Association of MTHFR C677T and A1298C polymorphisms with oral cancer susceptibility: evidence from a meta-analysis

Sui Jiang1,*
Jin-Dong Xu2
Zhen-Jian Zhuo3
Zhu-Ming Hua4,*

1Department of Oral and Maxillofacial Surgery, 2Department of Anesthesiology, Guangdong General Hospital, 3Guangdong Academy of Medical Sciences, 4School of Chinese Medicine, Faculty of Medicine, The Chinese University of Hong Kong, Hong Kong, People’s Republic of China

*These authors contributed equally to this work

Abstract: Methylenetetrahydrofolate reductase (MTHFR) is a central enzyme involved in folate metabolism and plays an important role in DNA synthesis and methylation. Several studies have been conducted to illustrate the associations between MTHFR C677T and A1298C polymorphisms with oral cancer susceptibility; however, the results are inconsistent. Therefore, we conducted an updated meta-analysis to obtain a more reliable estimation of the associations. We retrieved eligible studies from PubMed, EMBASE, and CBM databases through September 2016. Ultimately, pooled analyses involved 10 studies with 1443 cases and 1640 controls for the C677T polymorphism, as well as five studies with 973 cases and 1024 controls for the A1298C polymorphism. Risk estimates were presented as odds ratios (ORs) and 95% confidence intervals (95% CIs). Pooled results indicated that neither C677T nor A1298C polymorphism was associated with oral cancer susceptibility. However, a borderline significant association was detected between MTHFR C677T polymorphism and a decreased oral cancer risk (homogeneous model: OR=0.71, 95% CI=0.50–1.00) in hospital-based studies. Our results suggested that MTHFR C677T and A1298C polymorphisms might not be associated with oral cancer risk. However, more evidence is needed to further confirm these findings in the future.

Keywords: MTHFR, polymorphisms, oral cancer, susceptibility, meta-analysis

Introduction

Cancer is a major public health burden. An estimated 14.1 million new cancer cases and 8.2 million cases of cancer deaths arose worldwide, according to the data from GLOBOCAN 2012.1 Oral cancer, a subtype of head and neck cancer, is one of the most frequently diagnosed human malignancies in the world. Lines of evidence suggest that smoking,2 alcohol drinking,3 insufficient fruits and vegetables intake,4 and oral HPV infection5 are well-established risk factors for oral cancer. However, only a small part of exposed people eventually develop oral cancer. One acceptable explanation for this phenomenon is that genetic variations also modify individuals’ risk of developing cancer, beside health-risk environmental exposures and lifestyles.6

Previous studies demonstrated that folic acid deficiency resulting from low intake of fruits and vegetables increases the risk of developing cancer.7,8 In humans, folate provides the majority of methyl groups for de novo deoxynucleoside synthesis and intracellular methylation reactions.9 Folate deficiency may lead to uracil misincorporation during DNA synthesis, thus impairing the stability of DNA.10 Folate-metabolizing enzyme, methylenetetrahydrofolate reductase (MTHFR), is a key component in folic acid cycle and DNA synthesis. MTHFR catalyzes the irreversible reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, donating a methyl group for the
methyltransferase of homocysteine.\textsuperscript{11} Dysfunction of MTHFR may disrupt the dynamic equilibrium of methyl pool and consequently influence the deoxynucleoside synthesis and intracellular methylation reactions.

The human MTHFR gene is located on chromosome 1p36.3. By now, two common nonsynonymous MTHFR single-nucleotide polymorphisms (SNPs), C677T (Ala222Val, rs1801133) and A1298C (Glu429Ala, rs1801131), have been widely investigated.\textsuperscript{12,13} It has been shown that C677T and A1298C polymorphisms are associated with the risk of several types of cancer, including breast cancer,\textsuperscript{14} colorectal cancer,\textsuperscript{15} non-Hodgkin’s lymphoma,\textsuperscript{16} and cervical cancer.\textsuperscript{17} Different research groups have extensively assessed the association of C677T and A1298C polymorphisms with oral cancer risk, yet produce discrepant results.\textsuperscript{18,19} Four meta-analyses regarding such association have been conducted previously but somehow fail to establish reliable relationship between the two MTHFR SNPs and oral cancer risk.\textsuperscript{20-23} Therefore, we performed this evidence-based quantitative meta-analysis to provide a precise evaluation of the associations by including more eligible investigations.

Materials and methods

Literature search

We performed a comprehensive literature search in the PubMed and EMBASE, as well as Chinese databases (China National Knowledge infrastructure and WANFANG). No language limitation was applied in the literature search. The last research was updated in September 2016. The following search terms were adopted: “MTHFR or methylenetetrahydrofolate reductase”, “polymorphism or polymorphisms or SNP or single nucleotide polymorphism or variant”, and “oral cancer or oral carcinoma”. We also manually searched references listed in the retrieved articles after carefully reviewing. The latest or the largest study was included in the final meta-analysis, if there exist two or more articles containing overlapping data.

Inclusion/exclusion criteria

We used the following standards to select eligible articles: 1) studies evaluating the association of MTHFR C677T and A1298C polymorphisms with oral cancer risk; 2) case-control design; 3) sufficient data provided to compute odds ratios (ORs) and 95% confidence intervals (95% CIs); and 4) in the controls, genotype frequency of MTHFR C677T, A1298C, or other SNPs in agreement with Hardy–Weinberg equilibrium (HWE). Exclusion criteria were as follows: 1) case-only studies or case reports; 2) reviews or meta-analyses; 3) studies without detailed genotyping data; and 4) duplicate publications.

Data extraction

Two investigators (Zhu-Ming Hua and Zhen-Jian Zhuo) independently extracted data from the eligible studies. For conflicting results, a consensus was achieved after thorough discussion. The following characteristics were selectively extracted from each study: first author’s surname, year of publication, country, ethnicity, the source of controls, genotyping methods, and genetic distribution of cases and controls. The stratification analysis was conducted by ethnicity (Asians and Caucasians) and control source (hospital based and population based).

Statistical methods

Chi-square test was used to check the genotype frequency of SNPs among the controls, with P<0.05 suggesting a departure from HWE. The strength of association between MTHFR C677T and A1298C polymorphisms and oral cancer risk was assessed by calculating pooled ORs and 95% CIs. The following five genetic models were applied: homozygote model (C677T: TT vs CC; A1298C: CC vs AA), heterozygote model (C677T: CT vs CC; A1298C: AC vs AA), recessive model (C677T: TT vs CT/CC; A1298C: CC vs AC/AA), dominant model (C677T: CT/TT vs CC; A1298C: AC/CC vs AA), and allele contrast (C677T: T vs C; A1298C: C vs A). Stratification analyses were also performed by ethnicity (Asians and Caucasians) and source of control (hospital based and population based). We performed chi-square-based Q statistic test and inconsistency index statistics (F) to calculate between-study heterogeneity. If the studies were found to be homogeneous (with P<0.10 or F<50%), ORs were estimated using the fixed-effects model (the Mantel–Haenszel method). Otherwise, the random-effects model (the DerSimonian and Laird method) was adopted. Sensitivity analysis was performed by sequentially removing one study at a time and reanalyzing the pooled estimates, in order to exclude single studies that have significant influences on the overall ORs. Furthermore, potential publication bias was estimated by Begg’s funnel plot as well as Egger’s linear regression test. An asymmetric plot and a P-value <0.05 indicated the existence of publication bias. All the data management and statistical analysis were performed using STATA 11.0 software (Stata Corporation, College Station, TX, USA). All statistical tests were two-sided. A P-value of <0.05 was set as a significant threshold.
Trial sequential analysis (TSA)  
To avoid the random errors caused by dispersed data and repeated significance testing, we performed the TSA to obtain a more reliable conclusion.\textsuperscript{24} We only applied TSA to MTHFR C677T polymorphism, but not A1298C polymorphism, as the latter involves less than six studies. We calculated the required information size and estimated the sample size needed to make a robust conclusion. The required information size was evaluated by considering an overall type I error (a) of 5\% and type II error (b) of 20\%. Based on required information size as well as risk for type I and type II errors, TSA monitoring boundaries were constructed. If the cumulative Z-curve (blue line) crosses a TSA monitoring boundary (red lines sloping inward) before the required information size is reached, the robustness of evidence may be confirmed and no further trials are necessary. Otherwise, the evidence is inadequate to get a robust conclusion and it is necessary to continue to do trials. TSA software version 0.9 beta was used.

\section*{Results} 

\subsection*{Selection of studies} 
The identification and selection of studies are graphically presented in Figure 1. A total of 41 potentially relevant published records were initially retrieved from PubMed and EMBASE, and only one article was identified from Chinese databases. Among them, 25 articles were excluded after screening the titles and abstracts, and 17 remaining studies were further subjected to full-text assessment. Among them, seven studies were removed for the following reasons: five were meta-analyses or reviews,\textsuperscript{6,20–23} one was duplication publication,\textsuperscript{25} and one lacked description of oral cancer.\textsuperscript{26} Finally, 10 publications were included in the meta-analysis, of which 10 studies involved C677T polymorphism\textsuperscript{18,19,27–34} and five involved A1298C polymorphism.\textsuperscript{18,19,28,29,32}

\subsection*{Study characteristics} 
The study characteristics of the final selected studies are shown in Table 1. Ten studies with 1443 cases and 1640 controls for the C677T polymorphism were ultimately included in the meta-analysis. Among them, seven studies were conducted in Caucasians and three in Asians. As to the source of control, four were population-based studies and six were hospital based. Moreover, there were five studies for the A1298C polymorphism with 973 cases and 1024 controls. Of these studies, three were conducted in Caucasians and two in Asians. All of them were hospital-based design.

\subsection*{Meta-analysis results} 
The main results of the current meta-analysis are listed in Table 2 and Figure 2. As for C677T polymorphism, no

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{flowchart.png}
\caption{Flow diagram of the included studies for the associations between MTHFR C677T and A1298C polymorphisms and oral cancer susceptibility. \textbf{Abbreviation:} MTHFR, methylenetetrahydrofolate reductase.}
\end{figure}
significant association with overall oral cancer risk was observed under all the five genetic models: homozygote model (TT vs CC: OR = 0.92, 95% CI = 0.71–1.20), heterozygous model (CT vs CC: OR = 0.98, 95% CI = 0.72–1.33), recessive model (TT vs CC/CT: OR = 0.95, 95% CI = 0.74–1.23), dominant model (CT/TT vs CC: OR = 1.00, 95% CI = 0.74–1.37), and allele model (T vs C: OR = 1.00, 95% CI = 0.80–1.27). Stratified analysis by ethnicity did not reveal any significant association between C677T polymorphism and oral cancer risk among either ethnic group. In terms of source of controls, only a borderline significant association was detected between C677T polymorphism and a decreased oral cancer risk under the homozygous model (OR = 0.71, 95% CI = 0.50–1.00) in hospital-based studies.

Regarding the A1298C polymorphism, no association with overall oral cancer susceptibility was found (CC vs AA: OR = 0.76, 95% CI = 0.52–1.13; AC vs AA: OR = 0.97, 95% CI = 0.80–1.17; CC vs AC/AA: OR = 0.71, 95% CI = 0.49–1.03; AC/CC vs AA: OR = 0.93, 95% CI = 0.77–1.11; and C vs A: OR = 0.90, 95% CI = 0.78–1.05). Similarly, we could not observe any association between A1298C polymorphism and oral cancer risk in the stratified analysis by ethnicity.

Heterogeneity and sensitivity analysis

As shown in Table 2, substantial heterogeneities existed among the investigations for the MTHFR C677T polymorphism and oral cancer risk under the heterozygous (P = 0.001) and dominant (P < 0.001) models, as well as allele contrast (P = 0.001). Thus, the random-effects model was applied to calculate the pooled ORs and 95% CIs for these genetic models. The fixed-effect model was adopted for other two genetic models without heterogeneity.

The sequential leave-one-out sensitivity analysis was applied to investigate the influence of a single study on the pooled ORs. The similar recalculated ORs were obtained after the omission of each individual study, indicating the reliability and credibility of our results (data not shown).

Publication bias

We performed Begg’s funnel plot and quantitative Egger’s linear regression test to evaluate the publication bias. The shape of the Begg’s funnel plots appeared to be symmetrical for C677T and A1298C polymorphisms. Moreover, we did not observe significant publication bias as suggested by Egger’s test.

TSA

In this meta-analysis, 10 studies with 3083 individuals were included to investigate the association of C677T polymorphism with oral cancer susceptibility. The TSA for C677T polymorphism showed that the cumulative Z-curve did not cross the trial monitoring boundary before reaching the required information size, suggesting that additional trials were needed to further verify the conclusion (Figure 3). TSA was not applicable for A1298C polymorphism, since the number of eligible studies was too small.

Discussion

In this meta-analysis, we analyzed the association of MTHFR C677T and A1298C polymorphisms with oral cancer risk.
Table 2 Meta-analysis of the association between MTHFR C677T and A1298C polymorphisms and oral cancer risk

<table>
<thead>
<tr>
<th>Variables</th>
<th>No of studies</th>
<th>Sample size</th>
<th>Homozygous OR (95% CI)</th>
<th>Heterozygous OR (95% CI)</th>
<th>Recessive OR (95% CI)</th>
<th>Dominant OR (95% CI)</th>
<th>Allele OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>C677T</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>All</td>
<td>10</td>
<td>1,443/1,640</td>
<td>0.92 (0.71–1.20)</td>
<td>0.114</td>
<td>0.98 (0.72–1.33)</td>
<td>1.01 (0.74–1.37)</td>
<td>1.00 (0.80–1.27)</td>
</tr>
<tr>
<td>Ethnicity</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caucasian</td>
<td>7</td>
<td>596/782</td>
<td>1.14 (0.77–1.68)</td>
<td>0.744</td>
<td>1.15 (0.85–1.54)</td>
<td>1.06 (0.74–1.54)</td>
<td>1.15 (0.89–1.49)</td>
</tr>
<tr>
<td>Asian</td>
<td>3</td>
<td>847/858</td>
<td>0.77 (0.54–1.10)</td>
<td>0.014</td>
<td>0.69 (0.37–1.27)</td>
<td>0.86 (0.61–1.22)</td>
<td>0.72 (0.37–1.43)</td>
</tr>
<tr>
<td>Source of control</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hospital (HB)</td>
<td>6</td>
<td>976/1,112</td>
<td>0.71 (0.50–1.00)</td>
<td>0.278</td>
<td>0.78 (0.56–1.38)</td>
<td>0.006</td>
<td>0.77 (0.55–1.07)</td>
</tr>
<tr>
<td>Hospital (PB)</td>
<td>4</td>
<td>467/528</td>
<td>1.39 (0.91–2.12)</td>
<td>0.056</td>
<td>1.12 (0.76–1.65)</td>
<td>0.112</td>
<td>1.31 (0.88–1.96)</td>
</tr>
<tr>
<td><strong>A1298C</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>All</td>
<td>5</td>
<td>973/1,024</td>
<td>0.76 (0.52–1.13)</td>
<td>0.869</td>
<td>0.97 (0.80–1.17)</td>
<td>0.71 (0.49–1.03)</td>
<td>0.93 (0.77–1.11)</td>
</tr>
<tr>
<td>Ethnicity</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Caucasian</td>
<td>3</td>
<td>223/265</td>
<td>1.04 (0.45–2.39)</td>
<td>0.761</td>
<td>0.83 (0.57–1.21)</td>
<td>1.16 (0.52–2.61)</td>
<td>0.85 (0.60–1.22)</td>
</tr>
<tr>
<td>Asian</td>
<td>2</td>
<td>750/759</td>
<td>0.70 (0.45–1.10)</td>
<td>0.898</td>
<td>1.02 (0.82–1.29)</td>
<td>0.62 (0.41–0.95)</td>
<td>0.96 (0.77–1.18)</td>
</tr>
</tbody>
</table>

Abbreviations: het, heterogeneity; OR, odds ratio; CI, confidence interval; HB, hospital-based; PB, population-based.

**Discussion**

The meta-analysis of the association between MTHFR C677T and A1298C polymorphisms and oral cancer risk revealed conflicting results across different studies. The associations were found to vary significantly according to ethnicity, source of control, and study design. The role of each polymorphism in oral cancer risk was explored under five genetic models: homozygous, heterozygous, recessive, dominant, and allele. The heterogeneity among studies was assessed using Cochrane’s Q test and I² statistic. No significant association with oral cancer was observed for the two SNPs under all five genetic models. In addition, stratified analyses by ethnicity revealed null association in Caucasians and Asians. However, we detect a borderline significant association of C677T polymorphism with a decreased risk of oral cancer in hospital-based studies. This finding is consistent with previous studies that have identified C677T as a protective allele against oral cancer in Asians. Further investigations are needed to validate these findings and to elucidate the genetic basis of oral cancer susceptibility.

**Conclusion**

The meta-analysis of the association between MTHFR C677T and A1298C polymorphisms and oral cancer risk highlights the need for additional research to clarify the role of these genetic variations in the development of oral cancer. Future studies should focus on understanding the biological mechanisms underlying the observed associations and on validating these findings in larger and more diverse populations. This will contribute to the development of personalized prevention strategies for oral cancer.
by Zhu et al. in 2016, they suggested that MTHFR A1298C polymorphism was associated with decreased oral cancer risk. However, this association may not be convincible enough due to the relatively small sample; thus, it is necessary for us to update this research.

It should be noted that our stratified analyses revealed a borderline significant association of C677T polymorphism with a decreased oral cancer risk under the homozygous model in studies with hospital-based design. As the variant T alleles of MTHFR C677T polymorphism could reduce the
enzyme activity to nearly 50% compared to the wild-type C allele, we hypothesize that the reduced MTHFR activity will cause intracellular accumulation of 5,10-methylenetetrahydrofolate and result in a reduced incidence of DNA double-strand breakage. The reduced incidence of DNA double-strand breakage will maintain genetic stability and prevent oral cancer development.⁴³ Besides, we also observed that there seem to be different results from Asian and Caucasian studies for the association between C677T polymorphism and oral cancer risk. The discrepant results may be explained by the fact that different races may modify the genetic effect on oral cancer risk.

Compared to the previous meta-analyses, we have undertaken some critical measurements to assure the credibility of our conclusion. The publication bias analysis and sensitivity analysis indicated a lack of publication bias and the stability of the results. We also employed TSA to test the conclusion reliability of this meta-analysis. However, the Z-curve failed to cross the trial monitoring boundary before reaching the required information size, which indicated that more samples were needed to clarify the correlation between MTHFR C677T polymorphism and oral cancer risk.

In spite of the merits, some weaknesses of the study should be pointed out. First, the statistical power of the meta-analysis was restricted because of relative small sample size. Second, the existence of between-study heterogeneity in some comparisons might compromise the reliability of conclusion. Third, only relevant studies in English and Chinese were included, some investigations in other languages might be omitted. Forth, due to the utilization of unadjusted ORs, we were only able to examine the association of interest by single-factor estimation from genetic perspective. The impacts of other risk factors for oral cancer, including lifestyle, environment exposures, and gene–environment interactions, are also needed to be considered. Finally, there were some inherent limitations due to the retrospective nature of meta-analysis, such as inconsistent qualities of the included studies, misclassified genotypes, incomplete histological details, and unwell-matched sources of controls.

Conclusion

Despite some limitations, this meta-analysis indicated that there was no association observed between the two MTHFR polymorphisms (C677T and A1298C) and oral cancer risk. Further in-depth and well-designed investigations with larger sample sizes are warranted to explore the correlation, since this null correlation estimated by conventional meta-analysis failed to get the conformation of TSA.

Acknowledgment

This study was supported by grants from Science and Technology Planning Project of Guangdong Province (2007B031514005).

Disclosure

The authors report no conflicts of interest in this work.

References


