miRNA-146a rs2910164 C>G polymorphism increased the risk of esophagogastric junction adenocarcinoma: a case–control study involving 2,740 participants

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Purpose: The miRNA-146a rs2910164 C>G polymorphism may contribute to the development of cancer. However, the association between this polymorphism and the risk of esophagogastric junction adenocarcinoma (EGJA) remains unclear. In the present study, we carried out a case–control study to explore the potential relationship between miRNA-146a rs2910164 C>G polymorphism and EGJA risk.

Patients and methods: In total, 1,063 EGJA patients and 1,677 cancer-free controls were enrolled. The SNPscan™ genotyping assay, a patented technology, was used to test the genotyping of miRNA-146a rs2910164 C>G polymorphism.

Results: We found that miRNA-146a rs2910164 C>G polymorphism was associated with a risk of developing EGJA (additive model: adjusted odds ratio (OR), 1.27; 95% CI, 1.07–1.51; P=0.006; homozygote model: adjusted OR, 1.31; 95% CI, 1.03–1.65; P=0.027 and dominant model: adjusted OR, 1.36; 95% CI, 1.15–1.60; P<0.001). After adjustment for the Bonferroni correction, these associations were also found in additive and dominant genetic models. In the subgroup analyses, after adjustment by sex, age, alcohol consumption, and smoking status, results of multiple logistic regression analysis indicated that miRNA-146a rs2910164 C>G polymorphism increased the risk of EGJA in males, females, <64 years old, ≥64 years old, never smoking, and never drinking subgroups.

Conclusion: The current study highlights that the miRNA-146a rs2910164 C>G polymorphism increased the risk of EGJA in eastern Chinese Han population.

Keywords: miRNA-146a, polymorphism, esophagogastric junction adenocarcinoma

Introduction

Gastric carcinoma (GC) is the second most commonly diagnosed cancer and the second leading cause of cancer-related death in China,1 with an estimated 679,100 new GC cases and 498,000 related deaths in 2015.1 The esophagogastric junction adenocarcinoma (EGJA) was proposed by Siewert in 1999 as a unique disease: EGJA is considered as a special clinical malignancy and its clinicopathologic characteristic and biologic behavior are quite different from that of GC. EGJA may be a multifactorial disease, which is caused by a number of potential susceptibility factors, involving genetic predisposition, overweight, obesity, and environmental factors (eg, foods preserved by salting, smoking, drinking, and so on). The incidence and prevalence of EGJA are increasing worldwide in recent decades,2–4 most likely as a result of increases in the prevalence of overweight/obesity and of chronic gastroesophageal reflux disease.5 The
increase may also be related to the decreasing prevalence of *Helicobacter pylori* infection, which may be a protective factor for EGJA. Although these mentioned factors may contribute to the etiology of EGJA, hereditary factors may also influence the incidence of EGJA. As malignancy-related deaths can be decreased by controlling susceptibility factors, early diagnosis, and more effective treatment, the identification of new biomarkers may be beneficial for early detection and prevention of EGJA.

MicroRNAs (miRNAs) are a series of single-stranded noncoding-RNA molecule (including about 22 nucleotides), which are found in plants, animals, and some viruses. In general, miRNAs are similar to the small-interfering RNAs. The functions of miRNAs are RNA-silencing and suppression of translation. Previous studies suggested that miRNAs were implicated in a number of complex biologic processes (eg, cell differentiation, development, apoptosis, proliferation, and so on). Accumulating evidence demonstrates that the expression of many vital genes may be regulated by miRNAs. It was reported that most of the miRNAs acted on cancer-related genomic areas, and this might contribute to oncogenesis. Recently, Shin and Chu reported that miRNAs might act as important biomarkers and therapeutic targets of GC.

Single-nucleotide polymorphisms (SNPs) are a common genetic variation that occurs at a certain position in the genome. SNPs occur more frequently in noncoding regions than in coding regions. Results of previous investigations indicated that SNPs may influence susceptibility to human diseases. SNPs in miRNAs could influence both their expression and function, which might, therefore, alter the risk of cancer. In addition, several case–control studies and functional investigations reported that miRNA SNPs could affect GC susceptibility and their influence was closely related to their role in miRNAs’ expression. Although there are some case–control studies indicating that the rs2910164 C>G polymorphism in miRNA-146a could influence the risk for gastric cancer, the association between this polymorphism and the risk of EGJA remains unclear. To shed some light on this issue, we enrolled 2,740 participants to investigate the potential relationship between the miRNA-146a rs2910164 C>G polymorphism and EGJA susceptibility.

**Materials and methods**

**Subjects**

This hospital-based case–control study consisted of 280 EGJA patients who were consecutively recruited between January 2014 and May 2016 from the Affiliated Union Hospital and the Affiliated Cancer Hospital of Fujian Medical University. An additional 783 EGJA patients were consecutively recruited from the Affiliated People’s Hospital of Jiangsu University from January 2008 to November 2016. The EGJA patients were enrolled without any restriction of age. We have defined EGJA as tumors that have their center within 5 cm proximal and distal of the anatomical cardia. Siewert type I EGJA has its center within 1–5 cm proximal of the anatomical cardia. In addition, Siewert type II and III EGJA have their center within 1 cm proximal and 2 cm distal, and 2–5 cm distal of the anatomical cardia, respectively. In the present study, all Siewert type II EGJA cases were diagnosed by gastroscope and during surgery. All of the cases were recruited before their operation and pathologically confirmed.

Those EGJA cases who received chemotherapy or radiotherapy or had a history of other malignancy were excluded. For comparison, 1,677 cancer-free subjects matched with the EGJA cases were recruited as controls. All subjects were unrelated. Each participant answered a questionnaire by face-to-face interview. Experienced doctors collected the useful information on demographic variables and risk factors. The related data are listed in Table 1. A written informed consent was signed by each participant. This study protocol was in accordance with the Declaration of Helsinki and approved by the ethics committee of Jiangsu University (Zhenjiang, China) and Fujian Medical University (Fuzhou, China). In this study, each participant donated a blood sample, which was anticoagulated with EDTA.

**Selection of SNPs**

To determine the potential relationship between miRNA SNPs and EGJA risk, we selected the miRNA-146a rs2910164 C>G polymorphism according to the literature, which was significantly associated with cancer, type 2 diabetes, autoimmune diseases, and coronary artery disease in some studies. The corresponding information about the miRNA-146a rs2910164 C>G polymorphism is presented in Table 2.

**DNA extraction and genotyping**

Genomic DNA was extracted from the peripheral blood samples collected in EDTA test tubes using a DNA Purification Kit (Promega, Madison, WI, USA). SNPscan® genotyping assay (Genesky Biotechnologies Inc., Shanghai, China) was used to analyze the genotyping of miRNA-146a rs2910164.
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Table 1 Distribution of selected demographic variables and risk factors in esophagogastric junction adenocarcinoma cases and controls

<table>
<thead>
<tr>
<th>Variable</th>
<th>Overall cases (n=1,063)</th>
<th>Overall controls (n=1,677)</th>
<th>P-value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, mean (±SD)</td>
<td>64.19 (±8.63)</td>
<td>63.91 (±10.22)</td>
<td>0.451</td>
</tr>
<tr>
<td>Age (years)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;64</td>
<td>494 (46.47)</td>
<td>825 (49.19)</td>
<td>0.165</td>
</tr>
<tr>
<td>≥64</td>
<td>569 (53.53)</td>
<td>852 (50.81)</td>
<td></td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>759 (71.40)</td>
<td>1194 (71.20)</td>
<td></td>
</tr>
<tr>
<td>Female</td>
<td>304 (28.60)</td>
<td>483 (28.80)</td>
<td></td>
</tr>
<tr>
<td>Smoking status</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>773 (72.72)</td>
<td>1323 (78.89)</td>
<td></td>
</tr>
<tr>
<td>Ever</td>
<td>290 (27.28)</td>
<td>354 (21.11)</td>
<td></td>
</tr>
<tr>
<td>Alcohol use</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Never</td>
<td>908 (85.42)</td>
<td>1507 (89.86)</td>
<td></td>
</tr>
<tr>
<td>Ever</td>
<td>155 (14.58)</td>
<td>170 (10.14)</td>
<td></td>
</tr>
<tr>
<td>Lymph node status</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>625 (58.80)</td>
<td>170 (10.14)</td>
<td></td>
</tr>
<tr>
<td>Negative</td>
<td>438 (41.20)</td>
<td>170 (10.14)</td>
<td></td>
</tr>
<tr>
<td>Tumor–node–metastasis stage</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I+II</td>
<td>305 (28.69)</td>
<td>758 (71.31)</td>
<td></td>
</tr>
<tr>
<td>III+IV</td>
<td>758 (71.31)</td>
<td>710 (68.69)</td>
<td></td>
</tr>
</tbody>
</table>

Notes: aTwo-sided chi-square and Student’s t-test. Bold values are statistically significant (P<0.05).

Table 2 Primary information for hsa-miR-146a rs2910164 C>G polymorphism

<table>
<thead>
<tr>
<th>Genotyped polymorphism</th>
<th>hsa-miR-146a rs2910164 C&gt;G</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chr</td>
<td>5</td>
</tr>
<tr>
<td>Position_37</td>
<td>160485411</td>
</tr>
<tr>
<td>Region</td>
<td>nc transcript variant</td>
</tr>
<tr>
<td>MAF for Chinese in database</td>
<td>0.43</td>
</tr>
<tr>
<td>MAF in our controls (n=1,677)</td>
<td>0.38</td>
</tr>
<tr>
<td>P-value for HWE test in our controls</td>
<td>0.919</td>
</tr>
<tr>
<td>% Genotyping value</td>
<td>99.09</td>
</tr>
</tbody>
</table>

Abbreviations: Chr, chromosome; HWE, Hardy–Weinberg equilibrium; MAF, minor allele frequency; nc, noncoding.

C>G polymorphism. In brief, a 150 ng DNA sample was heated to 98°C and held for 5 minutes. The ligation reaction was carried out in an ABI 2720 thermal cycler. Then, a 48-plex fluorescence polymerase chain reaction (PCR) was conducted. In an ABI 3730XL sequencer, capillary electrophoresis was harnessed to analyze the PCR products. GeneMapper 4.1 software (Applied Biosystems, Foster City, CA, USA) was used to read the information of the genotype. For quality control, different technicians genotyped 4% of the genomic DNA samples that were randomly selected. And, the results were in full accord with the findings of the first assays.

Statistical analysis

The distribution of age was expressed as the mean ± SD. The age difference between EGJA patients and cancer-free controls was evaluated by using the Student’s t-test. Differences in the distributions of age, sex, smoking and drinking status, and frequencies of miRNA-146a rs2910164 C>G genotype between EGJA cases and controls were assessed using the χ²-test (for categorical variables). We used an online calculator (http://ihg.gsfc.nasa.gov/cgi-bin/hw/hwa1.pl) to assess Hardy–Weinberg equilibrium (HWE) in controls. The relationship between the miRNA-146a rs2910164 C>G polymorphism and susceptibility to EGJA was estimated by calculating crude and adjusted odds ratios (ORs) and 95% CIs. Adjustments were performed by age, sex, and smoking and drinking status using a multiple logistic regression model. A P-value <0.05 (two sided) was accepted as statistically significant. All analyses were conducted with the software SAS 9.4 (SAS Institute, Cary, NC, USA). The Power and Sample Size Calculator (http://biostat.mc.vanderbilt.edu/twiki/bin/view/Main/PowerSampleSize) was harnessed to obtain the power value (α=0.05). We used a Bonferroni correction to adjust for multiple testing.

Results

Baseline characteristics

A total of 2,740 individuals were enrolled for the present case–control study; out of those, 1,677 subjects were healthy participants (controls), and their mean age was 63.91±10.22 years (Table 1). Similarly, for the 1,063 EGJA patients, the mean age at diagnosis was 64.19±8.63 (Table 1). This study was fully matched by age and sex (P=0.451 and 0.909, respectively). The minor allelic frequency distribution of miRNA-146a rs2910164 C>G is 0.38 (Table 2). The success rate of genotyping was 99.09%. Genotype distribution of the miRNA-146a rs2910164 C>G polymorphism is shown in Table 3. The frequencies of miRNA-146a rs2910164 CC, CG, and GG were 38.47%, 47.07%, and 14.52% in control subjects compared to 31.41%, 52.16%, and 16.43% in EGJA patients, respectively. We found that the frequencies of the miRNA-146a rs2910164 CG, GG, and G allele were slightly higher in the EGJA cases than in the control group (52.16% vs 47.07%, 16.43% vs 14.52%, and 42.51% vs 38.47%, respectively).
For the miRNA-146a rs2910164 C>G polymorphism, the power value was 0.808 in the additive model, 0.604 in the homozygote model, and 0.960 in the dominant model.

**Association of miRNA-146a rs2910164 C>G polymorphism with EGJA in different subgroups**

In the subgroup analyses, the genotype frequencies of the miRNA-146a rs2910164 C>G polymorphism in different sex, age, alcohol consumption, and smoking subgroups are summarized in Table 5. After adjustment by sex, age, alcohol consumption, and smoking status, results of multiple logistic regression analysis indicated that the miRNA-146a rs2910164 C>G polymorphism increased risk of EGJA in several subgroups (male group: CG vs CC: \( P=0.012 \) and CG/GG vs CC: \( P=0.002 \); female group: CG/GG vs CC: \( P=0.040 \); <64 years subgroup: CG vs CC: \( P=0.009 \) and CG/GG vs CC: \( P=0.001 \); ≥64 years subgroup: CG/GG vs CC: \( P=0.042 \); never smoking group: CG vs CC: \( P=0.004 \) and CG/GG vs CC: \( P<0.001 \) and never drinking group: CG vs CC: \( P=0.009 \) and CG/GG vs CC: \( P<0.001 \) [Table 5]).

**Association of miRNA-146a rs2910164 C>G polymorphism with lymph node status in EGJA patients**

We found no statistically significant difference in genotype distribution of the miRNA-146a rs2910164 C>G polymorphism with different lymph node status (Table 6).

**Discussion**

As the miRNA SNPs potentially affect the miRNA biogenesis and change the target selection,39 people have paid more attention to the relationship of miRNA polymorphisms with risk of cancer. To the best of our knowledge, this case–control study is the largest sample size used to determine the association between the miRNA-146a rs2910164 C>G polymorphism and risk of EGJA.

**Table 3** The frequencies of miRNA-146a rs2910164 C>G polymorphisms in EGJA patients and controls

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Overall EGJA cases (n=1,063)</th>
<th>Overall controls (n=1,677)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>( n )</td>
<td>%</td>
</tr>
<tr>
<td>CC</td>
<td>327</td>
<td>31.41</td>
</tr>
<tr>
<td>CG</td>
<td>543</td>
<td>52.16</td>
</tr>
<tr>
<td>GG</td>
<td>171</td>
<td>16.43</td>
</tr>
<tr>
<td>CG+GG</td>
<td>714</td>
<td>68.59</td>
</tr>
<tr>
<td>CC+CG</td>
<td>870</td>
<td>83.57</td>
</tr>
<tr>
<td>GG</td>
<td>171</td>
<td>16.43</td>
</tr>
<tr>
<td>G allele</td>
<td>885</td>
<td>42.51</td>
</tr>
</tbody>
</table>

**Table 4** miRNA-146a rs2910164 C>G polymorphism with esophagogastric junction adenocarcinoma

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Crude OR (95% CI)</th>
<th>( P )-value</th>
<th>Adjusted OR* (95% CI)</th>
<th>( P )-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Additive model</td>
<td>1.28 (1.08–1.52)</td>
<td>0.005</td>
<td>1.27 (1.07–1.51)</td>
<td>0.006</td>
</tr>
<tr>
<td>Homozygote model</td>
<td>1.31 (1.03–1.65)</td>
<td>0.027</td>
<td>1.31 (1.03–1.65)</td>
<td>0.027</td>
</tr>
<tr>
<td>Dominant model</td>
<td>1.37 (1.16–1.61)</td>
<td>&lt;0.001</td>
<td>1.36 (1.15–1.60)</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Recessive model</td>
<td>1.16 (0.94–1.43)</td>
<td>0.178</td>
<td>1.16 (0.94–1.44)</td>
<td>0.166</td>
</tr>
</tbody>
</table>

**Notes:** *Adjusted for age, sex, smoking status, and alcohol use in a logistic regression model. Bold values are statistically significant (\( P<0.05 \)).

**Abbreviation:** OR, odds ratio.
In our study, it was established that the miRNA-146a rs2910164 C>G polymorphism significantly increased the risk of EGJA in overall comparison. Furthermore, in the subgroup analyses, results of multiple logistic regression analysis suggested that the miRNA-146a rs2910164 C>G polymorphism increased the risk of EGJA in male, female, <64 years, ≥64 years, never smoking, and never drinking subgroups. With the promoting application of gene-related studies, it is highly encouraged to assess the association between the miRNA-146a rs2910164 C>G polymorphism and cancer risk to obtain robust and replicable results. Considering the fact that most of the genetic variants usually have a low or moderate influence on future cancer susceptibility, this case–control study emphasizes the necessity of related large sample sizes to obtain a sufficiently precise estimate between the miRNA-146a rs2910164 C>G variants and the
development of EGJA. Recently, a number of case–control investigations focused on the relationship of the rs2910164 C>G variants with cancer risk. Subsequently, several quantitative assessment studies have reported positive signals of the miRNA-146a rs2910164 C>G polymorphism with cancer risk.41,44 In addition, several meta-analyses indicated that the miRNA-146a rs2910164 C>G polymorphism also increased the risk of GC.45–48 However, the association between this polymorphism and the risk of EGJA remains controversial. Xia et al reported that the miRNA-146a rs2910164 C>G polymorphism was not correlated with the development of gastric cardia adenocarcinoma,49 while Okubo et al found it associated with increased risk of upper third anatomic locations GC.50 Considering that only two case–control studies with related small sample sizes focusing on the relationship of this SNP with risk of EGJA, the results are still obscure. We recruited 2,740 participants to determine the potential relationship between the miRNA-146a rs2910164 C>G polymorphism and EGJA susceptibility. And we found that the C>G polymorphism increased the risk of overall EGJA susceptibility, which was very similar to the previous studies in Asians.23,51,52 However, the observed results should be interpreted with caution. An evident variation in allele frequency of the miRNA-146a rs2910164 G has been identified across different populations, ranging from 0.362 in Asians to 0.774 in Caucasians.53 In the future, more case–control studies with larger sample sizes and detailed gene–environment factors should be performed to confirm or refute these associations.

Some limitations in our study must be acknowledged. Firstly, in this study, only the miRNA-146a rs2910164 C>G polymorphism was included for exploring the association between this SNP and EGJA risk, and other SNP loci in the miRNA gene were not considered. Secondly, because of lack of sufficient EGJA samples, a replication study was not conducted. Thirdly, the relationship of the miRNA-146a rs2910164 C>G polymorphism with cancer subtypes or tumor stages was not analyzed. These limitations might decrease the validity of results because some potential susceptibility factors were not well considered. Finally, for the controls enrolled in local hospitals, they might not fully represent the whole Chinese population, and these possible biases may result in spurious findings.

In summary, the current study identifies the association between the miRNA-146a rs2910164 C>G polymorphism and EGJA risk in the eastern Chinese Han population. We have provided evidence for a potential cancer biomarker for EGJA early detection in the Chinese Han population and potentially for other countries. Well-designed case–control studies are needed to validate these primary findings and explore the potential interaction of gene–gene and gene–environment factors involved in miRNA-146a rs2910164 C>G polymorphism and EGJA.

Acknowledgments
We appreciate all subjects who participated in this study. We wish to thank Dr. Yan Liu (Genesky Biotechnologies Inc., Shanghai, China) for technical support. The project was supported by the Ministry of Health of the Peoples Republic of China (Grant No. WKJ2016–2-05), the Natural Science Foundation of Fujian Province (Grant No. 2016J01513, 2017J01259), the National Natural Science Foundation of China (Grant No. U1705282), the Fujian Provincial Health and Family Planning Research Talent Training Program (Grant No. 2015–CX–7, 2018–ZQN–13, 2016–1–11), Joint Funds for the Innovation of Science and Technology, Fujian Province (Grant No. 2017Y9077), and the National Clinical Key Specialty Construction Program.

Disclosure
The authors report no conflicts of interest in this work.

References
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MiRNA-146a rs2910164 C>G polymorphism and increased risk of EGJA


