GSTM1 Polymorphisms and Lung Cancer Risk in the Chinese Population: a Meta-Analysis Based on 47 Studies

Xin-Ping Chen¹,²&, Wei-Hua Xu²&, Da-Feng Xu³, Xian-He Xie⁴*, Jia Yao⁵, Sheng-Miao Fu²*

Abstract

Although a number of studies have been conducted on the association between GSTM1 polymorphisms and lung cancer in China, this association remains elusive and controversial. To clarify the effects of GSTM1 polymorphisms on the risk of lung cancer, a meta-analysis was performed in the Chinese population. Related studies were identified from PubMed, Springer Link, Ovid, Chinese Wanfang Data Knowledge Service Platform, Chinese National Knowledge Infrastructure (CNKI), and Chinese Biology Medicine (CBM) up to 5th April 2014. A total of 45 articles (47 studies) including 6,623 cases and 7,865 controls were involved in this meta-analysis. Overall, a significant association (OR = 1.45, 95%CI: 1.32-1.60) was found between the null GSTM1 and lung cancer risk when all studies in Chinese population pooled into the meta-analysis. In subgroup analyses stratified by quality score, geographic area and source of controls, the same results were observed under all the models. This meta-analysis showed that the null GSTM1 may be a potential biomarker for lung cancer risk in Chinese, but further studies with gene-gene and gene-environment interactions are required for definite conclusions.

Keywords: Meta-analysis - GSTM1 - polymorphism - lung cancer - Chinese population

Introduction

Lung cancer is the most commonly diagnosed cancer as well as the leading cause of cancer death in males globally, with 1.6 million newly confirmed cases and 1.4 million deaths from lung cancer annually (Jemal et al., 2011). Human cancers can be initiated by DNA damage caused by environmental chemical agents, such as polycyclic aromatic hydrocarbons (PAHs), and some adverse habits including tobacco smoking and alcohol use (Neumann et al., 2005).

Studies have shown that exposures to environmental and occupational PAHs are risk factors for lung cancer (Kriek et al., 1993; Li et al., 2004; Vineis & Husgafvel-Pursiainen, 2005). However, not all of those who have been exposed to the risk factors will develop lung cancer, suggesting that there is individual variation in cancer susceptibility in the general population (Neumann et al., 2005). To understand the contribution of genetic variations in lung cancer, genetic association approach has been widely used and has been fruitful. For example, studies have consistently associated the development of lung cancer with the genetic factors such as glutathione S-transferase M1 (GSTM1).

The association between GSTM1 gene and lung cancer has been investigated in numerous epidemiologic studies since glutathione S-transferase was first suggested as a potential marker for susceptibility to lung cancer in 1986 (Seidegard et al., 1986). Glutathione S-transferases consist five distinct families, namely alpha (GSTA), sigma (GSTS), mu (GSTM), pi (GSTP), and theta (GSTT) (Kiyohara et al., 2002). Located on the chromosome 1p13.3, the GSTM1 plays an important role in the xenobiotics’ detoxification. The most common genotype of GSTM1 gene is homozygous deletion (null genotype), which has been suggested to be associated with the loss of enzyme activity, increased vulnerability to cytogenetic damage and resulted in the increased susceptibility to cancer (Hayes et al., 2005; McIlwain et al., 2006).

Recently, the role of GSTM1 polymorphism in the etiology of different types of cancer has drawn more and more attention, including lung cancer. A number of studies in China have been conducted to explore whether GSTM1 polymorphism is associated with lung cancer susceptibility, but provided controversial or inconclusive results. Therefore, we conducted a meta-analysis to more precisely define the effect of GSTM1 polymorphism on risk for lung cancer in Chinese populations.

¹College of Agriculture, Hainan University, ¹Department of Breast Surgery, Hainan Province People’s Hospital, Haikou, Hainan Province, ²Department of Central Laboratory, ³Department of Hepatobiliary Surgery, ⁴Department of Chemotherapy, the First Affiliated Hospital of Fujian Medical University, Fuzhou, Fujian, China  *Equal contributors  *For correspondence: ShenmiaoFu@126.com and 13976868269@163.com
Materials and Methods

Search strategy
We searched databases containing PubMed, Springer Link, Ovid, Chinese Wanfang Data Knowledge Service Platform, Chinese National Knowledge Infrastructure (CNKI), and Chinese Biology Medicine (CBM) up to 5th April 2014, using combination of the following terms: (1) GSTM1 or GST M1; (2) lung cancer or lung neoplasm or lung tumor; (3) polymorphism or variant or variation; and (4) Chinese or China. We limited the languages to English and Chinese. Besides, the references from retrieved articles were also searched.

Eligibility criteria
Studies were included in this meta-analysis if they met the following criteria: (1) case-control study or cohort study studying on associations between GSTM1 polymorphism and lung cancer susceptibility; (2) all patients with the diagnosis of lung cancer confirmed by pathological or histological examination; (3) sufficient published data about sample size, odds ratio (OR), and their 95% confidence interval (CI); (4) published in English or Chinese language; (5) all participants were Chinese. Studies were excluded when they were: (1) not case-control study or cohort study; (2) duplicate of previous publication; (3) based on incomplete data; (4) meta-analyses, letters, reviews, case reports, or editorial articles.

Data extraction
Data were independently extracted by two reviewers (Xin-ping Chen and Wei-hua Xu) using a standardized data extraction form. Discrepancies were resolved by discussion and if consensus was not achieved the decision was made by the two raters. The title and abstract of all potentially relevant articles were screened to determine their relevance. Full articles were then scrutinized if the title and abstract were ambiguous. The following data were extracted from the identified studies: the first author, publication year, source of controls, geographic area, sample size, and the number of subjects with two GSTM1 genotypes. In this meta-analysis, the quality assessment of individual study was conducted according to the nine-star Newcastle-Ottawa Scale (Wells et al., 2009). For articles including different source of controls, data were extracted separately (Table 1).

Statistical analysis
Pooled odds ratios (ORs) and 95% confidence intervals (CIs) were used to assess the association of GSTM1 genetic polymorphism with lung cancer risk in Chinese population. Given that there was distribution of null/present heterozygote in only one study selected, the Hardy-Weinberg equilibrium (HWE) test could not be conducted. Cochrane’s Q test was performed to test the between-study heterogeneity. If there was heterogeneity, then the random-effects model was chosen to pool the ORs with 95% CIs, otherwise the fixed-effects model was used. Publication bias was investigated with the funnel plot, in which the Standard Error (SE) of log OR of each study was plotted against its OR. Funnel-plot asymmetry was further assessed by the method of Egger’s linear regression test (Egger et al., 1997). All the P values were two sided. P value less than 0.05 was considered statistically significant. All statistical analysis was conducted by using Stata version 10.0 (Stata Corp, College Station, Texas, USA).

Results

Study selection
We identified 114 articles that examined the association between GSTM1 polymorphism and risk of Lung cancer in Chinese. However, after screening of the titles and abstracts of all 114 articles, 50 were excluded. Of the 64 potentially relevant articles identified for further assessment, one article (Wu et al., 2003) was excluded because it did not provide sufficient data about the distribution of GSTM1 genotype, 18 (Gao et al., 1998; Gao & Zhang, 1998; Hu et al., 1998; Chen et al., 1999; Xue et al., 2001; Zhang et al., 2002; Wang et al., 2003; Gu et al., 2004; Luo et al., 2004; Ye et al., 2005; Zeng et al., 2005; Chang et al., 2006; Wang et al., 2006; Wang et al., 2007; Chang et al., 2009; Li et al., 2011; Li et al., 2012; Ma et al., 2013) were excluded because they concerned duplicate subjects. Finally, a total of 45 articles (47 studies) (Ge et al., 1996; Gao & Zhang, 1999; Lan et al., 2000; London et al., 2000; Chen et al., 2001; Zhao et al., 2001; Chan et al., 2002; Lu et al., 2002; Zhang et al., 2002; Zhang et al., 2002a; Chen et al., 2003; Wang et al., 2003; Xian et al., 2003; Chan-Yeung et al., 2004; Li et al., 2004; Liang et al., 2004; Yang et al., 2004; Chan et al., 2005; Li et al., 2005; Li et al., 2005a; Qiao et al., 2005; Wang et al., 2005; Chen et al., 2006; Qian et al., 2006; Wang et al., 2006; Yao et al., 2006; Gu et al., 2007; Lei et al., 2007; Liu et al., 2008; Xia et al., 2008; Wang et al., 2009; Fan et al., 2010; Jin et al., 2010; Song et al., 2010; Zheng et al., 2010; Zhu, 2010; Du et al., 2011; Zhang et al., 2011; Chen et al., 2012; Han et al., 2012; Liang et al., 2012; Liu et al., 2012; Wang et al., 2012; Yao et al., 2012; Lu, 2013) containing 6,623 cases and 7,865 controls were included in this meta-analysis, and the characteristics of these studies are shown in Table 1. Among 45 included articles, 22 articles provided ethnic information, with 18 being Han, the others being Mongolian, Zhuang and Man, respectively. Unfortunately, the ethnic information of the rest 23 articles was unknown.

Overall analysis
There was evidence of between-study heterogeneity in all included studies ($\chi^2=88.54, p<0.001$). Therefore, the random-effects model was used in overall analysis. The results showed that the pooled OR with 95% CI for lung cancer in Chinese with null GSTM1 was 1.45 (1.32-1.60) (Figure 1)

Subgroup analysis
In the subgroup analysis based on source of control, the results showed that the GSTM1 polymorphism was significantly related to lung cancer risk among population-based population (OR = 1.55, 95%CI: 1.39-1.73), as well
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As among hospital-based studies (OR = 1.26, 95% CI: 1.08-1.46) (Table 2). In addition, we also performed stratified analysis based on the quality score and geographic area, it revealed the similar results with all the studies (Table 2).

Sensitivity analysis
To evaluate the stability of the results, we performed a sensitivity analysis by different model. All the results were not materially altered (Table 2). Hence, results of the sensitivity analysis suggest that the data in this meta-analysis are relatively stable and credible.

Bias diagnosis
The Begg’s funnel plot and Egger’s test were performed to access the publication bias of literatures. As showed in Figure 2, the shape of the funnel plots did as among hospital-based studies (OR = 1.26, 95% CI: 1.08-1.46) (Table 2). In addition, we also performed stratified analysis based on the quality score and geographic area, it revealed the similar results with all the studies (Table 2).

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The pathways of carcinogen metabolism are complex, mediated by the activities of multiple genes. The effect of any single gene might have a limited impact on lung cancer risk than have so far been anticipated. Many controversial data are present in literature. Positive associations were found in certain populations and not confirmed in others. In addition to an expected interethnic variability in allele frequencies, variability has also been found within an ethnic group, resulting in heterogeneity in association studies. Gene-environment interactions could be a confounding factor in these studies, with controversial findings on cancer risk. Studies taking these factors into account may eventually lead to a better, comprehensive understanding of the association between the GSTM1 polymorphism and lung cancer risk.

This study has some limitations. First, we didn’t perform subgroup analysis on smoking status and other exposure history. Second, our results were based on unadjusted estimates. Therefore, the confounding factors might influence the estimates. Third, some publication bias was detected. Because the papers included in our meta-analysis were limited to those published in either English or Chinese only in the periods between 1989 and 2014, it is possible that some relevant published studies and unpublished studies that are likely to have null results were not included, which may have biased the results.

In summary, although studies investigating the association between GSTM1 polymorphism and the risk of lung cancer arrived at different conclusions (Piao et al., 2013; Shukla et al., 2013), this meta-analysis suggested that there was a significant association between null GSTM1 variant and lung cancer risk in the Chinese. Several recommendations on the future association studies of GSTM1-lung cancer can be made from this meta-analysis. First, a well thought-out study design is crucial for an association study. Second, it is important to make an effort to control risk factors, preferably in the design stage. Third, larger research articles in other populations with consistent results are required. Lastly, care should be exercised in genotyping and in checking for abnormality, such as the deviation from HWP.

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