Original Article CX3CR1 polymorphisms and the risk of age-related macular degeneration

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Abstract: Background: Age-related macular degeneration (AMD), a most common eye disease, can lead to irreversible visual impairment. Age, genetic and environmental factors have been implicated in AMD. Chemokine (C-X3-C motif) receptor 1 (CX3CR1) gene polymorphisms could influence the susceptibility of AMD. Methods: We tested the association between AMD and single nocleotide polymorphisms (SNPs) of CX3CR1 gene (rs3732378 and rs3732379) in 102 cases and 115 controls from China. Genotypes were determined by MassArray genotyping assay method. Association between CX3CR1 gene polymorphisms and AMD were examined by x² test and logistic regression. Results: Genotype distribution of CX3CR1 gene polymorphisms were in accordance with HWE examination. No obvious differences were observed in the genotypes of rs3732378 polymorphism between case and control groups (P>0.05), but A allele of it could increase the risk of AMD (P=0.025, OR=2.391, 95% CI=1.092-5.237). Both TT genotype and T allele of rs3732379 were significantly associated with the susceptibility of AMD (P=8.663, OR=8.663, 95% CI=1.044-71.874; P=0.021, OR=2.076, 95% CI=1.104-3.903). Age, gender and smoking status were used as common confounders to adjust the association between CX3CR1 gene polymorphism and AMD risk. Then we found that rs3732378 had no obvious association with AMD susceptibility. TT genotype of rs3732379 related to the occurrence of AMD, but the association was not significant (P=0.050, OR=8.274, 95% CI=1.002-69.963). T allele of rs3732379 might increase the susceptibility of AMD (P=0.029, OR=2.033, 95% CI=1.077-3.838). Conclusion: T allele of rs3732379 might have a positive association with the susceptibility of AMD.

Keywords: Age-related macular degeneration, CX3CR1 gene, polymorphisms

Introduction

Age-related macular degeneration (AMD) is the common eye disease which will lead to decreased vision even blindness in the elderly in developed countries [1, 2]. AMD is a progressive irreversible disorder of the central macular region of the retina, and categorized into early and late two stages. The development of drusen between retinal pigment epithelium (RPE) and underlying choroid is a harbinger of early AMD [3]. In early stage the symptoms of AMD are inconspicuous [4]. Drusen size and quantity have positive correlation with the risk of AMD [5]. AMD has dry and wet two forms. Dry AMD is characterized by geographic atrophy (GA) of RPE, and wet AMD result from abnormal choroidal neovascularization (CNV) in choriocapillaris. Few personal and environmental risk factors, aside from age have been identified for AMD. Some studies suggested that family history [6, 7], oxidative stress [8], lifestyle [9, 10], obesity [11], cytokines and their receptors [12, 13] may cause changes in the development of AMD.

Chemokine (C-X3-C motif) receptor 1 (*CX3CR1*), a receptor of chemokine, might implicate in macular degeneration development [14]. It was reported that *CX3CR1* protein level showed a significant alteration in AMD patients [15]. However, the genetic basis and molecular mechanism of *CX3CR1* in the occurrence and progression of AMD were unclear. Many efforts have been made to identify the mechanism of *CX3CR1* that can be used to forecast the probability of the onset of AMD. Several single nucleotide polymorphisms (SNPs) of *CX3CR1* gene have been discovered [16, 17]. However, most of the studies were focused on European descent. Because the distributions of genetic

	Case n=102	Control n=115	P value					
Status								
No AMD		115						
Wet AMD	65	-						
Dry AMD	16	-						
Mixed AMD	21	-						
Age (Mean ± SD)	66.17 ± 10.08	68.93 ± 10.59	0.051					
Gender			0.897					
Male	55	61						
Female	47	54						
Smoking			0.796					
Never	72	83						
Current or past	30	32						

variants exist distinction among ethnic groups, these SNPs of *CX3CR1* gene need to be tested in different ethnic groups.

In this study, we recruited AMD patients and healthy controls in Shandong Provincial Qianfushan Hospital and selected the rs3732378 (T280M) and rs3732379 (V249I) SNPs in *CX3CR1* gene to detect the association of *CX3CR1* gene and the susceptibility of AMD.

Methods

Study participants

This was a case-control designed study, and was approved by the ethic committee of Shandong Provincial Qianfoshan Hospital. Each participator signed the written informed consent form. 102 AMD patients and 115 age and gender-matched healthy controls were recruited from Shandong Provincial Qianfoshan Hospital. Participants were all older than 50 years. All subjects were diagnosed by two ophthalmologists and conducted a full ophthalmic examination. Independent grading of fundus photographs were used to confirm their disease status. Clinical diagnoses and categorization followed the guideline of National Eye Institute Age-Related Eye Disease Study [18]. Individuals had any eye disease were excluded from control group. All procedures were according to the principles of the Declaration of Helsinki. Demographic information of participants was listed in Table 1.

Genotyping

Genomic DNA was extracted from 1 ml peripheral blood of each fasting participant using a

TIANamp Blood DNA Kit (TianGen, China). The samples were genotyped by Mass-ARRAY method using a MassARRAY Analyzer 4 system (Sequenom, San Diego, CA, USA), according to the manufacturer's instructions.

Statistic analysis

All of the calculations were conducted by SPSS 18.0. We examined allele distributions of each SNP and Hardy-Weinberg equilibrium (HWE) using Chi square test in cases and controls. Difference of age between case and control groups was assessed by t test. Other demographic features were compared by χ^2 test between two groups. All the comparisons were adjusted for age, gender and smoking status by logistic regression. Odds ratios (ORs) and their corresponding 95% confidence intervals (95% CI) were used to evaluate the association strength between CX3CR1 gene and AMD risk. P value less than 0.05 was considered to be statistically significant.

Results

Subject features and HWE test

As **Table 1** shows, individual characteristics had no significant difference between case and control groups. In order to evaluate the role of *CX3CR1* gene in AMD, we recorded the genotype distribution of *CX3CR1* gene polymorphisms (rs3732378 and rs3732379) in case and control groups. The distribution frequencies of *CX3CR1* gene polymorphisms did not deviate from HWE in control group.

Association of CX3CR1 gene polymorphisms and AMD risk

Table 2 has showed the genotype distributions of rs3732378 polymorphism had no significant difference between case and control groups. A allele frequency of rs3732378 was significantly higher in cases than that in controls, which might relate to the susceptibility of AMD (P=0.025, OR=2.391, 95% CI=1.092-5.237). No significant difference was observed in TC genotype of rs3732379 between case and control groups. Genotype distribution of rs3732379 TT genotype was significantly associated with AMD risk (P=8.663, OR=8.663, 95% CI = 1.044-71.874). Meanwhile T allele frequency of

SNP	Case n=102 (%)	Control n=115 (%)	P value	OR (95% CI)	P* value	OR (95% CI)*
Rs3732378						
GG	85 (83.33)	106 (92.17)	-	-		-
GA	14 (13.73)	8 (6.96)	0.088	2.182 (0.875-5.445)	0.909	2.293 (0.879-5.980)
AA	3 (2.94)	1 (0.87)	0.225	3.741 (0.382-36.616)	0.344	3.073 (0.301-31.401)
G	184 (90.20)	220 (95.65)	-	-		-
А	20 (9.80)	10 (4.35)	0.025	2.391 (1.092-5.237)	0.065	2.157 (0.953-4.880)
Rs3732379						
CC	80 (78.43)	99 (86.09)	-	-		-
СТ	15 (14.71)	15 (13.04)	0.589	1.238 (0.571-2.683)	0.622	1.217 (0.557-2.658)
TT	7 (6.86)	1 (0.87)	0.018	8.663 (1.044-71.874)	0.050	8.274 (1.002-69.963)
С	175 (85.78)	213 (92.61)	-	-		-
Т	29 (14.22)	17 (7.39)	0.021	2.076 (1.104-3.903)	0.029	2.033 (1.077-3.838)

Table 2. Genotype distributions of rs3732378 and rs3732379 SNPs of CX3CR1 gene

Notes: *adjusted by age, gender and smoking status.

rs3732379 also higher in cases, and the allele might increase the risk of AMD (P=0.021, OR=2.076, 95% CI=1.104-3.903).

Adjusted result about the association of CX3CR1 gene polymorphisms and AMD risk

In order to get an accurate result, we took age, gender and smoking status as common confounders in the analysis of the association between *CX3CR1* genotype and AMD risk. Adjusted results indicated that the rs3732378 polymorphism not relate to AMD susceptibility (*P*>0.05). Although the TT genotype of rs3732379 may increase the risk of AMD but the relation was not significant (*P*=0.05, OR=8.274,95% CI=1.002-69.963). Additionally, T allele of rs3732379 might increase the AMD risk (*P*=0.029, OR=2.033, 95% CI= 1.077-3.838).

Discussion

AMD is a degenerative change of the eye, usually affect elder adults in developed countries. This disease is a common cause of visual impairment. AMD mainly influence retina, choroid and Bruch's membrane. As a complex disease, AMD derive from genetic and environmental factors [19, 20], and genetic factors play a substantial role [21]. Accumulation of microglial cell (MC) in subretinal space might evoke cardinal characteristics of AMD [17]. No positive *CX3CR1* protein was detected in retina in healthy MC [17]. *CX3CR1* gene might implicate in the pathogenesis of AMD. *CX3CR1* gene locates in chromosome 3p21.3, and has 5 exons. As the third generation genetic marker, SNP plays an important role in the exploration of the pathogenesis of many disease.

In order to understand the mechanism by which *CX3CR1* gene may contribute to the development of AMD, we analyzed the *CX3CR1* gene polymorphisms. T280M (rs3732378) and V2491 (rs3732379) were widely researched SNPs of *CX3CR1* gene. It was reported that the two polymorphisms were associated with the risk of AMD in USA cohort [22]. However, there were very few studies focused on Chinese lineage. The distribution of SNP had a difference among different ethnicity and region. So we genotyped the rs3732378 and rs3732379 polymorphisms of *CX3CR1* gene in Chinese Han AMD patients.

In this study, we observed association between CX3CR1 gene polymorphisms (rs3732378 and rs3732379) and AMD. There was no significant difference in the genotype distributions of rs3732378 between case and control groups. But A allele of rs3732378 was obviously increased the risk of AMD with the OR of 2.391. However, the age, gender and smoking status adjusted genotype and allele analysis of rs3732378 had no significant association with the development of AMD. Additionally, TC genotype of rs3732379 did not related to AMD risk. Both TT genotype and T allele of rs3732379 were significantly associated with the susceptibility of AMD, and might 8.663 and 2.076 times increase the AMD risk. After adjusted by age,

gender and smoking status, TT genotype of rs3732379 was not significantly associated with the risk of AMD. T allele of rs3732379 related to the risk of AMD as before, with the OR of 2.033. The results showed that rs3732379 mutation in *CX3CR1* gene is associated with the susceptibility of AMD, and we failed to find association of rs3732378 SNP of *CX3CR1* gene with AMD risk.

The results of present study are partially in accordance with previous study which suggested that V249I had approximately 2.928 times increased risk of dry AMD in Greek [16]. In another study, it reported that both rs3732378 and rs3732379 were found to be with an increased incidence of AMD in Chinese population [23], the same result also detected in another study in USA [22]. In contrast, a study performed by Combadière et al. indicated that A allele of rs3732378 was associated with an increased risk of AMD, but V249I polymorphism had no significant influence on the occurrence of AMD [17]. However, Debra et al. demonstrated that both rs3732378 and rs3732379 had no significant association with the development of AMD in USA after adjusted multiple factors [24].

In summary, polymorphisms of CX3CR1 gene had a positive association with the risk of AMD. However, a limitation of this study was notably. Frequencies of minor allele of rs3732378 and 3732379 of CX3CR1 gene were much lower in Chinese than that in American [25]. So it should be noted that the sample size of this study was not large enough to detect the potential role of variant alleles of CX3CR1 gene polymorphisms in the development of AMD. Nevertheless, the strengths of our study are as follows: firstly, the participators were selected randomly, therefore the potential selection bias may be diminished; secondly, all of the results were adjusted, so it was more accurate. However, the result was also insufficient to understand the mechanism of CX3CR1 gene in AMD, and further study was necessary.

Disclosure of conflict of interest

None.

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