RESEARCH ARTICLE

Relationship Between GSTT1 Gene Polymorphism and Hepatocellular Carcinoma in Patients from China

Jie Chen, Liang Ma, Ning-Fu Peng, Shi-Jun Wang, Le-Qun Li*

Abstract

Objective: The results from studies on associations of the glutathione S-transferase T1 (GSTT1) gene polymorphism and hepatocellular carcinoma (HCC) risk in Chinese populations are still conflicting. This meta-analysis was performed to evaluate the relationship in detail. Methods: Eligible reports were recruited into this meta-analysis from the databases of PubMed, Embase, Cochrane Library and CBM-disc (China Biological Medicine Database). Results were expressed with odds ratios (OR) for dichotomous data, and 95% confidence intervals (CI) were also calculated. Results: Eighteen investigations were identified for the analysis of association between polymorphic deletion of GSTT1 and HCC, consisting of 2,693 patients with HCC and 4,696 controls. Null genotype of GSTT1 was associated with HCC susceptibility in Chinese (OR=1.53, 95% CI: 1.28-1.82; P<0.00001). Conclusion: The GSTT1 null genotype is associated with HCC susceptibility in Chinese.

Keywords: Hepatocellular carcinoma - glutathione S-transferase T1 - gene polymorphism - meta-analysis

Asian Pacific J Cancer Prev, 13 (9), 4417-4421

Introduction

Hepatocellular carcinoma (HCC) is the sixth most common cancer and prevalent cancers in the human population, more than 50% of the world’s HCC cases occur in China (Li & Jiang, 2011). It is well-documented that multiple risk factors contribute to hepatocarcinogenesis, including chronic hepatitis B virus (HBV) or hepatitis C virus (HCV) infections, cirrhosis, carcinogen exposure (such as aflatoxin B1), excessive alcohol drinking (Bayram et al., 2011). China is an important country in the Asia-Pacific region, and the HBV is the mainly risk factor for the onset of HCC. The present evidences show that the factor of gene polymorphism is associated with the risk of HCC susceptibility (Yuan et al., 2011; Dong et al., 2012). Glutathione-S-transferases (GSTs) are an enzyme superfamily involved in the Phase II metabolism, acting as primary intracellular detoxifiers and contributing to a broad range of physiological processes including cellular defense (Masoudi et al., 2011; Wang et al., 2012). Glutathione-S-transferase T1 (GSTT1) is a most important sub-group type of GSTs, and its gene polymorphism takes part in the pathogenesis of cancers. There were some investigations reporting that GSTT1 deletion was associated with cancer susceptibility (Xu et al., 2011; Aguiar et al., 2012; Ramalhinho et al., 2012).

In the past decades, most of the epidemiologic studies investigating the association of GSTT1 gene polymorphism with HCC susceptibility were conducted in Chinese populations. Unfortunately, the available evidence is weak at present, due to sparseness of data or disagreements among the reported studies. The evidence from meta-analysis may be powerful than the individual investigation. This meta-analysis was performed to investigate whether the GSTT1 gene polymorphism was associated with the risk of HCC in Chinese population, by widely collect the reported investigations.

Materials and Methods

Search strategy for the association of GSTT1 gene polymorphism with HCC risk

The relevant studies were searched from the electronic databases of PubMed, Embase, Cochrane Library and CBM-disc (China Biological Medicine Database) on May 1, 2012. The retrieval strategy of (glutathione S-transferase T1 OR GSTT1) and (hepatocellular carcinoma OR liver cancer OR HCC) was entered into these databases mentioned above for search. The searches in Pubmed and Embase were limited in Human. Additional articles were identified through references cited in retrieved articles.

Inclusion and Exclusion Criteria

Inclusion criteria: (1) The outcome had to be HCC; (2) There had to be at least two comparison groups (HCC group vs control group); (3) Investigation should provide the data of GSTT1 genotype distribution.

Exclusion criteria: (1) Review articles and editorials; (2) Case reports; (3) Preliminary result not on GSTT1 gene polymorphism or outcome; (4) Investigating the
Table 1. Characteristics of the Studies Evaluating the Effects of GSTT1 on HCC Risk in Chinese

<table>
<thead>
<tr>
<th>Year</th>
<th>First author</th>
<th>Language</th>
<th>Location</th>
<th>Hepatitis virus</th>
<th>Control</th>
<th>Case</th>
<th>Control</th>
<th>Null frequency(%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1997</td>
<td>Dong</td>
<td>Chinese</td>
<td>Jiangsu, Guangxi, Hebei</td>
<td>HBV Population</td>
<td>63  47  110  42  70  112</td>
<td>57.27 37.01</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1999</td>
<td>Yu</td>
<td>English</td>
<td>Taiwan</td>
<td>HBV Hospital</td>
<td>41  42  83  181  194  375</td>
<td>49.4 48.28</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2001</td>
<td>Sun</td>
<td>English</td>
<td>Taiwan</td>
<td>HBV Population</td>
<td>30  37  67  77  51  128</td>
<td>44.78 60.16</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2002</td>
<td>Liu</td>
<td>Chinese</td>
<td>Jiangsu</td>
<td>HBV Population</td>
<td>34  50  84  36  108  144</td>
<td>40.48 20.01</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2003</td>
<td>Liu</td>
<td>Chinese</td>
<td>Guangxi</td>
<td>HBV Hospital</td>
<td>28  23  51  18  35  53</td>
<td>54.9 33.96</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2003</td>
<td>McGlynn</td>
<td>English</td>
<td>Taiwan</td>
<td>HBV Population</td>
<td>116 115 231 100 156 256</td>
<td>50.16 38.96</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2004</td>
<td>Li</td>
<td>Chinese</td>
<td>Jiangsu</td>
<td>HBV Population</td>
<td>108 99 207 97 110 207</td>
<td>52.17 46.87</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Zhang</td>
<td>Chinese</td>
<td>Hubei</td>
<td>HBV Population</td>
<td>38  22  60  34  39  73</td>
<td>63.33 46.58</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>He</td>
<td>Chinese</td>
<td>Guangxi</td>
<td>HBV Population</td>
<td>43  62  105  50 101 151</td>
<td>40.95 33.12</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Chen</td>
<td>English</td>
<td>Taiwan</td>
<td>HBV Population</td>
<td>289 279 577 199 190 389</td>
<td>50.09 51.17</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Deng</td>
<td>English</td>
<td>Guangxi</td>
<td>HBV Population</td>
<td>108 73 181 154 206 360</td>
<td>59.67 42.79</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Guo</td>
<td>Chinese</td>
<td>Henan</td>
<td>HBV Population</td>
<td>58 37 95 45 58 103</td>
<td>61.05 43.69</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Long</td>
<td>Chinese</td>
<td>Guangxi</td>
<td>HBV Hospital</td>
<td>82 58 140 234 302 536</td>
<td>58.71 43.67</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Ma</td>
<td>Chinese</td>
<td>Guangxi</td>
<td>HBV Population</td>
<td>35 27 62 21 52 73</td>
<td>56.45 28.77</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Long</td>
<td>English</td>
<td>Guangxi</td>
<td>HBV Hospital</td>
<td>146 111 257 297 352 649</td>
<td>56.81 45.77</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>Yang</td>
<td>Chinese</td>
<td>Guangxi</td>
<td>HBV Hospital</td>
<td>33 67 100 11 49 60</td>
<td>33 18.33</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2010</td>
<td>Kao</td>
<td>English</td>
<td>Taiwan</td>
<td>HBV Hospital</td>
<td>51 51 102 200 186 386</td>
<td>50 51.82</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2010</td>
<td>Wei</td>
<td>Chinese</td>
<td>Guangxi</td>
<td>HBV Population</td>
<td>104 77 181 276 365 641</td>
<td>57.46 43.06</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 2. Meta Analysis of the Association of GSTT1 Gene Polymorphism with Risk of HCC

<table>
<thead>
<tr>
<th>Group</th>
<th>Non-sensitivity analysis</th>
<th>Sensitivity analysis</th>
<th>OR(95%CI)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Overall: 1-19</td>
<td>1-1 Random</td>
<td>1.53(1.28,1.82)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Hospital: 1-12</td>
<td>1-1 Random</td>
<td>1.56(1.23,1.98)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>≥ 100: 1-12</td>
<td>1-1 Random</td>
<td>1.46(1.12,1.92)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>&lt; 100: 1-8</td>
<td>1-1 Random</td>
<td>1.62(1.03,2.53)</td>
</tr>
</tbody>
</table>

Results

Study characteristics for GSTT1 null genotype with HCC risk

Eighteen studies (Dong et al., 1997; Yu et al., 1999; Sun et al., 2001; Liu et al., 2002; Liu et al., 2003; McGlynn et al., 2003; Li et al., 2004; Chen et al., 2005; Deng et al., 2005; Guo et al., 2005; He et al., 2005; Long et al., 2005; Ma et al., 2005; Zhang et al., 2005; Long et al., 2006; Yang et al., 2009; Kao et al., 2010; Wei et al., 2010) were recruited into our investigation to study the relationship between GSTT1 null genotype and HCC risk. Eleven studies were published in Chinese and others were reported in English (Table 1). The data of our interest were extracted, and the frequencies of null genotype of GSTT1 for case group and control group were calculated (Table 1). Those 18 investigations contained 2693 case series and 4696 controls. The average distribution frequency of GSTT1 null genotype in HCC case was 52.04% and the average frequency in controls was 40.78%. The average distribution frequency of GSTT1 null genotype in cases was markedly increased when compared with that in control group (HCC/Control = 1.28).

Association of GSTT1 null genotype with HCC risk

In this meta-analysis, we found that GSTT1 null genotype was associated with HCC risk in Chinese (OR=1.53, 95%CI: 1.28-1.82; P<0.0001; Figure 1 and Table 2).

Sub-group analysis

Sub-group analysis for GSTT1 was also performed...
GSTT1 Null Gene Polymorphism Association with HCC in China

Figure 1. Association Between GSTT1 Null Genotype and HCC Susceptibility

Figure 2. Association Between GSTT1 Null Genotype and HCC Susceptibility (according to the population source of the controls)

Evaluation of publication bias

No significant publication bias was showed for overall Chinese population (P=0.112; Figure 4). In the sub-group analysis, there was also no significant publication bias for the meta-analysis according to the population source of the controls (P=0.244), and for the meta-analysis according to the sample size of case ≥ 100; Table 2).

Discussion

In our study, we found that the null genotype of GSTT1 was associated with the HCC risk in Chinese. Our results indicated that GSTT1 null genotype was associated with the susceptibility of HCC in Chinese, and it might become a useful indicator to predict the risk of HCC in Chinese population. In our study, we found that the average distribution frequency of GSTT1 null genotype in cases have a 1.28-fold increase when compared with that in control group. In the sub-group study according to according to source of the controls (population vs hospital), sample size of case (< 100 vs ≥ 100), we found that the results were consistent with the previous. There was no publication bias for overall Chinese population, the population source of the controls and the sample size of case more than 100.

Three meta-analyses were performed to investigate the association of GSTT1 gene polymorphism and HCC risk. White et al. (2008) performed a meta-analysis and included 13 eligible studies to study the relationship between GSTT1 genetic variants and found that there was no statistical difference in the null genotype distribution of GSTT1 between the HCC group and control group, and they did not performed the analysis for Chinese population or Asians. Wang et al. (2010) up-dated the meta-analysis from White et al. (2008) and included 18 studies for the association of GST gene polymorphism with HCC risk in Asians and found that null genotype of GSTT1 was associated with the risk of HCC. The conclusions were similar with ours. However, this meta-analysis not performed a sub-group study in Chinese population. Yu et al. (2011) conducted a meta-analysis in Chinese and included 16 studies for the relationship between GSTT1 gene polymorphism and HCC risk in Chinese, and they found that the null genotypes of GSTT1 was associated with increased risk of HCC. The number of included studies in our meta-analysis was larger than the previous meta-analyses. The conclusion from our study might be more robust.

GSTT1 null genotype might be an important factor for the morbidity and progression of cancers in Chinese population.

Figure 3. Funnel Plot to Assess Publication bias for GSTT1 in Overall Chinese Population. No significant funnel asymmetry was observed which could indicate publication bias. The horizontal line in the funnel plot indicates the random effects summary estimate, while the sloping lines indicate the expected 95% CI for a given standard error, assuming no heterogeneity between studies. logor, natural logarithm of the OR; s.e. of: logor, standard error of the logOR

Figure 4. Funnel Plot to Assess Publication bias for GSTT1 in Overall Chinese Population. No significant funnel asymmetry was observed which could indicate publication bias. The horizontal line in the funnel plot indicates the random effects summary estimate, while the sloping lines indicate the expected 95% CI for a given standard error, assuming no heterogeneity between studies. logor, natural logarithm of the OR; s.e. of: logor, standard error of the logOR

Figure 5. Funnel Plot to Assess Publication bias for GSTT1 in Overall Chinese Population. No significant funnel asymmetry was observed which could indicate publication bias. The horizontal line in the funnel plot indicates the random effects summary estimate, while the sloping lines indicate the expected 95% CI for a given standard error, assuming no heterogeneity between studies. logor, natural logarithm of the OR; s.e. of: logor, standard error of the logOR

Figure 6. Funnel Plot to Assess Publication bias for GSTT1 in Overall Chinese Population. No significant funnel asymmetry was observed which could indicate publication bias. The horizontal line in the funnel plot indicates the random effects summary estimate, while the sloping lines indicate the expected 95% CI for a given standard error, assuming no heterogeneity between studies. logor, natural logarithm of the OR; s.e. of: logor, standard error of the logOR
population. Wang et al. (2012) conducted a prospective study in Chinese population to detect the association between GSTT1 gene polymorphisms and survival of gastric cancer, and found that individuals carrying null-GSTT1 had a moderate higher risk of death from gastric cancer. Liu et al. (2012) performed a meta-analysis to explore the association between GSTT1 null genotype and risk for cervical cancer, and reported a modification on the association between GSTT1 null genotype and cervical cancer. Wang et al. (2010) conducted a meta-analysis to evaluate the association between polymorphism of GSTT1 and the risk of lung cancer in Chinese population, and this meta-analysis suggested that GSTT1 deletion polymorphisms might have an effect on the susceptibility of lung cancer in Chinese population. Those studies mentioned above might give us a message that GSTT1 null-genotype might be a risk factor to cause cancer in Chinese population. However, more studies should be performed in the future.

Our results indicated that there was an association between null genotypes of GSTT1 and HCC risk in Chinese population. The outcome might be robust to some extent. The GSTT1 null genotype might become a valuable indicator to predict the risk of HCC in Chinese population. Once it is confirmed, the early prevention would be conducted and the high mortality in Chinese would be improved. However, those findings should be regarded cautiously because many other ingredients, such as small sample size of the included report, limited statistical power, heterogeneity of enrolled cases, variable study designs and different interventions, were closely related to affect the results.

In conclusion, the results in our study support that null genotype of GSTT1 is associated with the risk of HCC in Chinese population. However, more association investigations are required to further clarify the role of the GSTT1 gene polymorphism in predicting the risk of HCC in Chinese population.

Acknowledgements

The author(s) declare that they have no competing interests.

References


