceptibility to carcinogenesis via balances between the methyl group provision and dTMP synthesis in individuals with the variant MTHFR genotypes. It has been suggested that cancer risk associated with MTHFR polymorphisms may be modulated by folate intake (25, 26). When folate intake is sufficient, individuals carrying the variant MTHFR genotypes may have a decreased risk because under these conditions, while adequate provision of methyl donors could still be ensured, enhanced genomic integrality would be achieved via conserving folate within a cyclic pathway inside cells by shunting methyl groups toward nucleotide synthesis due to diminished MTHFR activity. However, in the population where folate intake is low, both DNA methylation and DNA synthesis/repair might be impaired in the carriers of variant MTHFR genotypes, which, in turn, results in increased risk of carcinogenesis. This hypothesis for gene-nutrient interaction may explain the conflicting reports showing reduced risk of leukemia (27, 28) and colorectal cancer (25, 26) or elevated risk of endometrial cancer (29), cervical intraepithelial neoplasia (30), breast and/or ovarian cancer (31), esophageal cancer (20), and GCA (Ref. 21 and this study). However, alternative mechanisms may also exist to explain these conflicting results. For example, this may reflect the variation of different cancer sites and histology in response to the aberrant methylation resulting from MTHFR polymorphisms. It is possible that in the case of cancer types for which MTHFR polymorphisms increase the risk, activation of proto-oncogenes by aberrant methylation may be predominant mechanism, whereas in the case of cancers for which MTHFR polymorphisms reduce the risk, deficiency in methyl donors may protect against hypermethylation-induced silencing of tumor suppressor genes and thus lower the risk. It is interesting to note that folic acid deficiency-induced uracil incorporation into primary human lymphocyte DNA was not altered in vitro by the MTHFR C677T polymorphism (32). Additional studies to test the effects of MTHFR polymorphisms and folate deficiency on different types of cells would be helpful to clarify the mechanisms.

Folate deficiency has been shown to be common in various regions of China including Beijing (33–35), and a number of epidemiological studies conducted in the Chinese population have consistently indicated an inverse association between consumption of vegetables and fruits, an major source of folate, and risk of gastroesophageal cancer (2, 3, 19). Based on these data and findings observed in our present study, DNA hypomethylation should be considered as a possible molecular mechanism by which MTHFR polymorphisms increase the risk of GCA development. Consistent with this postulation, a recent study has shown that genomic DNA methylation was significantly lower in subjects with the MTHFR 677TT genotype compared with those with the 677CC genotype and that the methylation status in subjects with the MTHFR 677TT genotype was directly correlated with RBC folate levels (11, 12). DNA hypomethylation can result in chromosome instability and aberrant gene expression, which are commonly observed in many human cancers and in the early stages of carcinogenesis (13, 14, 36, 37). For instance, it has been shown that global genomic DNA hypomethylation caused by folate depletion is often accompanied by overexpression of oncogenes such as c-myc and c-Ha-ras (38, 39) and mutations in tumor suppressor genes such as Apo and p53 (40) in carcinogenesis. Taken together, these data provide very plausible molecular mechanisms through which suboptimal cellular folate levels and MTHFR polymorphisms could increase the risk for development of GCA.

In conclusion, our study demonstrates a significant association between the MTHFR C677T variant genotypes and risk of GCA in an at-risk Chinese population. These results are consistent with the findings in our previous study for esophageal cancer and strongly indicate that folate deficiency and/or impaired folate metabolism may play a role in gastroesophageal carcinogenesis. A larger population-based case-control study designed to determine interactions between folate/homocysteine metabolism genes and between these genes and folate intake on elevated risk of gastroesophageal cancers is under way in our laboratory.

References
MTHFR Polymorphism and Gastric Cardia Cancer


Susceptibility to Gastric Cardia Adenocarcinoma and Genetic Polymorphisms in Methylene-tetrahydrofolate Reductase in an At-Risk Chinese Population

Xiaoping Miao, Deyin Xing, Wen Tan, et al.


Updated version
Access the most recent version of this article at:
http://cebp.aacrjournals.org/content/11/11/1454

Cited articles
This article cites 38 articles, 14 of which you can access for free at:
http://cebp.aacrjournals.org/content/11/11/1454.full#ref-list-1

Citing articles
This article has been cited by 8 HighWire-hosted articles. Access the articles at:
http://cebp.aacrjournals.org/content/11/11/1454.full#related-urls

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.