Susceptibility to Esophageal Cancer and Genetic Polymorphisms in Glutathione S-Transferases T1, P1, and M1 and Cytochrome P450 2E1

Dong-Xin Lin, Yong-Ming Tang, Qiong Peng, Shi-Xin Lu, Christine B. Ambrosone, and Fred F. Kadlubar

Department of Chemical Etiology and Carcinogenesis, Cancer Institute, Chinese Academy of Medical Science and Beijing Union Medical College, Beijing 100021, People’s Republic of China [D-X. L., Q. P., S-X. L.], and Division of Molecular Epidemiology, National Center for Toxicological Research, Jefferson, Arkansas 72079 [Y-M. T., C. B. A., F. F. K.]

Abstract

Genetic polymorphisms in enzymes involved in carcinogen metabolism have been shown to influence susceptibility to cancer. Cytochrome P450 2E1 (CYP2E1) is primarily responsible for the bioactivation of many low molecular weight carcinogens, including certain nitrosamines, whereas glutathione S-transferases (GSTs) are involved in detoxifying many other carcinogenic electrophiles. Esophageal cancer, which is prevalent in China, is hypothesized to be related to environmental factors involved in the early events leading to the development of esophageal cancer.


Introduction

Cancer of the esophagus is one of the most common fatal diseases in certain regions of China such as Linxian County, where the mortality rate is as high as 150/100,000 (1). The risk for esophageal cancer in these areas has been associated with exposure to environmental carcinogens, particularly nitrosamines (2–4). However, even in high-risk regions, only certain individuals develop esophageal cancer. Most people live a normal life span, suggesting that host susceptibility factors may play an important role in cancer development. Most chemical carcinogens require metabolic activation for DNA-damaging capabilities, a step widely believed to be essential in carcinogenesis (5,6). On the other hand, carcinogens may also be detoxified before damaging DNA by in vivo metabolic detoxifying systems (7,8). Thus, it has been suggested that individual differences in carcinogen metabolism, which may be heritable or due to sustained environmental exposure to agents that affect the expression of enzymes involved in carcinogen activation or detoxification, may determine the susceptibility to chemically induced cancers. The major enzymes involved in the metabolic activation of chemical carcinogens are CYPs (4), a multigene superfamily of enzymes. Of the 25 or more CYP enzymes known to be expressed in human tissues, CYP2E1 is believed to be involved in the activation of most carcinogenic nitrosamines (9–12). Furthermore, this enzyme has the ability to metabolically activate many low molecular weight carcinogens (9) and to produce reactive free radicals from ethanol (13,14), which also might be of importance in cancer etiology.

CYP2E1 represents a major CYP isofrom in the human liver and is also expressed in extrahepatic tissues (15–17). Although the enzyme can be induced by certain chemicals such as ethanol, large interindividual variations have been observed before and after induction (18–20), suggesting that the variation may be due to genetic polymorphisms. RFLPs of the human CYP2E1 gene have been identified, and a polymorphism within the upstream region of the gene detected by Rsal has been shown to be associated with the transcriptional regulation of gene expression (21). Another genetic polymorphism that is detectable with DraI is located in intron 6 (22), and this allele has been found to contain a number of functional mutations affecting protein expression and catalytic activity (23). Associations between these genetic polymorphisms in CYP2E1 and the susceptibility to some types of cancer have been reported in case-control studies (22,24–29), although some negative results have been reported (30–40). To date, one study in Japan has evaluated the role of the Rsal polymorphism in relation to...
esophageal cancer and found no association (36). However, an increased risk of both oral (41) and nasopharyngeal (42) cancer has been associated with the prevalence of this variant allele in Taiwan.

The GSTs are a family of multifunctional enzymes that play a central role in the detoxification of toxic and carcinogetic electrophiles (43). Individuals who are homozygous for the null GSTM1 or GSTT1 alleles lack the respective enzyme function (44, 45), and these genotypes have been associated with an increased risk of cancer at many sites (44, 46–49). GSTP1, which is a major GST isozyme expressed in the human esophagus (17, 50), has also been shown to be genetically polymorphic (51, 52). A mutation of A to G within exon 5 results in an I to V change at position 105 in the amino acid sequence of the protein, which alters the specific activity and affinity for the electrophilic substrates of the enzyme (52, 53). Therefore, the GSTP1 polymorphism may also have potential effects on cancer susceptibility (51). Whereas numerous studies have been undertaken to examine the association between genetic polymorphisms in CYPs and/or GSTs and cancer susceptibility (vide supra), there is limitation information on their association with esophageal cancer (36, 54). In this study, we analyzed genetic polymorphisms in GSTM1, GSTT1, GSTP1, and CYP2E1 in subjects with esophageal cancer and severe epithelial hyperplasia, which is a precancerous lesion, and frequency-matched controls from Linxian County, China, an area where dietary nitrosamine exposures are known to be high (3).

Materials and Methods

Study Subjects. A pilot case-control study was designed to evaluate the possible role of genetic polymorphisms in carcinogen-metabolizing enzymes in the susceptibility to esophageal cancer. All subjects were residents of Linxian County, Henan Province, China. Smoking status was not available; however, recent studies with a similar population indicate that smoking prevalence is comparable between cases and controls. The diagnoses of esophageal cancer and epithelial hyperplasia were confirmed either histologically or cytologically. Cases were grouped as follows: (a) those with advanced dysplasia or severe hyperplasia (n = 45); (b) those with squamous cell carcinoma or adenocarcinoma (n = 45); and (c) those with squamous cell carcinoma, adenocarcinoma, or advanced dysplasia (n = 62). DNA samples were isolated from surgically removed esophageal tissues using standard methods (55) or from epithelial cells scraped from the esophagus. The yields of DNA varied with the amount of tissue available, and the analysis of each sample for all genotypes was not possible.

GSTM1 and GSTT1 Genotyping. GSTM1 and GSTT1 genotyping for gene deletions was carried out by a multiplex PCR using primer pairs 5′-GAACCTCCCTGAAAGCTAAAAGC-3′ and 5′-GGTGTGCCCTCAATATACGGTG-3′ for GSTM1, which produced a 219-bp product, and 5′-TCTCTTAGTGGC-3′ and 5′-GGATGGTACATGGC-3′ for GSTT1, which produced a 459-bp product.

Amplification of the albumin gene (5′-GCCCTCT-GCTAACAAGTCTTAC-3′ and 5′-GCCCTAAGAGAAGAAA-TCCCCAACATC-3′) was used as an internal control and produced a 350-bp product (36). PCR was performed in a 50-μl mixture consisting of sample DNA (0.1 μg), dNTP (0.2 mM; Boehringer Mannheim, Indianapolis, IN), MgCl2 (2.5 mM), each primer (1.0, 0.3, and 0.1 μM for GSTM1, GSTT1, and albumin, respectively), Taq polymerase (1.25 units; Promega, Madison, WI), and reaction buffer [10 mM Tris-HCl, 50 mM KCl (pH 9), 1% Triton X-100, and 2% DMSO]. Thirty-five cycles of amplification were performed at 94°C for 1 min (denaturation), 62°C for 1 min (annealing), and 72°C for 1 min (extension) using a GeneAmp 9600 thermal cycler (Perkin-Elmer Corp., Norwalk, CT). A 15:1 dilution of the amplified products was visualized by electrophoresis in an ethidium-bromide-stained 1.5% agarose gel (NuSieve 3:1; American Bioanalytical, Natick, MA) in TBE buffer (89 mM Tris-HCl, 0.89 mM boric acid, and 2 mM EDTA (pH 8.0; Fig. 1)).

GSTP1 RFLP Analysis. The primer pair 5′-AGCCACATC-CYTCTCCCTC-3′ and 5′-TACTGGCTGTTGATGTC-C-3′ was used to amplify exon 5 in the GSTP1 gene that includes the Alw26I enzyme recognition site (cf. Ref. 49). PCR reactions were carried out in a 50-μl mixture containing sample DNA (0.1 μg), reaction buffer, dNTP (0.2 mM), MgCl2 (2.5 mM), each primer (1.0 μM), and Taq polymerase (1.25 units). Amplification, which resulted in a 440-bp fragment, was achieved by 35 cycles of 30 s at 94°C, 30 s at 66°C, and 2 min at 72°C. Ten μl of the PCR reaction products were subjected to digestion with 20 units of the Alw26I enzyme in the buffer, as recommended by the manufacturer (Fermentas, Vilnius, Lithuania), for 2 h at 37°C. The samples were then analyzed by electrophoresis in 2% agarose gels. The presence of the polymorphic Alw26I restriction site yielded two fragments of 213 and 227 bp (GSTP1*A), whereas the absence of the polymorphic site was determined by the presence of a 440-bp fragment (GSTP1*).

CYP2E1 RFLP Analysis. The RFLPs in the 5′-flanking region and in intron 6 of the CYP2E1 gene were determined by PCR amplification followed by digestion with Rsal or DraI, using the methods described previously (21, 22). The PCR primers used for the 5′-flanking region (the Rsal site) were 5′-CTTCCTTGGTACATGGC-3′ and 5′-AGACCTC-CACATTGAC-3′ and produced a 459-bp product. The predominant allele (c1) was sensitive to Rsal digestion and yielded two products at 201 and 258 bp. The c2 allele was resistant to Rsal digestion. The PCR primers for intron 6 (the DraI site) were 5′-CTGGTGTTACATGGC-3′ and 5′-GGAGTGTTAGC-3′, which produced a 686-bp product. Only the D allele was sensitive to DraI cleavage, resulting in fragments of 335 and 351 bp. All PCR amplifications were performed in a total volume of 50 μl. The mixture used reaction buffer and contained each primer (1.0

\[ \text{M} \begin{array}{cccccccc} 1 & 2 & 3 & 4 & 5 & 6 & 7 & \text{GSTT1 (459 bp)} \\ & & & & & & & \text{Albumin (350 bp)} \\ & & & & & & & \text{GSTM1 (219 bp)} \end{array} \]

Fig. 1. An ethidium bromide-stained gel of electrophoresed products of the amplification of GSTM1, GSTT1, and albumin genes. Lanes 1–7 correspond to individual subjects. The absence of the PCR product indicates the null genotype. M, the molecular weight markers.

\[ ^{\text{W. Tan, Z. Li, and P. Lin, unpublished observations.}} \]
The characteristics of study subjects are presented in Table 1. Age and gender distributions among cases with cancer, cases with hyperplasia, and controls were very similar, reflecting the matching criteria used in this case-control study. DNA samples subjected to PCR and enzymatic digestion with RsaI revealed the expected fragment lengths, resulting in three genotypes of CYP2E1 (Fig. 2). The three genotypes of CYP2E1 recognized by PCR and Dral restriction fragment length analyses were readily discerned (Fig. 3). Distinctions of the CYP2E1 genotypes identified by these two restriction endonucleases were similar to those described previously (21, 22), as shown in Tables 2 and 3 for controls, cancer cases, and hyperplasia cases. The frequencies of the homozygous RsaI-sensitive allele (cl/cl) and the combined genotypes (c1/c2 + c2/c2) detected by RsaI were found to be 44 and 56%, respectively, in the control subjects, and those for the CC genotype and the CD + DD genotypes recognized by Dral were found to be 42 and 58%, respectively. As shown in Table 2, the frequency of variant genotypes of CYP2E1 detected by RsaI was significantly higher (χ² = 20.8; P < 0.001) in controls (56%) than in epithelial hyperplasia and dysplasia cases (17%) or in cases with cancer (20%). Subjects with the cl/c1 genotype had a 6-fold increased risk of developing epithelial hyperplasia and dysplasia (OR, 6.0; 95% CI, 2.3–16) and an almost 5-fold increased risk for cancer (OR, 4.8; 95% CI, 1.8–12.4) as compared to subjects with variant genotypes. The frequencies of the CD and DD genotypes detected by Dral were also slightly higher in control subjects (58%) than in cases with epithelial hyperplasia and dysplasia (41%) or in cases with cancer (45%), although the differences were not statistically significant. When cases with cancer and advanced dysplasia (n = 62) were analyzed together, the results for the RsaI (OR, 6.0; 95% CI, 1.8–24.4) and Dral (OR, 1.5; 95% CI, 0.7–3.6) polymorphisms were similar to that described for the cancer cases only.

The distributions of the GSTM1, GSTT1, and GSTP1 genotypes in cases and controls are shown in Table 4. GSTM1 and GSTT1 gene deletion was common in both controls and cases. The distribution of the genotypes of the three GST genes did not differ significantly between the controls and either group of cases, although the frequencies of the GSTT1 gene deletion and the frequencies of the GSTP1*B minor alleles were slightly lower in the cancer and hyperplasia cases than in the controls. No interactions were observed for combined contributions of GST genetic polymorphisms, together and with CYP2E1, on the risk of developing epithelial hyperplasia and esophageal cancer.

Results

The characteristics of study subjects are presented in Table 1. Age and gender distributions among cases with cancer, cases with hyperplasia, and controls were very similar, reflecting the matching criteria used in this case-control study. DNA samples subjected to PCR and enzymatic digestion with RsaI revealed the expected fragment lengths, resulting in three genotypes of CYP2E1 (Fig. 2). The three genotypes of CYP2E1 recognized by PCR and Dral restriction fragment length analyses were readily discerned (Fig. 3). Distinctions of the CYP2E1 genotypes identified by these two restriction endonucleases were similar to those described previously (21, 22), as shown in Tables 2 and 3 for controls, cancer cases, and hyperplasia cases. The frequencies of the homozygous RsaI-sensitive allele (cl/cl) and the combined genotypes (c1/c2 + c2/c2) detected by RsaI were found to be 44 and 56%, respectively, in the control subjects, and those for the CC genotype and the CD + DD genotypes recognized by Dral were found to be 42 and 58%, respectively. As shown in Table 2, the frequency of variant genotypes of CYP2E1 detected by RsaI was significantly higher (χ² = 20.8; P < 0.001) in controls (56%) than in epithelial hyperplasia and dysplasia cases (17%) or in cases with cancer (20%). Subjects with the cl/c1 genotype had a 6-fold increased risk of developing epithelial hyperplasia and dysplasia (OR, 6.0; 95% CI, 2.3–16) and an almost 5-fold increased risk for cancer (OR, 4.8; 95% CI, 1.8–12.4) as compared to subjects with variant genotypes. The frequencies of the CD and DD genotypes detected by Dral were also slightly higher in control subjects (58%) than in cases with epithelial hyperplasia and dysplasia (41%) or in cases with cancer (45%), although the differences were not statistically significant. When cases with cancer and advanced dysplasia (n = 62) were analyzed together, the results for the RsaI (OR, 6.0; 95% CI, 1.8–24.4) and Dral (OR, 1.5; 95% CI, 0.7–3.6) polymorphisms were similar to that described for the cancer cases only.

The distributions of the GSTM1, GSTT1, and GSTP1 genotypes in cases and controls are shown in Table 4. GSTM1 and GSTT1 gene deletion was common in both controls and cases. The distribution of the genotypes of the three GST genes did not differ significantly between the controls and either group of cases, although the frequencies of the GSTT1 gene deletion and the frequencies of the GSTP1*B minor alleles were slightly lower in the cancer and hyperplasia cases than in the controls. No interactions were observed for combined contributions of GST genetic polymorphisms, together and with CYP2E1, on the risk of developing epithelial hyperplasia and esophageal cancer.

Discussion

Because the etiology of esophageal cancer has been hypothesized to be associated with environmental nitrosamine exposure, we investigated whether genetic factors that might modulate the activation and/or detoxification of these carcinogens could have an impact on the risk of developing this malignant disease. We analyzed genetic polymorphisms at the CYP2E1, GSTM1, GSTT1, and GSTP1 loci and found that the CYP2E1 genotype was associated with susceptibility to esophageal cancer. Subjects who were homozygous c1/c1 for CYP2E1 were at a more than 4-fold excess risk of developing epithelial hyper-
CYP2E1 and Esophageal Cancer Susceptibility

Table 2  RsaI polymorphisms of CYP2E1 in controls and cases with severe hyperplasia and esophageal cancer

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Controls (%)</th>
<th>Hyperplasia and dysplasia (%)</th>
<th>Cancer (%)</th>
<th>Cancer and dysplasia (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(n = 45)</td>
<td>(n = 32)</td>
<td>(n = 45)</td>
<td>(n = 58)</td>
</tr>
<tr>
<td>c1/c1</td>
<td>20 (44)</td>
<td>25 (83)</td>
<td>36 (80)</td>
<td>48 (80)</td>
</tr>
<tr>
<td>c1/c2</td>
<td>22 (49)</td>
<td>7 (17)</td>
<td>11 (26)</td>
<td>11 (24)</td>
</tr>
<tr>
<td>c2/c2</td>
<td>3 (7)</td>
<td>0 (0)</td>
<td>3 (7)</td>
<td>4 (7)</td>
</tr>
<tr>
<td>OR (Cl)</td>
<td>1.0</td>
<td>6.0 (2.3-16.0)</td>
<td>4.8 (1.8-12.4)</td>
<td>4.0 (1.8-12.4)</td>
</tr>
</tbody>
</table>

* ORs and 95% CIs were calculated by logistic regression, with the c1/c1 genotype as the reference category, adjusted for age and sex.

Table 3  Frequencies of DraI CYP2E1 genotypes among controls and cases with severe hyperplasia and esophageal cancer

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Controls (%)</th>
<th>Hyperplasia and dysplasia (%)</th>
<th>Cancer (%)</th>
<th>Cancer and dysplasia (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(n = 45)</td>
<td>(n = 38)</td>
<td>(n = 45)</td>
<td>(n = 56)</td>
</tr>
<tr>
<td>CC</td>
<td>19 (42)</td>
<td>21 (59)</td>
<td>25 (55)</td>
<td>34 (57)</td>
</tr>
<tr>
<td>CD</td>
<td>23 (51)</td>
<td>16 (39)</td>
<td>16 (36)</td>
<td>16 (33)</td>
</tr>
<tr>
<td>DD</td>
<td>3 (7)</td>
<td>1 (2)</td>
<td>4 (9)</td>
<td>6 (10)</td>
</tr>
<tr>
<td>OR (Cl)</td>
<td>1.0</td>
<td>2.0 (0.9-4.4)</td>
<td>1.5 (0.7-3.6)</td>
<td>1.5 (0.7-3.6)</td>
</tr>
</tbody>
</table>

* CC, homozygous for the common allele; CD, heterozygous; DD, homozygous for the rare allele.

The mechanisms involved in CYP2E1 expression and the resulting amount and activity of the enzyme are not well characterized. Hu et al. (23) recently identified several mutations in the flanking regions in the DraI C allele using single-strand conformational polymorphism and found determinants of mRNA stability in some motifs. The Psrl or RsaI site is located in the 5'-flanking region and may affect gene transcription. Based on experiments with an in vitro expression system, Hayashi et al. (21) and Watanabe et al. (58) suggested that the c2/c2 genotype detected by RsaI produced higher enzyme activity than the c1/c1 genotype. However, this suggestion could not be confirmed in several in vivo and in vitro studies using chlorozoxazone and other specific substrates as probes for enzyme activity (59–61). Moreover, in view of the role of CYP2E1 in the metabolic activation of carcinogens and our results showing a protective effect of the c2/c2 genotype against esophageal cancer, we suggest that this genotype may result in less CYP2E1 activity toward esophageal carcinogens in Linxian County than the corresponding c1/c1 genotype.

The basal expression of CYP2E1 seems to be relatively low, but it can be highly induced. The polymorphism in the 5'-flanking region might be expected to modify the inducibility of the enzyme. Although the mechanism of CYP2E1 induction...
A significant association of the variant genotype recognized by DraI with increased lung cancer risk was also reported in a Japanese case-control study (22). In addition, contrary results with increased lung cancer risk was also reported in a Japanese study (23). A significant association of the variant genotype recognized by DdeI in this population could make such studies difficult to evaluate. Interracial difference in CYP2E1 activity may also account for the discrepancy. It is worthy to note that CYP2E1 activity was lower in Japanese subjects than it was in Caucasian subjects (61). Again, it is possible that the risk associated with polymorphisms alone is not evident without relevant exposure data.

GSTs, as an enzyme class, show activity against a broad range of DNA-damaging chemical substrates. Although several polycyclic aromatic hydrocarbon epoxides, such as benzo(a)pyrene diol-epoxide, are known substrates for GSTM1 and GSTP1 (65), there is little information on the detoxification of nitrosamines by these GSTs. It seems that genetic polymorphisms of GSTM1 and GSTP1 are mainly associated with an increased susceptibility for tobacco smoke-related cancers (44, 46, 48, 51). GSTT1 has significant activity in human erythrocytes and is implicated in the conjugation of natural and synthetic haloalkanes. The association between GSTT1 genetic polymorphisms and cancer risk has not been studied as extensively. Our results in the present study did not indicate an association between polymorphisms at the three GST genes and susceptibility to esophageal cancer. On the basis of what is known about substrates for human GSTM1, GSTP1, and GSTT1 and given the present findings, we suggest that the carcinogen(s) involved in the etiology of esophageal cancer in this high-incidence region may not be substrates for these GSTs. For example, previous epidemiological data already show that tobacco smoke plays a negligible role in the etiology of esophageal cancer in this area (66, 67).

In summary, we report a significant role of CYP2E1 but not GST polymorphisms in the development of esophageal cancer in Linxian County, China. Although the number of individuals with the CYP2E1 c2 allele was small, the differences in allele frequencies between cases and controls were striking. Of particular note was the apparent similarity in the frequencies of alleles in cases with esophageal cancer and in those with severe epithelial hyperplasia, in contrast to those among controls. Because this is one of the few reports on the association between genetic polymorphisms in carcinogen-metabolism enzymes and susceptibility to cancer of the esophagus, studies in larger populations would be desirable to confirm the findings of this pilot study.

References


Susceptibility to esophageal cancer and genetic polymorphisms in glutathione S-transferases T1, P1, and M1 and cytochrome P450 2E1.

D X Lin, Y M Tang, Q Peng, et al.


Access the most recent version of this article at:
http://cebp.aacrjournals.org/content/7/11/1013

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

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

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