Association Between MTHFR Genetic Variants and Multiple Sclerosis in a Southern Iranian Population

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Multiple sclerosis (MS) is a demyelinating neuro-inflammatory autoimmune disease of the central nervous system. Genetic predisposition has long been suspected in the etiology of this disease. The association between MTHFR polymorphisms and MS has been investigated in different ethnic groups. We investigated the association between MTHFR C677T and A1298C missense variants and MS in 180 patients and 231 age- and gender-matched healthy controls in a Southern Iranian population. The mutagenically separated PCR (MS-PCR) and PCR-RFLP methods were used to genotype MTHFR at position 677 and 1298, respectively. Compared with controls, we observed a strong association between two MTHFR variants and the risk of developing MS. Subjects carrying 677T allele (CT and TT genotypes) had increased susceptibility to MS as compared to those carrying CC genotype (odds ratio (OR) for CT= 2.9, 95% confidence interval (95% CI)= 1.88-4.49; OR for TT= 6.23, 95% CI= 3.08-12.59). The variant 1298AC genotype also increased the risk for MS among our study population (OR= 2.14, 95% CI= 1.37-3.34). Combined genotype analysis for two MTHFR SNPs revealed that compared to the wild type genotypes (677CC/1298AA), 3 genotypes including TT/AC, CT/AC, and TT/AA were significantly at increased risk for MS development (OR= 13.9, 5.3, and 4.9, respectively). Our results suggest a possible gene dose-dependent association between MTHFR mutant alleles and the risk of MS development.

Key words: Multiple sclerosis, MTHFR, SNP, genotype

Multiple sclerosis (MS) is a complex autoimmune disease of the central nervous system (CNS) resulting in CNS inflammation and demyelination of nerve axons (1, 2). A significant increase in MS incidence has been reported in Iran over the last decade, especially in females (3).

The MS etiology is not well-understood; however, several studies suggest that environmental and genetic factors might be involved in the etiology of this disease (4, 5). Age-dependant exposure to viral infection may also play a role in MS susceptibility (6).
Previous studies have indicated that MS patients have elevated plasma and cerebrospinal fluid (CSF) levels of neurotoxic amino acid homocysteine (7). Other studies have suggested that hyperhomocysteinemia is a risk factor for dementia and Alzheimer’s disease (8, 9) and might be associated with cognitive impairment in MS patients (10). Increased blood homocysteine was shown to be associated with the sensitization of neurons to oxidative stress that promotes apoptosis and hypersensitivity to excitotoxicity (11). Homocysteine may induce neurotoxicity through the oxidation of sulfhydryl groups resulting in generation of reactive oxygen species (11) and overstimulation of N-methyl-D-aspartate (NMDA) receptors resulting in neuronal damage due to excessive Ca\(^{2+}\) influx (12).

Methylenetetrahydrofolate reductase (MTHFR) is a key folate metabolizing enzyme that functions at the junction between two critical pathways regulating one carbon metabolism, nucleotide synthesis and synthesizing the universal methyl donor S-adenosyl methionine (SAM). MTHFR gene is polymorphic and two common non-synonymous mutations, C677T (A222V; rs1801133) and A1298C (E429A; rs1801131), have been associated with decreased enzyme activity and the increased levels of plasma homocysteine (13-16). As a result, the MTHFR genotypes may play a role in MS susceptibility. Both of the above-mentioned MTHFR polymorphisms have been extensively studied for associations with several diseases including neural tube defects (15, 17), and cardiovascular disease (18, 19). A few studies have also investigated the relationship between these polymorphisms and MS (20-22). The aim of this study was to investigate the association between functional polymorphisms of the MTHFR gene with MS among Southern Iranian population.

**Materials and methods**

**Study population**

This case-control study consisted of 180 unrelated patients and 231 healthy controls. The MS population was obtained from patients in university hospitals in Shiraz, Southern Iran, and the diagnosis was made by a neurologist according to the revised McDonald criteria (23). The associated MS population was comprised of three clinical subtypes: 128 relapsing-remitting MS (RR-MS; 71.1%), 43 secondary progressive MS (SP-MS; 23.9%), and 9 primary progressive MS (PP-MS; 5%). The control group was also obtained from healthy volunteers from the general population, which had been matched for age, gender, and ethnicity. Ethics approval for experimentation on humans was obtained from the Institutional Ethics Committee.

**Genotype analysis**

Genomic DNA was extracted from peripheral blood using a standard salting-out procedure (24). Genotyping of MTHFR at position 677 of DNA from healthy subjects (control) and multiple sclerotic patients was performed using the mutagenically separated PCR (MS-PCR) method, as previously described (25). The A1298C mutation of MTHFR was also examined by PCR-RFLP of DNA samples using the enzyme MboII (MBI Fermentas, Lithuania) as described previously (26).

**Statistical analysis**

All statistical analyzes were performed using the SPSS version 16 software package (SPSS Inc., Chicago, IL). Genotype and allele frequencies for the MTHFR genotype variants were investigated using standard Chisquare (\(\chi^2\)) analysis. In addition, conditional multivariate logistic regression analysis for matched case-control groups was used to calculate odds ratio (OR) and 95% confidence intervals (95% CI). A p-value <0.050 was considered as statistically significant.

**Results**

We investigated the association between two common functional polymorphisms of MTHFR
MTHFR Genetic Variants and Multiple Sclerosis

(C677T and A1298C) and MS incidence among Iranian patients. The case-control populations consisted of 180 patients and 231 healthy controls. The cases were more likely to be females (74%) older than 26 years (54.4%). The mean age of patients was 26.0± 12.3 years. The groups of patients and controls did not significantly differ concerning gender or age.

MTHFR C677T and A1298C genotyping was performed by MS-PCR and PCR-RFLP methods, respectively. Illustrative examples of genotype analysis of the two MTHFR variant genotypes are shown in Fig. 1. The results of genotype frequencies and odds ratios for MTHFR genotypes and MS are presented in Table 1. There was no significant Hardy-Weinberg disequilibrium concerning the MTHFR 677 and 1298 genotypes in controls. The distribution of MTHFR 677 genotypes among patients also agreed with that expected from the Hardy-Weinberg equilibrium ($\chi^2 = 0.5$, $P=0.47$). However, significant departures from Hardy-Weinberg equilibrium were observed for MTHFR 1298 genotypes among cases ($P=0.00$).

In our study, the allele frequency distributions of MTHFR C 677T were significantly different between patient and control groups (41.9% versus 20.3%, $P= 0.00$). The frequencies of the MTHFR C677T genotypes in the patients (CC, 35%; CT, 46.1%; TT, 18.9%) were also significantly different from controls (CC, 65%; CT, 29.5%; TT, 5.5%) ($P=0.00$; Table 1). The MS patients were presented with higher homozygous TT genotype than control group, as manifested by an odds ratio of 6.23 (95% CI= 3.08- 12.59). This could be translated into that people having the TT genotype are 6.23-fold more at risk of developing MS, in the multivariate logistic regression analysis (Table 1). Under the codominant model of inheritance, the CT genotype was also associated with an increased risk for MS with an odds ratio lower than recessive model (adjusted OR= 2.9, 95% CI= 1.88- 4.49).

When we combined heterozygous and homozygous variant genotypes, the adjusted OR for the CT/TT genotypes was 3.4 (95% CI= 2.29- 5.17). In case-case comparisons, we observed no differences in frequencies of MTHFR C677T genotypes in patients stratified by the clinicopathologic variables, including age, sex, and disease type (data not shown).
For the A1298C polymorphism, while the allele frequency distribution in MS patients was almost the same as that of controls (36.7% versus 34.7%), the genotype frequency distributions were significantly different (P = 0.001; Table 1). Analysis of the MTHFR A1298C frequency data obtained in this study showed that the heterozygotes (AC) were overrepresented in MS patients (67.8% versus 45.7%, P= 0.00) and a small trend for a higher frequency of the homozygous mutant genotype (CC) was observed in controls (11.8% versus 2.8%, P= 0.04). According to the logistic regression model, in the entire group of patients, MTHFR AC and AC+CC genotypes were strongly associated with a higher risk of MS incidence (Table 1). The adjusted OR for AC and AC+CC genotypes were 2.14 (95% CI 1.37- 3.34) and 1.77 (95%CI 1.15- 2.73), respectively. In case-case comparison, no statistically significant differences in frequencies of the MTHFR A1298C genotypes were found in patients stratified by age, sex, and disease type (data not shown).

### Table 1. Distribution of MTHFR C677T and A1298C genotypes and alleles in MS patients and controls

<table>
<thead>
<tr>
<th>MTHFR Genotypes &amp; alleles</th>
<th>Patients N (%)</th>
<th>Controls N (%)</th>
<th>OR (95% CI)</th>
<th>P*</th>
</tr>
</thead>
<tbody>
<tr>
<td>C677T</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CC (ref)</td>
<td>63 (35)</td>
<td>150 (65)</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>CT</td>
<td>83 (46.1)</td>
<td>68 (29.5)</td>
<td>2.9 (1.88- 4.49)</td>
<td>0.00</td>
</tr>
<tr>
<td>TT</td>
<td>34 (18.9)</td>
<td>13 (5.5)</td>
<td>6.23 (3.08-12.59)</td>
<td>0.00</td>
</tr>
<tr>
<td>CT+TT</td>
<td>117 (65)</td>
<td>81 (35.1)</td>
<td>3.44 (2.29-5.17)</td>
<td>0.00</td>
</tr>
<tr>
<td>C</td>
<td>209 (58.1)</td>
<td>368 (79.7)</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>T</td>
<td>151 (41.9)</td>
<td>94 (20.3)</td>
<td>2.83 (2.08-3.85)</td>
<td>0.00</td>
</tr>
<tr>
<td>A1298C</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>AA (ref)</td>
<td>53 (29.4)</td>
<td>79 (42.5)</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>AC</td>
<td>122 (67.8)</td>
<td>85 (45.7)</td>
<td>2.14 (1.37-3.34)</td>
<td>0.001</td>
</tr>
<tr>
<td>CC</td>
<td>5 (2.8)</td>
<td>22 (11.8)</td>
<td>0.34 (0.12-0.950)</td>
<td>0.04</td>
</tr>
<tr>
<td>AC+CC</td>
<td>127 (70.6)</td>
<td>107 (57.5)</td>
<td>1.77 (1.15-2.73)</td>
<td>0.04</td>
</tr>
<tr>
<td>A</td>
<td>223 (63.3)</td>
<td>243 (65.3)</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>C</td>
<td>132 (36.7)</td>
<td>129 (34.7)</td>
<td>1.09 (0.81-1.48)</td>
<td>0.574</td>
</tr>
<tr>
<td>Combined genotypes (677/1298)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CC/AA (ref)</td>
<td>22 (12.2)</td>
<td>46 (24.7)</td>
<td>1</td>
<td>0.28</td>
</tr>
<tr>
<td>CC/AC</td>
<td>39 (21.7)</td>
<td>57 (30.8)</td>
<td>1.43 (0.75- 2.74)</td>
<td>0.50</td>
</tr>
<tr>
<td>CC/CC</td>
<td>2 (1.1)</td>
<td>14 (7.5)</td>
<td>0.30 (0.06-1.43)</td>
<td>0.00</td>
</tr>
<tr>
<td>CT/AA</td>
<td>17 (9.4)</td>
<td>27 (14.5)</td>
<td>1.32 (0.60- 2.91)</td>
<td>0.77</td>
</tr>
<tr>
<td>CT/AC</td>
<td>63 (35)</td>
<td>25 (13.4)</td>
<td>5.27 (2.65-10.48)</td>
<td>0.004</td>
</tr>
<tr>
<td>CT/CC</td>
<td>3 (1.7)</td>
<td>5 (2.7)</td>
<td>1.26 (0.28-5.73)</td>
<td>0.00</td>
</tr>
<tr>
<td>TT/AA</td>
<td>14 (7.8)</td>
<td>6 (3.2)</td>
<td>4.87 (1.65-14.41)</td>
<td>ND</td>
</tr>
<tr>
<td>TT/AC</td>
<td>20 (11.1)</td>
<td>3 (1.6)</td>
<td>13.94 (3.74-10.48)</td>
<td>ND</td>
</tr>
<tr>
<td>TT/CC</td>
<td>0(0.00)</td>
<td>3 (1.6)</td>
<td>51.95 (1.65-14.41)</td>
<td>ND</td>
</tr>
</tbody>
</table>

*For OR and 95% CI calculations, controls with the wild-type CC and AA MTHFR genotypes were used as reference category. ND: not determined.

For MTHFR 677 and 1298 combined genotypes, double heterozygotes (677 CT/1298 AC) had 5.3- fold (95% CI 2.65- 10.48) increased risk compared with the wild-type (677 CC/1298 AA) genotypes of controls (Table 1). Individuals with the 677TT/1298AC and 677TT/1298AA genotypes...
were also at higher risk of developing MS in comparison to controls. The adjusted OR for \textit{TT/AC} and \textit{TT/AA} combined genotypes were 13.94 (95% CI 3.74- 51.95) and 4.87 (95% CI 1.65- 14.41), respectively. Due to the small number of cases in the current study, it was not possible to perform the analyses of MS risk associated with double homozygous mutants of \textit{677TT/1298CC} genotypes.

**Discussion**

Previous studies have suggested an influence of genetic factors in the aetiology of multiple sclerosis; however, the underlying molecular mechanisms of MS remain unidentified (27, 28). It has been reported that MS patients have elevated levels of plasma and cerebrospinal fluid homocysteine, a neurotoxic metabolite (7, 10, 29-31).

\textit{MTHFR} deficiency is the most common genetic cause of hyperhomocysteinemia (13, 16). \textit{MTHFR} enzyme reduces 5, 10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, which is required for remethylation and conversion of homocysteine to methionine.

The results of previous studies with regard to the association between two polymorphisms of \textit{MTHFR} with reduced enzyme activity (\textit{C677T} and \textit{A1298C}) and MS risk have been inconsistent. We examined the relationship between \textit{MTHFR C677T} and \textit{A1298C} polymorphisms and the risk of MS in a Southern Iranian population. According to the logistic regression model, in the entire group of patients, \textit{MTHFR C677T} and \textit{A1298C} polymorphisms were strongly associated with a higher risk of MS (Table 1). Compared with controls, the \textit{MTHFR C677T} genotype showed a higher risk of MS incidence both in the recessive and codominant models (for \textit{TT} versus \textit{CC}: OR= 6.23, 95% CI= 3.08-1 2.59 and \textit{CT} versus \textit{CC}: OR= 2.9, 95% CI= 1.88- 4.49, respectively). We also found a higher risk associated with the \textit{MTHFR I298AC} genotypes when the MS patients were compared with controls and the wild-type \textit{AA} genotype was used as a reference category (OR= 2.14, 95% CI= 1.37-3.34). However, under the recessive model of inheritance, the homozygous \textit{CC} genotype was slightly associated with a decreased risk for MS (OR= 0.34, 95% CI= 0.12-0.950). Such result could be due to low statistical power because of the limited number of homozygous subjects (5 out of 180 cases). It has been previously reported that compared to the \textit{677T} allele, \textit{1298 C} allele has a minor effect on \textit{MTHFR} activity. Neither the homozygous nor the heterozygous state of the \textit{MTHFR 1298C} genotype is associated with higher plasma homocysteine or a lower plasma folate concentration— that was observed with the homozygous \textit{677T} allele. However, double heterozygosity for both \textit{MTHFR} mutations results in similar features as observed in homozygotes for the \textit{677T} allele (15). When we considered both \textit{MTHFR 1298CC} and \textit{CT} genotypes, we found the increased risk of MS incidence associated with the \textit{AC/CC} genotypes in the entire group of patients (Table 1). Our finding is consistent with most previous reports in which an increased risk of MS was observed associated with the \textit{MTHFR A1298C} genotype (20, 32). This is in contrast to another study (21) that found no association between the \textit{MTHFR A1298C} polymorphism and MS in Australian population. In agreement with a previous report from Iran (33), we also found increased risk of MS associated with the \textit{MTHFR C677T} genotype. A non-significant increased MS risk associated with the \textit{C677T} variant genotype was also reported in a group of Australian population (22). However, some studies conducted on relatively small groups of cases, observed no association between MS and \textit{MTHFR C677T} polymorphism (20, 22, 32). Both the \textit{C677T} and \textit{A1298C} variant genotypes of \textit{MTHFR} have been associated with decreased enzyme activity, with the
C677T having a more severe effect than the A1298C variant. In vitro studies have shown that the 677TT and 1298CC variant genotypes have 60% and 30% reduced enzyme activity in comparison to the wild type MTHFR genotypes, respectively (16, 18, 34). Inconsistency of findings across studies could be explained with the differences in study designs, sample size, genotyping methods, racial, nutritional, and other environmental factors.

To examine the joint effect of MTHFR 677 and 1298 genotypes on MS risk, we analyzed the relationship between combined MTHFR SNPs at these loci and MS risk. Out of five major combined genotypes (CC/AC, CT/AA, CT/AC, TT/AA, and TT/AC) that constitute almost 80% of all genotypic diversity in our study group, the distribution of three genotypes was significantly different between cases and controls (Table 1). Based on our findings, 3 genotypes with the mutant alleles (TT/AC, CT/AC, and TT/AA) are high-risk genotypes for developing MS (13.9, 5.3, and 4.9-fold increased risk, respectively). According to a previous study, subjects with the combined 677CT/1298AC heterozygosity had significantly higher fasting serum homocysteine levels compared to those that were C677T heterozygous (16). Since both C677T and A1298C mutations can influence MTHFR activity and plasma homocysteine concentrations (15, 35), it is intriguing to believe that mutated alleles of MTHFR increase the risk for developing MS in a gene dose-related manner. To our knowledge, the combined effect of MTHFR genotypes has not been previously analyzed in MS populations and further studies are necessary to understand the dose-dependent association of MTHFR alleles with MS risk.

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Conflict of interests

The authors declared no conflict of interests.

References

MTHFR Genetic Variants and Multiple Sclerosis


