Association of glutathione S-transferase TI, M1, and P1 polymorphisms in the breast cancer risk: a meta-analysis

Zhiwang Song1, Chuan Shao2, Chan Feng1, Yonglin Lu1, Yong Gao1, Chunyan Dong1

1Department of Oncology, Shanghai East Hospital, Tongji University, Shanghai, 2Department of Neurosurgery, The Second Clinical Medical College of North Sichuan Medical College, Nanchong, Sichuan, People’s Republic of China

Background: Several case–control studies investigating the relationship between genetic polymorphisms of glutathione S-transferase (GST) M1, GSTT1, and GSTP1 (rs1695) and the risk of breast cancer have reported contradictory results. We therefore performed a meta-analysis to clarify this issue.

Materials and methods: An updated meta-analysis using PubMed and Web of Knowledge databases for the eligible case–control studies was performed. Random- or fixed-effects model was used.

Results: A total of 10,067 cancer cases and 12,276 controls in 41 independent case–control studies from 19 articles were included in this meta-analysis. Significant increase in risk of breast cancer for Asians was found in GSTM1-null genotype ($P=0.012$, odds ratio [OR] = 1.17, 95% confidence interval [CI] = 1.04–1.32) and GSTT1-null genotype ($P=0.039$, OR = 1.19, 95% CI = 1.01–1.38). In addition, our results showed that the GSTP1 (rs1695) polymorphisms can significantly increase the risk among Caucasians ($P=0.042$, OR = 1.16, 95% CI = 1.01–1.34). Sensitivity analysis and publication bias further confirmed the dependability of the results in this meta-analysis.

Conclusion: Our results demonstrate that both GSTM1- and GSTT1-null polymorphisms are associated with an increased risk of breast cancer in Asians and that GSTP1 Val105Ile (rs1695) polymorphism is associated with an increased breast cancer risk in Caucasians.

Keywords: GSTM1, GSTT1, GSTP1, polymorphism, breast cancer, meta-analysis

Background

Breast cancer, one of the most common cancers, has shown a steady increase in incidence worldwide in recent years. It remains the major cause of cancer-related mortality among women.1,2 According to earlier reports, there are ~1.15 million breast cancer patients diagnosed every year, and the highest incidence of breast cancer is found in Europe and USA.3,4 In the People’s Republic of China, the incidence of breast cancer has been growing rapidly. Patients with breast cancer, meanwhile, tend to be younger.5,6 Its pathogenesis is still unclear, although some studies have shown that breast cancer is caused by environmental and genetic factors.7,8

As a vital Phase II isoenzyme, the glutathione S-transferase (GST) family can identify environmentally hazardous materials and regulate the level of other enzymes and proteins in the cell. Thus, it plays an important role in many basic physiological processes of the human body.9–11 According to their distinct isoelectric points, human GSTs can be divided into seven classes, alpha ($\alpha$), mu ($\mu$), omega ($\omega$), pi ($\pi$), sigma ($\sigma$), theta ($\theta$), and zeta ($\zeta$). There are also microsomal GST isoenzymes.12 It is reported that there are at least three genes of them with common functional polymorphisms, which
are GSTT1 (θ), GSTM1 (μ), and GSTP1 (π). Every mutation in each of them may potentially lead to a loss of enzymatic function. Many researchers have shown that GSTs are crucial to cellular protection from a great deal of damage, and the polymorphism of GSTs could result in cancers of the esophagus, kidney, and liver, and glioma. A large number of studies have indicated that the GSTT1, GSTM1, and GSTP1 (rs1695) polymorphisms are associated with breast cancer. However, the results of these studies are inconclusive. Therefore, we performed this meta-analysis of published case–control studies to solve the conflicting results and draw a relatively reliable conclusion.

Materials and methods

Literature search
All related studies published before May 31, 2015, were identified independently by two reviewers through a computer-based search of PubMed and Web of Knowledge databases. The search terms used in this study were as follows: (“glutathione S-transferase” OR “GST” OR “GSTT1” OR “GSTM1” OR “GSTP1”) AND (“breast cancer” OR “breast neoplasm” OR “breast carcinoma”) AND “polymorphism”. There was no language restriction. For this meta-analysis, the included studies had to meet the following criteria: 1) a case–control study on the polymorphism of GSTT1, GSTM1, or GSTP1 polymorphism and the risk of breast cancer; 2) reported genotype frequencies of cases and controls; and 3) the genotypes of control subjects in accordance with the Hardy–Weinberg equilibrium (HWE).

Data extraction
Two investigators extracted carefully the relevant information independently, and any discrepancy was settled by consensus. The following data were extracted from articles: first author’s name, year, country, ethnicity, the source of controls, and the genotype attribution of cases and controls.

Statistical analysis
The odds ratio (OR) and their 95% confidence interval (CI) were adopted to evaluate the strength of association between the polymorphism of GSTT1, GSTM1, and GSTP1 (rs1695) and the risk of breast cancer. First, we examined GSTT1 and GSTM1 genotypes using the null vs present model. Then, the relationship between the GSTP1 (rs1695) polymorphism and risk of breast cancer was estimated with allelic (V vs I) model, the recessive (VV vs II + VI), the dominant (VV + VI vs II), and the codominant (VV vs II). The statistical significance of the pooled OR was determined by the Z-test, and a P<0.05 was considered statistically significant. HWE was estimated using the chi-squared test among controls, where P<0.05 was considered a significant departure from HWE. We evaluated heterogeneity among included studies with chi-squared-based Q-test and I² statistic. If the heterogeneity was obvious, with P<0.1, random-effects model was used to calculate the pooled OR; otherwise, the fixed-effects models were adopted. Moreover, subgroup analysis was conducted by ethnicity.

We performed sensitivity analysis by omitting single study every time to assess the robustness of the results. Funnel plots and Egger’s tests were used to explore the potential publication bias; P>0.05 was considered to indicate no significant publication bias. All P-values were based on two-sided tests.

Results

Study characteristics
Our meta-analysis was conducted according to guidelines of the “Preferred Reporting Items for Systematic Reviews and Meta-Analyses” (PRISMA) statement (checklist) and “Meta-analysis on Genetic Association Studies” statement (checklist). The flowchart is illustrated in Figure 1. A total of 171 potentially relevant articles were found by the literature search, and among these 121 articles were excluded because of obvious irrelevance after a preliminary screening of the titles and abstracts. In addition, after full-text reviews

![Flowchart of study selection in this meta-analysis](Image)

**Figure 1** Flowchart of study selection in this meta-analysis.

**Abbreviation:** HWE, Hardy–Weinberg equilibrium.
of the remaining 33 articles, 14 articles were excluded for the following reasons: articles were based on studies on prognosis or chemotherapy sensitivity (n=9), article was a quantitative analysis (n=1), article was a case report (n=1), articles had insufficient data (n=3), and studies deviated from HWE (n=2). Articles reporting data for different kinds of GST ethnicity were treated as independent studies. Finally, 19 articles involving 41 independent case–control studies with 10,067 cancer cases and 12,276 controls completely met the inclusion criteria. The detailed data collected from the included studies are summarized in Table 1.

Association of GSTM1-null polymorphism with breast cancer risk
Seventeen studies including 4,046 cases and 5,344 controls studied the association between GSTM1-null polymorphism and breast cancer.\(^6,19,21–26,28,30–31,34–36\) Our meta-analysis showed that there was no significant association of GSTM1-null polymorphism with breast cancer risk (OR =1.13, 95% CI =0.97–1.32) (Table 2). When stratifying for ethnicity, we found that GSTM1-null polymorphism could increase the breast cancer risk for Asians (OR =1.17, 95% CI =1.04–1.32) (Figure 2). However, no significant association was found for Caucasians (OR =1.13, 95% CI =0.85–1.52) or mixed ethnicity (OR =0.90, 95% CI =0.62–1.30) (Table 2).

Association of GSTT1-null polymorphism with breast cancer risk
Fourteen studies including 2,788 cases and 3,686 controls studied the association of GSTT1-null polymorphism with breast cancer.\(^8,19,21–23,25,28,30–31,34–36\) Totally, our meta-analysis showed that there was no significant association between GSTT1-null polymorphism and the risk of breast cancer (OR =1.15, 95% CI =0.93–1.42) (Table 2). When stratifying for ethnicity, we found that GSTT1-null polymorphism could increase the breast cancer risk among Asians (OR =1.19, 95% CI =1.01–1.41) (Figure 3). However, we found that there was no significant association of GSTT1-null polymorphism with breast cancer risk for Caucasians (OR =1.17, 95% CI =0.96–1.42) or mixed ethnicity (OR =0.88, 95% CI =0.57–1.34) (Table 2).

Association of GSTP1 Val105Ile polymorphism with breast cancer risk
Ten studies including 3,233 cases and 3,246 controls studied the association between GSTP1 Val105Ile (rs1695) polymorphism and breast cancer.\(^20,23–25,27,29–32,34,36\) In the allelic model, our meta-analysis showed that GSTP1 Val105Ile (rs1695) polymorphism was not associated with breast cancer risk overall (OR =1.21, 95% CI =0.99–1.48) (Table 2). When stratifying for ethnicity, similarly, we found that GSTP1 Val105Ile polymorphism could increase breast cancer risk for Caucasians (OR =1.16, 95% CI =1.01–1.34) (Figure 4). However, we found that there was no significant association between GSTP1 Val105Ile (rs1695) polymorphism and breast cancer risk for Asians (OR =1.26, 95% CI =0.91–1.75) (Table 2).

In the recessive model, we found that GSTP1 Val105Ile (rs1695) polymorphism was not associated with breast cancer risk overall (OR =1.16, 95% CI =0.83–1.62) (Table 2). When stratifying for ethnicity, we found that GSTP1 Val105Ile (rs1695) polymorphism had no significant association with the risk of breast cancer for Caucasians (OR =1.14, 95% CI =0.86–1.52) (Table 2) or for Asians (OR =1.28, 95% CI =0.70–2.35) (Table 2).

Similarly, we did not find any significant association of GSTP1 Val105Ile (rs1695) polymorphism with breast cancer risk overall (OR =1.19, 95% CI =0.93–1.52) and for Caucasians (OR =1.19, 95% CI =0.85–1.25) or Asians (OR =1.34, 95% CI =0.94–1.93) (Table 2) in the dominant model.

In codominant model, we found that there was no significant association of GSTP1 Val105Ile (rs1695) polymorphism with breast cancer risk overall (OR =1.24, 95% CI =0.81–1.89) and for Caucasians (OR =1.14, 95% CI =0.84–1.57) or Asians (OR =1.45, 95% CI =0.69–3.05) (Table 2).

Sensitivity analysis
A single study was excluded each time to reflect the effect of an individual study on the pooled OR and 95% CI. The deletion of any single study did not qualitatively alter the corresponding pooled ORs; these findings confirmed the stability of our meta-analysis results (data not shown).

Publication bias
We performed both Begg’s and Egger’s tests and generated a funnel plot to evaluate any potential publication bias. The symmetry of the funnel plots indicated no statistical evidence of publication bias in this meta-analysis (data not shown).

Discussion
Large-scale epidemiological studies on gene polymorphisms can contribute to uncovering the role and the corresponding mechanism of genes in the development of many diseases. To the best of our knowledge, this is the most comprehensive meta-analysis that evaluated the association of GSTM1-null, GSTT1-null, and GSTP1 Val105Ile (rs1695) polymorphisms with the risk of breast cancer. The obvious strength
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<th>Ethnicity</th>
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<th>Controls</th>
<th>GSTT1</th>
<th>Controls</th>
<th>GSTP1</th>
<th>Controls</th>
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**Abbreviations:** GST, glutathione S-transferase; Ile, isoleucine; Val, valine; “-”, no data; HWE, Hardy–Weinberg equilibrium.
null, and GSTT1-null polymorphisms are not significantly associated with breast cancer risk among Caucasians. However, no significant associations were found among Caucasian and mixed populations for GSTM1-null and GSTT1-null polymorphism. Similarly, no significant associations were found among Asians for GSTP1 Val105Ile (rs1695) polymorphism.

In 2013, Liu et al performed a meta-analysis, which showed that GSTP1 Val105Ile (rs1695) polymorphism was associated with the susceptibility of breast cancer in Asians under the allelic and recessive model. In another meta-analysis study, the GSTM1 and GSTP1 polymorphisms (under allelic and dominant model) were found to be associated with increased breast cancer risk Asian population, especially in East Asians, and that the GSTT1 polymorphism might not be associated with breast cancer. These differences between different meta-analyses might have been due to the relatively small number of samples in each study.

There are several possible causes for the differences between different ethnicities. First of all, the frequencies of the genotype vary sharply between different ethnicities. For instance, the homozygous null genotype distributions of the GSTT1 polymorphism change greatly between Asian and Caucasian populations, with a prevalence of 79.6% and

### Table 2 Meta-analysis of the association between GSTM1, GSTT1, and GSTP1 polymorphisms and breast cancer risk

<table>
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<tr>
<th>Comparisons</th>
<th>Odds ratio</th>
<th>95% CI</th>
<th>P-value</th>
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#### Abbreviations:
- GSTT1: glutathione S-transferase T1
- GSTM1: glutathione S-transferase M1
- GSTP1: glutathione S-transferase P1
- OR: odds ratio
- CI: confidence interval
- **P**: value

#### Study ID | OR (95% CI) | % weight
---|------------------|
Sohail et al | 0.96 (0.55–1.87) | 5.34 |
Zghieb et al | 1.05 (0.65–1.68) | 7.02 |
Sakoda et al | 1.15 (0.93–1.41) | 35.47 |
Chang et al | 1.11 (0.79–1.57) | 12.86 |
Syamala et al | 1.55 (1.08–2.22) | 10.03 |
Luo et al | 0.98 (0.76–1.27) | 24.16 |
Hashemi et al | 2.04 (1.27–3.29) | 5.02 |
Overall | 1.17 (1.04–1.32) | 100 |

#### Study ID | OR (95% CI) | % weight
---|------------------|
Zhou et al | 1.31 (0.97–1.77) | 20.15 |
Van Emburgh et al | 1.14 (0.93–1.41) | 45.43 |
Rangel et al | 1.30 (0.95–1.77) | 19.62 |
Ramalirinho et al | 0.81 (0.54–1.22) | 14.71 |
Overall | 1.16 (1.01–1.34) | 100 |

#### Abbreviations:
- S-Transferase M1, M2, and P1 polymorphisms in the breast cancer risk
- OR: odds ratio
- CI: confidence interval
- **P**: value

#### Figure 2 Forest plot for the association of GSTM1 null polymorphism and breast cancer risk for Asians.

**Abbreviations:** GSTM1, glutathione S-transferase M1; OR, odds ratio; CI, confidence interval.
19.0%, respectively.23,41 Therefore, more studies with larger sample sizes are needed to further confirm ethnic difference in the association between these polymorphisms and breast cancer risk. Second, different lifestyles may explain partially the ethnic difference, as Asians and Caucasians adopt different food preferences. Previous studies have demonstrated that high intake of certain fruits, vegetables, milk, and eggs may have important effects on breast cancer risk.42–44 Different lifestyles, such as maintaining body mass index, physical exercise, and intake of sugary drinks, red meat, and alcohol, also have important influence in breast cancer susceptibility.45,46 Finally, the finding of an increasing breast cancer risk only in Asians is a chance of finding because of the relatively small number of the studies among each ethnicity included in this meta-analysis.

GSTs are important Phase II detoxification enzymes involved in the metabolism of a large number of potential carcinogens. Mutations in all of the three GST genes may lead to oxidative stress and the accumulation of reactive quinone intermediates in cells. In the GST family, it is well known that the proteins GSTM1, GSTT1, and GSTP1 (rs1695) have important influence on the modification of some vital enzymes. Many studies have shown that these enzymes may combine with glutathione and affect the detoxification of electrophilic compounds, including carcinogens, therapeutic drugs, environmental toxins, and products of oxidative stress.47,48

Limitations

Several limitations of our study should be acknowledged when interpreting the results. First, due to the failure in acquiring detailed original information, all the results of this meta-analysis is based on single-factor calculation without adjustment by other important co-variables, such as menopausal state, age of menarche, tobacco smoking habit, lifestyle factors, and family history. Second, some heterogeneity was observed in this study due to uncontrolled confounding factors and selection bias. We solved this problem by adopting a random-effects model and performing sensitivity analysis. Third, only articles published and written in English were included this meta-analysis, which might have resulted in some degree of publication bias. However, no significant publication bias was detected, indicating that no noticeable harm was done by potential publication bias.

Conclusion

Our meta-analysis demonstrates that GSTM1- and GSTT1-null polymorphisms can increase breast cancer risk for Asians, and GSTP1 Val105Ile (rs1695) polymorphism can increase breast cancer risk for Caucasians.

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Disclosure

The authors report no conflicts of interest in this work.

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