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

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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 nitroamine exposure. Thus, we conducted a pilot case-control study to examine the association between CYP2E1, GSTM1, GSTT1, and GSTP1 genetic polymorphisms and esophageal cancer susceptibility. DNA samples were isolated from surgically removed esophageal tissues or scraped esophageal epithelium from cases with cancer (n = 45), cases with severe epithelial hyperplasia (n = 45), and normal controls (n = 46) from a high-risk area, Linxian County, China. RFLPs in the CYP2E1 and the GSTP1 genes were determined by PCR amplification followed by digestion with RsaI or DraI and Alw26I, respectively. Deletion of the GSTMI and GSTTI genes was examined by a multiplex PCR. The CYP2E1 polymorphism detected by RsaI was significantly different between controls (56%) and cases with cancer (20%) or severe epithelial hyperplasia (17%; P < 0.001). Persons without the RsaI variant alleles had more than a 4–6-fold risk of developing severe epithelial hyperplasia (adjusted odds ratio, 6.0; 95% confidence interval, 2.3–16.0) and cancer (adjusted odds ratio, 4.8; 95% confidence interval, 1.8–12.4). Polymorphisms in the GSTs were not associated with increased esophageal cancer risk. These results indicate that CYP2E1 may be a genetic susceptibility factor 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 CYPs2 (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 extrhepatic 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 in the upstream region of the gene detected by RsaI 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 RsaI polymorphism in relation to

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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 carcinogenic 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 limited 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 epithelial 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 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'-ACGCACATC-CCCTCCCCCAATGC-3' and 5'-TCTTGGTCTGTTAGGTGGC-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'-CTTCTTGGTCTAGGAGGAGGACG-3' and 5'-AGACCTCCAACGGAGGACG-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'-CTGTGCTAAGGATGCTACCTCAGGAGGACG-3' and 5'-GGAGTCTAAGGAGGACG-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

\[ W. Tan, Z. Li, and P. Lin, unpublished observations. \]
The RFLPs of PCR-amplified fragments obtained using *Dra*I and subjected to agarose gel electrophoresis. *Lanes 1–5, 9*, *CC* homozygotes; *Lanes 6, 7*, *DD* homozygotes; *Lanes 2, 8, 10*, *CD* heterozygote.

**Fig. 2.** The RFLPs of PCR-amplified fragments obtained using *Rsa*I and subjected to agarose gel electrophoresis. *Lanes 1–4, 9, 11, and 12*, *cc*/*cc* homozygotes; *Lanes 6 and 8*, *c2/c2* homozygotes; *Lane 5*, *c1/c2* heterozygote.

**Table 1** Demographic characteristics of the study subjects

<table>
<thead>
<tr>
<th>Age (yr)</th>
<th>Sample size</th>
<th>Controls</th>
<th>Hyperplasia and dysplasia</th>
<th>Cancer and dysplasia</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean</td>
<td>53.3</td>
<td>46</td>
<td>45</td>
<td>45</td>
</tr>
<tr>
<td>Range</td>
<td>40–65</td>
<td>45</td>
<td>54.8</td>
<td>55.5</td>
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<tr>
<td></td>
<td></td>
<td>12</td>
<td>47–65</td>
<td>47–55</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>35–70</td>
<td>35–70</td>
</tr>
<tr>
<td>Gender</td>
<td></td>
<td>Male (%)</td>
<td>50</td>
<td>47</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Female (%)</td>
<td>50</td>
<td>53</td>
</tr>
</tbody>
</table>

μM), dNTP (0.2 mM), MgCl2 (2.5 mM), and Taq polymerase (1.5 units/50 μL). The PCR conditions for amplifying the 5′-flanking region for the *Rsa*I site were 35 cycles of 30 s at 94°C, 30 s at 59°C, and 2 min at 72°C; for amplifying intron 6 with the *Dra*I site, the PCR conditions were 35 cycles of 30 s at 94°C, 30 s at 64°C, and 2 min at 72°C. Fifteen μL of each amplified product were digested with 10 units of *Rsa*I or 10 units of *Dra*I (New England Biolabs, Inc., Beverly, MA), respectively, at 37°C for 4 h, and the products were analyzed by electrophoresis in a 2.5% agarose gel.

**Statistical Analysis.** The χ² test was used to examine the differences in the distribution of genotypes between cases and controls. ORs with 95% CIs were computed using unconditional logistic regression (SPSS Inc., Chicago, IL) and adjusted for age and gender (57). DNA analyses of all of the genotypes for all study participants were not possible due to sample limitations; thus, the number of participants varies for each polymorphism.

**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 *Rsa*I revealed the expected fragment lengths, resulting in three genotypes of *CYP2E1* (Fig. 2). The three genotypes of *CYP2E1* recognized by PCR and *Dra*I restriction fragment length analyses were readily discerned (Fig. 3). Distributions 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 *Rsa*I-sensitive allele (c1/c1) and the combined genotypes (c1/c2 + c2/c2) detected by *Rsa*I 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 *Dra*I were found to be 42 and 58%, respectively. As shown in Table 2, the frequency of variant genotypes of *CYP2E1* detected by *Rsa*I was significantly higher (χ² = 20.8; P < 0.001) in controls (56%) than in epithelial hyperplasia and dysplasia cases (17%) or in cancer cases (20%). Subjects with the c1/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 *Dra*I 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 *Rsa*I (OR, 6.0; 95% CI, 1.8–2.4) and *Dra*I (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*, *GSTTI*, and *GSTP1* genotypes in cases and controls are shown in Table 4. *GSTM1* and *GSTTI* 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 *GSTTI* 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*, *GSTTI*, 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-
ORs and 95% CIs were calculated by logistic regression, with the genotype CC, homozygous for the common allele; CD, heterozygous; DD, homozygous for the rare allele.

Biologically plausible. Accordingly, it is expected that a lower epithelial hyperplasia of the esophagus is a precancerous lesion, in view of the fact that epithelial hyperplasia of the esophagus is a precancerous lesion, our results indicate that CYP2E1 is a genetic susceptibility factor involved in the early events of esophageal cancer. Because CYP2E1 is a major enzyme that catalyzes the activation of various nitrosamines and other low molecular weight carcinogens present in the diet, tobacco smoke, and the environment (9–12), its involvement in esophageal carcinogenesis is biologically plausible. Accordingly, it is expected that a lower level of CYP2E1 activity would reduce individual susceptibility to the cancer.

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 RsaI C allele using single-strand conformational polymorphism and found determinants of mRNA stability in some motifs. The PstI 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 PstI 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 remains controversial and seems to be mediated by different mechanisms, transcriptional activation of the gene is likely to be involved (62, 63). It is interesting that Lucas et al. (20) observed that chlorozoxazone metabolism did not differ for either polymorphism across the genotypes for the basal rates present in controls or in withdrawn alcoholics. However, after alcohol induction, chlorozoxazone metabolism was significantly lower in heterozygous genotypes than it was in homozygous c1 genotypes detected by analysis using either RsaI or DraI. These results indicate that the c2 genotypes might be associated with a lack of inducibility in CYP2E1 activity (20). To date, there has been no evidence showing that enhanced CYP2E1 activity in vivo is related to the c2 genotypes.

Several case-control studies have been conducted to examine the associations between CYP2E1 polymorphisms and the susceptibility to a number of cancers, although the results are inconsistent. In a Swedish study, Persson et al. (26) found that the frequency of the c2 genotype was significantly lower in lung cancer cases than it was in controls and suggested that this could constitute a protective factor against the disease. These data were also supported by recent data from a study by Wu et al. (64). Yu et al. (29) recently showed that the risk of developing hepatocellular carcinoma in cigarette smokers in Taiwan was significantly associated with the genotypes of CYP2E1 detected by PstI or RsaI, but not by DraI. They found that the frequency of the c1/c1 genotype detected by PstI or RsaI was higher in cases than it was in controls, and this difference was more pronounced among smokers. The data reported herein are consistent with these previous studies. Another case-control study conducted in Taiwan on CYP2E1 genetic polymorphisms and the risk of nasopharyngeal cancer, which is also hypothesized to be associated with exposure to nitrosamines, showed an increased risk of the c1/c1 genotype (42). However, in contrast to our results and those reported by Yu et al. (29) and Persson et al. (26), an excess risk of the cancer was associated with variant genotypes detected by both RsaI and DraI (28). In another recent study in Taiwan (41), the c2 allele was found to increase the risk of oral cancer among those who did not chew betel quid. In a case-control study of breast cancer, Shields et al. (27) also found the DraI polymorphism C alleles to be associated with increased risk among premenopausal smokers.

### Table 2 Rsal 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>6 (13)</td>
<td>6 (13)</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.

**ORs** and **95% CIs** were calculated by logistic regression, with the **CC** genotype as the reference category and groups (CD + DD) combined, adjusted for age and sex.
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 
showing no association between CYP2E1 genotypes and cancer 
risk in Caucasians were reported by other investigators (30, 31, 
33–35). The reasons for these discrepancies are not clear, and 
specific exposures may need to be further addressed. However, 
the very limited statistical power in Caucasian studies due to 
the extreme rarity of the variant genotypes of 
CYP2E1 makes 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 with-
out 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 polymor-
phisms 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 erythro-
cytes and is implicated in the conjugation of natural and syn-
thetic haloalkanes. The association between GSTT1 genetic 
polymorphisms and cancer risk has not been studied as exten-
sively. 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 genotypes in the development of esophageal cancer in 
Linxian County, China. Although the number of individuals 
with the CYP2E1 c2 alleles was small, no 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 en-
zymes and susceptibility to cancer of the esophagus, studies in 
larger populations would be desirable to confirm the findings 
of this pilot study.

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