

# Association of GSTM1 Null Allele with Prostate Cancer Risk: Evidence from 36 Case-Control Studies

Bingbing Wei<sup>1\*</sup>, Zhuoqun Xu<sup>1\*</sup>, You Zhou<sup>2\*</sup>, Jun Ruan<sup>1</sup>, Huan Cheng<sup>3</sup>, Bo Xi<sup>4</sup>, Ming Zhu<sup>1</sup>, Ke Jin<sup>1</sup>, Deqi Zhou<sup>1</sup>, Qiang Hu<sup>1</sup>, Qiang Wang<sup>1</sup>, Zhirong Wang<sup>1</sup>, Zhiqiang Yan<sup>1</sup>, Feng Xuan<sup>1</sup>, Xing Huang<sup>1</sup>, Jian Zhang<sup>1</sup>, Hongyi Zhou<sup>1</sup>

**1** Department of Urology, Affiliated Wuxi People's Hospital, Nanjing Medical University, Wuxi, China, **2** Faculty of Medicine, University of Helsinki, Finland, **3** Department of Urology, First Affiliated Hospital of Nanjing Medical University, Nanjing, China, **4** Department of Maternal and Child Health Care, School of Public Health, Shandong University, Jinan, China

## Abstract

**Background:** Glutathione S-transferase M1 (GSTM1) is thought to be involved in detoxifying several carcinogens and may play a vital role in tumorigenesis. Numerous studies have evaluated the association between GSTM1 null/present polymorphism and risk of prostate cancer (PCa). However, the results remain inconsistent. To derive a more precise estimation, we performed a meta-analysis.

**Methodology/Principal Findings:** A comprehensive search was conducted to identify all eligible case-control studies. We used odds ratios (ORs) with 95% confidence intervals (CIs) to assess the strength of the association. The overall association was significant (OR=1.28, 95% CI: 1.11–1.48,  $P=0.001$ ). Moreover, subgroup analyses showed GSTM1 null genotype significantly associated with PCa risk among Asians (OR=1.35, 95% CI: 1.03–1.78,  $P=0.03$ ) but not among Caucasians (OR=1.12, 95% CI: 0.96–1.31,  $P=0.16$ ). In addition, we did not find that smoking modified the genotype effect on the risk of PCa.

**Conclusions/Significance:** The present meta-analysis suggested that GSTM1 null allele was a low-penetrant risk factor for PCa among Asians.

**Citation:** Wei B, Xu Z, Zhou Y, Ruan J, Cheng H, et al. (2012) Association of GSTM1 Null Allele with Prostate Cancer Risk: Evidence from 36 Case-Control Studies. PLoS ONE 7(10): e46982. doi:10.1371/journal.pone.0046982

**Editor:** Olga Y. Gorlova, The University of Texas M. D. Anderson Cancer Center, United States of America

**Received:** April 21, 2012; **Accepted:** September 7, 2012; **Published:** October 10, 2012

**Copyright:** © 2012 Wei et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

**Funding:** No current external funding sources for this study.

**Competing Interests:** The authors have declared that no competing interests exist.

\* E-mail: xuzq@live.com

† These authors contributed equally to this work.

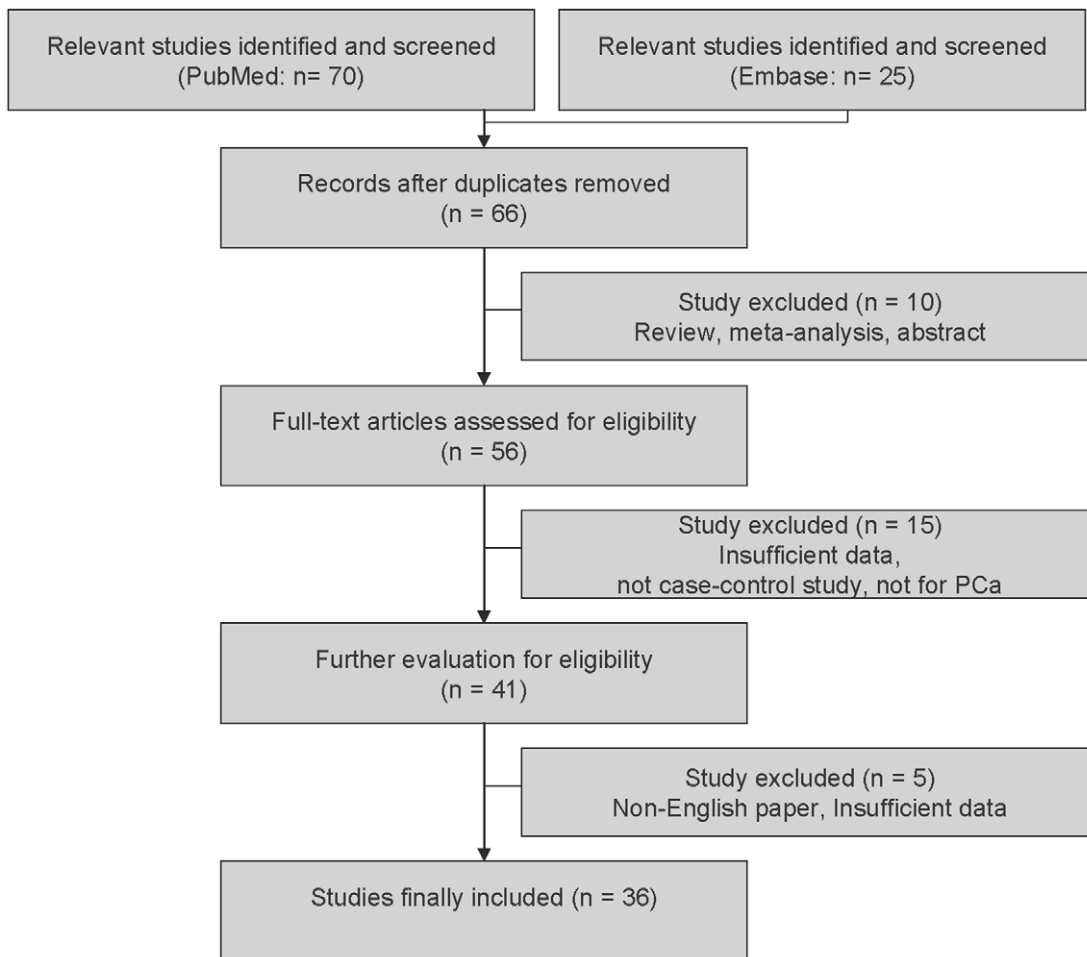
## Introduction

Prostate cancer (PCa) is now thought to be one of the most important medical problems in the male population [1]. In European countries, it is recognized as the most common solid neoplasm, with an incidence rate of 214 cases per 1000 men, outnumbering lung and colorectal cancer [2]. Furthermore, PCa is currently the second most common cause of cancer death in men [3]. Genetic predisposition and environmental factors are likely to contribute to the risk of PCa [4]; however, the etiology of PCa remains unclear. PCa incidence rate varies remarkably in different populations, highest among Africans, intermediate among Caucasians and lowest among Asians [5]. The variation in different ethnicities suggests that the genetic and environmental factor may play an important role in the etiology of PCa.

Generally, genetic susceptibility could modify the effect of environmental exposure, possibly explaining the difference of PCa incidence rate throughout the world. It is possible that the susceptibility to PCa is determined by the interindividual differences in the bioactivation of procarcinogens and detoxification of carcinogens because of the polymorphisms in metabolic genes. Glutathione S-transferase M1 (GSTM1) is thought to be

involved in detoxification of carcinogens, which has been considered as a PCa susceptibility gene [6].

GSTM1, located on chromosome 1p13.3, detoxifies numerous electrophilic substances, including carcinogens such as polycyclic aromatic hydrocarbons, ethylene oxide, epoxides, and styrene. GSTM1 expression could be hormonally controlled and induced by phenobarbital or propylthiouracil [7]. Three genetic polymorphisms, namely GSTM1\*0 (GSTM1 null polymorphism), GSTM1\*A and GSTM1\*B, have been identified. GSTM1\*0 is a deleted allele, and the homozygous allele (GSTM1 null genotype) is thought to be associated with low ability to detoxify several xenobiotics, reduced defense ability against oxidative stress, and free radical-mediated cellular damage [8–10]. Many studies on GSTM1 null genotype and PCa have compared the homozygous deletion genotype with the genotypes containing at least one functional allele (Null versus Present) [11–44]. Because GSTM1 null genotype could affect PCa risk by mediating the detoxification of activated tobacco carcinogens, it is with great interest that the tobacco smoking might affect the association between GSTM1 null genotype and PCa risk. Recent years, several studies have evaluated this possible effect [11–44].



**Figure 1. Flow chart of study selection based on the inclusion and exclusion criteria.**  
doi:10.1371/journal.pone.0046982.g001

However, the results are contradictory because of relatively small sample size with low statistical power. We therefore conducted a meta-analysis in order to provide an accurate estimate of the association.

## Methods

### Identification and Eligibility of Studies

PubMed (1956 to July 2012) and Embase (1947 to July 2012) database search was conducted using the following search terms: “GSTM1 or GST”, “polymorphism or variant”, and “prostate or prostatic”. Additional relevant studies were identified by a hand search of the references of original studies. Of these studies with the same or overlapping data, we selected the most recent ones with the largest number of subjects. Studies included in this meta-analysis should meet the following criteria: (a) evaluation the association of GSTM null/present polymorphism and PCa risk published in English language, (b) case-control study, (c) containing sufficient data for estimation of odds ratio (OR) with 95% confidence interval (95% CI).

### Data Extraction

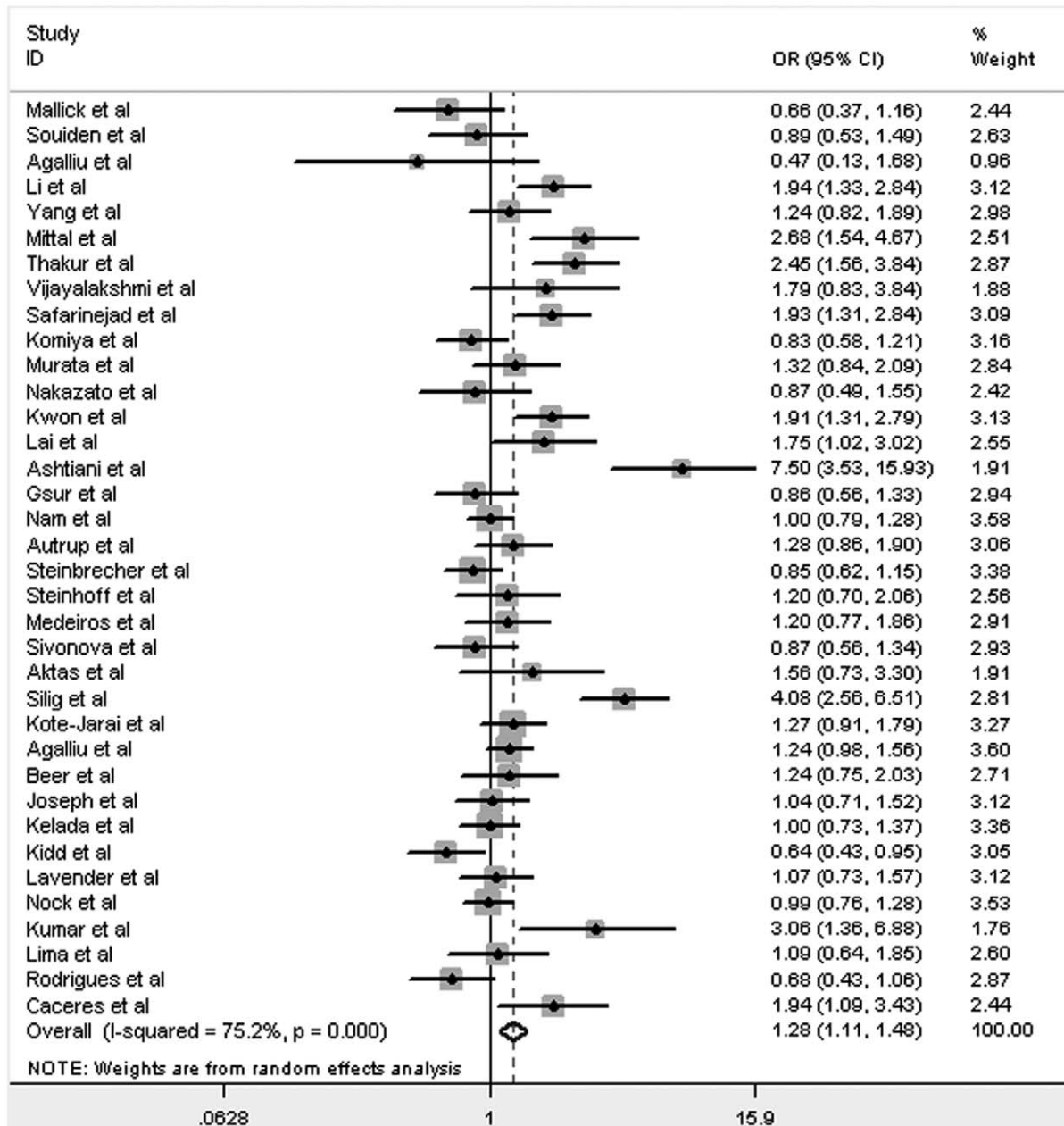
Two authors independently extracted the data and reached a consensus on all the items. For each study, the following information was collected: first author, publishing year, ethnicity

of subjects, source of controls, number of cases and controls, genotyping method. Different ethnic descents were categorized as Caucasians, Asians, and Africans. If a study did not specify the ethnicity or if it was not possible to separate participants according to such phenotype, the group was termed “mixed ethnicity”. For study [21] including subjects of different ethnic populations, data were collected separately whenever possible and recognized as an independent study.

### Statistical Analysis

The strength of the association between GSTM1 null/present polymorphism and PCa risk was measured by ORs with 95% CIs. The statistical significance of the summary OR was determined by the Z-test. For GSTM1 null polymorphism, we estimated the risk of the “Null” genotype on PCa risk, compared with the “Present” genotype. Stratified analyses were performed by ethnicities and smoking status.

Heterogeneity was evaluated by  $\chi^2$ -based Q-test. A *P* value of greater than 0.10 indicates a lack of heterogeneity among studies and the fixed-effects model was used to estimate the pooled OR of each study (the Mantel-Haenszel method). Otherwise, the random-effects model (the DerSimonian and Laird method) was used [45,46]. Sensitivity analysis was performed to assess the stability of results. Begg’s funnel plot and Egger’s test were



**Figure 2. Forest plot of PCa risk associated with GSTM1 null polymorphism (for Null versus Present).** The squares and horizontal lines correspond to the study-specific OR and 95% CI. The area of the squares reflects the weight (inverse of the variance). The diamonds represent the summary OR and 95% CI.

doi:10.1371/journal.pone.0046982.g002

performed to assess the publication bias of literatures;  $P < 0.05$  was considered statistically significant.

All statistical tests for this meta-analysis were performed with STATA (version 10.0; Stata Corporation, College Station, TX).

**Results**

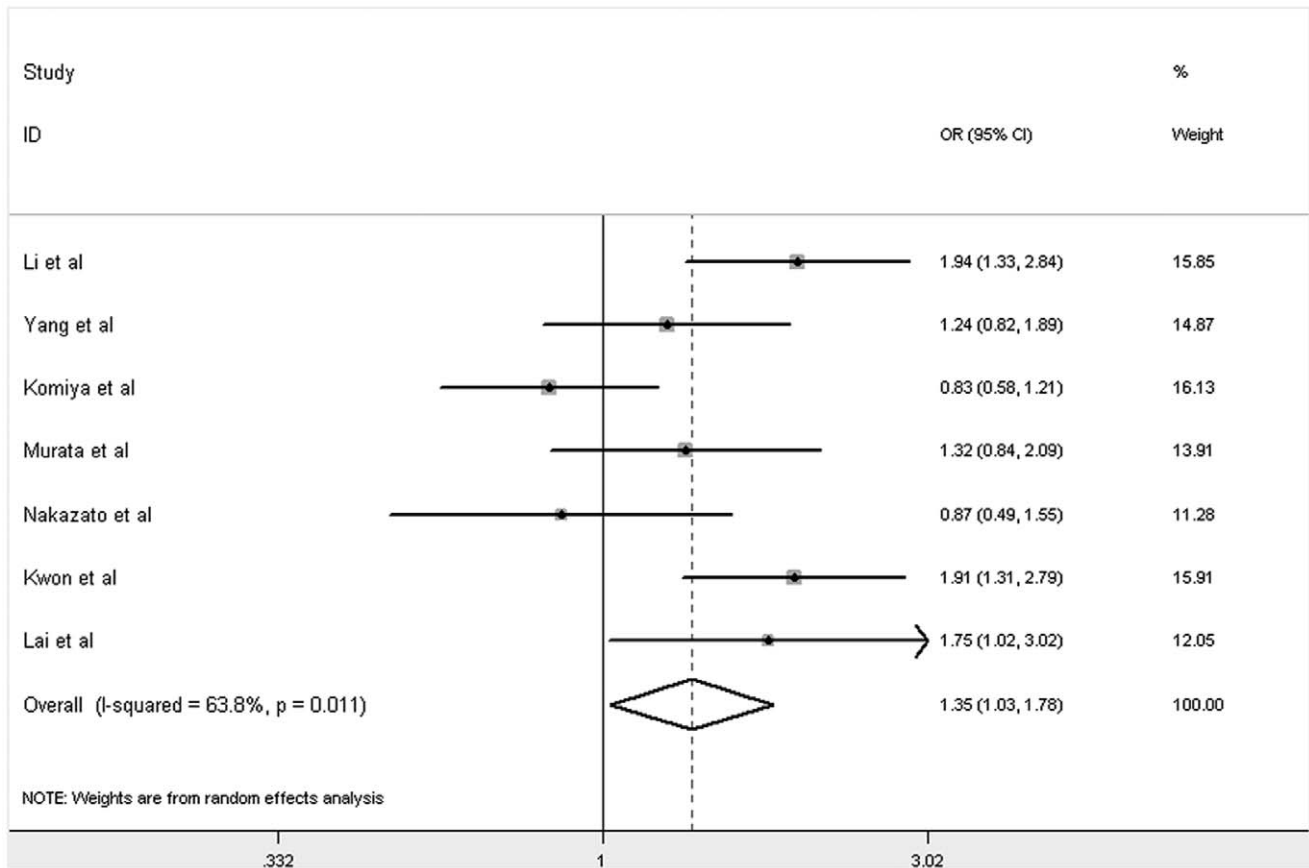
**Eligible Studies**

For PCa risk related to GSTM1 null polymorphism, articles were retrieved based on the search criteria above. Study selection process is shown in Figure 1. Ninety-five articles were retrieved. However, there were obvious overlapping data among a number of studies [23,34,39,42,47–51]. According to our inclusion criteria,

some of them were included [23,34,39,42,51]. Finally, a total of 36 studies including 6,202 cases and 8,209 controls were eligible for the meta-analysis. Study characteristics are summarized in Table S1. There were 7 studies on subjects of Asian, 17 of Caucasian, 3 of African and 9 of mixed ethnicity. Among them, 6 studies evaluated the effect of smoking status on the association. The controls from all eligible studies were frequency-matched controls to cases by age and ethnicity. A classical PCR or multiple PCR assay was conducted in 31 studies.

**Meta-analysis**

Overall, we found that GSTM1 null genotype was significantly associated with increased risk of PCa (Null versus Present:



**Figure 3. Forest plot of PCa risk associated with GSTM1 null polymorphism among Asians (for Null versus Present).** The squares and horizontal lines correspond to the study-specific OR and 95% CI. The area of the squares reflects the weight (inverse of the variance). The diamonds represent the summary OR and 95% CI. doi:10.1371/journal.pone.0046982.g003

OR = 1.28, 95% CI: 1.11–1.48,  $P = 0.001$ ; Table S2, Figure 2). In addition, subgroup analyses showed that there was significant association among Asians (Null versus Present: OR = 1.35, 95% CI: 1.03–1.78,  $P = 0.03$ ; Table S2, Figure 3), but neither in Caucasians (Null versus Present: OR = 1.12, 95% CI: 0.96–1.31,  $P = 0.16$ ; Table S2, Figure 4) nor Africans (data not shown).

**GSTM1-smoking Interaction**

The data on GSTM1 null genotype stratified by smoking status were available in six studies. Non-smokers with the GSTM1 null genotype did not have a significantly increased PCa risk, compared to Present genotype (Null versus Present: OR = 1.25, 95% CI: 0.64–2.45,  $P = 0.52$ ; Table S2). In addition, there was no significant association between GSTM1 null polymorphism and PCa risk among smokers (Null versus Present: OR = 1.16, 95% CI: 0.95–1.43,  $P = 0.15$ ; Table S2). This result was further confirmed by logistic regression analyses (data not shown).

**Test of Heterogeneity**

The heterogeneity was reckoned between each of the studies using Q-test. Overall significant heterogeneity was detected across studies (Null versus Present:  $P_{heterogeneity} < 0.01$ ; Table S2). In stratified analysis by ethnicity, there was significant heterogeneity among Asians ( $P_{heterogeneity} = 0.01$ ), Caucasians ( $P_{heterogeneity} < 0.01$ ; Table S2).

**Sensitivity Analysis**

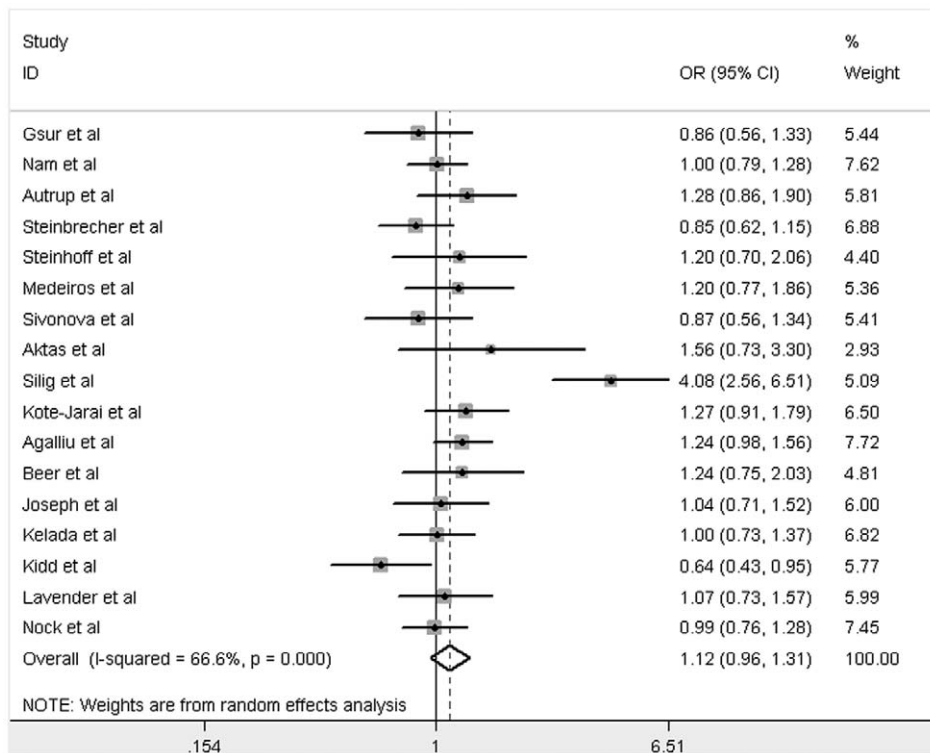
In the sensitivity analysis, the influence of each study on the pooled OR was examined by repeating the meta-analysis while omitting each study, one at a time. This procedure confirmed the stability of our overall result (data not shown).

**Publication Bias**

Begg’s funnel plot and Egger’s test were conducted to assess a possible publication bias in the literature. The shapes of funnel plots did not reveal any evidence of funnel plot asymmetry. The results Egger’s test from showed no indication of publication bias ( $P = 0.08$ ; Figure 5).

**Discussion**

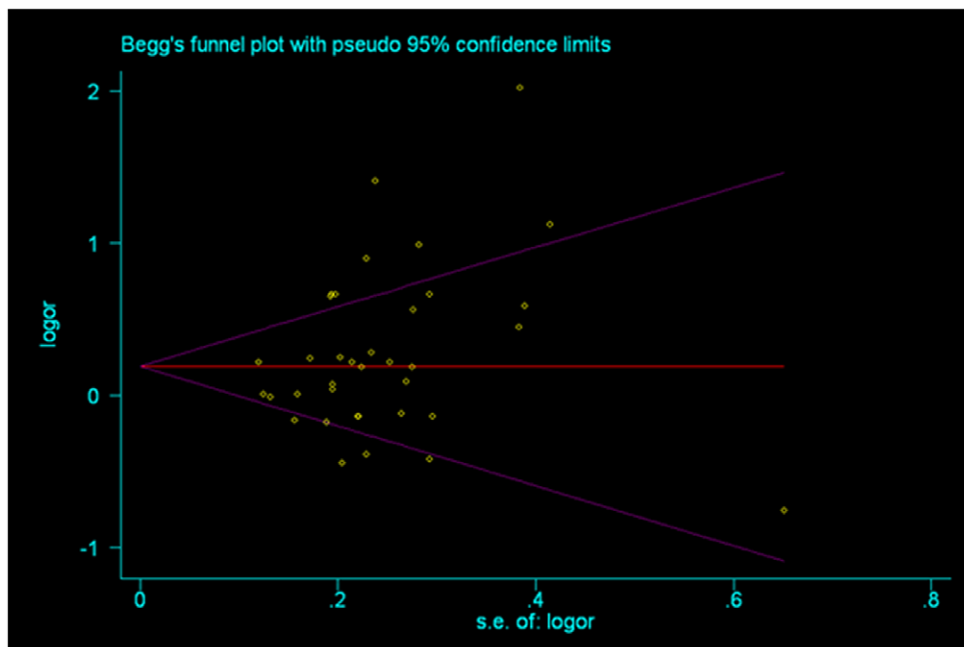
We performed a systematic literature search and combined the available results in the present meta-analysis, which is a useful strategy for elucidating genetic factors in cancer [52]. GSTM1 is thought to be involved in detoxification of hydrophobic electrophiles or oxidized lipids derived from the metabolism of xenobiotics [53,54]. The association of GSTM1 null polymorphism with different cancers, such as lung cancer [55], gastric cancer [56], and bladder cancer [57], has been extensively explored. The results of published studies on the association between GSTM1 null polymorphism and PCa risk remain conflicting and contradictory. The inconclusive results may be due to a small effect of GSTM1 null polymorphism on PCa risk.



**Figure 4. Forest plot of PCa risk associated with GSTM1 null polymorphism among Caucasians (for Null versus Present).** The squares and horizontal lines correspond to the study-specific OR and 95% CI. The area of the squares reflects the weight (inverse of the variance). The diamonds represent the summary OR and 95% CI. doi:10.1371/journal.pone.0046982.g004

The relatively low statistical power of published studies with small sample size might be a reason as well. Mo et al [58] evaluated the association between GSTM1 null polymorphism and PCa risk by

meta-analysis 3 years ago, but their study included overlapping data which might cause the bias. In addition, their use of scales for assessing quality or risk of bias is explicitly discouraged in



**Figure 5. Begg's funnel plot for publication bias test (for Null versus Present).** Each point represents a separate study for the indicated association. Log[or], natural logarithm of OR. Horizontal line, mean effect size. doi:10.1371/journal.pone.0046982.g005

Cochrane reviews [59]. Moreover, recently many original studies have come out and provided a variety of results. Hence, we conducted an updating meta-analysis to provide a quantitative approach for combining all the available within same topic. Concerning the reason methodology rules of meta-analysis [60,61], our study might provide a more accurate estimation.

The present meta-analysis, including 6,202 cases and 8,209 controls, explored the association between GSTM1 null/present polymorphism and PCa risk. Overall, we found that GSTM1 null genotype was significantly associated with PCa risk. Moreover, the association remained significant among Asians but not Caucasians. GSTM1 is thought to be involved in detoxification of hydrophobic electrophiles or oxidized lipids derived from the metabolism of xenobiotics [53,54], and play a vital role in carcinogenesis. The GSTM1 null genotype has no enzymatic activity and may affect the detoxification of carcinogens. Thus, it might be capable to alter the susceptibility to PCa among Asians. Given the important biological roles, the significant association between GSTM1 null polymorphism and PCa risk is reasonable and convincing.

In this study, we reported a significant association between GSTM1 null polymorphism and PCa risk among Asians, but not Caucasians. Ethnicity is a well established confounding factor for PCa. Our result suggested a possible role of ethnic difference in genetic backgrounds and the environment they lived in [62]. Actually, a number of studies have demonstrated that GSTM1 null genotype is significantly associated with some other cancers only in Asians. Zhuo et al [63] found that GSTM1 null genotype significantly increased susceptibility to oral cancer among Asians, but not Caucasians. Wang et al [64] reported that the null genotype of GSTM1 was a risk factor in cervical cancer among Asians, but not Caucasians. A recent study by Wang et al [65] showed that an increased hepatocellular carcinoma risk was significantly affected by the null genotype of GSTM1 among Asians. In addition, a meta-analysis by Qiu et al [66] provided evidences that the GSTM1 null genotype is a low-penetrant risk factor for gastric cancer development only in the Asian population.

To date, there is no reasonable molecular mechanism to explain the result. In the Caucasian population, the effect of the null genotype of GSTM1 on PCa risk might be masked by the presence of other as-yet unidentified causal genes involved in the development of PCa. In addition, heterogeneous exposure patterns to chemicals and environmental risk factors might also be taken account into account for the difference. Because there was

relatively small sample size for African population, the result on Africans should be interpreted with caution.

GSTM1 is involved in detoxification of epoxides from carcinogenic polycyclic aromatic hydrocarbons and combination of exposure to cigarette smoking. Lack of GSTM1 activity would increase the burden with ultimate carcinogenic epoxides [33]. In subgroup analyses by smoking status, the significant association was neither detected among non-smokers nor smokers. This suggested that smoking might not significantly modify the effect of GSTM1 null polymorphism on PCa risk. However, the result on undetected effect should be interpreted with caution because of a relatively small sample size included in the study.

Several limitation of our study should be addressed. (i) Although case misclassification bias was unlikely to exist in this study because all PCa cases were confirmed on the basis of histological criteria, we could not exclude the possibility that some control subjects had latent PCa which had not been detectable by PSA analysis or digital rectal examination (DRE). The undetected PCa in controls might produce bias estimates toward the null, and the strength of positive correlation might be underestimated. (ii) Our result was based on unadjusted estimates because of the limited information available. A more precise analysis should be conducted on the basis of adjustment for confounders such as age. (iii) Data on Africans was limited.

In summary, this meta-analysis provided the evidence that GSTM1 null genotype might be a low-penetrant susceptibility marker for PCa among Asians.

## Supporting Information

### Table S1 The characteristics of studies included in the meta-analysis.

(DOC)

### Table S2 Main result of pooled ORs in the meta-analysis.

(DOC)

## Author Contributions

Conceived and designed the experiments: BW ZX. Performed the experiments: BW ZX JR MZ. Analyzed the data: BW JR MZ. Contributed reagents/materials/analysis tools: BW ZX YZ JR HC BX MZ KJ DZ QH QW ZW ZY FX XH JZ HZ. Wrote the paper: BW ZX YZ.

## References

- Heidenreich A, Bellmunt J, Bolla M, Joniau S, Mason M, et al. (2011)EAU guidelines on prostate cancer. Part 1: screening, diagnosis, and treatment of clinically localised disease. *Eur Urol* 59: 61–71.
- Boyle P, Ferlay J (2005) Cancer incidence and mortality in Europe, 2004. *Ann Oncol* 16: 481–8.
- Jemal A, Siegel R, Ward E, Hao Y, Xu J, et al. (2008) Cancer statistics, 2008. *CA Cancer J Clin* 58: 71–96.
- Schaid DJ (2004) The complex genetic epidemiology of prostate cancer. *Hum Mol Genet* 13 Spec No 1: R103–21.
- Hsing AW, Tsao L, Devesa SS (2000) International trends and patterns of prostate cancer incidence and mortality. *Int J Cancer* 85: 60–7.
- Katoh T, Yamano Y, Tsuji M, Watanabe M (2008) Genetic polymorphisms of human cytosol glutathione S-transferases and prostate cancer. *Pharmacogenomics* 9: 93–104.
- Mannervik B, Awasthi YC, Board PG, Hayes JD, Di Ilio C, et al. (1992) Nomenclature for human glutathione transferases. *Biochem J* 282 (Pt 1): 305–6.
- Azarpira N, Nikeghbalian S, Geramizadeh B, Darai M (2010) Influence of glutathione S-transferase M1 and T1 polymorphisms with acute rejection in Iranian liver transplant recipients. *Mol Biol Rep* 37: 21–5.
- Rafiee L, Saadat I, Saadat M (2010) Glutathione S-transferase genetic polymorphisms (GSTM1, GSTT1 and GSTO2) in three Iranian populations. *Mol Biol Rep* 37: 155–8.
- Saadat I, Saadat M (2010) Influence of genetic polymorphisms of glutathione S-transferase T1 (GSTT1) and M1 (GSTM1) on hematological parameters. *Mol Biol Rep* 37: 249–53.
- Steinbrecher A, Rohrmann S, Timofeeva M, Risch A, Jansen E, et al. (2010) Dietary glucosinolate intake, polymorphisms in selected biotransformation enzymes, and risk of prostate cancer. *Cancer Epidemiol Biomarkers Prev* 19: 135–43.
- Lavender NA, Benford ML, VanCleave TT, Brock GN, Kittles RA, et al. (2009) Examination of polymorphic glutathione S-transferase (GST) genes, tobacco smoking and prostate cancer risk among men of African descent: a case-control study. *BMC Cancer* 9: 397.
- Sivonova M, Waczulikova I, Dobrota D, Matakova T, Hatok J, et al. (2009) Polymorphisms of glutathione-S-transferase M1, T1, P1 and the risk of prostate cancer: a case-control study. *J Exp Clin Cancer Res* 28: 32.
- Lima MM Jr, Oliveira MN, Granja F, Trindade AC, De Castro Santos LE, et al. (2008) Lack of association of GSTT1, GSTM1, GSTO1, GSTP1 and CYP1A1 polymorphisms for susceptibility and outcome in Brazilian prostate cancer patients. *Folia Biol (Praha)* 54: 102–8.
- Li M, Guan TY, Li Y, Na YQ (2008) Polymorphisms of GSTM1 and CYP1A1 genes and their genetic susceptibility to prostate cancer in Chinese men. *Chin Med J (Engl)* 121: 305–8.

16. Mallick S, Romana M, Blanchet P, Multigner L (2007) GSTM1 and GSTT1 polymorphisms and the risk of prostate cancer in a Caribbean population of African descent. *Urology* 69: 1165–9.
17. Yang J, Wu HF, Zhang W, Gu M, Hua LX, et al. (2006) Polymorphisms of metabolic enzyme genes, living habits and prostate cancer susceptibility. *Front Biosci* 11: 2052–60.
18. Nock NL, Liu X, Cicek MS, Li L, Macarie F, et al. (2006) Polymorphisms in polycyclic aromatic hydrocarbon metabolism and conjugation genes, interactions with smoking and prostate cancer risk. *Cancer Epidemiol Biomarkers Prev* 15: 756–61.
19. Silig Y, Pinarbasi H, Gunes S, Ayan S, Bagci H, et al. (2006) Polymorphisms of CYP1A1, GSTM1, GSTT1, and prostate cancer risk in Turkish population. *Cancer Invest* 24: 41–5.
20. Vijayalakshmi K, Vetriselvi V, Krishnan M, Shroff S, Vishwanathan KN, et al. (2005) Polymorphisms at GSTM1 and GSTP1 gene loci and risk of prostate cancer in a South Indian population. *Asian Pac J Cancer Prev* 6: 309–14.
21. Agalliu I, Langeberg WJ, Lampe JW, Salinas CA, Stanford JL (2006) Glutathione S-transferase M1, T1, and P1 polymorphisms and prostate cancer risk in middle-aged men. *Prostate* 66: 146–56.
22. Lai MT, Chen RH, Tsai FJ, Wan L, Chen WC (2005) Glutathione S-transferase M1 gene but not insulin-like growth factor-2 gene or epidermal growth factor gene is associated with prostate cancer. *Urol Oncol* 23: 225–9.
23. Caceres DD, Iturrieta J, Acevedo C, Huidobro C, Varela N, et al. (2005) Relationship among metabolizing genes, smoking and alcohol used as modifier factors on prostate cancer risk: exploring some gene-gene and gene-environment interactions. *Eur J Epidemiol* 20: 79–88.
24. Joseph MA, Moysich KB, Freudenheim JL, Shields PG, Bowman ED, et al. (2004) Cruciferous vegetables, genetic polymorphisms in glutathione S-transferases M1 and T1, and prostate cancer risk. *Nutr Cancer* 50: 206–13.
25. Komiya Y, Tsukino H, Nakao H, Kuroda Y, Imai H, et al. (2005) Human glutathione S-transferase A1, T1, M1, and P1 polymorphisms and susceptibility to prostate cancer in the Japanese population. *J Cancer Res Clin Oncol* 131: 238–42.
26. Aktas D, Hascicek M, Sozen S, Ozen H, Tuncbilek E (2004) CYP1A1 and GSTM1 polymorphic genotypes in patients with prostate cancer in a Turkish population. *Cancer Genet Cytogenet* 154: 81–5.
27. Beer TM, Evans AJ, Hough KM, Lowe BA, McWilliams JE, et al. (2002) Polymorphisms of GSTP1 and related genes and prostate cancer risk. *Prostate Cancer Prostatic Dis* 5: 22–7.
28. Medeiros R, Vasconcelos A, Costa S, Pinto D, Ferreira P, et al. (2004) Metabolic susceptibility genes and prostate cancer risk in a southern European population: the role of glutathione S-transferases GSTM1, GSTM3, and GSTT1 genetic polymorphisms. *Prostate* 58: 414–20.
29. Acevedo C, Opazo JL, Huidobro C, Cabezas J, Iturrieta J, et al. (2003) Positive correlation between single or combined genotypes of CYP1A1 and GSTM1 in relation to prostate cancer in Chilean people. *Prostate* 57: 111–7.
30. Kote-Jarai Z, Easton D, Edwards SM, Jefferies S, Durocher F, et al. (2001) Relationship between glutathione S-transferase M1, P1 and T1 polymorphisms and early onset prostate cancer. *Pharmacogenetics* 11: 325–30.
31. Gsur A, Haidinger G, Hinteregger S, Bernhofer G, Schatzl G, et al. (2001) Polymorphisms of glutathione-S-transferase genes (GSTP1, GSTM1 and GSTT1) and prostate-cancer risk. *Int J Cancer* 95: 152–5.
32. Steinhoff C, Franke KH, Golka K, Thier R, Romer HC, et al. (2000) Glutathione transferase isozyme genotypes in patients with prostate and bladder carcinoma. *Arch Toxicol* 74: 521–6.
33. Autrup JL, Thomassen LH, Olsen JH, Wolf H, Autrup H (1999) Glutathione S-transferases as risk factors in prostate cancer. *Eur J Cancer Prev* 8: 525–32.
34. Murata M, Shiraishi T, Fukutome K, Watanabe M, Nagao M, et al. (1998) Cytochrome P4501A1 and glutathione S-transferase M1 genotypes as risk factors for prostate cancer in Japan. *Jpn J Clin Oncol* 28: 657–60.
35. Nakazato H, Suzuki K, Matsui H, Koike H, Okugi H, et al. (2003) Association of genetic polymorphisms of glutathione-S-transferase genes (GSTM1, GSTT1 and GSTP1) with familial prostate cancer risk in a Japanese population. *Anticancer Res* 23: 2897–902.
36. Safarinejad MR, Shafiei N, Safarinejad SH (2011) Glutathione S-transferase gene polymorphisms (GSTM1, GSTT1, GSTP1) and prostate cancer: a case-control study in Tehran, Iran. *Prostate Cancer Prostatic Dis* 14: 105–13.
37. Thakur H, Gupta L, Sobti RC, Janmeja AK, Seth A, et al. (2011) Association of GSTM1/T1 genes with COPD and prostate cancer in north Indian population. *Mol Biol Rep* 38: 1733–9.
38. Soudien Y, Mahdouani M, Chaieb K, Elkamel R, Mahdouani K (2010) Polymorphisms of glutathione-S-transferase M1 and T1 and prostate cancer risk in a Tunisian population. *Cancer Epidemiol* 34: 598–603.
39. Kelada SN, Kardia SL, Walker AH, Wein AJ, Malkowicz SB, et al. (2000) The glutathione S-transferase-mu and -theta genotypes in the etiology of prostate cancer: genotype-environment interactions with smoking. *Cancer Epidemiol Biomarkers Prev* 9: 1329–34.
40. Kidd LC, Woodson K, Taylor PR, Albanes D, Virtamo J, et al. (2003) Polymorphisms in glutathione-S-transferase genes (GST-M1, GST-T1 and GST-P1) and susceptibility to prostate cancer among male smokers of the ATBC cancer prevention study. *Eur J Cancer Prev* 12: 317–20.
41. Nam RK, Zhang WW, Trachtenberg J, Jewett MA, Emami M, et al. (2003) Comprehensive assessment of candidate genes and serological markers for the detection of prostate cancer. *Cancer Epidemiol Biomarkers Prev* 12: 1429–37.
42. Mittal RD, Srivastava DS, Mandhani A, Kumar A, Mittal B (2004) Polymorphism of GSTM1 and GSTT1 genes in prostate cancer: a study from North India. *Indian J Cancer* 41: 115–9.
43. Rodrigues IS, Kuasne H, Losi-Guembarovski R, Fuganti PE, Gregorio EP, et al. (2011) Evaluation of the influence of polymorphic variants CYP1A1\*2B, CYP1B1\*2, CYP3A4\*1B, GSTM1\*0, and GSTT1\*0 in prostate cancer. *Urol Oncol* 29: 654–63.
44. Kumar V, Yadav GS, Datta SK, Singh S, Ahmed RS, et al. (2011) Association of GSTM1 and GSTT1 polymorphism with lipid peroxidation in benign prostate hyperplasia and prostate cancer: a pilot study. *Dis Markers* 30: 163–9.
45. Mantel N, Haenszel W (1959) Statistical aspects of the analysis of data from retrospective studies of disease. *J Natl Cancer Inst* 22: 719–48.
46. DerSimonian R, Laird N (1986) Meta-analysis in clinical trials. *Control Clin Trials* 7: 177–88.
47. Mittal RD, Mishra DK, Mandhani A (2006) Evaluating polymorphic status of glutathione-S-transferase genes in blood and tissue samples of prostate cancer patients. *Asian Pac J Cancer Prev* 7: 444–6.
48. Srivastava DS, Mandhani A, Mittal B, Mittal RD (2005) Genetic polymorphism of glutathione S-transferase genes (GSTM1, GSTT1 and GSTP1) and susceptibility to prostate cancer in Northern India. *BJU Int* 95: 170–3.
49. Murata M, Watanabe M, Yamanaka M, Kubota Y, Ito H, et al. (2001) Genetic polymorphisms in cytochrome P450 (CYP) 1A1, CYP1A2, CYP2E1, glutathione S-transferase (GST) M1 and GSTT1 and susceptibility to prostate cancer in the Japanese population. *Cancer Lett* 165: 171–7.
50. Rebbeck TR, Walker AH, Jaffe JM, White DL, Wein AJ, et al. (1999) Glutathione S-transferase-mu (GSTM1) and -theta (GSTT1) genotypes in the etiology of prostate cancer. *Cancer Epidemiol Biomarkers Prev* 8: 283–7.
51. Ashtiani ZO, Hasheminasab SM, Ayati M, Goulian BS, Modarressi MH (2011) Are GSTM1, GSTT1 and CAG repeat length of androgen receptor gene polymorphisms associated with risk of prostate cancer in Iranian patients? *Pathol Oncol Res* 17: 269–75.
52. Wei B, Zhou Y, Xu Z, Ruan J, Zhu M, et al. (2011) XRCC1 Arg399Gln and Arg194Trp polymorphisms in prostate cancer risk: a meta-analysis. *Prostate Cancer Prostatic Dis* 14: 225–31.
53. Strange RC, Fryer AA (1999) The glutathione S-transferases: influence of polymorphism on cancer susceptibility. *IARC Sci Publ*: 231–49.
54. Landi S (2000) Mammalian class theta GST and differential susceptibility to carcinogens: a review. *Mutat Res* 463: 247–83.
55. Benhamou S, Lee WJ, Alexandria AK, Boffetta P, Bouchardy C, et al. (2002) Meta- and pooled analyses of the effects of glutathione S-transferase M1 polymorphisms and smoking on lung cancer risk. *Carcinogenesis* 23: 1343–50.
56. Chen B, Zhou Y, Yang P, Wu XT (2010) Glutathione S-transferase M1 gene polymorphism and gastric cancer risk: an updated analysis. *Arch Med Res* 41: 558–66.
57. Zhang R, Xu G, Chen W, Zhang W (2011) Genetic polymorphisms of glutathione S-transferase M1 and bladder cancer risk: a meta-analysis of 26 studies. *Mol Biol Rep* 38: 2491–7.
58. Mo Z, Gao Y, Cao Y, Gao F, Jian L (2009) An updating meta-analysis of the GSTM1, GSTT1, and GSTP1 polymorphisms and prostate cancer: a HuGE review. *Prostate* 69: 662–88.
59. Higgins J, Green S (2011) *Cochrane Handbook for Systematic Reviews of Interventions* Version 5.1.0 [updated March 2011]. In: Higgins J, Green S, editors: The Cochrane Collaboration.
60. Geng J, Zhang Q, Zhu C, Wang J, Chen L (2009) XRCC1 genetic polymorphism Arg399Gln and prostate cancer risk: a meta-analysis. *Urology* 74: 648–53.
61. Wei B, Xu Z, Ruan J, Zhu M, Hu Q, et al. (2011) Re: Geng, et al.: XRCC1 Genetic Polymorphism Arg399Gln and Prostate Cancer Risk: A Meta-analysis (Urology 2009;74:648–653). *Urology* 78: 481–2.
62. Hirschhorn JN, Lohmueller K, Byrne E, Hirschhorn K (2002) A comprehensive review of genetic association studies. *Genet Med* 4: 45–61.
63. Zhuo W, Wang Y, Zhuo X, Zhu Y, Wang W, et al. (2009) CYP1A1 and GSTM1 polymorphisms and oral cancer risk: association studies via evidence-based meta-analyses. *Cancer Invest* 27: 86–95.
64. Wang D, Wang B, Zhai JX, Liu DW, Sun GG (2011) Glutathione S-transferase M1 and T1 polymorphisms and cervical cancer risk: a meta-analysis. *Neoplasma* 58: 352–9.
65. Wang B, Huang G, Wang D, Li A, Xu Z, et al. (2010) Null genotypes of GSTM1 and GSTT1 contribute to hepatocellular carcinoma risk: evidence from an updated meta-analysis. *J Hepatol* 53: 508–18.
66. Qiu LX, Wang K, Lv FF, Chen ZY, Liu X, et al. (2011) GSTM1 null allele is a risk factor for gastric cancer development in Asians. *Cytokine* 55: 122–5.