Lack of Association of Glutathione S-transferase T1 Gene Null and Susceptibility to Lung Cancer in China: a Meta-analysis

Hong-Zhou Liu1, Jie Peng2, Fang Zheng1*, Chun-Hong Wang3, Ming-Jun Han1

Abstract

**Background:** Variation in metabolic genes is regarded as an important factor in processes leading to cancer. However, the effect of GSTT1 null genotype is divergent in the form of lung cancer. **Methods:** Studies were conducted at different research databases from 1990 to 2013 and the total odds ratio (OR) and 95% confidence interval (CI) were calculated for lung cancer. Review Manager 5.2 and STATE 12 are employed. **Results:** Total OR value is calculated from 17 articles with 2,118 cases and 2,915 controls. We discovered no significant increase in lung cancer risk among subjects carrying GSTT1 null genotype [OR = 1.15; 95% CI 0.97-1.36] in this meta-analysis. **Conclusion:** The GSTT1 deletion polymorphism does not have a significant effect on the susceptibility to lung cancer overall in China.

**Keywords:** Glutathione S-transferase T1 gene (GSTT1) - genetic polymorphism - lung cancer

**Introduction**

According to World Health Organization (WHO), lung cancer is one of the most important cancers because of its high morbidity and mortality. Lung cancer increases roughly 400% during the past 30 years in China (Zhao et al., 2010). The WHO forecasts that over a million Chinese will be diagnosed in each year by the year 2025 (Zhao et al., 2010). Researchers think that there are many factors that can lead to lung cancer in our surroundings. Cigarettes are regarded as the most important environmental factor. However, not all of those who smoked get lung cancer. This phenomenon indicates that other factors also can contribute to the etiology of lung cancer, such as genetic variation. Variation of metabolic genes which involve in carcinogens metabolism is known as an important cause in the formation of cancer. As we all know that there are many metabolic genes can metabolize carcinogens. These genes include cytochrome P450 (CYP450), microsomal epoxide hydrolase, glutathione S-transferase and N-acetyltransferase. Glutathione S-transferase (GST) consists of GSTM1, GSTP1 and GSTT1. GSTT1 gene is situated at 22q11.23. It has eight thousand base pairs and consists of 5 exons and 4 introns. It encodes a protein that consists of 240 amino acids. GSTT1 has similar function to GSTM1, but it has lower binding activity. Although some researchers think that GSTT1 is involved in some carcinogens metabolism, there is no clear evidence that GSTT1 takes part in detoxifying nicotine. Besides, GSTT1 has two alleles. It consists of functional and non-functional genotypes. The distribution of GSTT1 null genotype is in great differences among different ethnic groups. Some researchers consider that the susceptibility of lung cancer is different because the distribution of GSTT1 null genotype varies in different populations. However, GSTM1 and CYP450 maybe have a more important role in detoxification of carcinogens, and GSTM1 and CYP450 can compensate the function of GSTT1. We doubt that GSTT1 null genotype is the etiology of lung cancer.

A number of studies have investigated the association between GSTT1 null genotype and lung cancer, but the results are divergent. Dongxu He et al. found that the distribution of GSTT1 null genotype was not significantly higher in lung cancer group than that in control group (OR=0.69 and 95% CI [0.32, 1.51]) (He et al., 2006). Tianzhu Yuan et al. found that the distribution frequency of GSTT1 null genotype was significantly higher in group with lung cancer than that in control group (OR=1.95 and 95% CI [1.24, 3.09]) (Yuan et al., 2005) without consideration of smoking. When it took cigarettes into account, OR value became 0.47 and 95% CI became [0.22, 1.00] in the non-smokers. This outcome makes us doubt that GSTT1 is the etiology of lung cancer. Furthermore, smoking is a major factor that can not be ignored. In the meta-analysis published in 2010, it caught a conclusion that there was a significant association between GSTT1 null genotype and the susceptibility of lung cancer (Wang et al., 2010). However, there are a small number of articles and a fewer cases and controls in that study. Especially, it does not rule out the impact of smoking. We enlarge the number of cases and controls to rule out publish bias, and eliminate the influence of cigarettes by using the subgroup of non-smokers.

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Figure 1. Forest Plot of Without Consideration of Smoking

Figure 2. Forest Plot of All 17 Papers

Figure 3. Forest Plot of All 17 Papers

Statistical analysis methods

Statistical analysis was done by using Review Manager 5.2 and STATA 12. Adjusted OR value and 95% CI were calculated for each study, and crude OR value should be calculated if adjusted OR value was not available. The meta-analysis was carried out on adjusted odds ratios, because the adjusted odds ratios were comparable. The Cochrane Q statistics test was performed for heterogeneity in this meta-analysis. A fixed effects model was used when P<0.10 and I²<50%, simultaneously, while a random effects model was selected when P>0.10 or I²>50%. The funnel plot was drawn to evaluate publication bias. Egger’s test and Begg’s test were also done to check the publication bias. All the tests were two-sided, a P value of 0.05 for any test or model was considered to be statistically significant.

Results

Overview of included studies

According to the search strategy, 34 papers were selected. We had read all the papers and 25 papers were included because they had complete data. However, 8 papers were excluded owing to duplicate data. Therefore, 14 papers were included in Figure 1, and this group took
Table 1. Literature Inclusion and Exclusion

<table>
<thead>
<tr>
<th>First author</th>
<th>Year</th>
<th>cases</th>
<th>controls</th>
<th>OR(95%CI)</th>
<th>Remark</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tianzhu Yuan</td>
<td>2005</td>
<td>150(52)</td>
<td>152(100)</td>
<td>1.95 [1.24,3.09]</td>
<td>inclusion (non-smoking subgroup)</td>
</tr>
<tr>
<td>Geyu Liang</td>
<td>2005</td>
<td>227</td>
<td>227</td>
<td>1.77 [1.22,2.58]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Geyu Liang</td>
<td>2004</td>
<td>152</td>
<td>152</td>
<td>2.06 [1.30,3.25]</td>
<td>exclusion (duplication of data)</td>
</tr>
<tr>
<td>Yanfei Cao</td>
<td>2004</td>
<td>104</td>
<td>205</td>
<td>2.67 [1.63,4.37]</td>
<td>exclusion (duplication of data)</td>
</tr>
<tr>
<td>Chan Yeung</td>
<td>2004</td>
<td>229</td>
<td>197</td>
<td>1.58 [1.07,2.32]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Lan</td>
<td>2000</td>
<td>122</td>
<td>122</td>
<td>1.35 [0.81,2.24]</td>
<td>inclusion</td>
</tr>
<tr>
<td>London</td>
<td>2000</td>
<td>232</td>
<td>710</td>
<td>0.91 [0.67,1.23]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Zhaobin</td>
<td>2001</td>
<td>233</td>
<td>187</td>
<td>1.09 [0.74,1.60]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Jikai Zhang</td>
<td>2002</td>
<td>161</td>
<td>165</td>
<td>1.10 [0.71,1.70]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Wang J</td>
<td>2003</td>
<td>112</td>
<td>119</td>
<td>1.08 [0.64,1.81]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Na Wang</td>
<td>2006</td>
<td>77</td>
<td>107</td>
<td>1.31 [0.73,2.36]</td>
<td>inclusion (duplication of data)</td>
</tr>
<tr>
<td>Wu Yao</td>
<td>2006</td>
<td>77</td>
<td>107</td>
<td>1.31 [0.73,2.36]</td>
<td>exclusion (duplication of data)</td>
</tr>
<tr>
<td>Xuesong Qi</td>
<td>2008</td>
<td>53</td>
<td>72</td>
<td>0.79 [0.37,1.66]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Juan Fan</td>
<td>2010</td>
<td>58</td>
<td>60</td>
<td>2.03 [0.97,4.26]</td>
<td>exclusion (duplication of data)</td>
</tr>
<tr>
<td>Daiyuan Ma</td>
<td>2011</td>
<td>100</td>
<td></td>
<td></td>
<td>exclusion (no control)</td>
</tr>
<tr>
<td>Mingjie Wang</td>
<td>2009</td>
<td>106(44)</td>
<td>250(134)</td>
<td>0.74 [0.37,1.46]</td>
<td>inclusion (non-smoking subgroup)</td>
</tr>
<tr>
<td>Shuangfei Li</td>
<td>2007</td>
<td>42</td>
<td>103</td>
<td>0.78 [0.38,1.61]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Jikai Zhang</td>
<td>2002</td>
<td>42</td>
<td>55</td>
<td>0.51 [0.23,1.15]</td>
<td>exclusion (duplication of data)</td>
</tr>
<tr>
<td>Dongxu He</td>
<td>2006</td>
<td>61</td>
<td>46</td>
<td>0.69 [0.32,1.51]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Qing Lan</td>
<td>1991</td>
<td>86</td>
<td>86</td>
<td>1.00 [0.54,1.84]</td>
<td>exclusion (duplication of data)</td>
</tr>
<tr>
<td>Jingnan Liu</td>
<td>2012</td>
<td>100(51)</td>
<td>135(85)</td>
<td>1.29 [0.64,2.58]</td>
<td>inclusion (non-smoking subgroup)</td>
</tr>
<tr>
<td>Na wang</td>
<td>2012</td>
<td>209</td>
<td>256</td>
<td>1.18 [0.81,1.71]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Hanchun Chen</td>
<td>2006</td>
<td>97</td>
<td>197</td>
<td>2.05 [1.25,3.36]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Guobo Du</td>
<td>2011</td>
<td>125</td>
<td>125</td>
<td>1.03 [0.63,1.70]</td>
<td>inclusion</td>
</tr>
<tr>
<td>Xingzhou He</td>
<td>2001</td>
<td>122</td>
<td>122</td>
<td>1.35 [0.81,2.24]</td>
<td>exclusion (duplication of data)</td>
</tr>
<tr>
<td>Kecheng Liang</td>
<td>2012</td>
<td>68</td>
<td>70</td>
<td>2.07 [1.04,4.12]</td>
<td>inclusion</td>
</tr>
</tbody>
</table>

This table shows all useful details and the following information is extracted from the studies in this table. Inclusion and exclusion are determined by the information.

Table 2. Egger’s Test and Begg’s Test

| Egger’s test | Coef. | Std. Err. | t | P>|t| | [95% Conf. Interval] |
|--------------|-------|-----------|---|-----|------------------------|
| slope        | 0.63741 | 0.3908243 | 1.63 | 0.124 | -.1956123 1.470432 |
| bias         | -2.625242 | 1.588844 | -1.65 | 0.119 | -6.011774 .7612903 |

| Begg’s test | adj. Kendall’s Score (P-Q) | Std.Dev.of Score | Number of studies | z | Pr>|z| | (continuity corrected) |
|-------------|---------------------------|-----------------|------------------|---|------|-----------------------------|
| -34         | 24.28                     | 17              |                  | -1.4 | 0.161 |                             |
|             |                           |                 |                  | 1.36 | 0.174 |                             |

Two tests were done by STATE12 to test publication bias. The result of Egger’s test is $P=0.119>0.05$ and Begg’s test is $P=0.174>0.05$. It indicates there is no publication bias.

Details of the literature

Tianzhu Yuan et al., Minjie Wang et al. and Jingnan Liu et al. had non-smoking subgroups of GSTT1 and lung cancer susceptibility. Therefore, the data of non-smoking subgroup was used to exclude the influence of smoking factors. Geyu Liang et al.; Jikai Zhang et al.; Yanfei Cao et al. and Hanchun Chen et al.; Qing Lan et al., Lan et al. and Xingzhou He et al.; Na Wang et al. and Wu Yao et al.; Kecheng Liang et al.and Juan Fan et al. had the duplicate data and data of later articles was selected in Table 1.

Test of heterogeneity

The relationship between GSTT1 null genotype and lung cancer susceptibility was shown in Figure 3. The total heterogeneity was analyzed for 17 case–control studies and the results was $P=0.02$ and $I^2=46\%$. $P$ value was less than 0.10, so we analyzed the summary odds ratios with random effects model. There are many causes may lead to heterogeneity. The distribution of GSTT1 null genotype is different in various regions; the selection of control group is different among articles; the mean reason that generates heterogeneity is the factor of smoking and subtypes of lung cancer.

Data analysis

The result was 1.21 and 95% CI was [1.03-1.41] in Figure 1 and the group of non-smoking was 0.78 and 95% CI was [0.52-1.17] in Figure 2. Total OR value was calculated from 2118 cases and 2915 controls in Figure 3 and the result was 1.15 and 95% CI was [0.97-1.36]. When we combined Figure 1 and Figure 2, the OR declined and turned to be insignificant. If the factor of smoking was excluded in all papers, the conclusion that there was no consideration of smoking. Three articles had non-smoking subgroup, so the data of non-smoking subgroup was selected in Figure 2. All of 17 papers were analysis in Figure 3.
can consider that there is no publication bias

The distribution of data is uniform through
the funnel plot, and shape of the funnel plot is symmetrical, we can consider that there is no publication bias

no significant correlation between GSTT1 null genotype and lung cancer might be more convincible. We caught a conclusion that single GSTT1 null type and lung cancer risk did not have a significant correlation. However, it was significant in Figure 1. It indicated that GSTT1 null genotype and smoking might have a joint action, or might be the effect of smoking.

Sources of bias and evaluation

The distribution of data was uniform through the funnel plot, and shape of the funnel plot was symmetrical, we could consider that there was no publication bias in Figure 4. In addition, the Egger’s test and Begg’s test were selected to test publication bias in Table 2. We used the inverse of the standard error as the independent variable and the standardized estimate of the size effect as the dependent variable in this analysis. The result of egger’s test was $P=0.119>0.05$, and begg’s test was $P=0.174>0.05$. It indicated that there was no publication bias.

Discussion

The article published by Qing Lan et al. (Lan et al., 1991) is the fist paper about the relationship between GSTT1 null genotype and the susceptibility of lung cancer among Chinese in 1991. More than one hundred papers about GSTT1 have been published during the past twenty years. Several articles discussed the relationships between lung cancer and GSTT1 null genotypes, but the results were instable and controversial. The meta-analysis published by Wang et al. (2010) in 2010 found that GSTT1 null genotype and risk of lung cancer had a significant association. However, a few studies were included and the factor of smoking was not excluded in his study. In addition, it would be better to chose a random effects model because of $P=0.02<0.10$ in this meta-analysis. Therefore, we re-did a meta-analysis to analyze the relationship between GSTT1 null genotype and lung cancer risk. We discovered that there was no significant association between GSTT1 null genotype and lung cancer risk.

It indicates that the there is no link between GSTT1 and susceptibility of lung cancer in this meta-analysis. Many reasons can lead to this result. Firstly, GSTT1 may be not take part in detoxification of nicotine and formation of lung cancer. Secondly, GSTT1 genotype has weak effect on detoxification of nicotine, and GSTT1 null genotype is less important than GSTM1 and CYP450 in the etiology of lung cancer. Thirdly, the function of GSTT1 can be compensated by GSTM1 and CYP450, so the GSTT1 null genotype does not cause any effect alone.

There were some limitations in this meta-analysis. First, only published papers were included in this meta-analysis, and it will cause publication bias. However, funnel plot, Egger’s test and begg’s test indicated that publication bias was negligible. Second, there were a few cases and controls in non-smoking subgroup in this meta-analysis and this suggests that further analysis needs to gather complete data which includes gender, age, smoking and type of lung cancer.

In a word, we found that there was no significant association between GSTT1 null genotype and the susceptibility of lung cancer.

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References


Lan Q, Xingzhou He XZ, Costa DJ, et al (2000). Indoor coal combustion emissions, GSTM1 and GSTT1 genotypes, and


