Polymorphisms in GSTP1, GSTM1, and GSTT1 and Susceptibility to Colorectal Cancer

Mark Welfare, A. Monesola Adeokun, Margaret F. Bassendine, and Ann K. Daly

Department of Pharmacological Sciences [M. W., A. M. A., A. K. D.] and Medicine [M. W., M. F. B.], University of Newcastle upon Tyne, Newcastle upon Tyne NE298NH, England

Abstract

Polymorphisms in glutathione S-transferases (GSTs) may predispose to colorectal cancer through deficient detoxification of environmental carcinogens, although previous results are conflicting. A study with 178 matched case-control pairs was conducted to determine the effect of the GSTT1 and GSTM1 null genotypes and polymorphisms in GSTP1 on colorectal cancer susceptibility. In a secondary analysis, we examined interactions between genotypes and with the N-acetyltransferase 2 (NAT2) genotype. Heterogeneity by age, sex, site, and stage of cancer was also examined. No effect of any genotype for GSTM1, GSTT1, or GSTP1 on colorectal cancer susceptibility was detected. Secondary end points showed that individuals with both the GSTT1 null and NAT2 slow genotypes combined appeared to be at increased risk of colorectal cancer (odds ratio = 2.33; 95% confidence interval, 1.1–5.0). We conclude that GST polymorphisms alone do not predispose to colorectal cancer in northeast England. We also observed possible effects of the GSTT1 null genotype on the age and stage at presentation, and these, together with the findings of an apparent interaction with NAT2 genotypes, need to be confirmed in further studies.

Introduction

GSTs are a large and diverse family of enzymes, and in humans, there are at least 13 GST enzymes belonging to five families, namely α (GSTA), μ (GSTM), π (GSTP), σ (GSTS), and θ (GSTT; Refs. 1 and 2). GSTs detoxify diverse electrophiles, including carcinogens, chiefly by conjugating them with glutathione. Heterocyclic amines are carcinogens that have been implicated as a potential cause of colorectal cancer in humans and that have also been shown to be detoxified by GSTs (3). In addition, foods that are known to induce the expression of GSTs are also thought to be protective against colorectal cancer (4). If it could be confirmed that GSTs are protective against colorectal cancer, it might be possible to identify individuals at high risk of this disease or to manipulate the expression of GSTs to prevent colorectal cancer by either dietary or pharmacological means.

One method of investigating the protective role of GSTs has been to study the effect of polymorphisms in GST genes on susceptibility to colorectal cancer. Functional polymorphisms are known for three of the human genes, namely GSTM1, GSTT1, and GSTP1 (5–8). For both GSTM1 and GSTT1, the variant allele is a deletion of the gene, and individuals who are homozygous for the deleted allele are said to possess the “null” genotype and do not express the enzyme at all. For GSTP1, two genetic polymorphisms are known, Ile-105 → Val, resulting from an A → G transition at base 1578, and Ala-114 → Val, resulting from a C → T transition at base 2293 (8). The GSTP1* A allele possesses Ile-105 and Ala-114 and GSTP1*B has Val-105 and Ala-114, whereas GSTP1* C has both Val-105 and Val-114. Site-directed mutagenesis has been used to show the functional significance of the Ile-105 → Val polymorphism. Alleles with Ile-105 have greater activity with 3,4-dichloro-1-nitrobenzene, whereas those with the Val-105 allele have greater activity with ethacrynic acid and bromosulphthalein (8, 9).

Five published studies have examined the relationship between the GSTM1 null genotype and susceptibility to colorectal cancer or colorectal polyps (10–14). Only the study by Zhong et al. (10) found increased risk associated with the null genotype, particularly for cancers of the proximal colon. Three studies have examined whether possession of the null genotype for GSTT1 confers susceptibility to colorectal cancer (11–13). Only the largest study, with 148 cases and 577 controls, demonstrated an association between the null genotype and colorectal cancer, with an OR of 1.88 (95% CI, 1.28 – 2.77; Ref. 13). Two studies have examined the frequency of the Ile-105 → Val GSTP1 polymorphism, and one the frequency of the Ala-114 → Val GSTP1 polymorphism in colorectal cancer; neither study reported any association (15, 16).

The enzyme NAT2 is responsible for the polymorphism in the metabolism of drugs such as isoniazid (17). Individuals can be classified as fast or slow acetylators using metabolic probes such as sulfamethazine (phenotyping) or by analyzing sequence polymorphisms in the NAT2 gene (genotyping). The fast acetylator phenotype of NAT2 has been reported to be associated with susceptibility to colorectal cancer (18, 19), although studies that classified acetylator status using genotyping techniques have mostly shown no overall association (20–22). Recently several studies have that shown that the risk in fast acetylators appears to be influenced by their consumption of dietary heterocyclic amines (21, 23).

The main hypotheses investigated in this paper were that polymorphisms in any of the GSTM1, GSTT1, or GSTP1 genes predispose to colorectal cancer. The secondary questions investigated were whether there was any interaction between various combinations of GSTP1, GSTT1, GSTM1, and NAT2 genotypes.
Materials and Methods

This study was a case-control study using a matched pair design so that biases due to age, sex, and area of residence were minimized. Power calculation, assuming that the GSTM1 null genotype would be present in ~45% of controls, showed that, using 1:1 matching, 160 cases were required for the study to have 90% power to detect an OR of 2.0 for the GSTM1 null genotype at the 0.05 significance level. For the GSTT1 polymorphism, 155 cases were required to detect an OR of 2.0 with 80% power, assuming that the population frequency of GSTT1 null genotype would be 20%. At the time the study was designed, the GSTP1 polymorphisms were not known, so no power calculation was made.

All patients with histologically proven colorectal cancer diagnosed in the Newcastle and North Tyneside health district (covering an area ~30 × 15 miles) in the time period December 1994–September 1995 were invited to participate if they did not meet any exclusion criteria. The main exclusion criteria were the inability to give informed consent and cancers occurring in inherited syndromes or in patients with colitis. A total of 230 cases that matched the inclusion criteria were identified, and 201 cases agreed to participate (87% recruitment). Age- and sex-matched community controls were recruited for each case. They were identified from the records of the general practitioner (primary care physician) that the matched case usually attended in an attempt to match for social circumstances. Three potential controls were identified for each case but because there was a participation rate of ~50% among controls only 178 matched case-control pairs were actually recruited (77% of the original cases). The median age of the matched case and controls was identical (69 years), and 58% of the cases and controls were men. The cases for whom no control was found were younger than those for whom a control was found (59 versus 69 years, P = 0.01), but the sex distribution was not significantly different.

The study received approval from the Newcastle and North Tyneside Ethics Committee, and all subjects gave informed, written consent.

The GSTM1 null genotype was detected using the method of Zhong et al. (24), and the GSTT1 null genotype was detected using a multiplex PCR method, as described by Chenevix-Trench et al. (11) using the GSTT1 primers described by Pembile et al. (7).

The A1578→G substitution, which is present in the GSTP1*B and GSTP1*C alleles and which gives rise to the base substitution of valine for alanine at position 105, was detected using the restriction enzyme Alw26I. The primers were 5’-GGCTCTATGGGAAGGACCAGGAGG-3’ (1323–1346 bp) and 5’-GCACCTCCATCCAGAAACTGGCGGCGG3’ (1746–1768 bp), and the PCR was carried out using the general methods described previously (25) in a total volume of 50 μl with 30 cycles of 1 min at 94°C, 1 min at 64°C, and 2 min at 72°C. A product of 445 bp was obtained, and a 20-μl aliquot was digested with 1 unit of Alw26I. The GSTP1*A and GSTP1*B alleles were allocated on the assumption that the GSTP1*A genotype at the 0.05 significance level. For the GSTT1 polymorphism, 155 cases were required to detect an OR of 2.0 with 80% power, assuming that the population frequency of GSTT1 null genotype would be 20%. At the time the study was designed, the GSTT1 null genotype was not known, so no power calculation was made.

There were four primary end points (the frequency of null GSTT1 and GSTM1 and the frequency of the two polymorphisms of GSTP1 in cases and controls). There were six main secondary analyses of the combination genotypes between GSTM1, GSTT1, GSTP1, and NAT2. Because other authors had suggested that there may be differences in the genotype pattern at different ages or sites or stage of tumor, the frequency of the genotypes was also examined by sex, in three age subgroups, and by stage and site of the tumor. However, there was no prior hypothesis to support any of these latter analyses, which were only performed to compare with previously published data. The frequencies of genotypes in cases and controls were compared using McNemar’s test for matched case-control studies which provides greater power than an unmatched study. In addition, heterogeneity and contingency table analysis and χ² test for trend were used.

Data were analyzed using the program SPSS Release 6.0 (SPSS Inc., Chicago, IL) and EpiInfo Version 6.02 (Centers for Disease Control, Atlanta, GA; WHO, Geneva, Switzerland). ORs were calculated using the CIA software program (Confidence Interval Analysis Version 1.1; Martin Gardner and the BMJ, 1991).

Results

GSTP1. The overall frequency of GSTP1 alleles and genotypes is shown in Table 1. The frequencies for the Val-105 allele were 0.33 for controls and 0.31 for cases. The frequencies for the Val-114 allele were 0.1 for controls and 0.08 for cases. No individuals were detected who were positive for Val-114 but not for Val-105.

In the controls, 11.7% of individuals were homozygous and 42.7% were heterozygous for Val-105, and 44.9% were homozygous for Ile-105. In the cases, the figures were 7.6, 45.2, and 46.9%, respectively. This compares to a homozygous rate for Val-105 of 6.5% in the normal Edinburgh population and 9.1% in Norway and heterozygous rates of 42.5 and 39.4%, respectively (15, 27). There was no difference between cases and individually matched controls in the frequency of homozygotes for Val-105 (OR = 0.57; 95% CI, 0.25–1.2) or the frequency of individuals who possessed at least one Val-105 allele (OR = 1.01; 95% CI, 0.65–1.6).

In the controls, 15.6% of individuals possessed the Val-114 variant (GSTP1*C allele), and in the cases, 14.3% of individuals (OR = 1.0; 95% CI, 0.5–1.9). There were six individuals homozygous for Val-114 (all but one in the control group), but this difference was not significant (OR = 0.18; 95% CI, 0.01–1.58).

GSTT1. For GSTT1, 19.8% of cases and 16.9% of controls were null. There was no difference in the frequency of the null genotype between matched cases and controls by McNemar’s test (OR = 1.21; 95% CI, 0.63–2.0). Analysis by sex showed no difference between cases and their matched controls.

There was no significant difference between cases and controls for any of three age bands by McNemar’s test, but for three age bands, the frequency of the GSTT1 null genotype appeared to become less with increasing age. This is represented in Table 2. A χ² test for trend of the GSTT1 null
**Table 1** Allele and genotype frequencies of the GSTP1 gene in cases and controls

<table>
<thead>
<tr>
<th>Allele frequency</th>
<th>Cases (n = 196)</th>
<th>Controls (n = 178)</th>
</tr>
</thead>
<tbody>
<tr>
<td>GSTP1*AA</td>
<td>278 (0.70)</td>
<td>238 (0.67)</td>
</tr>
<tr>
<td>GSTP1*AB</td>
<td>91 (0.23)</td>
<td>83 (0.23)</td>
</tr>
<tr>
<td>GSTP1*AC</td>
<td>28 (0.07)</td>
<td>35 (0.10)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Genotype frequency</th>
<th>Cases (n = 196)</th>
<th>Controls (n = 178)</th>
</tr>
</thead>
<tbody>
<tr>
<td>*A/*A</td>
<td>92 (0.47)</td>
<td>82 (0.45)</td>
</tr>
<tr>
<td>*A/*B</td>
<td>69 (0.35)</td>
<td>54 (0.31)</td>
</tr>
<tr>
<td>*A/*C</td>
<td>20 (0.10)</td>
<td>20 (0.11)</td>
</tr>
<tr>
<td>*B/*B</td>
<td>6 (0.03)</td>
<td>12 (0.07)</td>
</tr>
<tr>
<td>*B/*C</td>
<td>8 (0.04)</td>
<td>5 (0.02)</td>
</tr>
<tr>
<td>*C/*C</td>
<td>1 (0.005)</td>
<td>5 (0.03)</td>
</tr>
</tbody>
</table>

* The values given are actual numbers, with frequencies in parentheses. The genotype frequencies were in Hardy-Weinberg equilibrium for both the cases and controls.

**Table 2** Frequency of GSTT1 null genotype by age

<table>
<thead>
<tr>
<th>Age, yr (no. of matched pairs)</th>
<th>Cases</th>
<th>Controls</th>
</tr>
</thead>
<tbody>
<tr>
<td>&lt;65 (n = 54)</td>
<td>15/54 (27.7%)</td>
<td>12/54 (22%)</td>
</tr>
<tr>
<td>65–75 (n = 73)</td>
<td>14/73 (19%)</td>
<td>13/73 (16.4%)</td>
</tr>
<tr>
<td>&gt;75 (n = 50)</td>
<td>6/50 (12%)</td>
<td>6/50 (12%)</td>
</tr>
</tbody>
</table>

* The values given are actual numbers with percentage frequencies in parentheses. χ² test for trend gave P = 0.14 for the cases.

Discussion

This population-based study suggests that variant alleles in the GSTT1, GSTM1, and GSTP1 genes are unlikely to convey moderate increase in susceptibility to colorectal cancer, although the possibility of a small effect was not excluded. There has been conflicting evidence concerning the role of GST polymorphisms in susceptibility to colorectal cancer. Single studies have demonstrated an association between the GSTT1 or GSTM1 null genotype and colorectal cancer, although these have not been confirmed in further studies (10–14).

The study that has found a significant difference between cases and controls with respect to the GSTM1 null genotype was only marginally statistically significant (OR = 1.8; 95% CI 1.2–2.7) and was performed using cases recruited in Edinburgh and controls from three localities throughout the United Kingdom (10). The reasons for the differences between studies are not clear but could be related to methods of recruitment or type I statistical errors. Similar considerations could apply to the discrepancies seen in the studies of GSTT1 null genotype. It seems unlikely that the GSTM1 null genotype could predispose to colorectal cancer because GSTM1 is only expressed at low levels in the colon (28). There appears to be no information available at present concerning GSTT1 expression in human colon.

GSTP1 seems a more likely candidate susceptibility gene because it is expressed at high levels in the colon and because it has been demonstrated to play a role in heterocyclic amine deactivation (3, 28). In fact, in one previous publication on the Ile-105→Val polymorphism in relation to colorectal cancer, it appears that homozygous possession of the Ile-105 variant may actually protect from colorectal cancer, although the authors only examined for the effect of homozygous Val-105 (37 of 100 colorectal cancer cases and 79 of 155 controls homozygous for Ile-105; OR = 0.56 95% CI, 0.33–0.97; Ref. 15). It would be interesting to know the in vitro effect of the GSTP1 polymorphisms on heterocyclic amine detoxification.

The population frequency of the Val-114 variant has been reported in two recent reports (15, 29). The frequency of both the GSTP1 polymorphisms was remarkably similar in the present study to that reported in Australian and American Caucasians (34, 33, and 33% Val-105 in Australia, England, and America, respectively; and 7, 8, and 9% Val-114, respectively). We did not find any individuals with Val-114 but not Val-105, and we allocated genotype on the basis that the two polymorphisms are in strong linkage disequilibrium. However, it has recently been reported that there is a rare allele (GSTP1*D) that has the Val-114 polymorphism with Ile-105 (29). Our assay will have classified any subjects with the genotype GSTP1*B/GSTP1*A as GSTP1*A/GSTP1*C, but because the *B/D genotype is very rare (15, 29)
and the majority of *A/B/C* genotype assignments will be correct, this is unlikely to have affected the overall outcome of the study.

Individuals with the combination slow acetylator-GSTT1 null genotype were also more frequent in cases than controls. The relationship between acetylator status and colorectal cancer susceptibility is complicated, with some studies showing increased risk to individuals with the fast acetylator type and others showing no increased risk (18-23). In one study, fast acetylator individuals with high fried meat intake had an OR of 6.04 (95% CI, 1.34-55) of developing colorectal cancer, although fast acetylator status alone was not a risk factor (21). This suggests that slow acetylators must be at increased risk from other factors. This study suggests that this factor may be the GSTT1 null genotype, and if this finding is confirmed in larger studies, it could help to explain some of the heterogeneity between previous studies of colorectal cancer and acetylator status.

Further analyses, which were performed for comparison with previous studies but for which there was no prior hypothesis, showed a number of interesting findings, although because of the small sample size these are best regarded as preliminary and need confirming in other studies. The GSTT1 null genotype appeared to be less common with advancing age in both cases and controls, although this failed to reach statistical significance. This is particularly interesting because similar findings were noted in another study of colorectal cancer (11). It may be that the GSTT1 null genotype gets less frequent with increasing age, although it is unlikely that a single genetic polymorphism could be responsible for such a significant increase in overall mortality. Because the finding was stronger in cases than controls, it is possible that individuals with the null genotype develop their tumors at a younger age than individuals that do express the enzyme. This finding needs to be investigated further in prospective studies. The GSTT1 null genotype was also found more frequently in early rather than late tumors. This observation may have arisen by the differential catalytic activity of the encoded proteins. J. Biol. Chem., 274: 409–414, 1991.

In general, this study has not confirmed previous suggestions of a role for GST polymorphisms in colorectal cancer susceptibility. However, secondary analyses have revealed some interesting associations that justify further investigation.

References


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