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A novel polymorphism of the GP78 gene is associated with coronary artery disease in Han population in China

Erdenbat Cha^{1†}, Zhen-Yan Fu^{1†}, Yi-Tong Ma^{1*}, Qing Zhu¹, Xiang Xie¹ and Fen Liu²

Abstract

Background: GP78 is a membrane-anchored ubiquitin ligase mediating the degradation of 3-hydroxy-3-methylglutaryl-CoA coenzyme A reductase (HMGCR) and Insig-1, which was very essential for the synthesis of cholesterol process. Cholesterol levels have a causal role in the development of cardiovascular disease. The aim of the present study was to assess the association between the human gp78 gene polymorphism and coronary artery disease (CAD) in a Han and Uygur population of China.

Methods: We used two independent case-control studies: a Han population (602 CAD patients and 572 control subjects) and a Uygur population (374 CAD patients and 376 control subjects). All CAD patients and controls were genotyped for the same three single nucleotide polymorphisms (SNPs) (rs731119, rs2617849 and rs2440472) of gp78 gene by a Real-time PCR instrument.

Results: In the Han population, for total and men, the distribution of SNP3 (rs2440472) alleles and the dominant model (AA vs AG + GG) and recessive model (GG vs AG + AA) showed a significant difference between CAD and control participants (for allele: $P = 0.003$ and $P = 0.002$, respectively; for dominant model: $P = 0.041$ and $P = 0.026$, respectively; for recessive model: $p = 0.004$ and $p = 0.004$, respectively). The significant difference in both the two models was retained after adjustment for covariates (for dominant model OR: 0.760, 95% confidence interval [CI]: 0.584-0.99, $P = 0.042$; OR: 0.686, 95% CI: 0.498-0.946, $P = 0.022$, respectively; for recessive model OR: 1.451, 95% CI: 1.067-1.974, $P = 0.018$; OR: 1.789, 95% CI: 1.219-2.627, $P = 0.000$). Our data was also assessed via haplotype-based case-control studies. For the Han population, for total, The G-T-G haplotype in CAD was significantly higher than that in the control group ($P = 0.02$), and the G-C-A haplotype in CAD was significantly lower than that in the control group ($P = 0.0443$). And for man, the G-T-G haplotype in CAD was significantly higher than that in the control group ($P = 0.0048$).

Conclusions: The GG genotype and G allele of rs2440472 in gp78 gene could be a risk genetic marker of CAD in Han population in China.

Keyword: gp78, Single nucleotide polymorphism, Coronary artery disease, Case-control study, Haplotype

Introduction

The etiology and pathogenesis of coronary artery disease (CAD) are likely to comprise a multifactorial disorder resulting from inheritance of several susceptibility genes, as well as multiple environmental determinants [1,2]. Experimental, genetic, and epidemiologic data support the concept that an elevated plasma level of low-density

lipoprotein (LDL) cholesterol is a primary causal factor in the pathogenesis of coronary artery disease [3], a main underlying pathology is atherosclerosis, a process of cumulative deposition of LDL cholesterol in the arteries supplying blood to the heart and brain that eventually leads to impaired or absent blood supply and myocardial infarction or stroke [4]. Consistent and compelling evidence has demonstrated association between lipid concentrations and cardiovascular disease incidence worldwide [5-7]. HMGCR catalyzes the conversion of 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) to mevalonate

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that is a rate limiting step in cholesterol biosynthesis [8]. Sterol promotes the degradation of HMGCR through the ubiquitin-proteasome pathway, and therefore slows down cholesterol biosynthesis [9]. gp78 (also known as autocrine motility factor receptor [AMFR]), an ER (endoplasmic reticulum) membrane-anchored ubiquitin ligase, has been identified as the E3 that ubiquitinates HMGCR [10,11]. Through its transmembrane domain, gp78 interacts with another ER membrane protein, Insig-1 or Insig-2 [11]. When the cholesterol level is low, HMGCR is kept apart from the Insig-gp78 complex and stabilized. A high level of sterol promotes the interaction between HMGCR and Insig-1/-2, which causes the ubiquitination of HMGCR by gp78 and subsequent degradation [11]. So it has been hypothesized that gp78 may suppress cholesterol biosynthesis by targeting HMGCR to degradation. Besides HMGCR, gp78 also mediates the degradation of Insig-1 protein. Destruction of Insig-1 releases its inhibition on SREBP and stimulates the expression of lipogenic genes. Thus, gp78 has opposite effects on lipid biosynthesis [12].

Originally, gp78 was identified as the tumor autocrine motility factor receptor that mediates tumor invasion and metastasis [13,14]. The transcript for gp78 is widely expressed in a variety of tissues, and immunoblot analysis with a monoclonal antibody indicates that an increase in levels of gp78 correlates with the metastatic potential of a variety of human tumors. GP78 was very essential for the synthesis of cholesterol process. Cholesterol levels have a causal role in the development of cardiovascular disease. The aim of the present study was to assess the association between the human gp78 gene and CAD.

Methods

Ethical approval of the study protocol

This study was approved by the Ethics Committee of the First Affiliated Hospital of Xinjiang Medical University (Urumqi, China). Written informed consent was obtained from all participants. All participants explicitly provided permission for DNA analyses as well as collection of relevant clinical data. It was conducted according to the standards of the Declaration of Helsinki.

Subjects

The subjects were from a Han population and a Uygur population who lived in the Xinjiang Uygur Autonomous Region of China. All patients and controls had a differential diagnosis for chest pain encountered in the Cardiac Catheterization Laboratory of First Affiliated Hospital of Xinjiang Medical University from 2006 to 2013. All of the procedures of coronary angiography were undertaken by highly skilled physicians using the Judkins approach. The findings of coronary angiography were interpreted by at least two experienced imaging

specialists and the final diagnosis of CAD was made according to the angiography report.

We selected randomly 602 Han patients and 374 Uygur patients with CAD and a control group of 572 and 376, respectively, of ethnically and geographically matched individuals. CAD diagnosed by angiography, which was defined as the presence of at least one significant coronary artery stenosis of $\geq 50\%$ luminal diameter on coronary angiography. All control subjects also underwent a coronary angiogram and have no coronary artery stenoses and did not show clinical or electrocardiogram evidence of myocardial infarction (MI) or CAD. Control subjects were not healthy individuals, some of them have hypertension, some of them have diabetes mellitus (DM), some of them have hyperlipidemia, which means the control group were exposed to the same risk factors of CAD while the results of coronary angiogram is normal. Data and information about traditional coronary risk factors, including hypertension, DM, and smoking, were collected from all study participants. Hypertension was defined as having a systolic blood pressure above 140 mmHg or/and diastolic blood pressure above 90 mmHg or any anti-hypertensive agent used. Diabetes mellitus was diagnosed according to the criteria of the American Diabetes Association [15]. In addition, individuals with fasting plasma glucose >7.0 mmol/L or with a history of diabetes or treatment with insulin were considered diabetic. Smoking was classified as smokers (including current and ex-smokers) or non-smokers. All patients with impaired renal function, malignancy, connective tissue disease, valvular disease or chronic inflammatory disease were excluded.

Blood collection and DNA extraction

Fasting Blood samples drawn by venepuncture in the catheter-room were taken from all participants before cardiac catheterization. The blood samples were drawn into a 5 ml ethylene diamine tetraacetic acid (EDTA) tube and centrifuged at $4000 \times g$ for 5 min to separate the plasma content. Genomic DNA was extracted from the peripheral leukocytes using standard phenol-chloroform method. The DNA samples were stored at -80°C until use. While used, the DNA was diluted to 50 ng/ μL concentration.

Genotyping

The gp78 gene spans 64.08 kb, in this study using the Haploview 4.2 software and the HapMap phase II database, we identified three tag SNPs (rs731119, rs2617842 and rs2440472) by using minor allele frequency (MAF) ≤ 0.1 and linkage disequilibrium patterns with $r^2 \geq 0.5$ as a cut off. The position of the SNP1, SNP2 and SNP3 (rs731119, rs2617842 and rs2440472) was by order of increasing distance from the GP78 gene 5' end [Figure 1].

Genotyping was undertaken using the TaqMan[®] SNP Genotyping Assay (Applied Bio systems). The primers

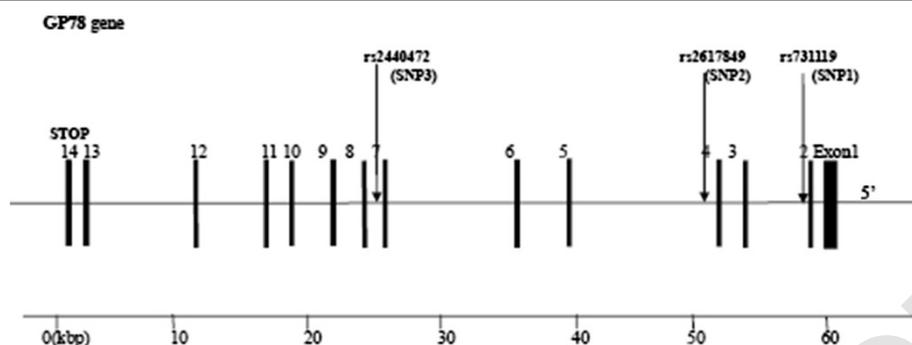


Figure 1 Structure of the human GP78 gene. This gene consists of 14 exons separated by 13 introns. Boxes indicate exons, and lines indicate introns and intergenic regions. Arrows mark the locations of polymorphisms.

and probes used in the TaqMan[®] SNP Genotyping Assays (ABI) were chosen based on information at the ABI website (<http://myscience.appliedbiosystems.com>). Thermal cycling was done using the Applied Biosystems 7900HT Standard Real-Time PCR System. Plates were read on Sequence Detection Systems (SDS) automation controller software v2.3 (ABI). PCR amplification was performed using 2.5 μ l of TaqMan Universal Master Mix, 0.15 μ l probes and 1.85 ddH₂O in a 6- μ l final reaction volume containing 1 μ l DNA. Thermal cycling conditions were as follows: 95°C for 5 min; 40 cycles of 95°C for 15 s; and 60°C for 1 min. All 96 wells Plates were read on Sequence Detection Systems (SDS) automation controller software v2.3 (ABI).

Biochemical analysis

Serum concentrations of total cholesterol (TC), triglyceride (TG), glucose (Glu), high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), Creatinine (Cr), blood urea nitrogen (BUN), were measured using standard methods in the Central Laboratory of First Affiliated Hospital of Xinjiang Medical University.

Statistical analysis

All continuous variables are expressed as means \pm standard deviation (S.D.). The difference between the CAD and Control groups was analyzed using an independent-sample T-Test. The differences in the frequencies of smoking, hypertension, diabetes mellitus, and GP78 genotypes were analyzed using χ^2 test or Fisher's exact test where appropriate. Hardy-Weinberg equilibrium was assessed by χ^2 analysis. Logistic regression analyses with effect ratios (odds ratio [OR] and 95% CI) were used to assess the contribution of the major risk factors. All statistical analyses were performed using SPSS 17.0 for Windows (SPSS Institute, Chicago, USA). P-values of less than 0.05 were considered to statistically significant.

Results

Table 1 shows the clinical characteristics of the study participants. For Han and Uygur population, there was no significant difference in age between CAD patients and control subjects it means the study was age-matched case-control study. In the Han and Uygur population, for total, men, and women, the plasma concentration of Glu, and the prevalence of essential hypertension (EH), and diabetes mellitus (DM), were significantly higher for patients with CAD than for control participants. In the Han population, for total and men, body mass index (BMI), and smoking were significantly higher for patients with CAD than for control participants. The LCL were significantly higher for patients with CAD than for control participants only in the Han population for total. In the Uygur population, for total and men the HDL were significantly lower for patients with CAD than for control participants. The smoking were significantly higher for patients with CAD than for control participants in the Uygur population for total.

Table 2 shows the distribution of genotypes and alleles of SNP1, SNP2 and SNP3 for the GP78 gene, (Table 2: Han population; Table 3: Uygur population). The genotype distributions for each of the SNPs were in agreement with the predicted Hardy-Weinberg equilibrium values (data not shown). In the Han population, for total and man, the distribution of SNP3 (rs2440472) genotypes showed a significant difference between CAD and control participants (for total: $P = 0.008$, for males: $P = 0.007$). The distribution of SNP3 (rs2440472) alleles and the dominant model (AA vs AG + GG) and recessive model (GG vs AG + AA) showed a significant difference between CAD and control participants (for allele: $P = 0.003$ and $P = 0.002$, respectively; for dominant model: $P = 0.041$ and $P = 0.026$, respectively; for recessive model: $p = 0.004$ and $p = 0.004$, respectively). G allele of rs2440472 was significantly higher in CAD patients than in control participants (total: 48.3% vs 42.2%; men: 48.1% vs 38.9%).

Table 1 Characteristics of study participants

| | Han | | | | | | | | | Uigur | | | | | | | | |
|--------------------------|---------------|------------------------|---------|---------------|----------------------|---------|---------------|------------------------|---------|---------------|------------------------|---------|---------------|----------------------|---------|---------------|------------------------|---------|
| | CAD patients | Total control subjects | p value | CAD patients | Men control subjects | p value | CAD patients | Women control subjects | p value | CAD patients | Total control subjects | p value | CAD patients | Men control subjects | p value | CAD patients | Women control subjects | p value |
| Number (n) | 602 | 572 | | 388 | 341 | | 214 | 231 | | 374 | 376 | | 279 | 225 | | 95 | 151 | |
| Age (years) | 60.94 ± 9.18 | 60.25 ± 8.37 | 0.18 | 59.60 ± 9.628 | 59.70 ± 8.905 | 0.88 | 60.18 ± 8.58 | 61.44 ± 8.38 | 0.12 | 59.24 ± 7.72 | 58.96 ± 7.28 | 0.61 | 58.79 ± 7.65 | 59.36 ± 7.24 | 0.4 | 58.97 ± 8.07 | 59.46 ± 7.97 | 0.64 |
| BMI (kg/m ²) | 27.15 ± 3.21 | 26.03 ± 2.67 | 0.000* | 26.96 ± 2.57 | 26.31 ± 3.01 | 0.002* | 25.15 ± 3.02 | 25.61 ± 3.46 | 0.14 | 26.91 ± 3.39 | 26.76 ± 4.59 | 0.61 | 27.0 ± 3.39 | 26.74 ± 4.86 | 0.48 | 26.65 ± 3.40 | 26.79 ± 4.17 | 0.77 |
| Pulse (beats/min) | 74.02 ± 8.17 | 74.62 ± 7.86 | 0.2 | 74.03 ± 8.407 | 75.28 ± 7.776 | 0.04 | 74.01 ± 7.74 | 73.65 ± 7.90 | 0.62 | 75.88 ± 10.62 | 71.33 ± 9.51 | 0.000* | 74.96 ± 10.39 | 71.25 ± 9.92 | 0.000* | 78.59 ± 10.88 | 71.44 ± 8.89 | 0.000* |
| Glu (mmol/L) | 6.24 ± 2.42 | 5.60 ± 1.65 | 0.000* | 6.03 ± 2.15 | 5.68 ± 1.73 | 0.016* | 6.62 ± 2.81 | 5.47 ± 1.50 | 0.000* | 6.11 ± 2.64 | 5.10 ± 1.79 | 0.000* | 6.11 ± 2.68 | 5.11 ± 1.82 | 0.000* | 6.13 ± 2.53 | 5.09 ± 1.76 | 0.000* |
| TG (mmol/L) | 1.97 ± 1.28 | 1.93 ± 1.33 | 0.63 | 1.94 ± 1.55 | 2.03 ± 1.42 | 0.36 | 2.02 ± 1.49 | 1.84 ± 1.54 | 0.20 | 1.95 ± 1.08 | 1.82 ± 2.41 | 0.36 | 1.92 ± 1.08 | 2.01 ± 2.99 | 0.68 | 2.05 ± 1.09 | 1.55 ± 1.08 | 0.001* |
| TC (mmol/L) | 4.27 ± 1.11 | 4.31 ± 0.98 | 0.46 | 4.12 ± 1.05 | 4.22 ± 0.95 | 0.21 | 4.52 ± 1.17 | 4.45 ± 0.99 | 0.48 | 4.30 ± 1.07 | 4.35 ± 1.11 | 0.51 | 4.20 ± 0.95 | 4.37 ± 1.24 | 0.1 | 4.60 ± 1.35 | 4.33 ± 0.89 | 0.11 |
| HDL (mmol/L) | 1.13 ± 0.36 | 1.15 ± 0.38 | 0.29 | 1.08 ± 0.33 | 1.10 ± 0.39 | 0.56 | 1.22 ± 0.38 | 1.24 ± 0.35 | 0.63 | 0.97 ± 0.43 | 1.15 ± 0.69 | 0.000* | 0.94 ± 0.28 | 1.14 ± 0.76 | 0.000* | 1.07 ± 0.71 | 1.18 ± 0.58 | 0.2 |
| LDL (mmol/L) | 2.69 ± 1.09 | 2.53 ± 0.92 | 0.009* | 2.61 ± 0.98 | 2.53 ± 0.92 | 0.33 | 2.84 ± 1.26 | 2.53 ± 0.92 | 0.04 | 2.63 ± 1.01 | 2.70 ± 0.96 | 0.34 | 2.59 ± 1.02 | 2.66 ± 0.93 | 0.48 | 2.72 ± 0.98 | 2.76 ± 1.00 | 0.8 |
| Cr (mmol/L) | 76.37 ± 23.92 | 74.06 ± 17.93 | 0.06 | 81.62 ± 24.68 | 79.36 ± 16.55 | 0.14 | 66.85 ± 19.14 | 66.18 ± 16.99 | 0.7 | 74.49 ± 23.16 | 70.54 ± 18.75 | 0.03 | 78.43 ± 21.39 | 77.43 ± 16.35 | 0.63 | 63.03 ± 24.39 | 57.99 ± 16.22 | 0.12 |
| BUN (mmol/L) | 5.33 ± 1.68 | 5.22 ± 1.73 | 0.22 | 5.42 ± 1.67 | 5.44 ± 1.65 | 0.89 | 5.18 ± 1.69 | 4.89 ± 1.78 | 0.07 | 5.29 ± 1.74 | 5.07 ± 1.53 | 0.12 | 5.27 ± 1.71 | 5.33 ± 1.475 | 0.72 | 5.33 ± 1.81 | 4.59 ± 1.52 | 0.01 |
| EH (%) | 56.9 | 46.9 | 0.001* | 54.5 | 46.0 | 0.022* | 61.2 | 48.1 | 0.005* | 52.3 | 39.6 | 0.001* | 49.3 | 37.3 | 0.007* | 61.1 | 43 | 0.006* |
| DM (%) | 26.6 | 11.7 | 0.001* | 24.0 | 14.7 | 0.002* | 31.3 | 7.4 | 0.000* | 18.8 | 6.4 | 0.000* | 18.8 | 7.1 | 0.000* | 21.1 | 5.3 | 0.000* |
| Smoke (%) | 42.6 | 35.1 | 0.00* | 69.3 | 58.1 | 0.002* | 4.2 | 1.3 | 0.06 | 44.9 | 32.4 | 0.000* | 59.9 | 53.8 | 0.17 | 1.1 | 0.7 | 0.74 |

BMI, body mass index; BUN, blood urea nitrogen; Cr, creatinine; Glu, glucose; TG, triglyceride; TC, total cholesterol; HDL, high density lipoprotein; LDL, low density lipoprotein; EH, essential hypertension; DM, diabetes mellitus. Continuous variable were expressed as mean ± standard deviation. P value of continuous variables was calculated by independent T-T test. The P value of categorical variable was calculated by Fisher's exact test. *P<0.05.

Table 2 Genotype and allele distributions in patients with CAD and control subjects (Han population)

| | | | Total | | | Men | | | Women | | |
|------------------|-----------------|------------|-------------|---------------|------------|------------|---------------|------------|------------|---------------|---------|
| | | | CAD n (%) | Control n (%) | P value | CAD n (%) | Control n (%) | P value | CAD n (%) | Control n (%) | P value |
| rs731119 (SNP1) | Genotype | G/G | 369 (60.8) | 375 (64.1) | 0.236 | 237 (61.2) | 227 (63.9) | 0.695 | 132 (60) | 148 (64.3) | 0.283 |
| | | A/A | 21 (3.5) | 26 (4.4) | | 11 (2.8) | 11 (3.1) | | 10 (4.5) | 15 (6.5) | |
| | | A/G | 217 (35.7) | 184 (31.5) | | 139 (35.9) | 117 (33) | | 78 (35.5) | 67 (29.1) | |
| | Dominant model | GG | 369 (60.8) | 375 (64.1) | 0.238 | 237 (61.2) | 227 (63.9) | 0.447 | 132 (60) | 148 (64.3) | 0.342 |
| | | AG + AA | 238 (39.2) | 210 (35.9) | | 150 (38.8) | 128 (36.1) | | 88 (40) | 82 (35.7) | |
| | Recessive model | AA | 21 (3.5) | 26 (4.4) | 0.382 | 11 (2.8) | 11 (3.1) | 0.837 | 10 (4.5) | 15 (6.5) | 0.36 |
| | | AG + GG | 572 (99.83) | 455 (100) | | 376 (97.2) | 344 (96.9) | | 210 (95.5) | 215 (93.5) | |
| | Additive model | AG | 217 (35.7) | 184 (31.5) | 0.117 | 139 (35.9) | 117 (33) | 0.447 | 78 (35.5) | 67 (29.1) | 0.342 |
| | | GG + AA | 390 (64.3) | 401 (68.5) | | 237 (61.2) | 227 (63.9) | | 132 (60) | 148 (64.3) | |
| | Allele | G | 955 (78.7) | 934 (79.8) | 0.484 | 613 (79.2) | 571 (80.4) | 0.558 | 342 (77.7) | 363 (78.9) | 0.666 |
| A | | 259 (21.3) | 236 (20.2) | | 161 (20.8) | 139 (19.6) | | 98 (22.3) | 97 (21.1) | | |
| rs2617849 (SNP2) | Genotype | T/T | 222 (39.9) | 181 (38.8) | 0.046 | 132 (37.8) | 102 (31.1) | 0.159 | 90 (43.3) | 79 (35.3) | 0.234 |
| | | C/C | 74 (13.3) | 87 (15.8) | | 49 (14) | 56 (17.1) | | 25 (12) | 31 (13.8) | |
| | | C/T | 261 (46.9) | 284 (51.4) | | 168 (48.1) | 170 (51.8) | | 93 (44.7) | 114 (50.9) | |
| | Dominant model | TT | 222 (39.9) | 181 (38.8) | 0.014* | 132 (37.8) | 102 (31.1) | 0.066 | 90 (43.3) | 79 (35.3) | 0.89 |
| | | CC + CT | 335 (60.1) | 371 (67.2) | | 217 (62.2) | 226 (68.9) | | 118 (56.7) | 145 (64.7) | |
| | Recessive model | CC | 74 (13.3) | 87 (15.8) | 0.242 | 49 (51.9) | 56 (17.1) | 0.276 | 25 (12) | 31 (13.8) | 0.574 |
| | | TT + CT | 483 (86.7) | 465 (84.2) | | 300 (86) | 272 (82.9) | | 183 (88) | 193 (86.2) | |
| | Additive model | CT | 261 (46.9) | 284 (51.4) | 0.126 | 168 (48.1) | 170 (51.8) | 0.337 | 93 (44.7) | 114 (50.9) | 0.199 |
| | | CC + TT | 296 (53.1) | 268 (48.6) | | 181 (51.9) | 158 (48.2) | | 115 (55.3) | 110 (49.1) | |
| | Allele | C | 409 (37.7) | 458 (41.5) | 0.021* | 266 (38.1) | 282 (43) | 0.068 | 143 (34.4) | 176 (39.3) | 0.135 |
| T | | 705 (63.3) | 646 (58.5) | | 432 (61.9) | 374 (57) | | 273 (65.6) | 272 (60.7) | | |
| rs2440472 (SNP3) | Genotype | A/A | 164 (27.2) | 187 (32.7) | 0.008* | 110 (28.4) | 123 (36.1) | 0.007* | 54 (25.2) | 64 (27.7) | 0.582 |
| | | G/G | 144 (23.9) | 98 (17.1) | | 95 (24.5) | 54 (15.8) | | 49 (22.9) | 44 (19) | |
| | | A/G | 294 (48.8) | 287 (50.2) | | 183 (47.2) | 164 (48.1) | | 111 (51.9) | 123 (53.2) | |
| | Dominant model | A/A | 164 (27.2) | 187 (32.7) | 0.041* | 110 (28.4) | 123 (36.1) | 0.026* | 54 (25.2) | 64 (27.7) | 0.555 |
| | | GG + AG | 438 (72.8) | 385 (67.3) | | 278 (71.6) | 218 (63.9) | | 160 (74.8) | 167 (72.3) | |
| | Recessive model | GG | 144 (23.9) | 98 (17.1) | 0.004* | 95 (24.5) | 54 (15.8) | 0.004* | 49 (22.9) | 44 (19) | 0.318 |
| | | AA + AG | 458 (76.1) | 474 (82.9) | | 293 (75.5) | 287 (84.2) | | 165 (77.1) | 187 (81) | |
| | Additive model | AG | 294 (48.8) | 287 (50.2) | 0.647 | 183 (47.2) | 164 (48.1) | 0.802 | 111 (51.9) | 123 (53.2) | 0.771 |
| | | AA + GG | 308 (51.2) | 285 (49.8) | | 205 (52.8) | 177 (51.9) | | 103 (48.1) | 108 (46.8) | |
| | Allele | A | 622 (51.7) | 661 (57.8) | 0.003* | 403 (51.9) | 410 (60.1) | 0.002* | 219 (51.2) | 251 (54.3) | 0.345 |
| G | | 582 (48.3) | 483 (42.2) | | 373 (48.1) | 272 (39.9) | | 209 (48.8) | 211 (45.7) | | |

CAD, coronary artery disease.

The P value of genotype was calculated by Fisher's exact test. *P<0.05.

And the A allele of rs2440472 was significantly lower in CAD patients than in control participants (total: 51.7% vs 57.8%; males: 51.9% vs 39.9%). The recessive model (GG vs AG + AA) of rs2440472 was significantly higher in CAD patients than in control participants (total: 23.9% vs 17.1%; men: 24.5% vs 15.8%). The dominant model (AA vs AG + GG) of rs2440472 was significantly lower in CAD patients than in control participants (total: 27.2% vs 32.7%; males: 28.4% vs 36.1%). For the Uygur population, the

distribution of the three SNPs genotypes and alleles showed no significant difference between the CAD patients and control subjects.

Table 4 shows that multiple logistic regression analyses were done with Glu, EH, DM, BMI, LDL, and smoking because these variables were the major confounding factors for CAD, (Table 4: In dominant model; Table 5: In recessive model. For total and men, the significant difference of rs2440472 in both models was retained after

Table 3 Genotype and allele distributions in patients with CAD and control subjects (Uygur population)

| | | | Total | | | Men | | | Women | | |
|------------------|-----------------|---------|------------|---------------|---------|------------|---------------|---------|------------|---------------|---------|
| | | | CAD n (%) | Control n (%) | P value | CAD n (%) | Control n (%) | P value | CAD n (%) | Control n (%) | P value |
| rs731119 (SNP1) | Genotype | G/G | 269 (63) | 244 (64.4) | 0.811 | 202 (62.7) | 146 (63.8) | 0.873 | 67 (63.8) | 98 (65.3) | 0.968 |
| | | A/A | 18 (4.2) | 18 (4.7) | | 12 (3.7) | 10 (4.4) | | 6 (5.7) | 8 (5.3) | |
| | | A/G | 140 (32.8) | 117 (30.9) | | 108 (33.5) | 73 (31.9) | | 32 (30.5) | 44 (29.3) | |
| | Dominant model | GG | 269 (63) | 244 (64.4) | 0.684 | 202 (62.7) | 146 (63.8) | 0.806 | 67 (63.8) | 98 (65.3) | 0.802 |
| | | AG + AA | 158 (37) | 135 (35.6) | | 120 (37.3) | 83 (36.2) | | 38 (36.2) | 52 (34.7) | |
| | Recessive model | AA | 18 (4.2) | 18 (4.7) | 0.714 | 12 (3.7) | 10 (4.4) | 0.705 | 6 (5.7) | 8 (5.3) | 0.895 |
| | | AG + GG | 409 (95.8) | 361 (95.3) | | 310 (96.3) | 219 (95.6) | | 99 (94.3) | 142 (94.7) | |
| | Additive model | AG | 140 (32.8) | 117 (30.9) | 0.56 | 108 (33.5) | 73 (31.9) | 0.682 | 32 (30.5) | 44 (29.3) | 0.844 |
| | | GG + AA | 287 (67.2) | 262 (69.1) | | 214 (66.5) | 156 (68.1) | | 73 (69.5) | 106 (70.7) | |
| | Allele | G | 678 (79.4) | 605 (79.8) | 0.833 | 512 (79.5) | 365 (79.7) | 0.938 | 166 (79) | 240 (80) | 0.793 |
| | | A | 176 (20.6) | 153 (20.2) | | 132 (20.5) | 93 (20.3) | | 44 (21) | 60 (20) | |
| rs2617849 (SNP2) | Genotype | T/T | 152 (39.7) | 128 (35.4) | 0.576 | 120 (42.6) | 78 (36.1) | 0.346 | 32 (31.7) | 50 (34.2) | 0.869 |
| | | C/C | 57 (14.9) | 58 (16) | | 36 (12.8) | 31 (14.4) | | 21 (20.8) | 27 (18.5) | |
| | | C/T | 174 (45.4) | 176 (48.6) | | 126 (44.7) | 107 (49.5) | | 48 (47.5) | 69 (47.3) | |
| | Dominant model | TT | 152 (39.7) | 128 (35.4) | 0.223 | 120 (42.6) | 78 (36.1) | 0.145 | 32 (31.7) | 50 (34.2) | 0.674 |
| | | CC + CT | 231 (60.3) | 234 (64.6) | | 162 (57.4) | 138 (63.9) | | 69 (68.3) | 96 (65.8) | |
| | Recessive model | CC | 57 (14.9) | 58 (16) | 0.667 | 36 (12.8) | 31 (14.4) | 0.607 | 21 (20.8) | 27 (18.5) | 0.653 |
| | | TT + CT | 326 (85.1) | 304 (84) | | 246 (87.2) | 185 (85.6) | | 80 (79.2) | 119 (81.5) | |
| | Additive model | CT | 174 (45.4) | 176 (48.6) | 0.384 | 126 (44.7) | 107 (49.5) | 0.282 | 48 (47.5) | 69 (47.3) | 0.967 |
| | | CC + TT | 209 (54.6) | 186 (51.4) | | 156 (55.3) | 109 (50.5) | | 53 (52.5) | 77 (52.7) | |
| | Allele | C | 288 (37.6) | 292 (40.3) | 0.279 | 198 (35.1) | 169 (39.1) | 0.193 | 90 (44.6) | 123 (42.1) | 0.592 |
| | | T | 478 (62.4) | 432 (59.7) | | 366 (64.9) | 263 (60.9) | | 112 (55.4) | 169 (57.9) | |
| rs2440472 (SNP3) | Genotype | A/A | 85 (22.7) | 78 (20.7) | 0.269 | 57 (20.4) | 43 (19.1) | 0.316 | 28 (29.5) | 35 (23.2) | 0.513 |
| | | G/G | 120 (32.1) | 106 (28.2) | | 94 (33.7) | 64 (28.4) | | 26 (27.4) | 42 (27.8) | |
| | | A/G | 169 (45.2) | 192 (51.1) | | 128 (45.9) | 118 (52.4) | | 41 (43.2) | 74 (49) | |
| | Dominant model | A/A | 85 (22.7) | 78 (20.7) | 0.51 | 57 (20.4) | 43 (19.1) | 0.712 | 28 (29.5) | 35 (23.2) | 0.271 |
| | | GG + AG | 289 (77.3) | 298 (79.3) | | 222 (79.6) | 182 (80.9) | | 67 (70.5) | 116 (76.8) | |
| | Recessive model | GG | 120 (32.1) | 106 (28.2) | 0.245 | 94 (33.7) | 64 (28.4) | 0.207 | 26 (27.4) | 42 (27.8) | 0.939 |
| | | AA + AG | 254 (67.9) | 270 (71.8) | | 185 (66.3) | 161 (71.6) | | 69 (72.6) | 109 (72.2) | |
| | Additive model | AG | 169 (45.2) | 192 (51.1) | 0.107 | 128 (45.9) | 118 (52.4) | 0.143 | 41 (43.2) | 74 (49) | 0.371 |
| | | AA + GG | 205 (54.8) | 184 (48.9) | | 151 (54.1) | 107 (47.6) | | 54 (56.8) | 77 (51) | |
| | Allele | A | 339 (45.3) | 348 (46.3) | 0.71 | 242 (43.4) | 204 (45.3) | 0.533 | 97 (51.1) | 144 (47.7) | 0.467 |
| | | G | 409 (54.7) | 404 (53.7) | | 316 (56.6) | 246 (54.7) | | 93 (48.9) | 158 (52.3) | |

CAD, coronary artery disease.

The P value of genotype was calculated by Fisher's exact test. *P<0.05.

adjustment for Glu, EH, DM, BMI, LDL, and smoking in Han population (for dominant model OR: 0.760, 95% confidence interval [CI]: 0.584-0.99, P = 0.042; OR:0.686, 95% CI: 0.498-0.946, P = 0.022, respectively; for recessive model OR:1.451, 95% CI: 1.067-1.974, P = 0.018; OR:1.789, 95% CI: 1.219-2.627, P = 0.000, respectively).

Table 6 shows the patterns of linkage disequilibrium in the GP78 gene with their |D'| and r² values. All three

SNPs were located in one haplotype block because all the |D'| values were >0.5. r² values of the three SNPs were all <0.5, it means the three SNPs can not replace each other [16,17]. We then used the three SNPs to establish haplotypes in Han subjects in order of SNP1-SNP2-SNP3.

Table 7 shows the distribution of haplotypes in CAD patient and control participants. We found eight haplotypes

Table 4 Multiple logistic regression analysis for CAD patients and control subjects of Han population in dominant model

| | Total | | | Men | | | Women | | |
|--------------------------------|-------|-------------|--------|-------|-------------|--------|-------|-------------|--------|
| | OR | 95% CI | P | OR | 95% CI | P | OR | 95% CI | P |
| Dominant model (AA vs AG + GG) | 0.76 | 0.584–0.99 | 0.042* | 0.686 | 0.498–0.946 | 0.022* | 1.027 | 0.64–1.647 | 0.913 |
| Glu | 1.1 | 1.027–1.178 | 0.006* | 1.062 | 0.974–1.158 | 0.172 | 1.152 | 1.021–1.299 | 0.021 |
| BMI | 1.134 | 1.086–1.183 | 0.000* | 1.099 | 1.039–1.162 | 0.001* | 1.182 | 1.103–1.267 | 0.000* |
| EH | 1.307 | 1.024–1.669 | 0.032* | 1.244 | 0.918–1.685 | 0.159 | 1.377 | 0.9–2.106 | 0.14 |
| LDL | 1.131 | 1.002–1.277 | 0.046* | 1.045 | 0.891–1.225 | 0.59 | 1.311 | 1.075–1.6 | 0.008* |
| DM | 2.185 | 1.542–3.098 | 0.000* | 1.637 | 1.07–2.505 | 0.023* | 4.265 | 2.239–8.123 | 0.000* |
| Smoking | 1.657 | 1.295–2.12 | 0.000* | 1.674 | 1.223–2.291 | 0.001* | 2.259 | 0.516–9.895 | 0.28 |

EH, essential hypertension; DM, diabetes mellitus; CAD, coronary artery disease; BMI, body mass index; Glu, glucose; LDL, low density lipoprotein.
 *P<0.05.

in all subjects. The overall distribution of the haplotypes were significantly different between the CAD patients and the control subjects (all P = 0.001). For total and male, the frequency of the 001(G-T-G) haplotype was significantly higher for CAD patients than for control subjects (P = 0.02 and P = 0.0048). In addition, the frequency of the 010 (G-C-A) haplotype was lower in the CAD patients than in the control subjects in total (P = 0.0443).

Table 8 shows the distribution of genotypes and alleles of SNP1, SNP2 and SNP3 for the GP78 gene between the Han and Uyghur populations. In the CAD group, for total and man, the distribution of SNP3 (rs2440472) genotypes and allele showed a significant difference between Han and Uyghur population (genotypes: for total: P = 0.008, for males: P = 0.011; allele: for total: P = 0.006, for males: P = 0.002). In the Control group, for total and man, the distribution of SNP3 (rs2440472) genotypes and allele showed a significant difference between Han and Uyghur population (genotypes: for total: P = 0.00, for males: P = 0.00; allele: for total: P = 0.00, for males: P = 0.00). In the CAD group, GG genotype and G allele of rs2440472 was significantly higher in Han population than Uyghur population. In the Control group, GG genotype and G allele of rs2440472 was significantly lower in Han population than Uyghur population.

Discussion

Cholesterol is an essential component of most biological membranes and is the precursor for synthesis of steroid hormones and bile acids. However, high levels of cholesterol cause severe problems including coronary heart disease [18]. Cholesterol is synthesized from acetyl-CoA through a cascade of enzymatic reactions. The biosynthesis of cholesterol is tightly regulated, mainly through two feedback regulatory mechanisms: sterol-regulated degradation of HMG-CoA reductase (HMGCR) and maturation of sterol-regulatory element-binding protein (SREBP) [19]. Sterol-regulated degradation of 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGCR) is a rapid feedback regulatory mechanism by which cell employs to control the cholesterol biosynthesis. This process is initiated by the sterol induced interaction between HMGCR and Insig-1/gp78, a membrane-bound ubiquitin ligase complex [20]. When the concentration of cellular sterol is high, the membrane domain of HMGCR can sense the excessive sterols and the whole protein is rapidly degraded, therefore the cholesterol biosynthesis is shut down [21]. This sterol promotes the degradation of HMGCR through the ubiquitin-proteasome pathway, and therefore slows down cholesterol biosynthesis [9]. This was very important negatively feedback regulatory

Table 5 Multiple logistic regression analysis for CAD patients and control subjects of Han population in recessive model

| | Total | | | Men | | | Women | | |
|-------------------------------|-------|-------------|--------|-------|-------------|--------|-------|-------------|--------|
| | OR | 95% CI | P | OR | 95% CI | P | OR | 95% CI | P |
| Recessive model (GGvsAG + AA) | 1.451 | 1.067–1.974 | 0.018* | 1.789 | 1.219–2.627 | 0.000* | 1.024 | 0.604–1.736 | 0.929 |
| Glu | 1.098 | 1.024–1.177 | 0.009* | 1.058 | 0.97–1.154 | 0.2 | 1.152 | 1.021–1.299 | 0.021 |
| BMI | 1.136 | 1.089–1.185 | 0.000* | 1.098 | 1.038–1.161 | 0.000* | 1.182 | 1.103–1.267 | 0.000* |
| EH | 1.311 | 1.026–1.676 | 0.03* | 1.42 | 1.03–1.932 | 0.026* | 1.377 | 0.9–2.106 | 0.14 |
| LDL | 1.214 | 1.038–1.42 | 0.015* | 1.015 | 0.864–1.192 | 0.856 | 1.307 | 1.068–1.601 | 0.009* |
| DM | 2.225 | 1.565–3.162 | 0.000* | 1.842 | 1.197–2.834 | 0.005* | 4.251 | 2.238–8.073 | 0.000* |
| Smoking | 1.633 | 1.274–2.093 | 0.000* | 1.703 | 1.242–2.333 | 0.000* | 2.279 | 0.524–9.916 | 0.272 |

EH, essential hypertension; DM, diabetes mellitus; CAD, coronary artery disease; BMI, body mass index; Glu, glucose; LDL, low density lipoprotein.
 *P<0.05.

Table 6 Pairwise linkage disequilibrium ($|D'|$ above diagonal and r^2 below diagonal) for the three SNPs

| r ² | SNP | $ D' $ | | | | | |
|----------------|------|--------|-------|-------|---------|-------|------|
| | | CAD | | | Control | | |
| | | SNP1 | SNP2 | SNP3 | SNP1 | SNP2 | SNP3 |
| | SNP1 | 0.965 | 0.961 | | 0.99 | 0.99 | |
| | SNP2 | 0.155 | | 0.922 | 0.176 | | 0.99 |
| | SNP3 | 0.267 | 0.492 | | 0.363 | 0.485 | |

mechanism that cells use to control their cholesterol level. Sterol regulatory element-binding proteins (SREBPs) are major transcription factors activating the expression of genes involved in biosynthesis of cholesterol, fatty acid and triglyceride [22]. The SREBP is first synthesized as membrane bound transcription precursor (pre-SREBP), which forms a complex with SREBP cleavage-activating protein (SCAP). When cellular cholesterol level is high, Insig-1/-2 binds SCAP and retains the SCAP-SREBP complex in ER [23]. When the cholesterol level is low, SCAP dissociates from Insig-1/-2 and escorts SREBP to Golgi to undergo protease cleavages. The released N-terminal transcriptional domain of SREBP (nSREBP) enters the nucleus to activate transcription of genes encoding proteins in lipid biosynthesis and uptake. Meanwhile, Insig-1 is ubiquitinated by gp78 and degraded, therefore creating a rapid and convergent regulation on cholesterol biosynthesis and uptake [24,25]. From this angle, degradation of Insig-1 by gp78 should release the inhibition on SREBP and increase the biosynthesis of lipid.

The essential function of the gp78 in the cholesterol synthesis process was ubiquitination, that is a process during which proteins are modified with a single ubiquitin or a chain of ubiquitin monomers. It occurs through a cascading action of E1 ubiquitin-activating enzyme, E2 ubiquitin-conjugating enzyme and then E3 ubiquitin ligase [26]. Bao-Liang Song and his colleagues found gp78 as the ubiquitin ligase (E3) that initiates sterol-

dependent degradation of reductase, and Insig-1 as a bridge between gp78/VCP and the reductase substrate [11]. DeBose-Boyd and coworkers have shown that sterols induce the binding of ER-embedded HMG CoA reductase to Insig-1, and this interaction induces the ubiquitination and degradation of the reductase [27]. Later, they have shown that ubiquitination is mediated by gp78, which forms a complex with Insig-1 [11]. In the presence of sterols, this bound gp78 ubiquitinates HMG CoA reductase. It is tempting to speculate that in the absence of sterols, when neither Scap nor HMG CoA reductase is bound to Insig-1, gp78 ubiquitinates Insig-1, accelerating its degradation. When sterols induce HMGCoA reductase to bind to Insig-1, the ubiquitination reaction is diverted toward HMG CoA reductase, on the other hand, when sterols induce Scap to bind to Insig-1, the gp78 no longer ubiquitinates Insig-1. Perhaps Scap displaces gp78 from Insig-1 in a sterol dependent reaction [25]. In sterol-depleted cells, cholesterol dissociates from the Scap/SREBP complex, and this causes Insig-1 to dissociate well. The liberated Insig-1 undergoes ubiquitination by gp78 at lysines 156 and 158, which leads to proteasomal degradation. The liberated Scap/SREBP complex binds to COPII proteins, which cluster it into COPII-coated vesicles for transport to the Golgi [28]. In the Golgi, the SREBP is processed by proteases to release the transcriptionally active NH₂-terminal domain, which moves to the nucleus, where it activates transcription of all of the genes that encode enzymes required for cholesterol synthesis and for uptake through the LDL receptor [29]. It means that gp78 gene promotes the synthesis of cholesterol.

In the Han population, for total and men, there was a significant difference in the genotypic distribution of SNP3 (rs2440472) between CAD patients and control subjects, the distribution of SNP3 (rs2440472) alleles and the dominant model (AA vs AG + GG) and recessive model (GG vs AG + AA) showed a significant difference

Table 7 The distribution of haplotype in CAD patient and control participants

| | ID | Haplotype | Total | | | Men | | | Women | | |
|---|-----|-----------|---------|-------------|---------|---------|-------------|---------|---------|-------------|---------|
| | | | CAD (%) | Control (%) | P value | CAD (%) | Control (%) | P value | CAD (%) | Control (%) | P value |
| 1 | 100 | A T A | 0.3 | 0 | - | 0.4 | 0 | - | 0 | 0 | - |
| 2 | 101 | A T G | 21.2 | 20.2 | 0.495 | 20.8 | 19.7 | 0.52 | 21.8 | 21 | 0.738 |
| 3 | 010 | G C A | 36.2 | 41 | 0.044 | 36.5 | 42.4 | 0.058 | 35.8 | 38.8 | 0.386 |
| 4 | 000 | G T A | 15.1 | 16.6 | 0.422 | 14.5 | 17.7 | 0.154 | 16.2 | 15 | 0.619 |
| 5 | 001 | G T G | 26.2 | 22.2 | 0.02 | 26.4 | 20.2 | 0.005 | 25.9 | 25.2 | 0.816 |
| 6 | 110 | A C A | 0 | 0 | - | 0 | 0 | - | 2.34 | 2.02 | 0.354 |
| 7 | 111 | A C G | 0.3 | - | - | 0.3 | 0 | - | 0.3 | 0 | - |
| 8 | 011 | G C G | 0.7 | - | - | 1.1 | 0 | - | - | - | - |

The P value of genotype was calculated by Fisher's exact test, and revised by False discovery rate. *P<0.05; 0 represent Maximum gene frequency, 1 represent Minimum gene frequency.

The P value of each haplotype by the order of SNP1-SNP2-SNP3 is relative to the other haplotypes as a group (overall P =0.001).

Table 8 Genotype and allele distributions between Han and Uygur population

| | | | CAD | | | | | | | | | Control | | | | | | | | |
|---------------------|----------|-----|-------|---------|---------|-------|---------|---------|-------|---------|---------|---------|---------|---------|-------|---------|---------|-------|---------|---------|
| | | | Total | | | Men | | | Women | | | Total | | | Men | | | Women | | |
| | | | Han n | Uygur n | P value | Han n | Uygur n | P value | Han n | Uygur n | P value | Han n | Uygur n | P value | Han n | Uygur n | P value | Han n | Uygur n | P value |
| rs731119 (SNP1) | Genotype | G/G | 369 | 269 | 0.545 | 237 | 202 | 0.68 | 132 | 67 | 0.642 | 375 | 244 | 0.96 | 227 | 146 | 0.714 | 148 | 98 | 0.893 |
| | | A/A | 21 | 18 | | 11 | 12 | | 10 | 6 | | 26 | 18 | | 11 | 10 | | 15 | 8 | |
| | | A/G | 217 | 140 | | 139 | 108 | | 78 | 32 | | 184 | 117 | | 117 | 73 | | 15 | 8 | |
| | Allele | G | 955 | 678 | 0.69 | 613 | 512 | 0.888 | 342 | 166 | 0.703 | 934 | 605 | 0.99 | 571 | 365 | 0.761 | 363 | 240 | 0.718 |
| | | A | 259 | 176 | | 161 | 132 | | 98 | 44 | | 236 | 153 | | 139 | 93 | | 97 | 60 | |
| rs2617849 (SNP2) | Genotype | T/T | 222 | 152 | 0.772 | 132 | 120 | 0.159 | 90 | 32 | 0.234 | 181 | 128 | 0.68 | 102 | 78 | 0.422 | 79 | 50 | 0.476 |
| | | C/C | 74 | 57 | | 49 | 36 | | 25 | 21 | | 87 | 58 | | 56 | 31 | | 31 | 27 | |
| | | C/T | 261 | 174 | | 168 | 126 | | 93 | 48 | | 284 | 176 | | 170 | 107 | | 114 | 69 | |
| | Allele | C | 409 | 288 | 0.697 | 266 | 198 | 0.271 | 143 | 90 | 0.014 | 458 | 292 | 0.62 | 282 | 169 | 0.205 | 176 | 123 | 0.442 |
| | | T | 705 | 478 | | 432 | 366 | | 273 | 112 | | 646 | 432 | | 374 | 263 | | 272 | 169 | |
| rs2440472 (SNP3) | Genotype | A/A | 164 | 85 | 0.008* | 110 | 57 | 0.011* | 54 | 28 | 0.582 | 187 | 78 | 0.00* | 123 | 43 | 0.00* | 64 | 35 | 0.125 |
| | | G/G | 144 | 120 | | 95 | 94 | | 49 | 26 | | 98 | 106 | | 54 | 64 | | 44 | 42 | |
| | | A/G | 294 | 169 | | 183 | 128 | | 111 | 41 | | 287 | 192 | | 164 | 118 | | 123 | 74 | |
| | Allele | A | 622 | 339 | 0.006* | 403 | 242 | 0.002* | 219 | 97 | 0.979 | 661 | 348 | 0.00* | 410 | 204 | 0.00* | 251 | 144 | 0.072 |
| | | G | 582 | 409 | | 373 | 316 | | 209 | 93 | | 483 | 404 | | 272 | 246 | | 211 | 158 | |

CAD, coronary artery disease.

The P value of genotype was calculated by Fisher's exact test. *P<0.05.

between CAD and control participants. G allele and the recessive model (GG vs AG + AA) of rs2440472 was significantly higher in CAD patients than in control participants, A allele and the dominant model (AA vs AG + GG) of rs2440472 was significantly lower in CAD patients than in control participants. The significant difference in the two models of SNP3 between CAD patients and control subjects was retained after adjustment for covariates such as Glu, BMI, EH, DM, LDL and smoking (Table 4). This indicated in Han population, for total and males, the risk of CAD was increased with the GG genotype of rs2440472, and the AA genotype of rs2440472 was lowering the risk of CAD. In our study we also identifying two susceptible haplotypes (G-T-G; G-C-A) in the Han population, this result is consistent with the distribution of genotype results that the GG genotype of rs2440472 is a risk factor of CAD and the AA genotype is a protective factor of CAD, because G allele and A alleles of SNP3 was involved in haplotypes 001 and 010. Although, the gp78 has opposite effects on lipid biosynthesis, but the net effect was to increase the biosynthesis of cholesterol [13]. We speculated that Han subjects with the GG genotype of rs2440472 (SNP3) and G-T-G haplotype may be make the gp78 gene have a high ability for synthesizing cholesterol, thus increasing the chances of CAD; in contrast, that with the AA genotype of rs2440472 (SNP3) and G-C-A haplotype may be attenuate the synthesizing function of gp78 gene, which was decreasing the chances of CAD. For the Uygur population, we did not find an association between the three SNPs of the gp78 gene and CAD. In addition, in the Table 8 we have analysed the distribution of genotypes and alleles of SNP1, SNP2 and SNP3 for the GP78 gene between the Han and Uygur populations. From the table we can see both in the CAD and Control subjects the frequency of SNP3 (rs2440472) genotypes and alleles showed a significant difference between Han and Uygur population. We consult the national center for biotechnology information (NCBI) Web site then found the distribution of rs2440472 genotypes showed a significant difference between the European and Asian population. The Uygur population is one of the minorities residing mainly in northwest China (The Xinjiang Uygur Autonomous Region of China). They originate from intermarriage between Caucasians and Mongolians, and have their own language culture and the unique genetic background. The Han and Uygur are two different races, they has a different genetic background, maybe it was the reason why the distribution of rs2440472 genotypes have differences between the two populations.

In our study when analyzing men and women separately, there was only an association between the SNP3 (rs2440472) and CAD in men, however, in the women we did not find any association between the three SNPs

of the gp78 gene and CAD. We can't find any report about the gp78 gene and gender relation, so we unable to explain why there are gender differences in the distribution of genotypes, thus further studies are needed to explore this issue.

Conclusion

This was the first demonstration of the relationship between the gp78 gene polymorphisms and CAD. We found that rs2440472 may be a novel polymorphism of the gp78 gene associated with CAD in Han population in China. The GG genotype and G allele of rs2440472 in gp78 gene could be a risk genetic marker of CAD and the AA genotype and A allele may be a protective genetic marker of CAD in Han population in China, which supported the hypothesis that gp78 gene variations were involved in the pathogenesis of CAD. Certainly it needs further studies are warranted to replicate our results as well as elucidate the biological mechanism.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

EC and Z-YF performed statistical analyses and wrote the manuscript. QZ and EC extracted DNA. XX and FL collected blood samples and contributed to the acquisition of clinical data. Y-TM; Z-YF and EC conceived the study and participated in its design and coordination and helped to draft the manuscript. All authors read and approved the final manuscript.

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