Research Article

Association of Apolipoprotein E Polymorphisms and Risks of Ischemic Stroke in Chinese Patients with Type 2 Diabetes Mellitus

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Background. The apolipoprotein E (APOE) gene polymorphisms have been intensively studied in patients with type 2 diabetes mellitus (T2DM) and ischemic stroke (IS) in recent years. However, it is unclear whether APOE gene polymorphisms are correlated with increased risk for developing IS in T2DM patients. Thus, this study was designed to examine the association between APOE gene polymorphisms and risks of IS in Chinese patients with T2DM.

Methods. This case-control study enrolled 243 subjects with T2DM as controls, and 210 subjects with T2DM complicated with IS as case patients. The genotypes were determined using real-time PCR while HbA1c and lipid levels were detected using commercially available kits.

Results. The systolic blood pressure (SBP), diastolic blood pressure (DBP), and the proportion of patients with a history of hypertension were higher in the case patients than that in the controls. We confirmed that the ε2/ε3 genotype, as well as SBP and history of hypertension, was the independent risk factor for developing IS in T2DM patients.

Conclusions. We conclude that the ε2/ε3 genotype might contribute to the increased risk for developing IS in Chinese patients with T2DM.

1. Introduction

China has the highest number of diabetes in the world. According to the International Diabetes Federation (IDF) report, there were 116 million Chinese diagnosed with diabetes in 2019, and the number will increase to 141 million by 2030 [1]. Ischemic stroke (IS) is a cerebrovascular complication of type 2 diabetes mellitus (T2DM) due to accelerated atherosclerosis and carotid artery disease development [2]. Both macrovascular and microvascular systems of the brain are severely affected in T2DM [3]. T2DM exacerbates ischemic brain injury and worsens functional outcome after stroke [4]. Patients with T2DM have a two- to four-fold increase in the risk of IS compared with the general population [5, 6]. Moreover, stroke patients with diabetes have a poor prognosis after stroke onset [7]. Thus, it is of great importance to investigate the risk factors of T2DM patients complicated with IS.

Mounting evidence indicates that the apolipoprotein E (APOE) gene located at chromosome 19q13.32 is a candidate gene in the development of T2DM and IS [8–10]. The protein encoded by the APOE gene consists of 299 amino acid residues and contains amphipathic α-helical lipid-binding structural domains which enable APOE to interact with members of the low-density lipoprotein receptor family. Through the interaction, APOE plays an essential role in lipid transport in both plasma and brain [11]. The dysregulation of the APOE expression and genetic variance of the APOE influence the APOE functions and lead to the pathogenesis of nervous and cardiovascular diseases eventually [11–13]. The common gene variants, epsilon-2 (ε2), epsilon-3 (ε3), and epsilon-4 (ε4), are generated by the two single-nucleotide polymorphisms (SNPs) rs7412 (C/T) and rs429358 (C/T) in exon 4 of the APOE gene. The variants are different haplotypes of the APOE gene generated by the combination of the two SNPs at the APOE locus [14]. The most common allele iso-
form is ε3 with a frequency of 70-80%. The ε2 and ε4 have a frequency of 5-10% and 10-15%, respectively [15]. The 3 alleles of the APOE gene form 6 genotypes (ε2/ε2, ε2/ε3, ε2/ε4, ε3/ε3, ε3/ε4, ε4/ε4) [16]. The ε3/ε3 is the most common genotype with a frequency of approximately 67% [8]. The frequencies of ε3/ε4 and ε2/ε3 are lower than those of ε3/ε3, and ε2/ε2, ε4/ε4, and ε2/ε4 genotypes have the lowest frequencies [17].

Understanding the risk factors of T2DM patients complicated with IS may shed light into intervening the development of complications of T2DM. So far, studies on the association of APOE polymorphisms and IS risks in Chinese patients with T2DM are lacking. Thus, this study is designed to elucidate whether the APOE gene polymorphism is an essential determinant of Chinese patients with T2DM complicated with IS.

2. Materials and Methods

2.1. Subjects. A case-control study was carried out from July 2015 to July 2018. Informed consent was obtained from all enrolled subjects, and the design protocol was approved by the Ethics Committee of China-Japan Friendship Hospital. The data of the families, their medical history, and smoking habits of the patients was obtained by a questionnaire. Clinical examination including measurement of systolic blood pressure (SBP) and diastolic blood pressure (DBP) was applied. Anthropometric data (weight and height) were collected and used for BMI calculation. Hypertension was defined by clinical symptoms or signs, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²).

2.2. DNA Isolation and APOE Genotyping. Blood samples were collected in vacuum tubes and stored at -20°C until processed. DNA was extracted from each blood sample using the genomic DNA purification kit (Xi’an Tianlong Science and Technology Co., Ltd., Xi’an, Shaanxi, China). The concentration of DNA was quantified using a NanoDrop 1000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA). Three APOE alleles (ε2, ε3, and ε4) were detected by an APOE Genotyping Kit (Sinochips Bioscience Co., Ltd., Zuhuai, Guangdong, China). Polymorphic alleles were identified by the fluorescence intensity of the hybridization sites.

2.3. Biochemical Analysis. Plasma levels of fasting TG, TC, LDL-C, and HDL-C were measured using the AU5800 automated biochemical analyzer (Beckman Coulter, Brea, CA, USA). HbA1c was detected using the D-10 Hemoglobin Testing System (Bio-Rad, Hercules, CA, USA).

2.4. Statistical Analysis. The data were statistically analyzed using SPSS version 24.0 software (IBM, Chicago, IL, USA). Quantitative data were expressed as mean values ± standard deviation (SD). Normally distributed data were compared using Student’s t-test. The significance of differences in the proportion of patients with a history of hypertension between the two groups was tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²). The differences in the distribution frequencies of genotype and allele between the two groups, and the deviations from Hardy-Weinberg equilibrium were tested by the chi-square test (χ²).

3. Results

3.1. General Characteristics and Biochemical Variables of the Patients. 210 T2DM patients complicated with IS and 243 age- and sex-matched controls from the same demographic area were included in this study. Table 1 presents the general characteristics and biochemical variables of the patients in the control and the IS groups. No statistically significant differences were observed between the groups in age, gender, BMI, smoking, diabetes duration, HbA1c level, and plasma lipid level (P > 0.05). However, SBP, DBP, and the proportion of patients with a history of hypertension were higher in the IS group than in the control group (P < 0.05).

3.2. APOE Genotype and Allele Distribution Frequencies in the IS and the Control Groups. The APOE genotype distribution in the IS and the control groups were in Hardy-Weinberg equilibrium (P > 0.05). Distribution frequencies of the 6 genotypes and 3 alleles of APOE in the IS and the control groups are summarized in Table 2.
We observed that SBP, DBP, and the proportion of patients with a history of hypertension were higher in the IS group than in the control group. We also found that the ε2/ε3 genotype was an independent risk factor for developing IS in T2DM patients. SBP and history of hypertension were also independent risk factors for developing IS in T2DM patients after adjusting for age, gender, BMI, SBP, DBP, history of hypertension, smoking habits, diabetes duration, HbA1c, TG, TC, LDL-C, HDL-C, and history of dyslipidemia.

A prospective population-based study, with approximately 20-year follow-up, evaluated the effect of T2DM on cardiovascular disease in 13105 samples. The study revealed an increased relative risk for developing stroke of 1.5 to 6.5 fold in T2DM individuals [20]. The increased risk is seen even after early diagnosis. It is reported that the risk of stroke in newly treated patients with T2DM is 9.1% within the first 5 years. The stroke rate is double that of the general population [21]. Many studies have indicated that T2DM patients have residual neurological deficits and a worse functional outcome, along with worse long-term mortality [7, 22]. Therefore, patients and physicians need to aggressively control cardiovascular risk factors soon after T2DM diagnosis. The identification of susceptibility genes and other risk factors would be helpful for the management of IS in T2DM patients.

APOE gene is one of the most widely studied candidate genes of T2DM. In a case-control study recruiting of 451 Thais, it has been demonstrated that ε4 allele containing genotypes were the predictors of T2DM [23]. A meta-analysis of 30 studies including 5423 case patients and 8197 controls suggests that ε2 allele is associated with increased risk of T2DM [8]. Besides, the relation between APOE gene polymorphisms and IS has been intensively investigated in many studies. Most findings suggest that ε4 allele increases the odds of IS [24–26]. However, little is known about the link between APOE gene polymorphisms and developing IS in T2DM patients. So far, there is only one study conducted on the issue. The study displayed that APOE gene polymorphisms were not linked with IS in T2DM patients [27]. However, we found that T2DM patients who carried the ε2/ε3 genotype were at 1.90-fold increased risk to develop IS in the present study. After adjustment for other established risk factors, ε2/ε3 was an independent risk factor for developing IS in T2DM patients (Table 4).

4. Discussion

Many studies showed that patients suffering from T2DM are at a higher risk for IS than individuals without T2DM [4, 20]. Thus, it is essential to explore the predisposing risk factors for IS among T2DM patients. We carried out a case-control study to investigate the association of the APOE gene polymorphisms and risks of IS in Chinese patients with T2DM.

### Table 1: Demographic, clinical, and biochemical data of the IS and the control groups.

<table>
<thead>
<tr>
<th></th>
<th>IS (n = 210)</th>
<th>Control (n = 243)</th>
<th>P value</th>
</tr>
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<tbody>
<tr>
<td>Age (years)</td>
<td>65.41 ± 8.20</td>
<td>64.58 ± 10.21</td>
<td>0.338</td>
</tr>
<tr>
<td>Gender (male %)</td>
<td>47.62</td>
<td>52.26</td>
<td>0.324</td>
</tr>
<tr>
<td>BMI (kg/mm²)</td>
<td>25.29 ± 3.98</td>
<td>25.75 ± 3.19</td>
<td>0.175</td>
</tr>
<tr>
<td>SBP (mmHg)</td>
<td>142.67 ± 19.41</td>
<td>133.98 ± 18.63</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>DBP (mmHg)</td>
<td>81.64 ± 10.17</td>
<td>78.17 ± 10.67</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Hypertension (%)</td>
<td>84.28</td>
<td>70.20</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td>Smokers (%)</td>
<td>18.57</td>
<td>17.70</td>
<td>0.809</td>
</tr>
<tr>
<td>Diabetes duration (years)</td>
<td>14.44 ± 6.09</td>
<td>15.10 ± 8.32</td>
<td>0.332</td>
</tr>
<tr>
<td>IS duration (years)</td>
<td>3.65 ± 2.10</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>HbA1c (%)</td>
<td>7.66 ± 1.72</td>
<td>7.96 ± 1.88</td>
<td>0.084</td>
</tr>
<tr>
<td>HbA1c (mmol/mol)</td>
<td>60.25 ± 18.81</td>
<td>63.45 ± 20.59</td>
<td>0.084</td>
</tr>
<tr>
<td>TG (mmol/L)</td>
<td>1.88 ± 1.62</td>
<td>2.00 ± 1.46</td>
<td>0.433</td>
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<tr>
<td>TC (mmol/L)</td>
<td>4.20 ± 1.24</td>
<td>4.24 ± 1.14</td>
<td>0.697</td>
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<tr>
<td>LDL-C (mmol/L)</td>
<td>2.48 ± 0.95</td>
<td>2.52 ± 0.99</td>
<td>0.666</td>
</tr>
<tr>
<td>HDL-C (mmol/L)</td>
<td>1.05 ± 0.33</td>
<td>1.04 ± 0.31</td>
<td>0.880</td>
</tr>
<tr>
<td>Dyslipidemia (%)</td>
<td>64.29</td>
<td>64.20</td>
<td>0.984</td>
</tr>
</tbody>
</table>

3.3. Association of APOE Gene Polymorphisms and IS. The univariate analysis was used to evaluate the association from the perspective of the genotype and allele frequencies of APOE gene polymorphisms. The genotype of ε2/ε3 increased the risk of IS in T2DM patients, with unadjusted OR 1.901 (95% CI 1.117-3.297, P = 0.0179), while the genotype of ε3/ε4 showed no association with IS in T2DM patients, with unadjusted OR 1.629 (95% CI 0.943-2.756, P = 0.0694) (Table 3). The results displayed no significant difference in APOE gene allele frequencies between the two groups (Table 3). After being adjusted for age, gender, BMI, SBP, DBP, history of hypertension, smoking habits, diabetes duration, HbA1c, TG, TC, LDL-C, HDL-C, and history of dyslipidemia using multivariable binary logistic regression analysis as shown in Table 4, the ε2/ε3 genotype was an independent risk factor for developing IS in T2DM patients, with adjusted OR 2.225 (95% CI 1.244-3.980, P = 0.007). However, the genotype of ε3/ε4 was not found to be an independent risk factor for developing IS in T2DM patients, with adjusted OR 1.727 (95% CI 0.978-3.049, P = 0.060) (Table 4). SBP (95% CI 1.004-1.031, P = 0.013) and history of hypertension (95% CI 1.089-3.045, P = 0.022) were also independent risk factors for developing IS in T2DM patients (Table 4).
pressure management is a core issue for mitigating the development of IS in T2DM patients.

There are some limitations in our study which require further investigation. Firstly, the replicability of the data needs to be verified in a larger sample size involving different ethnic groups. Secondly, our study is inadequate in proving the causal relationship but merely an association research due to the study design of case-control. However, our findings indeed contribute to risk prediction for IS in T2DM patients. The genotype ε2/ε3 of APOE is possibly a genetic predisposition factor for IS in T2DM patients. Furthermore, it is of great significance to control the blood pressure for T2DM patients to avoid IS onset.

5. Conclusions

Our study indicates that the APOE gene polymorphisms are associated with the development of IS in T2DM patients. We also identify ε2/ε3 genotype, SBP, and history of hypertension as independent risk factors in the development of IS in T2DM patients.

This study provides data that may help to improve the ability to identify diabetic individuals at increased risk for IS and improve the clinical management of patients with T2DM.

Data Availability

The data used to support the findings of this study are available from the corresponding authors upon request.

Conflicts of Interest

The authors declared no conflict of interest.

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References


