

5,10-Methylenetetrahydrofolate Reductase C677T Gene Polymorphism Can Influence Age at Onset of Parkinson's Disease

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Abstract- A case-control study was designed to investigate a possible genetic susceptibility of the *MTHFR* C677T polymorphism and assess whether the genetic polymorphism could be a predictor of levodopa-induced adverse effects in patients with Parkinson's disease (PD) of Chinese descent living in Taiwan. There were 94 sporadic PD patients with levodopa therapy at least for five years and 146 control subjects, matched by sex and gender, in this study. Results revealed that there were no differences of the allelic and genotypic frequencies of the *MTHFR* C677T polymorphism between PD patients and the controls. Analysis of age at onset stratified by *MTHFR* C677T polymorphism showed a trend of early age at onset in the PD patients carrying with *T* allele. The genetic influence was particularly significant in late-onset PD (onset age at or older than 60 years) with an early age at onset for 3.4 years. However, the *MTHFR* C677T polymorphism was not associated with the risk to develop dyskinesia, motor fluctuation and psychosis induced by levodopa in PD patients. In conclusion, results of the study revealed that the *MTHFR* C677T polymorphism could significantly influence age at onset of PD in Chinese population, but neither as a genetic susceptibility nor as a predictor of levodopa-induced adverse effects in PD.

Key Words: Case-control study, Genetic polymorphism, Levodopa-induced adverse effect, 5,10-Methylenetetrahydrofolate reductase gene, Parkinson's disease

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INTRODUCTION

The combined effect of environmental precipitating factors and the presence of a genetic susceptibility may

contribute to the pathogenesis of Parkinson's disease (PD)⁽¹⁾. Increased evidence suggests that a high plasma level of homocysteine (Hcy) might contribute to these processes through direct neurotoxic effects^(2,3). In animal

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models of PD, injection of Hcy in the brain exacerbated 1-methyl-4-phenyl-1,2,3,6-tetrahydropyridine-induced motor dysfunction and loss of dopaminergic neurons⁽²⁾. Hcy has been also observed to cause DNA strand breaks and to enhance oxidative stress, mitochondrial dysfunction, and apoptosis induced by rotenone and iron in cultured human dopaminergic cells⁽³⁾.

Clinically, an increased plasma level of Hcy was initially identified as a risk factor for vascular diseases^(4,5) and was subsequently shown to be a risk factor for Alzheimer's disease⁽⁶⁾, cortical and hippocampal atrophy⁽⁷⁾, depression⁽⁸⁾, and nondemented elderly people with decreased cognitive performance⁽⁹⁾. Total plasma Hcy was also significantly higher among PD patients compared to nonparkinsonian controls^(10,11). The hyperhomocysteinemia in PD patients were principally the result of levodopa administration and from methylation of levodopa and dopamine by catechol O-methyltransferase⁽¹²⁻¹⁴⁾. The 5,10-methylenetetrahydrofolate reductase gene (*MTHFR*) is a folate-dependent enzyme that catalyzes remethylation of Hcy. Individuals with homozygous thermolabile (*TT*) genotype for the *MTHFR* C677T polymorphism display a reduced enzymatic activity, resulting in mild hyperhomocysteinemia⁽¹⁵⁾. A study by Yasui et al.⁽¹⁶⁾ demonstrated a higher plasma Hcy level in PD patients carrying *TT* genotype than those carrying with other genotypes. Therefore, the *MTHFR* could be a candidate gene responsible for the risk of PD through affecting Hcy level by *MTHFR* polymorphism. A recent study by de Lau et al.⁽¹⁷⁾ in a Caucasian population has shown that *TT* genotype of the *MTHFR* C677T polymorphism was associated with an increased risk for PD, particularly in smoker. To reproduce the genetic susceptibility of *MTHFR* polymorphism for PD in different populations, the present study investigated a possible association between *MTHFR* polymorphism and PD patients in a Chinese population living in Taiwan. In addition, this study also investigated the role of *MTHFR* polymorphism in the risk of developing levodopa-induced adverse effects in chronically treated PD patients, because genetic factors may contribute to the pathogenesis of adverse drug reaction⁽¹⁸⁻²⁰⁾.

PATIENTS AND METHODS

The enrolled PD patients were recruited from the Movement Disorders Clinic of Chushang Show-Chwan Hospital in Nantou, Taiwan from January 2004 to December 2005. They have received treatment with levodopa at least for five years. Idiopathic PD was diagnosed according to the UK Parkinson's Disease Society Brain Bank Clinical Diagnostic Criteria⁽²¹⁾. Clinical data were collected during the last office visit through physical examination, detailed history, and review of patient charts and outside documents. The precise duration of PD and duration of levodopa treatment had been given from the beginning of parkinsonian symptoms and levodopa therapy until blood sampling during the last office visit for genetic analysis, respectively. Dyskinesia was defined as drug induced hyperkinetic or dystonic movements or postures or both⁽²²⁾ or if patients had a score of ≥ 1 on items 32 to 39 of the Unified Parkinson's Disease Rating Scale (UPDRS) part 4⁽²³⁾. "On-off" phenomenon denoted sudden, unpredictable fluctuation of motor symptoms, and wearing-off effects were defined as reemergence of parkinsonian symptoms after a dose of levodopa⁽²⁴⁾. However, we recorded these two symptoms as one item (motor fluctuation) and did not differentiate between "on-off" and "wearing off" in the analysis. Finally, levodopa-induced psychosis was defined as PD patients having symptoms of disorder of perception, usually consisting of visual hallucinations with or without insight, and/or disordered thought with clear sensorium⁽²⁵⁾. Patients with previous psychiatric illness or whose hallucinations began before commencing antiparkinsonian medication were excluded. The control volunteers were selected by cluster sampling from the same community over the same period of time. They were all unrelated and received detailed interviews which consisted of a personal health history and family history of PD. A simple physical examination was performed to make sure that there were no parkinsonian symptoms. Participants who were aborigines or having a positive family history of PD were excluded. Therefore, PD patients and control subjects in this study came from the same ethnic origin of Chinese descent. Informed consent

was obtained from the PD patients and control subjects, according to a protocol approved by the Human Subjects Research Ethics Committee of the Hospital.

Genomic DNA was extracted from peripheral whole blood using the IsoQuick Nucleic acid extraction kit (ORCA Research Inc., Bothell, WA, USA), according to the manufacturer's protocol. The primers designed and procedure of the conventional polymerase chain reaction (PCR) and fragment restriction length polymorphism (FRLP) used for amplification of *MTHFR* C677T polymorphism was described by Frosst et al.⁽²⁶⁾, resulting in three genotypes (CC/TT homozygotes and CT heterozygote). Each blood specimen was tested in duplicate to ensure reproducibility of the results.

Statistical analysis was performed using the SPSS for Windows release 12.0, run on an IBM-compatible computer. Tests for the allelic and genotypic frequencies were performed using the chi-square (X^2) tests. Differences between the mean age at onset of PD and the genotypes were compared using one-way ANOVA. The demographic data of PD patients with and without levodopa-induced adverse effects were expressed as mean \pm S.D. and were compared by unpaired Student's *t* test. Tests for the difference in the *MTHFR* C677T polymorphism between PD patients with and without levodopa-

induced adverse effects were also performed using the X^2 tests. A *p*-value of < 0.05 was considered significant.

RESULTS

This study included 94 sporadic PD patients treated with levodopa and 146 control subjects matched by sex and gender. The demographic data of both study groups are shown in Table 1. The genotype frequencies of *MTHFR* C677T polymorphism in the controls were consistent with the Hardy-Weinberg equilibrium. Although the frequencies of both the homozygote TT genotype and T allele of the polymorphism in the PD patients were higher than those of the controls, these differences did not reach statistical significance ($X^2=2.848$, $p=0.241$ and $X^2=2.48$, $p=0.120$, respectively) (Table 1). Further analysis of the *MTHFR* C677T polymorphism between the PD patients and controls stratified by age at onset and gender did not reveal any significant differences.

The mean age at onset of PD patients in this study was 61.2 ± 10.0 years (mean \pm standard deviation, ranging from 32 to 90 years). When the mean age at onset of PD was stratified by the *MTHFR* genotype, age at onset of PD patients with T allele bearers (either *MTHFR*-TT

Table 1. Demographic characteristics and *MTHFR* C677T polymorphism for the study groups

	PD patients	Controls	<i>P</i> -value
Number of subjects	94	146	
Mean age (years)	69.5 \pm 11.0	68.5 \pm 6.1	
Gender (male/female)	1.12	1.11	
Mean age at onset of PD (years)	61.2 \pm 10.0	-	
Duration of PD (years)	8.3 \pm 2.7	-	
Duration of levodopa treatment (years)	7.0 \pm 2.3	-	
Mean levodopa dosage (mg/day)	627.5 \pm 322.7	-	
<i>MTHFR</i> C677T polymorphism			
Genotype frequency			
CC	55.3%	63.7%	0.241
CT	58.3%	33.6%	
TT	6.4%	2.7%	
CC	55.3%	63.7%	0.195
CT + TT	44.7%	36.3%	
Allele frequency			
C	74.5%	80.5%	0.120
T	25.5%	19.5%	

MTHFR: 5,10-methylenetetrahydrofolate reductase gene, PD: Parkinson's disease

Table 2. Correlation between C677T polymorphism of MTHFR and age at onset of PD

MTHFR polymorphism	No.	Mean age at onset of PD
Total PD patients	94	61.2 ± 10.0
CT + TT	54	59.5 ± 11.0 ^a
CC	52	63.3 ± 13.0
Early-onset PD (onset age < 60 years)	37	
CT + TT	14	49.0 ± 7.0 ^b
CC	23	47.3 ± 5.4
Late-onset PD (onset age > 60 years)	57	
CT + TT	28	67.9 ± 4.5 ^{c*}
CC	29	71.3 ± 6.6

Abbreviation as in Table 1; * p < 0.05.

a: No difference of mean age at onset between patients carrying T allele MTHFR and CC genotypes (t = -1.53, 95% CI = -8.71~1.121, p = 0.129); b: No difference of mean age at onset between early-onset PD patients carrying T allele MTHFR and CC genotypes (t = 0.77, 95% CI = -2.76 ~ 6.13, p = 0.447); c: Significant difference of mean age at onset between late-onset PD patients carrying T allele MTHFR and CC genotypes (t = -2.332, 95% CI = -6.43 ~ -0.48, p = 0.023)

Table 3. Frequencies of the MTHFR C677T polymorphism of the PD stratified by levodopa-induced adverse effects

Variable	No. (%)	Genotype frequency			Allele frequency		
		CC (%)	CT + TT (%)	p-value	T (%)	C (%)	p-value
Total PD	94 (100%)	52 (55.3%)	42 (44.7%)		48 (25.5%)	140 (74.5%)	
Dyskinesia							
with	15 (16.0%)	7 (46.7%)	8 (53.3%)	0.462	8 (26.7%)	22 (73.3%)	0.876
without	79 (84.0%)	45 (57.0%)	34 (43.0%)		40 (25.3%)	118 (74.7%)	
Motor fluctuation							
with	39 (41.5%)	26 (66.7%)	13 (33.3%)	0.062	16 (20.5%)	62 (79.5%)	0.184
without	55 (58.5%)	26 (47.3%)	29 (52.7%)		32 (29.1%)	78 (70.9%)	
Psychosis							
with	21 (22.3%)	12 (57.1%)	9 (42.9%)	0.849	9 (21.4%)	33 (78.6%)	0.489
without	73 (77.7%)	40 (54.8%)	33 (45.2%)		39 (26.7%)	107 (73.3%)	

Abbreviation as in Table 1.

or MTHFR-CT, 59.5 years of mean age) was 3.8 years earlier than that with T allele nonbearers (MTHFR-CC, 63.3 years of mean age), despite that the difference did not reach statistical significance (95% CI=-8.71~1.12, p=0.129). When PD patients were divided into two subgroups, early-onset (onset age < 60 years) and late-onset (onset age ≥ 60 years), further analysis revealed a statistical significance of 3.4 years early age at onset of PD in the late-onset group with T allele bearers (95% CI=-6.43 ~ -0.48, p=0.023) (Table 2). There was no statistical difference in the mean age at onset of PD between T allele bearers and nonbearers in the early-onset group. The cumulative percentage of the MTHFR genotype according to the age at onset of PD patients is shown in Fig.

In the study, mean duration of treatment with levodopa in those 94 sporadic PD patients was 7.1 ± 2.0 years (ranging from 5 to 18 years) and mean dosage of levodopa was 627.5 ± 322.7 mg/day. Fifteen PD patients (16.0%) developed dyskinesia, 39 PD patients (41.5%) showed motor fluctuation, and 21 PD patients (23.3%) had levodopa-induced psychosis. Patients with dyskinesia, motor fluctuation, or psychosis had a significantly longer duration of the disease, and had been treated longer with levodopa than all other patients. Patients with levodopa-induced dyskinesia or motor fluctuation had been younger at the age at onset than that in patients without these adverse effects, but patients with levodopa-induced psychosis had been older at the age at

onset. Analysis of the difference in the *MTHFR* C677T polymorphism in PD patients stratified by levodopa-induced adverse effects revealed that the genetic polymorphism was not associated with the risk to develop dyskinesia, motor fluctuation and psychosis induced by levodopa (Table 3).

DISCUSSION

Previous studies have shown associations of the *MTHFR* C677T polymorphism with a number of disorders, including vascular disorders (such as ischemic stroke, coronary arterial disease and peripheral arterial disease), psychiatric diseases (such as schizophrenia and depression), cancers (such as breast, gastric and colorectal cancer), and neurodegeneration disorders (such as Alzheimer's disease)⁽⁴⁻¹¹⁾. Theoretically, *TT* genotype of the *MTHFR* C677T polymorphism might be associated with a greater risk for PD, because the genotype would reduce enzymatic activity and result in hyperhomocysteinemia^(2,3,15,16). However, the former studies did not support the hypothesis and revealed an insignificant association between the *MTHFR* C677T polymorphism and the risk of PD in the English⁽²⁷⁾, Germans⁽²⁸⁾ and Polacks⁽²⁹⁾. Results of our study also revealed non-insignificance of the genetic polymorphism in the risk of PD in a Chinese population living in Taiwan. A recent study by de Lau et al.⁽¹⁷⁾ in Hollanders demonstrated that *TT* genotype of the *MTHFR* C677T polymorphism was associated with a borderline increased risk for PD and their further analysis showed a strong and significant increase in risk for PD with *TT* genotype in smoker (RR=3.74; 95% CI=1.78-7.85). The explanations for the significance restricted in smoker were that smoking could increase plasma Hcy levels and the *TT* genotype could interact with smoking to increase plasma Hcy level, particularly in smoker^(30,31). Unfortunately, information on smoking status in our present study was not available, therefore, multiplicative effects could not be analyzed as was done by de Lau et al.⁽¹⁷⁾

Plasma Hcy levels are kept low by remethylation to methionine, which require folate and vitamin B₁₂, and by conversion to cysteine, for which vitamin B₆ is an essen-

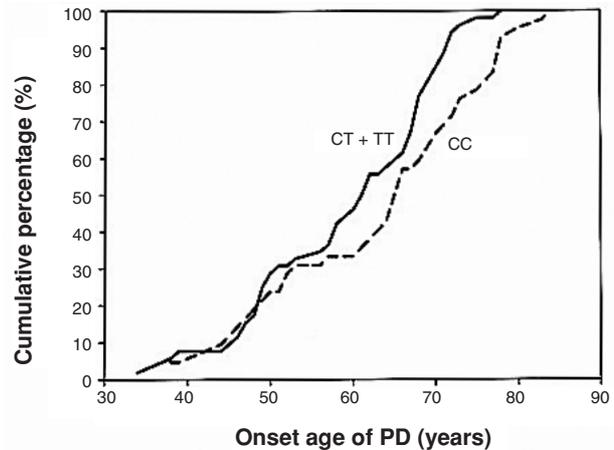


Figure. Cumulative percentage of the *MTHFR* genotype according to the age at onset of PD patients (n = 94)

tial cofactor⁽³²⁾. Increased plasma Hcy levels are associated with low plasma levels as well as low dietary intakes of folate, vitamin B₁₂, and vitamin B₆^(33,34). Considering the potential neurotoxicity of Hcy^(2,3), it is theoretically possible that higher intakes of folate and vitamin B₁₂ and B₆ might decrease the risk of PD by decrease of plasma Hcy levels. However, a retrospective study by Chen et al.⁽³⁵⁾ showed no significant association for either these vitamins. A prospective, population-based cohort study by de Lau et al.⁽³⁶⁾ revealed that a higher intake of either vitamin B₁₂ or folate did not significantly decrease risk of PD, but the association was found in the high vitamin B₆ intake. Although a potential effect of folate and vitamin is not completely ruled out, these findings may point toward a controversy of the hyperhomocysteinemia in the risk of PD and the *TT* genotype in the genetic susceptibility of PD. An alternative explanation for the non-association by Harmon et al.⁽²⁷⁾ indicated that brain could be protected in the situation of hyperhomocysteinemia by the preferential accumulation of folate in the CNS where its concentration was higher than that in serum.

Methodologic strengths of our study include the virtually complete long-term follow up at least five years, adequate stratification and control selection from the same geographic area. We attempted to minimize poten-

tial confounding variables by carefully matching controls to PD patients individually. Anyway, ethnic origin is an important issue for the genetic association study because there are significant discrepancies of genetic polymorphism among populations of different genetic backgrounds^(37,38). As a summation from the previous studies in the literature, the frequency of the *TT* genotype of *MTHFR* polymorphism in the Caucasian populations of healthy subjects was 7-13%^(17,27-29). Our study in Chinese showed 2.7% of the *TT* genotype frequency which was much lower in comparison with the Caucasian populations. Therefore, the discrepancy of genetic association studies in the different genetic background may result from the different *TT* genotype frequency. Another reason was that the result might be a false negative because there was a limited number of patients (94 of total cases studied) and a lack of statistical power in our study⁽³⁹⁾.

In this case-control study, we found a significant effect of the *MTHFR C677T* polymorphism on the age at onset in Chinese PD population. The *T* allele of the gene was associated with a trend of early age at onset of PD and the trend was particularly noted in late-onset PD patients. A study by Müller's et al.⁽²⁸⁾ also revealed the *CC* genotype of *MTHFR A1298C* was associated with the latest onset of disease in the German population. Generally, an interaction exists between genetic susceptibility and environmental exposure may contribute to the pathogenesis in sporadic PD and older onset PD⁽¹⁾. Because the enrolled patients in our study were all sporadic PD, we therefore proposed that the older *T*-allele carriers would be susceptible to other environmental factors, e.g. hyperhomocysteinemia, which is responsible to an early onset of PD. A study by Kalina and Czeizel^(40,4) showed that the *T* allele carriers of the *MTHFR C677T* polymorphism with congenital heart disease (CHD) died earlier due to myocardial infarction and the *C* allele carrier with a lower Hcy level may provide protection against fatal coronary artery occlusion.

To date, there have been only a few studies investigating the relationship between the genetic polymorphism and L-dopa-induced adverse effects in PD patients, but their results were inconsistent^(18-20,41,42). In

this study, genetic variation analysis of the *MTHFR C677T* polymorphism in PD patients with and without levodopa-induced adverse effects revealed the genetic marker was not associated with the risk to develop adverse effects. This finding may advise that, at least among Chinese, the *MTHFR C677T* polymorphism is unlikely to be a useful predictor for the occurrence of adverse effects in levodopa-treated PD patients.

In conclusion, the present case-control study demonstrated that *MTHFR C677T* polymorphism did not confer genetic susceptibility contributing the risk of PD among ethnic Chinese living in Taiwan, but the genetic polymorphism could influence onset age of PD. There may be other genetic risks or more than one susceptible gene contributing to the pathogenesis of PD in Chinese populations. Analysis of the underlying mechanism is required for prophylactic and therapeutic strategies.

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