Meta-analysis of the Association Between GSTM1 and GSTT1 Gene Polymorphisms and Cervical Cancer

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Abstract

Aim: We conducted a meta-analysis to analyze the influence of GSTM1 and GSTT1 gene polymorphisms on cervical cancer risk, and explore gene-environment interactions. Methods: Identification of relevant studies was carried out through a search of Medline and the EMbase up to Oct. 2011. All case-control studies that investigated the association between GSTM1 and GSTT1 gene polymorphisms and risk of cervical cancer were included. The pooled odds ratio (OR) was used for analyses of results and the corresponding 95% confidence intervals (CI) were estimated. Results: A total of 21 case-control studies were included in the meta-analysis of GSTM1 (2,378 cases and 2,639 controls) and GSTT1 (1,229 cases and 1,223 controls) genotypes. The overall results showed that the GSTM1 null was related to an increased risk of cervical cancer (OR=1.50, 95% CI=1.21-1.85). Subgroup analysis were performed based on smoking and ethnicity. Our results showed that smokers with null GSTM1 genotype had a moderate increased risk of cervical cancer (OR=1.85, 95% CI=1.07-3.20). For the ethnicity stratification, moderate significantly increased risk of null GSTM1 genotype was found in Chinese (OR=2.12, 95% CI=1.43-3.15) and Indian populations (OR=2.07, 95% CI=1.49-2.88), but no increased risk was noted in others. Conclusion: This meta-analysis provided strong evidence that the GSTM1 genotype is associated with the development of cervical cancer, especially in smokers, and Chinese and Indian populations. However, no association was found for GSTT1 null genotype carriers.

Keywords: GSTM1 - GSTT1 - polymorphism - cervical cancer - meta-analysis

Introduction

Cervical cancer is the third most common cancer in women, and the seventh overall, with an estimated 530,000 new cases in 2008. More than 85% of the global burden occurs in developing countries, where it accounts for 13% of all female cancers. High-risk regions are Eastern and Western Africa (ASR greater than 30 per 100,000), Southern Africa (26.8 per 100,000), South-Central Asia (24.6 per 100,000), South America and Middle Africa (ASRs 23.9 and 23.0 per 100,000 respectively). Rates are lowest in Western Asia, Northern America and Australia/New Zealand (ASRs less than 6 per 100,000) (IARC, 2011). The different incidence in different areas indicates the genetic factors and environmental factors play a role in the development of cervical cancer.

It is well established that human papilloma virus (HPV) infection is a necessary but insufficient event for the development of cervical cancer(Walboomers and Meijer, 1997; Herrington, 1999; Walboomers et al., 1999; Schiffman et al., 2007), because not all HPV-infected patients do develop cervical cancer. Therefore, there are other cofactors for cervical cancer development. Previous studies showed the glutathione S-transferases (GSTs) genetic variants is related to human phase II detoxification enzymes. Cytosolic GSTs (GSTM and GSTT) play a role in the detoxification of the carcinogenic electrophiles of aflatoxin and polycyclic aromatic hydrocarbons (PAHs) in tobacco smoke. The mode of action of GSTs is considered to co-effect with activation and detoxification of tobacco carcinogens. Therefore, several studies found the association between the genetic polymorphisms of GSTs and the risk of cancer development (Carlsten et al., 2008; Mo et al., 2009; Zhuo et al., 2009).

GSTM1 facilitates the excretion of a wide range of carcinogens, reactive oxygen species and chemotherapeutic agents with a variety of substrate specificities (Rebeck, 1997). The GSTT1 polymorphism is considered in the detoxification of environmental carcinogens, including 1,3 butadiene and ethylene oxide in tobacco smoke and ambient air (Landi, 2000). The null GST (GSTM-null genotype) results in a completely loss of enzyme activity to bind with genotoxic substrates, including epoxides derived from aflatoxin and PAHs (Hayes and Pulford, 1995). There are large number of epidemiological studies concerning the association between GSTM1 and GSTT1 and risk

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of cervical cancer in different populations, however, the results is inconsistent (Singh et al., 2006; Song et al., 2006; Agodi et al., 2010; Palma et al., 2010). Although there is a meta-analysis regarding on the two gene polymorphism and cervical cancer, no gene-environment interaction was explored, especially for smoking and ethnicity. Therefore, we conducted a meta-analysis regarding the effect of GSTM1 and GSTT1 gene polymorphisms on cervical cancer risk, and explore the gene-environment interaction on cervical cancer risk.

**Materials and Methods**

**Selection criteria and search strategy**

Identification of relevant studies was to carried out through a search of Medline and EMBase up to Oct. 2011 using the following terms without any restriction on language, including ‘cervical cancer’, ‘cervical tumor’, ‘cervical neoplasm’, ‘cervical adenocarcinoma’, ‘glutathione S-transferase’, ‘GST’, ‘GSTM’ and ‘GSTT’.

All studies that examined the association/non association of the GST gene polymorphisms with cervical cancer were identified. 215 potentially relevant studies were searched. Of the 215 literatures, 187 literatures were irrelevant, and 7 studies were excluded were excluded because of various reasons (3 studies were conducted on overlapping population, and 4 studies did not include controls in analysis). Finally, 21 literatures were met the inclusion criteria and included.

The literature search was performed up to Oct. 2011. The inclusion criteria were as following: case-control studies that investigated the association between GSTM1 and GSTT1 gene polymorphisms and risk of cervical cancer; Studies presented original data and the number of null genotype of GSTM1 and GSTT1 in cases and controls. For each study, the following information were excluded: author, publication year, country of origin, average years of cases and controls, number of cases and controls, number of null genotype for GSTM1 and GSTT1 in cases and controls and the adjusted ORs of selected studies. Two authors independently assessed the articles for inclusion/exclusion, resolved disagreements, and reached consistency.

**Statistical analysis**

The association between GSTM1 and GSTT1 gene polymorphisms and cervical cancer was estimated by calculating pooled ORs and 95% CIs. Odds ratio (OR) was used for analyses of results and their corresponding 95% confidence intervals(CI) were estimated. Heterogeneity across studies was estimated using Q statistic, and a p>0.05 suggested a lack of heterogeneity. Meta analysis was carried out by using random-effects or fixed effects methods (Der and Laird, 1986; Mantel and Haenszel, 1959) model based on the pooled effect estimates in the presence (p≤0.1) or absence (p>0.1) of heterogeneity. Potential publication bias was estimated by constructing funnel plots (Begg and Mazumdar, 1994). As asymmetric funnel plot indicated a relationship between effect and study size, which suggested the possibility of either publication bias or a systematic difference between smaller and larger studies (small study effects). Furthermore, publication bias was assessed by Egger’s test (Egger et al., 1997). Studies were categorized into subgroups based on ethnicity and smoking status. The data analysis was performed (STATA, version 10, StataCorp LP, College Station, TX).

**Results**

A total of 21 case-control studies were included in the meta-analysis of GSTM1 (2,378 cases and 2,639 controls)
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GSTM1 null was related to the increased risk of cervical cancer (OR=1.50, 95% CI=1.21-1.85). Moreover, an non-significant increased risk of cervical cancer was found in individual carrying GSTT1 null genotype (1.21-1.58).

Subgroup analysis were performed based on smoking and ethnicity (Figure 2-6). The results showed that smokers with null GSTM1 genotype had a moderate increased risk of cervical cancer (OR=1.85, 95% CI=1.07-3.20), while no significant increased risk was found in non-smokers. However, we only found a non-significant increased risk of cervical cancer in null GSTT1 genotype carriers (OR=1.43, 95% CI=0.97-2.09).

After stratification by smoking, the heterogeneity was significantly decreased (P=0.14 and P=0.54 for


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For example, the incidence of cervical cancer is high in populations with ethnic differences on genetic predisposition to human diseases. GSTs are considered to be involved in the conjugation reaction of phase II metabolism of xenobiotics, catalyzing reactions between glutathione and a variety of potentially toxic and carcinogenic electrophilic compounds (Der Simonian and Laird, 1986; Hayes and Pulford, 1995). Moreover, GSTs also play an important role in modulating the induction of other enzymes and proteins for cellular functions, such as DNA repair (Der Simonian and Laird, 1986). The relationship between GST gene polymorphisms and cervical cancer has been investigated in various studies (Singh et al., 2006; Songet al., 2006; Agodi et al., 2010; Palma et al., 2010). However, the association between them has been controversial, and these discrepancies could have been due to limited sample numbers and ethnic differences. In our meta-analysis, the role of GSTM1 polymorphism may promote the development of cervical cancer, and have interaction with smoking. This indicated the GSTM1 and GSTT1 gene deletions may promote the development of cervical dysplasia by inhibiting the detoxification of polycyclic hydrocarbons and other compounds that influence oxidative stress and DNA adduct formation (Parl, 2005).

Many studies have reported on the effect of ethnic differences on genetic predisposition to human diseases. For example, the incidence of cervical cancer is high in southern Africa, and is almost five-folds higher than in the Northern America and Australia (IARC, 2011). Our studies showed the GSTT1 and GSTM1 null genotypes had an increased risk of Chinese and Indian populations, and no risk in Japanese, European and American. These differences showed variations in cancer susceptibility by ethnicities. In addition, the data showed that the allele frequency of GSTM1 null genotype was higher in American and Japanese than in Chinese and India populations, which showed variation in the effect of the genotype might be due to different of lifestyle, nutrition, environmental factors, and genetic factors.

Our study showed tobacco constituents are modified by metabolizing enzymes and may promote malignant cellular growth (Prokopczyk et al., 1997). The mode of action is through the activation and detoxification of tobacco carcinogens, thus, one might expect the polymorphism of GSTs may alter the risk of cancer among smokers. The lack of GST activities caused by an inherited deletion of the GST have been reported to increase the risk of several tobacco-related cancers (Kietthubthew et al., 2001; Spurdle et al., 2001; Lee et al., 2002; van der Hel et al., 2003; Sweeney et al., 2003). It was therefore hypothesized that smoking and GST genotype may synergistically influence the cervical cancer development. Our study showed the null GSTM1 genotype may increased the cervical cancer risk among smokers, which provide strong evidences for the association between GSTs and cervical cancer risk.

A limitation of this study is that the environment and lifestyle of populations were not included in the influencing factors. The pathways of carcinogen metabolism are complex. Cervical cancer have major environmental determinations such as HPV infection, age and reproductive health. Secondly, the sample size reported in the literature is still relatively small and might not provide sufficient power to estimate the association between the null GSTM1 and GSTM1 polymorphism and cervical cancer risk.

In conclusion, this meta-analysis provided strong evidence that the GSTM1 genotype are associated with the development of cervical cancer, and especially in Chinese and Indian population, and smoking showed a modification on the association between GSTM1 null genotype and cervical cancer. However, no significant increased risk of cervical cancer was found in GSTT1 null genotype carriers. Further studies investigating the
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References


