

RESEARCH ARTICLE

The MTHFR C677T Polymorphism and Risk of Acute Lymphoblastic Leukemia: an Updated Meta-analysis Based on 37 Case-control Studies

Yuan Jiang¹, Jing Hou¹, Qiang Zhang¹, Shu-Ting Jia², Bo-Yuan Wang³, Ji-Hong Zhang², Wen-Ru Tang^{2*}, Ying Luo^{2*}

Abstract

Background: The C677T polymorphism of the methylenetetrahydrofolate reductase (MTHFR) has been associated with acute lymphoblastic leukemia (ALL). However, results were conflicting. The aim of this study was to quantitatively summarize the evidence for the MTHFR C677T polymorphism and ALL risk. **Methods:** Electronic searches of PubMed and the Chinese Biomedicine database were conducted to select case-control studies containing available genotype frequencies of C677T and the odds ratio (OR) with 95% confidence interval (CI) was used to assess the strength of any association. **Results:** Case-control studies including 6,371 cases and 10,850 controls were identified. The meta-analysis stratified by ethnicity showed that individuals with the homozygous TT genotype had decreased risk of ALL (OR= 0.776, 95% CI: 0.687~0.877, $p < 0.001$) in Caucasians (OR= 0.715, 95% CI: 0.655~0.781, $p = 0.000$). However, results among Asians (OR=0.711, 95% CI: 0.591~1.005, $p = 0.055$) and others (OR=0.913, 95% CI: 0.656~1.271, $p = 0.590$) did not suggest an association. A symmetric funnel plot, the Egger's test ($P=0.093$), and the Begg- test ($P=0.072$) were all suggestive of the lack of publication bias. **Conclusion:** This meta-analysis supports the idea that the MTHFR C677T genotype is associated with risk of ALL in Caucasians. To draw comprehensive and true conclusions, further prospective studies with larger numbers of participants worldwide are needed to examine associations between the MTHFR C677T polymorphism and ALL.

Keywords: MTHFR C677T - meta-analysis - acute lymphoblastic leukemia - risk factor

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Introduction

Acute lymphoblastic leukaemia (ALL) is the maximum common pediatric leukemia accounting for 25-30% of all cases of childhood malignancies (Krajinovic et al., 1999). The disease-free survival of childhood ALL has surpassed 80% in the developed countries over the last years. Nevertheless, almost 20% of the children with ALL either revert or do not respond to treatment (Karathanasis et al., 2011). Even though the scientific, pathological and immunophenotypic types of the disease are well acknowledged, about leukemogenesis is little known (Krajinovic et al., 1999). A range of factors might be related to the biologic mechanisms and etiology of ALL. It is generally considered that the development of ALL is a comprehensive result of environment, genetic risk factors, and gene-environment interactions (Robien et al., 2003; Scelo et al., 2009). Folate deficiency and aberrant metabolism have been reported to be associated with ALL

(Yang et al., 2011). Poly-morphisms in genes involved in folate transport, metabolism, and distribution in vivo drew widespread attention in the last decade (McNeer 2011). The polymorphisms in the methylenetetrahydrofolate reductase (MTHFR) gene C677T, has been associated with acute lymphoblastic leukemia because they reduced MTHFR enzyme activity, leading to enhanced availability of 5,10-methylenetetrahydrofolate in the DNA synthesis pathway and reduced uracil misincorporation into DNA (Skibola et al., 1999).

The human MTHFR gene contains 11 exons, located on chromosome 1p36.3, and encodes methylenetetrahydrofolate reductase (MTHFR) a key enzyme in folate and homocysteine metabolism. MTHFR catalyzes the biologically irreversible reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, which provides the methyl group for the remethylation of homocysteine to methionine (Bailey et al., 1999). In the MTHFR enzyme, several

¹Lab of Molecular Genetics of Aging & Tumor, Faculty of Life Science and Technology, ²Lab of Molecular Genetics of Aging & Tumor, Medical Faculty, ³Lab of Molecular Genetics of Aging & Tumor, Faculty of Life Science and Technology & Faculty of Environmental Science and Engineering, Kunming University of Science and Technology, Kunming, Yunnan, China *For correspondence: yingluo@kmust.edu.cn, twr@sina.com

Table 1. The Distribution of the MTHFR C677T Variant for Cases and Controls

Author, year	Case			Control			Ethnicity	Country	P ^a
	CC	CT	TT	CC	CT	TT			
Azhar et al., 2012	35	31	6	65	34	10	Other	Iran	0.089
Chan et al., 2011	140	43	2	122	51	4	Asian	Indonesia	0.620
Yang et al., 2011	96	180	96	84	168	115	Asian	china	0.136
Sood et al., 2010	54	38	3	173	71	11	other	India	0.290
Yeoh et al., 2010	184	111	23	163	150	32	Asian	Singapore	0.765
Lightfoot et al., 2010	374	341	90	359	314	84	Caucasian	UK	0.223
Damjanovic et al., 2010	45	28	5	163	190	59	Caucasian	Serbia	0.762
Tong et al., 2010	135	192	34	173	257	73	Asian	China	0.152
Lv et al., 2010	38	65	24	72	83	27	Asian	China	0.700
Jonge et al., 2009	130	93	22	219	223	54	Caucasian	New Zealand	0.805
Kim et al., 2009	29	51	27	540	863	297	Asian	Korea	0.133
Kantar et al., 2009	8	9	3	11	5	1	other	Turkey	0.679
Alcasabas et al., 2008	145	41	3	322	66	6	Asian	Philippines	0.227
Liu et al., 2008	34	23	26	38	36	9	Asian	China	0.914
Giovannetti et al., 2008	51	11	3	26	6	0	Asian	Indonesia	0.558
Giovannetti et al., 2008	26	6	0	51	11	3	Asian	Indonesia	0.039
Giovannetti et al., 2008	224	234	45	47	31	8	Caucasian	Surabaya	0.391
Kamel et al., 2007	39	42	7	156	135	20	other	Egypt	0.195
Petra et al., 2007	30	33	5	112	110	36	Caucasian	Slovenia	0.287
Oh et al., 2007	49	55	14	138	229	60	Asian	Korea	0.023
Kim et al., 2006	17	38	11	24	55	21	Asian	Korea	0.313
Reddy et al., 2006	51	77	7	79	58	5	other	India	0.148
Yu, 2006	30	14	7	20	23	10	Asian	China	0.466
Zanrosso et al., 2006	43	35	8	59	50	10	mixed	Brazil	0.897
Zanrosso et al., 2006	53	21	5	37	32	10	mixed	Brazil	0.462
Chatzidakis et al., 2006	31	18	3	32	47	9	Caucasian	Greece	0.169
Oliveira et al., 2005)	48	50	5	45	57	9	Caucasian	Portugal	0.120
Schnakenberg et al., 2005	195	201	47	184	152	43	Caucasian	Germany	0.179
Thirumaran et al., 2005	199	195	59	600	681	167	Caucasian	Germany	0.210
Gemmati et al., 2004	52	53	9	78	128	51	Caucasian	Italy	0.908
Balta et al., 2003	71	60	11	90	87	8	other	Turkey	0.020
Krajcinovic et al., 2004	112	127	31	126	128	46	Caucasian	Canada	0.159
Jiang et al., 2004	15	14	0	18	41	8	Asian	China	0.039
Deligezer et al., 2003	27	31	4	74	73	14	other	Turkey	0.501
Franco et al., 2001	36	28	6	22	36	13	mixed	Brazil	0.796
Wiemels et al., 2001	98	91	27	89	79	32	Caucasian	UK	0.047
Skibola et al., 1999	35	29	5	61	39	14	Caucasian	England	0.061

^ap value for Hardy–Weinberg equilibrium in control group

single nucleotide polymorphisms including the two most important, C677T and A1298C, can affect folate and total homocysteine (tHcy) status. The MTHFR C677T, which involves a cytosine (C) to a thymine (T) substitution at position 677, changes an alanine to a valine in the enzyme. The C677T increases thermolability of MTHFR and causes impaired folate binding and reduced activity of the MTHFR enzyme (Frosst et al., 1995). MTHFR C677T is associated with decreased concentrations of folate in serum, plasma, and red blood cells, and mildly increased plasma total homocysteine (tHcy) concentration (Frosst et al., 1995). Based on its biological functions, MTHFR C677T can be seen as a candidate gene for Acute lymphoblastic leukaemia. Accumulating studies have investigated the association between this polymorphism and Acute lymphoblastic leukaemia. However, the results were inconsistent. Therefore, we conducted a meta-analysis to quantitatively assess the effect of the MTHFR C677T polymorphism on the risk of Acute lymphoblastic leukaemia.

Materials and Methods

Publication Search

We searched the PubMed and Chinese biomedicine databases for all articles on the association between MTHFR C677T and acute lymphoblastic leukemia risk (last search update, March 1, 2013). The following key words were used: “MTHFR”, “polymorphism” and “Acute lymphoblastic leukaemia” or “leuki”. Case-control studies containing available genotype frequencies of C677T were chosen. Of the studies with overlapping data published by the same author, only the most recent or complete study was included in this meta-analysis.

Statistic analysis

For control group of each study, the observed genotype frequencies of the MTHFR C677T polymorphism were evaluated for Hardy Weinberg-Equilibrium (HWE) using the χ^2 test. The strength of association between MTHFR C677T gene and Acute lymphoblastic leukaemia was

Table 2. ORs and 95% CI for ALL and the MTHFR C677T Polymorphism under Different Genetic Models

Genetic model (population)	pooled OR [95% CI]	p	Heterogeneity		Publication Bias	
			I-squared	p	Begg	Egger
Additive (T vs. C)						
Caucasian	0.715[0.655~0.781]	0.000	0.260	0.493	0.218	
Asian	0.711[0.591~1.005]	0.055	0.000	0.392	0.580	
Others	0.913[0.656~1.271]	0.590	0.000	0.061	0.275	
overall	0.776[0.687~0.877]	0.000	0.000	0.072	0.093	
Dominant (T-carriers vs. CC)						
Caucasian	0.863[0.718~1.036]	0.114	0.001	0.273	0.197	
Asian	0.939[0.769~1.148]	0.540	0.025	0.815	0.584	
Others	1.122[0.776~1.622]	0.541	0.001	0.297	0.574	
overall	0.944[0.828~1.076]	0.386	0.000	0.289	0.447	
Recessive (TT vs. C-carriers)						
Caucasian	0.794[0.644~0.980]	0.031	0.143	0.131	0.002	
Asian	1.009[0.723~1.409]	0.956	0.005	0.392	0.464	
Others	0.861[0.593~1.251]	0.433	0.648	0.532	0.564	

accessed by calculating crude odds ratios (ORs) and 95% confidence intervals (CIs). The pooled ORs were performed for additive genetic model (T vs. C), dominant model (TT+CT vs. CC), and recessive model (TT vs. CT+ CC) respectively. Heterogeneity assumption was evaluated by a chi-square based Q-test. A P-value of <0.05 for the Q-test indicated heterogeneity among the studies, the summary OR estimate of each study was calculated by the random effects model (DerSimonian et al., 1986; Mantel et al., 1959). The potential for publication bias was examined by a Begg's test (funnel plot method) and Egger's linear regression test ($P < 0.05$ considered representative of statistical significance) (Egger et al., 1997). All analyses were performed using Stata software (version 8.2; Stata Corporation, College Station, TX).

Results

Eligible studies

We identified a total of 37 relevant publications that association between MTHFR C677T and Acute lymphoblastic leukaemia, including 6371 Acute lymphoblastic leukaemia cases and 10850 controls in our meta-analysis (Table 1). Since C677T genotypes in the control group by Giovannetti (Giovannetti et al., 2008), Oh (Oh et al., 2007), Balta (Balta et al., 2003), Jiang (Jiang et al., 2004), Wiemels (Wiemels et al., 2001), were not in HWE, these data (537 cases and 944 controls) were excluded from our meta-analysis. Therefore, our final data pooling consisted of 32 publications, including 5834 cases and 9906 controls.

Meta-analysis

Differences in allelic distribution by ethnicity could be partially responsible for the observed differences in the association between MTHFR C677T and acute lymphoblastic leukemia. The results of the association between the MTHFR C677T polymorphism and Acute lymphoblastic leukaemia and the heterogeneity test are shown in Table 2. The association was most pronounced for carriers of the T allelic gene (additive model: R=

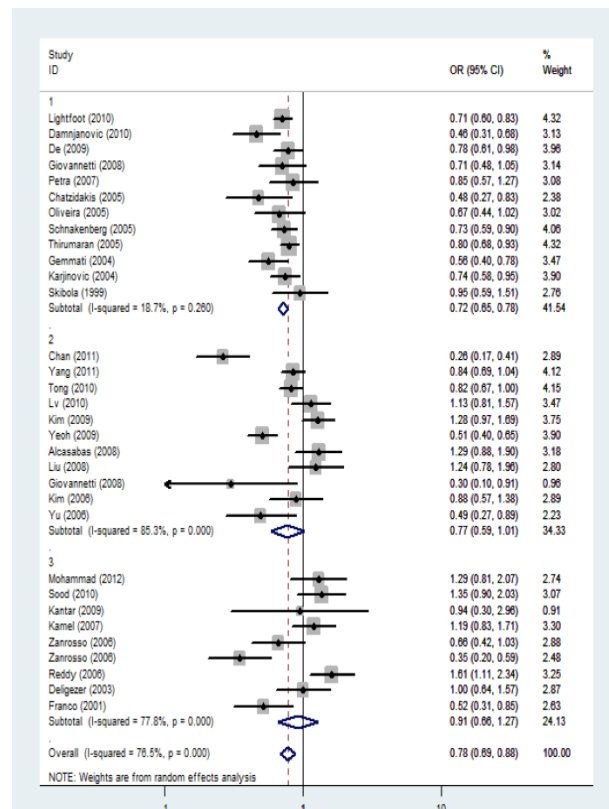


Figure 1. Forest Plot of ORs of Recurrent Pregnancy Loss for T Allele When Compared to the C Allele. The squares and horizontal lines correspond to the study-specific OR and 95% CI. The area of the squares reflects the study-specific weight. The diamond represents the pooled OR and 95% CI

0.776, 95% CI: 0.687~0.877, $p = 0.000$). The positive association was driven by a Caucasian additive model: (OR= 0.715, 95% CI: 0.655~0.781, $p = 0.000$, $P = 0.260$ for heterogeneity, Figure 1). No significant association was found in Asian (OR= 0.711, 95% CI: 0.591~1.005, $p = 0.055$) and other (OR=0.913, 95% CI: 0.656~1.271, $p = 0.590$).

Publication bias

Funnel plot and Egger's test were performed to quantitatively evaluate the publication bias of literatures on Acute lymphoblastic leukaemia. The results of Egger's test provided statistical evidence for funnel plot symmetry ($P = 0.285$) in overall results, suggesting the absence of publication bias.

Discussion

Acute lymphoblastic leukaemia, an important clinical problem, has been well-studied but the mechanism of ALL is still relatively unclear. Single nucleotide polymorphisms (SNPs) can be used as a implement in investigating genetic variations and disease susceptibility. ALL is speculated to be associated with inherited thrombophilias that encompass diverse conditions including the thermolabile variant of the MTHFR (Jilma et al., 2003). Methylene tetrahydrofolate reductase is an enzyme in homocysteine metabolism. The MTHFR C677T, which is found within the enzyme catalytic domain, result in both a thermolabile protein and increased tHcy. Through its effect

on tHcy levels, MTHFR C677T has been implicated as a risk factor in the pathogenesis of Acute lymphoblastic leukaemia.

The frequency of homozygous TT genotypes was found significantly higher among the childhood with Acute lymphoblastic leukaemia than the other two groups indicated that MTHFR C677T polymorphism would be expected to play a major role to bring about ALL. Some studies reported significantly decreased prevalence of MTHFR C677T among cases in distinct ethnicity (Wang et al., 2012; Yan et al., 2012). In contrast, other studies reported an insignificant association between the MTHFR C677T and ALL (Li et al., 2011; Wang et al., 2010). The variances in ethnicity may be one major reason for the controversy. A meta-analysis summarizing studies on association between the MTHFR C677T polymorphism and Acute lymphoblastic leukaemia until march 2011 found the TT genotype marginally significantly associated with reduced ALL risk in Children. However, five new studies have been published increasing the number of Acute lymphoblastic leukaemia and controls with genetic information. We excluded five studies in this meta-analysis after evaluating the articles in their entirety.

The summary OR from our meta-analyses revealed that individuals with the T allelic gene had decreased risk of Acute lymphoblastic leukaemia ($p=0.000$), especially in Caucasian ($p=0.000$). However, our data do not support the association for Asian ($p=0.055$).

The TT genotype of C677T polymorphism in MTHFR gene was associated with elevated plasma homocysteine level, increased risk of arterial stiffness (Trabetti 2008). Women with elevated total homocysteine concentrations showed a significant association with defective chorionic villous vascularization (Nelen et al., 2000). independently of hyperhomocysteinemia, was due to interference with red blood cell folate metabolism, as has been suggested (Golbahar et al., 2005). It is also possible that association of the MTHFR 677TT genotype with Acute lymphoblastic leukaemia. In the Govindaiah study, MTHFR genotype impacts more prominent in men than women (Govindaiah et al., 2009). However, the mechanism by which homocysteine causes DNA damage needs to be elucidated further.

There are limitations that are present in this analysis, which mainly relate to the lack of other risk factors between the subjects in the available studies. In these cases, few investigators reported results from subgroup analysis for other risk factors, such as age, environmental pollution, sexuality and so on; therefore, the association in these factors could not be assessed. There is a need for larger and wider case-control studies to explore the role of other factors that are likely to cause Acute lymphoblastic leukaemia.

This is a meta-analysis with sufficient individual data to stratify results by both ethnicity and the number of Acute lymphoblastic leukaemia, including a total of 5834 cases and 9906 controls from 32 independent publications, we examined the association between C677T of the MTHFR gene and Acute lymphoblastic leukaemia risk. We demonstrated that the T allele of the C677T polymorphism was associated with a significantly reduced

risk of Acute lymphoblastic leukaemia on Caucasians, whereas did not appear to have an effect in both Asians and Others. Future well designed large studies might be necessary to validate this association in different populations incorporated with environmental factors in the susceptibility of Acute lymphoblastic leukaemia.

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