Association of the -160 C>A Polymorphism in the CDH1 Promoter with Gastric Cancer: A Case-control Study

Majid Tafrihi1*, Sogand Kalantari1 and Mohammad Shokrzadeh2

1Molecular & Cell Biology Research Lab2, Department of Molecular and Cell Biology, Faculty of Basic Sciences, University of Mazandaran, Babolsar, Mazandaran, Iran
2Department of Toxicology, Faculty of Pharmacy, Mazandaran Pharmaceutical Sciences Research Center, Mazandaran University of Medical Sciences, Sari, Iran

ABSTRACT

E-cadherin is a tumor suppressor protein that plays a crucial role in cell-cell adherens junction and tissue architecture and it is hypothesized to participate in carcinogenesis. It has been shown that a polymorphism in the upstream of the transcription start site of the CDH1 gene affects E-cadherin transcriptional regulation and seems to be associated with a variety of cancers. For the first time, we investigated the association of the rs16260 in the 5'-untranslated region of the CDH1 gene with gastric cancer in Iranian population. Seventy-eight patients with gastric cancer and 72 healthy individuals were included and genotyped for this SNP using PCR-RFLP method. Our results showed that the frequency of the AA genotype in gastric cancer patients (16 of 78, 20.5%) was higher than healthy individuals (9 of 72, 12.5%), the frequency of the A allele in the patients group was higher than controls (OR=1.231, 95% CI= 0.772-1.962, p-value= 0.383), but statistical analysis revealed the absence of association between AA genotype and gastric cancer risk (OR=1.719, 95% CI= 0.656-4.502, p-value= 0.268). In conclusion, our results suggest that this substitution and the AA genotype have not a major impact on the individual’s susceptibility to gastric cancer, and therefore this SNP may be an ethnicity-dependent risk factor. Further works with a larger sample size and including other criteria such as H. pylori infection status are needed for more accuracy.

Introduction

Gastric cancer is the fifth most common cancer and the third leading cause of cancer-related death worldwide (Bray et al., 2018). The role of factors including age, sex, diet, alcohol, smoking, Helicobacter pylori, low socioeconomic status, genetic factors, and a positive family history in the incidence and development of gastric cancer have been established (Lu et al., 2015). According to morphological features, Laure’n classified gastric carcinomas into intestinal and diffuse type (Carcas, 2014). In Japanese classification, they are corresponding to differentiated and undifferentiated types, respectively (Ushijima and Sasaki, 2004). In intestinal type tumors, which commonly occur in elderly men, tumor cells express adhesion molecules and therefore, cell adhesions are established, tumor cells arranged in tubular or glandular formations and exhibit better prognosis. In contrast, in diffuse type which occurs in younger females, cells lack adhesions, and invade as single cells or collectively (Qiu et al., 2013; Ma et al., 2016). The CDH1 gene is located on chromosome 16q22.1, encodes the transmembrane glycoprotein E-cadherin. This protein is a calcium-dependent cell-cell adhesion molecule that has crucial roles in epithelial cell behavior and maintenance of tissue architecture and

integrity (Wong et al., 2018). In normal epithelial tissues, E-cadherin acts as a tumor suppressor, mainly by enhancing the membrane localization of β-catenin protein at cell adhesion contacts, and sequestering the β-catenin oncoprotein from binding to LEF/TCF factor and inhibits its transcriptional activity of Wnt signaling target genes (Tafrihy et al., 2007; Petrova et al., 2016; Tafrihi and Nakhaei Sistani 2017). Downregulation or loss of expression of E-cadherin in different epithelial tumors which is associated with poor prognosis and survival in patients of a variety of cancers leads to cancer cell invasion, epithelial-mesenchymal transition (EMT), and metastasis (Onder et al., 2008; Tafrihi et al., 2014).

So far, there are different single nucleotide polymorphisms (SNPs) have been identified in the regulatory and/or coding regions of the CDH1 gene that affect the expression and ability of E-cadherin protein to mediate cell-cell adhesion (Suriano et al., 2003; Corso et al., 2007). Accordingly, a C>A transversion at -160 from the transcription start site of the CDH1 promoter has been identified, repeatedly. In vitro studies using luciferase reporter gene showed that this substitution leads to lower luciferase activity in different cell lines (Cattaneo et al., 2006). It is suggested that this polymorphism is associated with increased susceptibility to various epithelial malignancies including gastric, colorectal, prostate, and breast cancer (Wang et al., 2008; Wang et al., 2012), and the minor allele is regarded as a cancer genetic marker (Cattaneo et al., 2006). However, so far, no study has been performed on the association of the rs16260 polymorphism with gastric cancer among the Iranian population. In this hospital-based, case-control study we have investigated the association of the rs16260 polymorphism in the promoter region of the CDH1 gene with the risk of gastric cancer among a population in the north of Iran.

**Materials and Methods**

**Samples**

In this study, the blood samples of the 78 clinically diagnosed gastric cancer patients including 48 males and 30 females and 72 age-matched healthy individuals consisting of 34 males and 38 females were recruited from Baghban medical center in Sari (Table 1). The blood samples were collected into EDTA_{Na2} containing complete blood count/CBC tubes and stored at -20°C before genomic DNA extraction. The study protocols were approved by the ethical review board of the University of Mazandaran. All patients and controls were from Mazandaran province, agreed to participate in this study and the written informed consent that is in accordance with the principles laid down in the Helsinki II declaration was obtained from all of them.

| Table 1. Demographic characteristics of patients and healthy individual's groups contributing this study |
|-----------|------------------|------------------|
| Samples   | Patients group (n= 78) | Healthy individuals group (n= 72) |
| Age (years) (Mean± SD) | 67.9 ± 13.18 | 68.5 ± 13.2 |
| Sex (Male/Female) | 48/30 | 43/38 |
| diffused / Intestinal type | 52/26 | - |

**PCR-RFLP and SNP genotyping**

Genomic DNA was extracted from peripheral blood leukocytes using the salting-out method (Shokrzadeh et al., 2017). The polymerase chain reaction-restriction length polymorphism (PCR-RFLP) method was performed to detect the rs16260 polymorphism. The PCR primers that were used in this study to amplify a fragment with 326 bp covering the CDH1 -160 (Fig. 1A), were forward primer 5’-TGATCCCAGGTCTTAGTGAGC-3’ and reverse primer 5’-TCTGAACTGACTTCCGCAAGC-3’ (Bioneer, South Korea). PCR was performed by Technne thermal cycler (Technne Co., UK) in a 25 μl reaction volume containing 20-80 ng of genomic DNA, 10 pM of each primer, and WizPure PCR 2X master mix (Wiz Bio Solutions, South Korea). The amplification process consisted of an initial denaturation step at 94 °C for 5 min, followed by 35 cycles of denaturation step at 94
˚C for 50 sec, annealing at 61.4 ˚C for 30 sec, polymerization at 72 ˚C for 40 sec, and with a final extension at 72 ˚C for 10 min. As a negative control, for each panel of PCR, distilled water was used instead of DNA in the reaction tube. For the RFLP analysis, PCR products were digested in a 10-μl reaction volume containing 2.5 U of HincII restriction enzyme (Thermo Fisher Scientific, USA) and 1X reaction buffer at 37 ˚C overnight. The C allele yielded an undigested fragment of 326 bp and the presence of the A allele produces fragments of 213 and 113 bp. The digestion products were separated on a 3% agarose gel with a 50 bp molecular weight marker (GeneDireX, Taiwan) and visualized under UV light using Red-Type AlphalImager system (Proteinsimple, USA) after staining with ethidium bromide.

**In silico analysis**

HaploReg software which is available at https://pubs.broadinstitute.org/mammals/haploreg.php is a tool that is used to explore annotations of noncoding variations in the genomes including SNPs at regulatory regions of the disease-associated loci. For this purpose, the reference SNP ID number was entered at the query sequence to looking for potential transcription factor binding sites. The PROMO ver. 3.0.2 software (using TRANSFAC ver. 6.4) that is available at http://alggen.lsi.upc.es/cgi-bin/promo_v3/promo/promoinit.cgi?dirDB=TF_8.3, was used to predict transcription factor binding sites in DNA sequences among those already experimentally verified. For this purpose, the sequence carrying the intended SNP was loaded at the query sequence to looking for potential transcription factor binding sites.

**Statistical analyses**

For both cases and healthy individuals, the Hardy-Weinberg equilibrium was tested. Odd ratios (OR) and 95% confidence interval (95% CI) for various genotypes were calculated. Differences between case and control groups were analyzed by chi-squared test. A probability of p < 0.05 was considered significant. Statistical analysis was carried out with the SPSS ver. 23 (SSPS Inc., USA).

**Results**

At first, the 226 bp fragment containing the rs16260 polymorphism was amplified using polymerase chain reaction (Fig. 1B). The agarose gel electrophoresis of some RFLP products is shown in figure 1C. The A allele that provides a restriction site for HincII is cut and produces 213 and 113 bp fragments, whereas the C allele was not cut by the restriction enzyme (Fig. 1C).

**Genotypes and allele frequencies**

Statistical analyzes showed that the genotype distribution of patients and controls were consistence with Hardy-Weinberg equilibrium. Genotype distribution and allele frequencies of the CDH1 rs16260 polymorphism in patients and healthy controls were shown in Table 2. Of the gastric cancer patients, 30 of 78 (38.5%) were homozygous for the C allele, 16 of 78 (20.5%) were for homozygous for the A allele and 32 of 78 (41%) were heterozygous (AC). In the healthy individual group, 29 of 72 (40.3%) had CC genotype, 9 of 72 (12.5%) had AA genotype and 34 of 72 (47.2%) were heterozygous (AC). The frequency of AA genotype in gastric cancer patients was higher than controls. The frequency of the A allele in the patients group was higher than controls (OR=1.231, 95% CI= 0.772-1.962, p-value= 0.383), but statistical analysis revealed absence of association between AA genotype and gastric cancer risk (OR=1.719, 95% CI= 0.656-4.502, p-value= 0.268).

**In silico analysis**

Using the HaploReg ver. 4.1 software we found that the rs16260 polymorphism is located in DNase hypersensitive site in different tissues and cell lines. Also, modified histones H3K4me1 and H3K27ac are found in this region that labels enhancers and H3K4me3 and H3K9ac histones are located in the promoter region of various cell lines and tissues. Our analysis using PROMO ver. 3.0.2 showed that this substitution changes the transcription factor binding sites (Fig. 2).
Fig. 1. The CDH1 gene map and PCR-RFLP results: Human CDH1 gene map was obtained from NCBI, the rs16260 polymorphism is located on the promoter region of the gene (A); Schematic representation of the digestion of the PCR products with HincII restriction enzyme (B); The gel electrophoresis of 326 bp fragments containing rs16260 (C).

Table 2. Genotype and allele frequencies of the CDH1 -160 C>A in cases and healthy individuals

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Patients (%)</th>
<th>Healthy individuals (%)</th>
<th>P-value</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>CC</td>
<td>30 (38.5)</td>
<td>29 (40.3)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>AC</td>
<td>32 (41.0)</td>
<td>34 (47.2)</td>
<td>0.792</td>
<td>0.910 (0.451 – 1.837)</td>
</tr>
<tr>
<td>AA</td>
<td>16 (20.5)</td>
<td>9 (12.5)</td>
<td>0.268</td>
<td>1.719 (0.656 – 4.502)</td>
</tr>
<tr>
<td>AC+AA</td>
<td>48 (61.5)</td>
<td>43 (59.7)</td>
<td>0.186</td>
<td>1.889 (0.731 – 4.878)</td>
</tr>
<tr>
<td>Allele</td>
<td>Patients (%)</td>
<td>Healthy individuals (%)</td>
<td>P-value</td>
<td>OR (95% CI)</td>
</tr>
<tr>
<td>C</td>
<td>92 (59.0)</td>
<td>92 (63.9)</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>A</td>
<td>64 (41.0)</td>
<td>52 (36.1)</td>
<td>0.383</td>
<td>1.231 (0.772 – 1.962)</td>
</tr>
</tbody>
</table>

Discussion

Single nucleotide polymorphisms are common DNA variations among people that may partly explain the individual’s susceptibility to various diseases including cancer (Deng et al., 2017). These variations, particularly in promoter or coding regions of a gene, may have serious effects on its transcription or protein function (Li et al., 2000). Several studies have investigated the role of genetic variations in different genes in the etiology of gastric cancer (Wu et al., 2002; Kiemeney et al., 2006; Qiu et al., 2009). It has been shown that several cancers are associated with rs16260 polymorphism of the CDH1 gene (Forszt et al., 2009; Memni et al., 2016).
The association of the rs16260 polymorphism with gastric cancer has been frequently investigated in different ethnic populations with conflicting results. For example, Humar et al. reported that in an Italian population, the -160 A allele is associated with an increased risk of sporadic diffused gastric cancer (Humar et al., 2002). On the other hand, in Taiwanese gastric cancer patients of mixed histology, a reduced frequency of the AA genotype compared to control group has been shown (Wu et al., 2002). It is suggested that, in diffused-type gastric cancer samples, the AA genotype has the protective role (Zhao et al., 2015). Also, there are no statistically significant differences in genotype and allele frequencies between non-cardia gastric cancer patients and controls in Caucasian and Chinese populations (Pharoah et al., 2001; Lu et al., 2005). On the other hand, several studies have reported that the AA genotype is associated with an increase in the gastric cancer risk (Al-Moundhri et al., 2010; Chu et al., 2014). Several reasons may account for these discrepancies including modifying genes, environmental factors, and different ethnicities (Chen et al., 2011; El-Husny et al., 2016). Meta-analyses suggested that the rs16260 polymorphism is an ethnicity-dependent risk factor for gastric cancer (Gao et al., 2008; Wang et al., 2008; Jiang et al., 2015) and also for other cancers (Geng et al., 2012; Wang et al., 2012). Due to controversial results from various ethnic populations, we aimed to study the association of the rs16260 polymorphism in the promoter region of the CDH1 gene and gastric cancer, for the first time among Iranian gastric cancer patients. In this study, we found that there is no statistically significant difference between cancer patients and control groups. Our analysis showed that patients with the CC genotype were more likely to contract gastric cancer than those with the AA genotype (OR= 0.582, 95% CI, 0.222-1.524, p-value = 0.268).

For more accurate analysis, linkage analysis of several tightly linked polymorphisms (Haplotypes) that modulate gastric cancer risk must be included. Depending on the combination of SNPs and genes, the influence of the rs16260 polymorphism may be varied (Zhang et al., 2008). The exact mechanism underlying the association of E-cadherin genotypes with gastric cancer remains to be well known, but this discrepancy may be related to differences in the affinity of DNA binding proteins to the two alleles of the E-cadherin promoter (Shin et al., 2004; Li et al., 2014).

The in silico analysis showed that this substitution eliminates the RXRα and T3Rβ binding sites and creates binding site for FOXP3 and C/EBP3 transcription factors. It has been shown that the rs16260 polymorphism in the promoter region of the CDH1 gene changes the methylation status, and eliminates a CF-1
binding site and creates binding sites for RC2 and MCBF transcription factors (Borges et al., 2010). Footprinting analyses showed that the C allele is protected from digestion by DNase I in the presence of the HeLa cell nuclear extracts. On the other hand, transfection of DU145 cells with plasmid carrying the A allele resulted in decreased transcripional activity (Li et al., 2000). Also, it has been shown that this SNP alters the secondary structure of paRNA and the risk allele facilitates the assembly of AGO1-isomiR-4534 complex that results in the CDH1 gene silencing (Pisignano et al., 2017).

In conclusion, the current study showed that the rs16260 polymorphism may not have an association with gastric cancer susceptibility in Mazandaran population. It is clear that this study have some limitations including low sample size and lack of information on smoking status, dietary habits and the prevalence of H. pylori infection in participants. Also analyzing other SNPs in the CDH1 gene may fortify our results.

**Research ethical approval**

All procedures performed in studies involving human participants were in accordance with the ethical standards of the institutional and/or national research committee and with the 1964 Helsinki declaration and its later amendments or comparable ethical standards.

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**Conflict of interest**

The authors declare that they have no competing interests for this publication.

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