Methylenetetrahydrofolate Reductase C677T Polymorphism and Cervical Cancer Risk: a Meta-Analysis

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Abstract

Background: Methylenetetrahydrofolate reductase (MTHFR) is a key enzyme in the metabolism of folate, and the role of MTHFR C677T polymorphism in cervical carcinogenesis is still controversial. Method: We performed a meta-analysis of all relevant case-control studies that examined any association between the C677T polymorphism and cervical cancer risk. We estimated summary odds ratios (ORs) with their confidence intervals (CIs) to assess links. Results: Finally, 10 studies with a total of 2113 cervical cancer cases and 2804 controls were included. Results from this meta-analysis showed that significantly elevated cervical cancer risk was associated with the MTHFR T allele in the Asian population under conditions of two genetic comparison models (for TT vs. CC, OR = 1.37, 95% CI 1.00-1.87, P = 0.050; for TT vs. TC+CC: OR = 1.34, 95% CI 1.01-1.77, P = 0.039). However, there was no obvious association between the MTHFR C677T polymorphism and cervical cancer risk in the other populations. Conclusion: The MTHFR C677T polymorphism is associated with cervical cancer risk in Asians, while any possible link in the Caucasian population needs further studies.

Keywords: Methylenetetrahydrofolate reductase - genetic polymorphism - cervical cancer - meta-analysis

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Introduction

Cervical cancer is the third most commonly diagnosed cancer and the fourth leading cause of cancer death in the females worldwide, accounting for 9% (529,800 cases) of the total new cancer cases and 8% (275,100 deaths) of the total cancer deaths among females in 2008 (Jemal et al., 2011). More than 85% of these cases and deaths occur in developing countries (Jemal et al., 2011, Li et al., 2011). Epidemiological studies have confirmed that oncogenic subtypes of the human papilloma virus (HPV) are a crucial etiological factor of cervical tumorigenesis (Walboomers et al., 1999; Munoz et al., 2003). However, this virus is cleared by the immune system in the majority of HPV infected women and only stays in the few individuals, with the oncogenic subtypes resulting in cervical cancer (Munger et al., 2004; Mun et al., 2011). Thus, this information suggests a remarkable interaction between the virus and the host’s genetic factors, which may increase the host’s susceptibility to cervical cancer (Magnusson et al., 1999; Baseman and Koutsky, 2005).

The 5, 10-methylenetetrahydrofolate reductase gene (MTHFR) maps to chromosome 1p36.3, and MTHFR plays a central role in folate metabolism, together with other enzymes by irreversibly catalyzing the conversion of 5, 10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, the primary circulating form of folate and a cosubstrate for homocysteine methylation to methionine (Goyette et al., 1994; Goyette et al., 1998). Many rare mutations of the MTHFR gene have been described in individuals, resulting in very low enzymatic activity, whereas the most common polymorphism is a C to T mutation in exon 4 at nucleotide 677, leading to Ala222Val and presenting in healthy individuals with lower enzyme activity (Frosst et al., 1995; Goyette et al., 1998). This MTHFR genetic polymorphism can lead to abnormal DNA methylation and DNA synthesis, possibly leading to an altered risk for cervical cancer (Frosst et al., 1995; Goyette et al., 1998). Recent studies have shown that the MTHFR 677 TT genotype is associated with an increased risk of cancer risk, suggesting an important role of folate levels and subsequent impaired chromosomal DNA synthesis and aberrant DNA methylation in carcinogenesis (Dong et al., 2008; Zhang et al., 2010). There are also many published studies investigating the association between C677T polymorphism and cervical cancer risk, but the effect of MTHFR C677T polymorphism on cervical cancer risk remains controversial (Shekari et al., 2008; Kohaar et al., 2010; Mostowska et al., 2011; Prasad and Wilkhoo, 2011; Tong et al., 2011; von Keyserling et al., 2011). With the present meta-analyses, we aimed to assess the overall effect of the MTHFR C677T polymorphism on cervical cancer by including all available published papers.

Materials and Methods

Study identification and selection criteria

We searched PubMed, Embase and CNKI database
using the following search strategy: (‘cervical carcinoma’ or ‘cervical cancer’) and (‘Methylenetetrahydrofolate reductase’ or ‘MTHFR’ or ‘C677T’) and (‘polymorphism’ or ‘polymorphisms’ or ‘mutation’ or ‘mutations’) for papers published (last search was done on November 12, 2011). The language of the papers was not restricted. All searched studies were retrieved, and their bibliographies were checked for other relevant publications. When more than one of the same patient population was included in several publications, only the most recent or complete study was used in this meta-analysis.

The following criteria were used to select the eligible studies: (1) case-control studies; (2) evaluation of the MTHFR C677T polymorphism and cervical cancer risk; (3) identification of cervical cancer was confirmed histologically or pathologically; (4) sufficient reported genotypic frequencies in both case and control populations for estimating an odds ratio (OR) with a 95% confidence interval (CI); (5) the genotype distribution among the control population was consistent with Hardy-Weinberg Equilibrium (HWE). The major reasons for exclusion of studies were: (1) case only studies; (2) review papers; (3) containing overlapping data.

Data extraction
Data retrieved from the articles included the following: first author’s name, publication year, country of origin, racial decent of the study population (categorized as Caucasian population, Asian population and others), the frequency for MTHFR C677T genotypes and the allele frequency of MTHFR C677T. Disagreements were resolved by reaching a consensus among all reviewers.

Statistical analysis
For the control group of each study, the distribution of genotypes was tested for HWE using the Chi-square test. If controls of studies were found not to be in HWE, sensitivity analyses were performed with and without these studies to test the robustness of the findings. The strength of association between MTHFR C677T polymorphism and cervical cancer risk was estimated by Odds ratios (ORs) with 95% confidence intervals (CIs). Five different comparison models of ORs were calculated: the allele model (T vs. C), the Homozygote comparison model (TT versus CC), the Heterozygote comparison model (CT versus CC), the Recessive genetic comparison model (TT versus CC), and the Dominant genetic comparison model (TT+TC versus CC). The \( \chi^2 \)-based Q statistic was used to investigate the degree of heterogeneity between the studies, and a \( P \) value < 0.05 was interpreted as significant heterogeneity among the studies (Cochran, 1954). To calculate the proportion of total variability attributed to between-study heterogeneity, the \( I^2 \) statistic was calculated, which statistic was useful when deciding whether there was too much heterogeneity to combine the studies and derive a pooled estimate (Higgins et al., 2003). \( I^2 \) values of 25%, 50%, and 75% were used as evidence of low, moderate, and high heterogeneity, respectively. If heterogeneity existed, the random effects model (the DerSimonian and Laird method) (DerSimonian and Laird, 1986), which yields wider confidence intervals, was adopted to calculate the overall OR value. Otherwise, the fixed effects model (the Mantel-Haenszel method) was used (Mantel and Haenszel, 1959). In order to assess the stability of the results, sensitivity analyses were performed by reanalyzing the significance of ORs after omitting each study in turn. An estimate of potential publication bias was carried out by the Begg’s funnel plot, in which the standard error of log (OR) of each study was plotted against its log (OR). An asymmetric plot suggested a possible publication bias. Besides, the funnel plot asymmetry was further assessed by the method of Egger’s linear regression test, a linear regression approach to measure funnel plot asymmetry on the natural logarithm scale of the OR (Egger et al., 1997). The significance of the intercept was determined with the t-test suggested by Egger (\( P < 0.05 \) was considered representative of statistically significant publication bias). We also calculated separate pooled estimates for different ethnic groups (Caucasian population, Asian population and the others). The analysis was conducted using STATA (version 9.2; Stata Corp, College Station, TX). All \( P \) values were two-sided and a \( P \) value of less than 0.05 was deemed statistically significant.

Results
Characteristics of includes studies
34 unique references were initially identified by the search. After discarding those which clearly did not meet the criteria, 19 studies were further assessed for eligibility (Piyathilake et al., 2000; Goodman et al., 2001; Gerhard et al., 2003; Lambropoulos et al., 2003; Sull et al., 2004; Kang et al., 2005; Zoodsma et al., 2005; Delgado-Enciso et al., 2006; Rao et al., 2006; Piyathilake et al., 2007; Nandan et al., 2008; Shekari et al., 2008; Agodi et al., 2010; Kohaar et al., 2010; Tong et al., 2010; Mostowska et al., 2011; Prasad and Wilkho, 2011; Tong et al., 2011; von Keyserling et al., 2011). After reviewing each original paper and extracting data, nine studies were excluded including five studies focusing on cervical intraepithelial neoplasia (Piyathilake et al., 2000; Goodman et al., 2001; Lambropoulos et al., 2003; Piyathilake et al., 2007; Agodi et al., 2010), three studies for not specifying genotypic frequencies of CC, CT, and TT (Gerhard et al., 2003; Nandan et al., 2008; Rao et al., 2006) and one study for overlapping data (Tong et al., 2010). Finally, 10 case-control studies with a total of 2113 cervical cancer cases and 2804 controls were included into this meta-analysis (Sull et al., 2004; Kang et al., 2005; Zoodsma et al., 2005; Delgado-Enciso et al., 2006; Shekari et al., 2008; Kohaar et al., 2010; Mostowska et al., 2011; Prasad and Wilkho, 2011; Tong et al., 2011; von Keyserling et al., 2011). The detailed characteristics of these studies are summarized in Table 1. There were three case-control studies from Caucasian population, four studies from Asian population, four studies from Indians and one study from Latino (Table 1). Besides, the distributions of genotypes were all consistent with HWE in the control groups of these 11 studies (All \( P_{\text{HWE}} \) were more than 0.05, Table 1).

Meta-analysis results
Table 1. Description of the studies included in the meta-analyses of the MTHFR C677T polymorphism and cervical cancer risk

<table>
<thead>
<tr>
<th>First author</th>
<th>Year</th>
<th>Study</th>
<th>Ethnicity</th>
<th>MTHFR C677T genotype distribution</th>
<th>P\textsubscript{HWE}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prasad VV</td>
<td>2011</td>
<td>Case-control</td>
<td>Indian(India)</td>
<td>Case: 0 TT, 5 CT, 57 CC</td>
<td>0.07</td>
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<td></td>
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<td></td>
<td>Control: 1 TT, 12 CT, 228 CC</td>
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<tr>
<td>von Keyserling H</td>
<td>2011</td>
<td>Case-control</td>
<td>Caucasian(Germany)</td>
<td>Case: 34 TT, 188 CT, 164 CC</td>
<td>0.9</td>
</tr>
<tr>
<td></td>
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<td></td>
<td></td>
<td>Control: 27 TT, 136 CT, 165 CC</td>
<td></td>
</tr>
<tr>
<td>Mostowska A</td>
<td>2011</td>
<td>Case-control</td>
<td>Caucasian(Poland)</td>
<td>Case: 9 TT, 59 CT, 56 CC</td>
<td>0.43</td>
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<td></td>
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<td></td>
<td></td>
<td>Control: 18 TT, 81 CT, 69 CC</td>
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<tr>
<td>Tong SY</td>
<td>2011</td>
<td>Case-control</td>
<td>East Asian</td>
<td>Case: 28 TT, 65 CT, 53 CC</td>
<td>0.37</td>
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<td></td>
<td>Control: 77 TT, 198 CT, 152 CC</td>
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<tr>
<td>Kohaar I</td>
<td>2010</td>
<td>Case-control</td>
<td>Indian</td>
<td>Case: 4 TT, 47 CT, 113 CC</td>
<td>0.6</td>
</tr>
<tr>
<td></td>
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<td></td>
<td></td>
<td>Control: 5 TT, 65 CT, 161 CC</td>
<td></td>
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<tr>
<td>Shekari M</td>
<td>2008</td>
<td>Case-control</td>
<td>Indian</td>
<td>Case: 2 TT, 28 CT, 170 CC</td>
<td>0.54</td>
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<td></td>
<td></td>
<td>Control: 7 TT, 68 CT, 125 CC</td>
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<tr>
<td>Delgado-Enciso I</td>
<td>2006</td>
<td>Case-control</td>
<td>Latino(Mexico)</td>
<td>Case: 18 TT, 34 CT, 18 CC</td>
<td>0.34</td>
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<tr>
<td></td>
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<td></td>
<td>Control: 20 TT, 49 CT, 20 CC</td>
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<tr>
<td>Zoodsma M</td>
<td>2005</td>
<td>Case-control</td>
<td>Caucasian(Netherlands)</td>
<td>Case: 49 TT, 230 CT, 164 CC</td>
<td>0.61</td>
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<td></td>
<td>Control: 57 TT, 262 CT, 273 CC</td>
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<tr>
<td>Kang S</td>
<td>2005</td>
<td>Case-control</td>
<td>East Asian(Korea)</td>
<td>Case: 20 TT, 32 CT, 27 CC</td>
<td>0.49</td>
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<tr>
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<td></td>
<td>Control: 12 TT, 32 CT, 30 CC</td>
<td></td>
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<tr>
<td>Sull JW</td>
<td>2004</td>
<td>Case-control</td>
<td>East Asian(Korea)</td>
<td>Case: 58 TT, 115 CT, 73 CC</td>
<td>0.99</td>
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<tr>
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<td></td>
<td></td>
<td>Control: 80 TT, 221 CT, 153 CC</td>
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</table>

*P\textsubscript{HWE}, the P value for Hardy-Weinberg equilibrium in the control group

Table 2 listed the main results of this meta-analysis. Overall, there was no association between the MTHFR C677T polymorphism and cervical cancer risk (All P values were more than 0.05, Table 2). A single study involved in the meta-analysis was deleted each time to define the influence of the individual data-set to the pooled ORs, and the corresponding pooled ORs were not materially altered, indicating that our results were statistically robust.

In the subgroup analyses by ethnicity, significantly elevated cervical cancer risk was associated with MTHFR T allele in the Asian population under two genetic comparison models (for TT vs. CC, OR = 1.37, 95%CI 1.00-1.87, P = 0.050; for TT vs. TC+CC: OR = 1.34, 95%CI 1.01-1.77, P = 0.039) (Table 2). However, there was no obvious association between the MTHFR C677T polymorphism and cervical cancer risk in the other population (Table 2).

Discussion

MTHFR regulates the metabolism of folate and it is an important factor in DNA methylation and synthesis (Goyette et al., 1998). A base change from C to T at
types of cancer, including colorectal cancer, gastric cancer and breast cancer (Taioli et al., 2009; Dong et al., 2010; Zacho et al., 2011).

Some limitations of this meta-analysis should be acknowledged. Firstly, the controls were not uniformly defined. The controls in some studies were selected mainly from healthy populations, while the others were selected mainly from individuals having benign diseases, such as cervical intraepithelial neoplasia, or non-cancer individuals. Secondly, potential cervical cases were possible because some studies may have included the control groups selected mainly from non-symptom populations. Thirdly, our results were based on unadjusted estimates, while a more precise analysis should be conducted if all individual data were available, which would allow for the adjustment by other co-variants including smoking status, environmental factors, and HPV infection status (Chansaenroj et al., 2012). Thus, further large sample size studies with gene-gene and gene-environment interactions need performing to identify this association more comprehensive.

In conclusion, this meta-analysis suggests that the MTHFR C677T polymorphism is associated with cervical cancer risk in the Asian population, while this possible association in the Caucasian population needs further study. Moreover, gene-gene and gene-environment interactions should also be considered in this association, and such studies taking these factors into account may eventually lead to our better and comprehensive understanding of the association between the MTHFR C677T polymorphism and cervical cancer risk.

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References


