

Association between *GSTM1* polymorphisms and lung cancer: an updated meta-analysis

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Genet. Mol. Res. 14 (1): 1385-1392 (2015) Received January 2, 2014 Accepted May 26, 2014 Published February 13, 2015 DOI http://dx.doi.org/10.4238/2015.February.13.17

ABSTRACT. The relationship between glutathione S-transferase M1 (GSTM1) genetic polymorphisms and lung cancer has been reported previously. However, the results are not consistent. Therefore, to clarify the association between GSTM1 polymorphisms and lung cancer, we performed a meta-analysis based on published studies. We used the Revman 5.0 software to perform literature retrieval, article selection, data collection, and statistical analysis. We utilized a random-effect model to pool the odds ratios (ORs) and 95% confidence intervals (CIs). A total of 38 eligible studies including 5737 lung cancer patients and 6843 cancer-free control subjects were analyzed. We found no association between GSTM1 genetic polymorphisms and lung cancer risk (OR = 1.15, 95%CI = 0.98-1.36, P = 0.08). Including only Chinese individuals, we found no association between GSTM1 genetic polymorphisms and lung cancer risk (OR = 1.13, 95%CI = 0.97-1.32, P = 0.13). In conclusion, we found that *GSTM1* polymorphisms are not associated with lung cancer risk.

Key words: GSTM1; Lung cancer; Meta-analysis; Polymorphism

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INTRODUCTION

Recently, lung cancer has become the most common cause of cancer-related death (Persson et al., 1999). Human cancers can be initiated by DNA damage resulting from environmental factors such as alcohol use and smoking (Ada et al., 2012). However, individuals not exposed to these risk factors can also develop lung cancer, indicating that a difference in cancer susceptibility exists among individuals (Ada et al., 2012). Previous studies indicate that genetic polymorphisms in the glutathione S-transferase M1 (GSTMI) gene may affect the risk of lung cancer (Nakachi et al., 1993; Cao et al., 2004; Chen et al., 2004a, 2012; Atinkaya et al., 2012; Han et al., 2012; Li et al., 2012; Liang et al., 2012; Liu et al., 2012). Subjects who have inherited specific variants in the GSTM1 gene may be susceptible to the effects of chemical carcinogens and thus at a high risk of developing lung cancer. GSTM1 is a member of the glutathione S-transferase family and is capable of detoxifying reactive electrophiles that can act as mutagens. In addition, the GSTM1 gene is polymorphic, and several studies have reported that a deletion mutation in the GSTM1 gene results in GSTM1 deficiency associated with lung cancer (Liang et al., 2012; Liu et al., 2012; López-Cima et al., 2012; Yao et al., 2012). Seidegård et al. (1986) first reported the association between GSTM1 deficiency and lung cancer. Since then, there have been more than 40 studies examining this topic (Li et al., 2012; Liang et al., 2012; Liu et al., 2012; López-Cima et al., 2012; Yao et al., 2012). However, there is disagreement among the results of these studies. The small sample sizes used in many studies may be one explanation for this. To clarify the effect of GSTM1 polymorphisms on the risk of lung cancer, we performed a meta-analysis of 38 studies to determine the association between GSTM1 status and lung cancer risk.

MATERIAL AND METHODS

Publication search

We searched the PubMed, EMbase, Chinese Biomedical Literature Database, China National Knowledge Infrastructure (CNKI), and Wanfang databases using the search terms "lung cancer" and "GSTM1" through July 31, 2013. The online search was accompanied by a manual check of the reference lists from the identified articles and reviews for potentially eligible original reports.

Inclusion criteria

The inclusion criteria were as follows: 1) the studies examined the association between *GSTM1* and lung cancer without restrictions on language or publication year; 2) the research design was a case-control study or cohort study without restrictions on age or race; 3) the size of the sample, odds ratios (ORs), and their 95% confidence intervals (CIs) were provided.

Exclusion criteria

Exclusion criteria were as follows: 1) duplicate data; 2) case reports, series, abstract, comment, review, and editorial; and 3) insufficient data.

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Literature quality assessment and data extraction

We collected the following information: the name of the first author, publication year, country, number of cases and controls, and genotyping method. In a few studies, some of the data had already been reported elsewhere; therefore, only novel data were included.

Data analysis

Meta-analysis was performed using the RevMan 5.0 software, which was provided by the Cochrane Collaboration. The *Q*-test and the I^2 test were used to directly examine the heterogeneity between each study. The OR value and its 95%CI was used to evaluate the relationship between *GSTM1* status and lung cancer risk. To test for publication bias, we used the RevMan 5.0 statistical software to construct a funnel plot. P < 0.05 was considered to be statistically significant.

RESULTS

Literature screening

A total of 464 studies were initially identified, and 402 studies were excluded because of duplicate publication and nonclinical-based research. Eighty-three studies were reviewed, and 24 publications were excluded because they did not include control subjects. A total of 38 studies were included, all of which were case-control studies (Table 1). The 38 studies included 5737 lung cancer patients and 6843 cancer-free control subjects.

Meta-analysis

From the 38 selected studies, OR values and 95%CIs were extracted and directly used to evaluate the relationship between *GSTM1* polymorphisms and lung cancer. There was heterogeneity (P < 0.001, $I^2 = 77\%$) among the publications; therefore, we utilized a random-effect model to merge OR values. We found no association between *GSTM1* polymorphisms and lung cancer (OR = 1.15, 95%CI = 0.98-1.36, P = 0.08; Figure 1). When only Chinese subjects were analyzed, we found no association between *GSTM1* genetic polymorphisms and lung cancer risk (OR = 1.13, 95%CI = 0.97-1.32, P = 0.13; Figure 2).

Publication bias analysis

We analyzed publication bias using the Revman 5.0 software. The funnel plots (Figures 3 and 4) show that the points were evenly distributed, symmetrical, and most were within the 95%CI. This indicates that no publication bias existed and that the study results were credible.

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Year	Country	Genotyping methods	Cases/Controls (N)	Genotypes	Case (N)	Genotypes	Control (N)
2012	Turkey	Multiplex PCR	213/231	12	123	107	124
							23
							56
							95 78
							65
							40
					99		246
2012	China	Multiplex PCR	200/200	97	123	79	110
2011	China	Multiplex PCR	125/125	54	71	52	73
2004	China		281/326				224
							359
							89
							57 200
							200 66
							39
				90			95
2012	China	Multiplex PCR	68/70	21	47	31	39
2012	China	PCR-RFLP	360/360	215	145	253	107
2008	China	Chips	110/125	44	66	68	57
	- F ···						418
							23
							53
							47 57
							31
							108
				40			42
2006	China	Multiplex PCR	91/91	56	35	51	40
2007	China	Multiplex PCR	58/131	24	34	55	76
							139
							68
							33
							91 22
							72
2010	Italy	Duplex PCR	75/121	33	42	53	68
	Ada 2012 Al 2011 Altinksy 2012 Altinksy 2012 Chang 2006 Chen CM 2012 Chen H 2008 Chen M 2004 Cu 92 2010 Cu 92 2010 Cu 92 2010 Cu 97 2004 Cu 97 2007 Han RL 2012 Lei FM 2007 Han RL 2012 Lei FM 2007 Li W 2012 Li W 2012 Li W 2014 Li W 2014	$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	LCI M.H. Bi 90] 93] 92] 93] 92] 93] 92] 93] 92] 93] 93] 93] 94] 93] 93] 93] 94] 93] 95] 94] 94] 94] 95] 93] 97] 97] 97] 97] 97] 97] 97] 92] 93] 44] - 92] 94] 94] - 94] -	dds Ratio andom, 95% CI		
	2012 2011 2004 2006 2004 2008 2012 2011 2007 2012 2007 2012 2007 2012 2007 2012 2007 2012 2012	2012 Тигкеу 2011 Сhina 2012 Тигкеу 2014 China 2004 China 2005 China 2011 China 2007 China 2007 China 2006 China 2007 China 2012 China 2008 China 2008 China 2006 China 2006 China 2007 China 2008 China 2009 Italy Abola China	2012 Turkey Multiplex PCR 2011 China Multiplex PCR 2012 Turkey Multiplex PCR 2004 China Multiplex PCR 2004 China Multiplex PCR 2004 China Multiplex PCR 2004 China Multiplex PCR 2005 China Multiplex PCR 2004 China Multiplex PCR 2005 China Multiplex PCR 2007 China Multiplex PCR 2007 China Multiplex PCR 2006 China Multiplex PCR 2007 China Multiplex PCR 2005 China Multiplex PCR 2012 China Multiplex PCR 2006 China Multiplex PCR 2008 Chin	2012 Turkey Multiplex PCR 213/231 2011 China Multiplex PCR 128/122 2012 Turkey Multiplex PCR 128/122 2004 China Multiplex PCR 104/205 2006 China Multiplex PCR 163/163 2004 China Multiplex PCR 91/91 2008 China PCR-RFLP 158/455 2012 China Multiplex PCR 200/200 2011 China Multiplex PCR 200/200 2007 China Multiplex PCR 128/214 2007 China Multiplex PCR 128/214 2004 China Multiplex PCR 128/214 2005 China Multiplex PCR 98/136 2012 China Multiplex PCR 98/136 2012 China Multiplex PCR 98/136 2012 China Multiplex PCR 789/789 2008 China Multiplex PCR 789/789	2012 Turkey Multiplex PCR 213/231 12 2011 China Multiplex PCR 50/50 14 2012 Turkey Multiplex PCR 104/205 39 2004 China Multiplex PCR 163/163 57 2004 China Multiplex PCR 91/318 56 2004 China Multiplex PCR 91/138 56 2004 China Multiplex PCR 200/200 97 2011 China Multiplex PCR 200/200 97 2012 China Multiplex PCR 200/200 97 2011 China Multiplex PCR 279/684 164 2012 China Multiplex PCR 28/1326 101 2007 China Multiplex PCR 29/684 164 2012 China Multiplex PCR 9/8/36 44 2012 China Multiplex PCR 9/8/36 215 2012 China Multiplex PCR	2012 Turkey Multiplex PCR 213/231 12 12 12 2011 China Multiplex PCR 50/50 14 36 2012 Turkey Multiplex PCR 128/122 72 53 2004 China Multiplex PCR 104/205 39 65 2004 China Multiplex PCR 104/205 39 65 2004 China Multiplex PCR 91/138 56 35 2004 China Multiplex PCR 200/200 97 123 2011 China Multiplex PCR 125/125 54 71 2004 China Multiplex PCR 128/214 49 79 2007 China Multiplex PCR 128/214 49 72 2007 China Multiplex PCR 217/193 112 118 24 2007 China Multiplex PCR 128/214 49 79 2006 China 116 115	2012 Turkey Multiplex PCR 213/231 12 12 12 13 107 2011 China Multiplex PCR 50/50 14 36 57 2004 China Multiplex PCR 104/205 39 65 110 2006 China Multiplex PCR 163/163 57 106 85 2004 China Multiplex PCR 91/138 56 35 51 2004 China Multiplex PCR 91/138 56 35 51 2004 China Multiplex PCR 200/200 97 12 79 2011 China Alliplex PCR 125/125 54 71 52 2004 China Alliplex PCR 125/126 101 180 102 20012 China Multiplex PCR 128/126 101 180 102 2004 China Multiplex PCR 98/136 44 56 61 <td< td=""></td<>

Figure 1. Forest plot of lung cancer risk associated with GSTM1 polymorphism (in total). The squares and horizontal lines correspond to the study-specific OR and 95%CI, respectively. The area of the squares reflects the study-specific weight. The diamond represents the pooled results of OR and 95%CI. In this analysis, random-effect model was used.

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	Case		Control			Odds Ratio	Odds Ratio
Study or Subgroup	Events	Total	Events	Total	Weight	M-H, Random, 95% CI	M-H, Random, 95% Cl
Cao 2004	65	104	95	205	3.4%	1.93 [1.19, 3.13]	
Chang 2006	106	163	78	163	3.6%	2.03 [1.30, 3.16]	
Chen CM 2012	35	91	65	138	3.1%	0.70 [0.41, 1.20]	+
Chen H 2008	35	91	40	91	2.9%	0.80 [0.44, 1.44]	
Chen M 2004	99	158	246	454	3.9%	1.42 [0.98, 2.06]	-
Chen SD 2004	123	220	110	189	3.8%	0.91 [0.61, 1.35]	+
Du G 2011	71	125	73	125	3.3%	0.94 [0.57, 1.55]	-
Gu YF 2004	180	281	224	326	4.1%	0.81 [0.58, 1.14]	
Gu YF 2007	115	279	359	684	4.3%	0.63 [0.48, 0.84]	+
Han RL 2012	79	128	89	214	3.5%	2.26 [1.45, 3.55]	
Lei FM 2007	24	42	57	103	2.4%	1.08 [0.52, 2.22]	_ _
Li D 2005	217	344	200	295	4.1%	0.81 [0.58, 1.13]	
Li W 2012	99	156	66	93	3.1%	0.71 [0.41, 1.24]	+
Li WY 2004	56	100	39	100	3.0%	1.99 [1.13, 3.50]	
Li Y 2006	127	217	95	200	3.8%	1.56 [1.06, 2.30]	
Liang KC 2012	47	68	39	70	2.5%	1.78 [0.89, 3.57]	<u> </u>
Liu D 2012	145	360	107	360	4.2%	1.59 [1.17, 2.17]	
Liu Q 2008	66	110	57	125	3.2%	1.79 [1.06, 3.01]	
Lu QF 2008	491	776	418	776	3.5%	0.92 [0.75, 1.12]	+
Qi XS 2008	19	53	31	72	2.4%	0.74 [0.36, 1.53]	
Qian BY 2006	108	177	108	161	3.6%	0.77 [0.49, 1.20]	
Wang DQ 2006	56	96	42	61	2.6%	0.63 [0.32, 1.25]	+
Wang QM 2006	35	91	40	91	2.9%	0.80 [0.44, 1.44]	
Xia Y 2007	34	58	76	131	2.8%	1.03 [0.55, 1.92]	
Ye WY 2004	186	294	139	214	3.9%	0.93 [0.64, 1.34]	+
Yao ZG 2012	96	150	68	150	3.5%	2.14 [1.35, 3.41]	
Ye WY 2004	23	58	33	62	2.4%	0.58 [0.28, 1.19]	
Zeng M 2005	91	147	91	142	3.4%	0.91 [0.56, 1.47]	-+-
Zhang JQ 2011	34	50	22	50	2.1%	2.70 [1.20, 6.11]	
Zhu XX 2010	93	160	72	160	3.6%	1.70 [1.09, 2.64]	
							L.
Total (95% CI)		5147		6005	100.0%	1.13 [0.97, 1.32]	•
Total events	2865		3179				
Heterogeneity: Tau² =	= 0.12; Chi); I² = 72%	0.01 0.1 1 10 100				
Test for overall effect:	Z=1.53 (P = 0.1	3)				
							Favors [case] Favors [control]

Figure 2. Forest plot of lung cancer risk associated with GSTM1 polymorphism (only in Chinese). The squares and horizontal lines correspond to the study-specific OR and 95%CI, respectively. The area of the squares reflects the study-specific weight. The diamond represents the pooled results of OR and 95%CI. In this analysis, random-effect model was used.

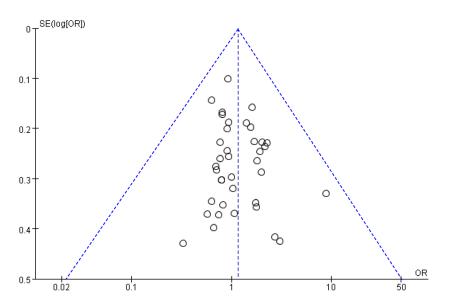


Figure 3. Funnel plot for publication bias test (in total). Each circle denotes an independent study for the indicated association. Log[OR], natural logarithm of OR. Horizontal line stands for mean effect size.

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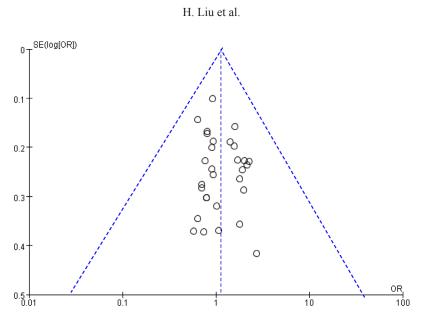


Figure 4. Funnel plot for publication bias test (only in Chinese). Each circle denotes an independent study for the indicated association. Log[OR], natural logarithm of OR. Horizontal line stands for mean effect size.

DISCUSSION

In the present meta-analysis, we found no association between *GSTM1* polymorphisms and lung cancer risk.

The biochemical function of GSTM1 suggests a plausible biochemical rationale for individual differences in the susceptibility to certain kinds of cancer, particularly those resulting from exposure to chemical carcinogens. Individuals with deletions of both copies of GSTM1 are completely deficient in the GST isoenzyme; this enables a greater fraction of the relevant chemical carcinogens from cigarette smoke to penetrate the cellular DNA and form carcinogenic adducts. According to this model, individuals with 1 or 2 copies of the GSTM1 gene express this GST isozyme and detoxifies a greater fraction of the carcinogen or carcinogens before adduct formation. Although various previous publications have suggested that the GSTM1 polymorphism is associated with lung cancer, our meta-analysis did not show this result. In this meta-analysis, a total of 38 case-control studies were analyzed to comprehensively assess the association between GSTM1 polymorphisms and lung cancer. Genotypes in all studies were detected using genetic DNA from blood samples. Most of these studies evaluated the genotypes for quality control. The genotype distribution of controls in all studies was consistent with Hardy-Weinberg equilibrium. However, according to our meta-analysis, there is no genetic association between GSTM1 and the susceptibility to lung cancer. In addition, exploring the heterogeneity between each study is an important goal of meta-analysis. In the present study, we found significant heterogeneity among the studies included, which may have resulted from the use of different genotyping methods. In addition, sensitivity analysis showed that omission of any single study did not significantly impact the combined ORs. Furthermore, the funnel plot did not reflect clear asymmetry, indicating no considerable publication bias in this meta-analysis. This indicated that our results were reliable.

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In summary, this meta-analysis of 38 studies showed that GSTM1 polymorphisms are not risk factors for lung cancer.

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