Original Article

# Cholesterol Ester Transfer Protein *Taq1B* Polymorphism and Its Association with Cardiovascular Risk Factors in Patients Undergoing Angiography in Yazd, Eastern Iran: A Cross-Sectional Study

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## What's Known

- The studies that were conducted in different populations in Iran lacked consistency. Furthermore, previous research did not investigate the relationship between the *Taq1B* variant and all of the metabolic syndrome components. Moreover, the observational studies on this issue in Iran are quite scarce, with small sample sizes that do not completely account for confounders.

## What's New

- In line with previous studies, the present study found no relationship between the *Taq1B* variant and plasma lipid levels or other cardiovascular disease risk factors in patients undergoing angiography in Yazd (Iran). This finding might be specific to this region.

## Abstract

**Background:** Several studies assessed the relationship between the *cholesterol ester transfer protein (CETP) Taq1B* gene polymorphism (rs708272) with risk factors of cardiovascular diseases (CVDs). However, their findings were inconsistent. The present study investigated the relationship between CVD risk factors and the *Taq1B* variant in patients undergoing coronary angiography.

**Methods:** This cross-sectional study was conducted on 476 patients aged 30-76 years old of both sexes from 2020-2021, in Yazd (Iran). The *Taq1B* polymorphism genotypes were evaluated using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) on DNA extracted from whole blood. Standard protocols were used to measure cardio-metabolic markers. To determine the association between CVDs risk factors and the rs708272 variant, binary logistic regression was used in crude and adjusted models.

**Results:** *Taq1B* polymorphism genotype frequencies were 10.7% for B1B1, 72.3% for B1B2, and 17% for B2B2. There was no significant association between abnormal levels of CVDs risk factors and different genotypes of the *Taq1B* variant, Gensini score (P=0.64), Syntax score (P=0.79), systolic blood pressure (P=0.55), diastolic blood pressure (P=0.58), and waist circumference (P=0.79). There was no significant association between genotypes of the rs708272 variant and any abnormal serum lipid levels. After adjusting for confounders, the results remained non-significant.

**Conclusion:** There was no significant association between CVDs risk factors and *CETP* rs708272 polymorphism. The relationship between *CETP* gene variants and CVD occurrences varied across groups, implying that more research in different regions is required.

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**Keywords** ● Polymorphism, single nucleotide ● Coronary angiography ● Polymorphism, genetic

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## Introduction

Cardiovascular diseases (CVDs) are a group of disorders that affect the heart and blood vessels, and are the leading cause of death worldwide, accounting for 22.2 million deaths per year by 2030.[1] Age, sex, family history, smoking, physical inactivity, unhealthy diet, impaired glucose and lipid levels, high blood pressure, and waist circumference (WC), and metabolic syndrome (MetS) are all CVD risk factors.[2, 3] Previous studies found a correlation between abnormal blood lipid levels such as elevated triglyceride (TG), low-density lipoprotein cholesterol (LDL-C), decreased high-density lipoprotein cholesterol (HDL-C), abdominal obesity, and the risk of CVD.[4, 5] Evidence suggests that lifestyle modifications such as a healthy diet, increasing physical activity, quitting smoking, and losing weight could improve and control risk factors of CVDs.[6]

Genetic variants, such as single nucleotide polymorphisms (SNPs), were also shown through lipid metabolism and could have an association with CVDs.[7] The *cholesterol ester transfer protein (CETP)* gene encodes the CETP, which transfers cholesteryl esters from HDL to iatrogenic lipoproteins in exchange for TG.[8] A silent mutation base in the 277$^{th}$ nucleotide of the first intron of the *CETP* gene might change the Guanine base (G) to Adenine base (A), resulting in the rs708272 (*Taq1B*) variation. G called as B1 allele (frequent allele) with a restriction site for *Taq1* endonuclease enzyme and A called as B2 allele (less common allele) without Taq1 restriction site.[9] Previous review studies suggested that the *Taq1B2* variant of the *CETP* gene may reduce the severity of blood vessel stenosis by increasing HDL-C levels and decreasing plasma CETP.[7, 10] However, the reported association between *CETP* gene variants and lipid levels was contradictory in different populations.[11-13] According to the findings of an epidemiological and clinical investigation, MetS was associated with an increased risk of CVDs.[14] However, the evidence on the association of MetS components and *Taq1B* polymorphism with CVDs was limited and inconsistent.[15, 16]

Since the evidence on the association between CVD risk factors and *Taq1B* polymorphism was inconsistent, it seemed necessary to investigate how genetic variations in different populations can lead to different findings. Therefore, since there were few studies in different regions of Iran, this study aimed to assess the relationship between the *CETP Taq1B* polymorphism and CVDs risk factors, such as WC, lipid profiles, fasting blood glucose (FBS), systolic blood pressure (SBP), diastolic blood pressure (DBP), and severity of stenosis coronary arteries across *Taq1B* genotypes in patients undergoing coronary angiography.

## Materials and Methods

### *Study Design and Participants*

The present cross-sectional study assessed 476 patients who were referred to Afshar Hospital (Yazd, Iran) for angiography between September 2020 and October 2021. The participant's age ranged from 35 to 75. All participants provided written informed consent before participating in the study. Subjects were excluded if they had a history of cancer, chronic heart failure (CHF), a history of myocardial infarction (MI), percutaneous coronary intervention (PCI), coronary artery bypass grafting (CABG), chronic kidney disease stage III or higher, liver disease or were receiving medication for liver disease, certain perceptual or psychological disorders, immune system failure, an acquired immunodeficiency syndrome (AIDS), or extreme obesity (body mass index [BMI] more than 40). Pregnant and lactating women, as well as those with oral intake restrictions were also excluded. This study was approved by the Ethics Committee of Shahid Sadoughi University of Medical Sciences, Yazd, Iran, (IR.SSU.SPH.REC.1400.079).

### *DNA Extraction and Genotyping*

Genome Deoxyribonucleic acid (DNA) was extracted from white blood cells in 100 µL of peripheral whole blood using the Kit protocol (SIMBIOLAB, IRAN). The extracted DNA was stored at -20 °C until analysis. The *CETP-Taq1B* variant was amplified using the polymerase chain reaction (PCR) method, with a 20 µL volume solution consisting of 2 µL genomic DAN, 6 µL water, 10 µL Master Mix (Amplicon, Denmark), and 1 µL of each primer 5'-ACTAGCCCAGAGAGAGGAGTG-3' and 5'-CAGCCGCACACTAACCCTA-3' synthesized by SinaClon, Iran. Amplification was applied with one denaturation cycle for 5 min denaturation cycle at 95 °C, followed by 40 cycles for 30 sec at 95 °C, annealing at 66 °C for 30 sec, and primary extension at 72 °C for 30 sec. The final extension was one cycle at 72 °C in 5 min. The PCR products were electrophoresed on 2% agarose gel (Sina Clon Co., Iran) and then digested by endonuclease enzyme of the Taq1 (Fermentase, Lithuania) after incubating at 37 °C for 24 h in a 30 µL (10 µL PCR products, 2 µL buffer, 0.5 µL Taq1 enzymes, and 17.5 µL water). Digested fragments of the 708272-*CETP* were

electrophoresed using 2% agarose gel with a voltage of 100 V for one hour. Finally, using ultraviolet transilluminationl, genotypes were identified on the gel based on fragment length.

The patient's weight and height were measured based on the standard protocols utilizing Omron BF-511 portable digital scales (with an accuracy of 100 gr) and a tape measure (with an accuracy of 0.1 cm). The WC was measured with a non-stretch tape in the middle of the iliac crown and the lowest rib in the standing position with an accuracy of 0.1 cm. Based on the National Cholesterol Education Program Adult Treatment Panel III (NCEP ATP III), abdominal obesity was defined as WC>102 for men and >88 cm for women.[17, 18] BMI was calculated by dividing weight (Kg) by squared height ($m^2$). All these variables were measured by nutrition-trained students.

*Physical Activity Assessment*

Daily physical activity was evaluated using the International Physical Activity Questionnaire (IPAQ).[19] Activity levels were measured in metabolic equivalent (MET) hours per week and categorized as sedentary, moderate, or active based on a list of regular daily activities throughout the previous week.

*Laboratory Measurements*

After overnight fasting, we collected 4 mL of venous blood from each participant. After being placed in tubes containing ethylenediaminetetraacetic acid (EDTA), the samples were centrifuged for 5 min at 5000 rpm. According to a standard laboratory protocol, biomarkers such as TG, HDL-C, LDL-C, total cholesterol (TC), and FBS were measured using Pars Azmun kits (Tehran, Iran). Abnormal levels of biochemical markers were defined as follows TG≥150 mg/dL, FBS≥110 mg/ dL; HDL-C<40 mg/ dL for men, and HDL-C<50 mg/dL for women; TC≥200 mg/dL and LDL-C≥130 mg/dL.[17, 18]

*Calculation Syntax and Gensini Scores*

The severity of coronary artery stenosis in participants undergoing angiography was determined using two scoring criteria: Syntax and Gensini. According to Gensini, the percentage of lumen obstruction in atherosclerotic lesions was 1 point for ≤25% obstruction, 2 points for 26-50% obstruction, 4 points for 51-75% obstruction, 8 points for 76-90% obstruction, 16 points for 91-99% obstruction, and 32 points for full obstruction. The scores were multiplied by coefficients ranging from1 to 5, depending on the number of coronary arteries and obstructed sections. A coefficient value of 5 was used for the main left coronary artery, 2.5 for the anterior descending and proximal of the left coronary artery, 1.5 for the mid-segment of the left anterior descending coronary artery, 1 for the proximal right section, and other segments received a coefficient of 0.5. The total Gensini score (GS) was calculated by adding the stenosis scores and coefficients for each duct.[20, 21] GS≥23 was considered as intermediate-high-risk severity of coronary artery stenosis and <23 as low-risk.[22]

A web-based computer program (http://www.syntaxscore.com) was used to calculate the SYNTAX score (SS).The questions on the list concerning SS were related to functional and anatomical parameters of the obstruction ≥50%, and stenosis of arteries with a diameter of ≥1.5 mm.[22, 23] The SYNTAX score (SS) was calculated as the sum of all obstruction scores. The SS lower than 22 was considered to be of low severity of coronary artery stenosis, while SS≥22 was of moderate-severe severity.[22] The coronary angiographies were analyzed by experienced cardiologists, who were anonymized to the patients' identity except for age and sex.

*Assessment of Other Variables*

Trained interviewers utilized a general questionnaire to collect other socioeconomic information including, age, sex, smoking status, job, educational levels, menstrual status, and drug use history. Prior to angiography, BP was measured by hospital-experienced nurses according to standard protocol. The patients with BP≥140 and ≥90 mmHg were classified as having systolic and diastolic BP, respectively.[17, 18]

*Statistical Analysis*

Data were analyzed using SPSS 24.0 (IBM Corporation, Chicago, IL). To assess CVD risk factors across *Taq1B* genotypes, one-way ANOVA analysis for continuous variables and the Chi square test for categorical variables were used. Odds Binary logistic regressions in crude and multivariable-adjusted models were used to evaluate the odds ratio (OR) and 95% confidence intervals (CIs) of CVD risk factors across genotypes. The univariate logistic test was used to identify confounders for adjustment, which were then entered into the multivariate models. According to the Hosmer-Lemeshow principle, variables with a P≤0.2 were considered confounders. Age, sex, BMI, physical activity, smoking status, used medications, job, education level, economic status, menopausal status, family size, and marital status were all included as confounders. Pearson's Chi square test was used for assessing the Hardy-Weinberg equilibrium (HWE). All analyses were conducted

using a statistical package for the social sciences (SPSS) software version 24 (IBM Corporation, USA). P<0.05 was considered statistically significant, except for HWE, where P value>0.05 was used.

## Results

*General Characteristics of Study Participants*

The basic characteristics of participants for each genotype of the *CETP-Taq1B* polymorphism is shown in table 1. The participant's mean age was 56.90±9.31 years. The frequency of the *CETP-Taq1B* genotypes was (10.7%), (72.3%), and (17%) for B1B1, B1B2, and B2B2, respectively. There was no statistically significant difference in age (P=0.73), BMI (P=0.52), weight (P=0.77), height (P=0.88), WC (P=0.61), physical activity (P=0.73), sex (P=0.93) across the *CETP-Taq1B* genotypes. The genotypes were all within the HWE (P>0.999). The electrophoresis results of the digested products showed the following fragments: homozygous B1B1 with two bands of 175 and 345 base pairs (bp), heterozygous B1B2 with three bands of 520, 175, and 345 bp, and homozygous B2B2 with one band of 520 bp (figure 1).

*Comparison of CVD Risk Factors Across Genotypes of the CETP-Taq1B*

The CVD risk factors according to genotypes of the *CETP-Taq1B* are presented in table 2. As shown, no significant difference was found between FBS (P=0.56), TC (P=0.99), LDL-C (P=0.59), TG (P=0.22), HDL-C (P=0.26), WC (P=0.61), SBP (P=0.72), DBP (P=0.88), and scores of severity of coronary artery stenosis (GS=0.59) and (SS=0.83) in different *Taq1B* genotypes.

*Association of CVD Risk Factors with Genotypes of CETP-Taq1B*

Table 3 shows the odds ratios (95% CIs) of CVD risk factors across *CETP-Taq1B* genotypes. The following OR (95% CIs) of abnormal biochemical profiles were not associated with genotypes: high serum LDL (OR: 1.12; 95% CI: 0.53-2.35, P=0.75), TG (OR: 0.97; 95% CI: 0.46-2.03, P=0.94), TC (OR: 1.29; 95% CI: 0.58-2.86, P=0.52), FBS (OR: 1.38; 95% CI: 0.67-2.84, P=0.37), and low HDL (OR: 0.58; 95% CI: 0.26-1.27, P=0.17). There

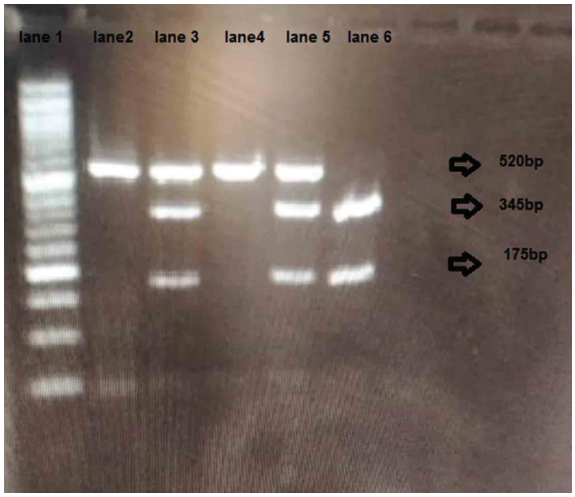


**Figure 1:** This figure shows the digested fragments of the 708272-*CETP* on 2% agarose gel electrophoresis. The ladder marker (lane 1) was 50 bp, the homozygous B1B1 genotype (lane 6) had two bands of 175 bp and 345 bp. The heterozygous B1B2 genotype (lanes 3 and 5) had three bands of 175 bp, 345 bp, and 520 bp. The homozygous B2B2 genotype (lanes 2 and 4) had one band of 520 bp.

**Table 1:** General characteristics of study participants according to the *CETP-Taq1B* genotypes

| Variables | | *CETP*-rs708272 | | | | |
|---|---|---|---|---|---|---|
| | | Total genotypes (n=476) | B1B1 n=51 (10.7%) | B1B2 n=344 (72.3%) | B2B2 n=81 (17%) | P value |
| Age (year, mean±SD) | | 56.90±9.31 | 57.84±10.03 | 56.74±9.07 | 56.99±9.91 | 0.73 |
| BMI (Kg/m$^2$, mean±SD) | | 27.42±4.28 | 27.30±3.99 | 27.31±4.37 | 27.93±4.08 | 0.52 |
| Weight (Kg, mean±SD) | | 74.02±12.92 | 74.07±14.99 | 73.79±12.78 | 74.99±12.13 | 0.77 |
| Height (cm, mean±SD) | | 164.41±9.89 | 164.24±11.29 | 164.54±9.85 | 163.95±9.16 | 0.88 |
| WC (cm, mean±SD) | | 99.62±10.95 | 100.64±11.29 | 99.29±11.13 | 100.30±10.01 | 0.61 |
| Physical activity, n (%) | Sedentary | 158 (33.2) | 17 (33.3) | 116 (33.7) | 25 (30.9) | 0.73 |
| | Moderate | 160 (33.6) | 20 (39.2) | 112 (32.6) | 28 (34.6) | |
| | Active | 158 (33.2) | 14 (27.5) | 116 (33.7) | 28 (34.6) | |
| Sex, n (%) | Male | 301 (63.2) | 33 (64.7) | 218 (63.4) | 50 (61.7) | 0.93 |
| | Female | 175 (36.8) | 18 (35.3) | 126 (36.6) | 31 (38.3) | |
| Smoking status, n (%) | Non-smoker | 307 (64.5) | 32 (62.7) | 218 (63.4) | 57 (70.4) | 0.66 |
| | Former smoker | 17 (3.6) | 2 (3.9) | 14 (4.1) | 1 (1.2) | |
| | Current smoker | 152 (31.9) | 17 (33.3) | 112 (32.6) | 23 (28.4) | |
| Medicine consumption; yes, n (%) | Anti-hypertensives | 208 (43.7) | 23 (45.1) | 151 (43.9) | 34 (42) | 0.93 |
| | Anti-hyperlipidemic | 172 (36.1) | 18 (35.3) | 121 (35.2) | 33 (40.7) | 0.63 |
| | Anti-diabetic | 156 (32.8) | 16 (31.4) | 114 (33.1) | 26 (32.1) | 0.95 |

BMI: Body mass index; WC: Waist circumference; One-way ANOVA was used for continuous variables, and Chi square test was used for categorical variables. P<0.05 was considered significant.

**Table 2:** Measures of CVDs risk factors across *CETP-Taq1B* genotypes

| Variable | Tertiles of *CETP-Taq1B* genotypes | | | | |
|---|---|---|---|---|---|
| | **Total genotypes (n=476) Mean±SD** | **B1B1 (n=51) Mean±SD** | **B1B2 (n=344) Mean±SD** | **B2B2 (n=81)** Mean±SD | **P value** |
| WC (cm) | 99.62±10.95 | 100.64±11.29 | 99.29±11.13 | 100.30±10.01 | 0.61 |
| TC (mg/dL) | 199.16±110.05 | 198.44±132.16 | 199.43±107.48 | 198.53±106.73 | 0.99 |
| LDL (mg/dL) | 98.03±41.86 | 92.22±38.42 | 98.67±40.51 | 99.07±48.95 | 0.59 |
| HDL (mg/dL) | 48.59±12.02 | 46.55±10.88 | 48.53±12.14 | 50.14±12.15 | 0.26 |
| TG (mg/dL) | 155.27±85.66 | 168.63±102.70 | 150.81±75.50 | 164.96±109.23 | 0.22 |
| FBS (mg/dL) | 134.24±63.62 | 129.93±59.64 | 133.27±61.80 | 140.79±72.89 | 0.56 |
| SBP (mgHg) | 128.53±13.91 | 127.61±11.84 | 128.85±14.30 | 127.72±13.53 | 0.72 |
| DBP (mgHg) | 79.01±11.16 | 78.48±8.80 | 79.17±10.16 | 78.68±15.88 | 0.88 |
| Gensini score | 34.62±42.12 | 32.69±46.58 | 35.82±40.98 | 30.61±44.19 | 0.59 |
| Syntax score | 10.65±12.96 | 9.93±14.88 | 10.88±12.39 | 10.14±14.13 | 0.83 |

TC: Total cholesterol; HDL-C: High-density lipoprotein cholesterol; FBS: Fasting blood sugar; LDL-C: Low-density lipoprotein cholesterol; TG; Triglyceride; SBP: Systolic blood pressure; DBP: Diastolic blood pressure; One-way ANOVA was used. P<0.05 was considered significant.

was no significant relationship between stenosis scores of coronary arteries across genotypes, GS (OR: 0.84; 95% CI: 0.40-1.74, P=0.64), and SS (OR: 0.88; 95% CI: 0.34-2.28, P=0.79). There was no relationship between other variables, including SBP (OR: 0.79; 95% CI: 0.37-1.68, P=0.55), DBP (OR: 0.76; 95% CI: 0.29-2.0, P=0.58), and WC (OR: 0.90; 95% CI: 0.43-1.89, P=0.79). After adjusting confounders, the associations remained non-significant in both models 1 and 2 for all outcomes.

## Discussion

The *Taq1B* variant was not associated with any CVD risk factors. As previously stated, CVDs were multifactorial, and genetic variants, in addition to environmental factors, can play an independent role in their incidence. Some studies, but not all, concurred that the *Taq1B2* variant can reduce the risk of CVD events by lowering CETP concentration and adjusting plasma lipid levels.[7, 10] In the present study, the frequency of the B2 allele was more than B1 allele (53% vs. 47%), which was similar to certain Asian studies,[11, 24] but contrary to others.[12, 13, 25, 26] We found no difference in plasma TG, or LDL-C levels between different genotypes of the *Taq1B* variant; which was consistent with the findings of previous research in Iran.[13, 26, 27] However, in contrast to our findings, they found that B2B2 genotype carriers had higher HDL-C levels than B1B1 genotype carriers. Besides, the present study found no correlation with HDL-C, which was similar to Rahimi and others.[13] According to an Egyptian study, subjects with the B2 allele had higher HDL-C levels and lower TG, LDL-C, and TC levels.[28] Similarly, studies in other populations supported the important role of the B2 allele in lipid metabolism and the severity of risk coronary stenosis.[25, 29, 30] They suggested that *Taq1B* might cause coronary arteries stenosis through abnormalities in HDL-C. However, the results of other studies were inconsistent.[11, 13, 31] Raina and others found no association between rs708272 variant and coronary stenosis in Jammu community,[11] with a similar allelic frequency to ours. Allelic heterogeneity in different populations, study design type, subjects' health status, ethnicities and races, sample sizes, genotyping methods and environmental factors, and other *CETP* gene SNPs may explain the disparity in findings.

In this study, no association between rs708272 genotypes and high blood pressure and fasting glucose was found. Hou and others conducted a case-control study in China and found no relationship.[16] Moreover, Corella and colleagues found no association between *Taq1B* polymorphism and systolic blood pressure.[32] Although they reported a small association, it was significant with diastolic blood pressure. The findings of a study in Thai population indicated that *CETP-Taq1B* might not be a genetic risk factor for MetS traits.[15] According to Porchay-Balderelli and others, there was no association between *Taq1B* genotypes and blood pressure.[33] El-Lebedy and colleagues conducted a study in an Egyptian population and reported that carriers of the B1 allele increased the risk for DM2 up to 1.75-fold.[34] In a Spanish population, Lopez and colleagues found that GG genotype carriers had higher blood sugar.[35] Similar to the findings of a study by Corella and others, the present study found no relationship between the *TaqIB* variant and serum FBS.[32] Different results were reported in different populations, which could be attributed to ethnic group differences in variation prevalence.

**Table 3:** Multi-variable adjusted OR for CVDs risk factors across *CETP-Taq1B* genotypes (n=476)

| Variable | B1B1 (n=51) | B1B2 (n=344) | B2B2 (n=81) | P value* | P trend |
|---|---|---|---|---|---|
| High WC | | | | | |
| Crude | 1.00 | 0.91 (0.49-1.69) | 0.90 (0.43-1.89) | 0.79 | 0.82 |
| Model 1 | 1.00 | 0.67 (0.25-1.83) | 0.44 (0.13-1.50) | 0.19 | 0.18 |
| Model 2 | 1.00 | 0.69 (0.24-2.01) | 0.45 (0.13-1.61) | 0.22 | 0.20 |
| High serum HDL | | | | | |
| Crude | 1.00 | 0.86 (0.46-1.62) | 0.58 (0.26-1.27) | 0.17 | 0.14 |
| Model 1 | 1.00 | 0.86 (0.44-1.65) | 0.54 (0.24-1.21) | 0.13 | 0.10 |
| Model 2 | 1.00 | 0.93 (0.47-1.85) | 0.61 (0.26-1.42) | 0.25 | 0.21 |
| High serum LDL | | | | | |
| Crude | 1.00 | 1.41 (0.75-2.65) | 1.12 (0.53-2.35) | 0.75 | 0.96 |
| Model 1 | 1.00 | 1.39 (0.74-2.61) | 1.00 (0.47-2.12) | 0.99 | 0.78 |
| Model 2 | 1.00 | 1.27 (0.66-2.44) | 0.78 (0.40-1.89) | 0.73 | 0.53 |
| Low serum TC | | | | | |
| Crude | 1.00 | 1.58 (0.80-3.12) | 1.29 (0.58-2.86) | 0.52 | 0.73 |
| Model 1 | 1.00 | 1.61 (0.80-3.24) | 0.99 (0.43-2.30) | 0.99 | 0.72 |
| Model 2 | 1.00 | 1.47 (0.70-3.10) | 0.72 (0.29-1.82) | 0.50 | 0.34 |
| High serum TG | | | | | |
| Crude | 1.00 | 0.92 (0.49-1.71) | 0.97 (0.46-2.03) | 0.94 | 0.99 |
| Model 1 | 1.00 | 0.95 (0.49-1.81) | 0.78 (0.35-1.71) | 0.54 | 0.51 |
| Model 2 | 1.00 | 0.82 (0.40-1.65) | 0.75 (0.32-1.75) | 0.50 | 0.52 |
| High serum FBS | | | | | |
| Crude | 1.00 | 1.01 (0.55-1.84) | 1.38 (0.67-2.84) | 0.37 | 0.29 |
| Model 1 | 1.00 | 1.14 (0.61-2.11) | 1.43 (0.66-3.02) | 0.34 | 0.32 |
| Model 2 | 1.00 | 1.13 (0.59-2.17) | 1.35 (0.61-2.96) | 0.44 | 0.43 |
| High SBP | | | | | |
| Crude | 1.00 | 0.95 (0.50-1.79) | 0.79 (0.37-1.68) | 0.55 | 0.50 |
| Model 1 | 1.00 | 0.97 (0.51-1.85) | 0.81 (0.38-1.74) | 0.59 | 0.54 |
| Model 2 | 1.00 | 1.07 (0.55-2.07) | 0.91 (0.42-1.99) | 0.82 | 0.73 |
| High DBP | | | | | |
| Crude | 1.00 | 1.03 (0.47-2.24) | 0.76 (0.29-2.0) | 0.58 | 0.52 |
| Model 1 | 1.00 | 1.03 (0.47-2.25) | 0.76 (0.29-2.01) | 0.58 | 0.52 |
| Model 2 | 1.00 | 1.09 (0.48-2.47) | 0.82 (0.30-2.25) | 0.71 | 0.63 |
| High Syntax score | | | | | |
| Crude | 1.00 | 1.09 (0.50-2.37) | 0.88 (0.34-2.28) | 0.79 | 0.90 |
| Model 1 | 1.00 | 1.17 (0.52-2.60) | 0.98 (0.36-2.62) | 0.97 | 0.90 |
| Model 2 | 1.00 | 1.25 (0.55-2.84) | 1.03 (0.38-2.81) | 0.94 | 0.97 |
| High Gensini score | | | | | |
| Crude | 1.00 | 1.46 (0.79-2.66) | 0.84 (0.40-1.74) | 0.64 | 0.48 |
| Model 1 | 1.00 | 1.53 (0.79-2.94) | 0.85 (0.38-1.90) | 0.70 | 0.49 |
| Model 2 | 1.00 | 1.40 (0.71-2.73) | 0.86 (0.38-1.96) | 0.73 | 0.58 |

HDL-C: High-density lipoprotein cholesterol; FBS: Fasting blood sugar, LDL-C: Low-density lipoprotein cholesterol; TG: Triglyceride; SBP: Systolic blood pressure; DBP: Diastolic blood pressure; *P value: Genotype B2B2 compared to genotype B1B1. For high WC: Confounders adjusted in model 1: age, sex, BMI, and physical activity; Confounders adjusted in model 2: Additionally, job, menopausal status, used medications, smoking status, education level, marital status. For high serum HDL: Confounders adjusted in model 1: sex, physical activity; Confounders adjusted in model 2: Additionally, job, menopausal status, used medications, smoking status, family size. For high serum LDL: Confounders adjusted in model 1: age; Confounders adjusted in model 2: Additionally, used medications, smoking status, education level. For high serum TC: Confounders adjusted in model 1: age, sex, BMI; Confounders adjusted in model 2: Additionally, used medications, economic status, smoking status, marital status, education level, family size. For high serum TG: Confounders adjusted in model 1: age, sex, BMI, physical activity; Confounders adjusted in model 2: Additionally, job, menopausal status, used medication. For high serum FBS: Confounders adjusted in model 1: age, BMI; Confounders adjusted in model 2: Additionally, job, used medications, economic status. For high SBP: Confounders adjusted in model 1: sex, physical activity; Confounders adjusted in model 2: Additionally, smoking status, menopausal status, education level, job, family size, marital status, and used medications. For high DBP: Confounders adjusted in model 1: sex; Confounders adjusted in model 2: Additionally, smoking status, menopausal status, family size. For high Syntax Score: Confounders adjusted in model 1: sex, age; Confounders adjusted in model 2: Additionally, family size, job, education level, menopausal status, smoking status, used medications. For a high Gensini Score: Confounders adjusted in model 1: sex, age, BMI; Confounders adjusted in model 2: Additionally, menopausal status, smoking status, economic status, and job.

Perez-Robles and others demonstrated that Mexican women with abdominal obesity, who carry the *Taq1B2* allele, might have impaired lipid metabolism due to environmental factors.[36] Another study suggested that B2B2 carriers with a BMI≥27 might have lower HDL-C levels.[37] The present study found no relation between the *Taq1B* variant and abdominal obesity. The location of the *Taq1B* polymorphism at the *CETP* locus, as well as its proximity to other *CETP* SNPs, may render it more vulnerable to various factors.[37, 38] However, as previously stated, the evidence supporting a relationship between rs708272-*CETP* and MetS components was contradictory. Hence, further studies on other *CETP* gene variants are required to clarify the observed relationships.

One of the major strengths of this study was that several confounders were measured and adjusted in the analysis. Nonetheless, the present study had some limitations. Since in this study we did not measure plasma CETP levels, which have a significant role in the metabolism of lipoproteins, the interpretations was rather challenging. Measuring HDL3[39] as a marker related to plasma CETP levels was essential. It is recommended to analyze all SNPs of the *CETP* gene associated with CVD risk factors and to their interactions with each other and other variables.

## Conclusion

There was no association between CVD risk factors and *Taq1B* genotypes. Given that the findings of the present study was inconclusive in other populations, more extensive research are required to account for all possible relevant factors.

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## Authors' Contribution

A.SA, AN, A.AV, Z.D, M.T, M.M, V.A, S.BR, M.MN, MY, SS.KH, F.M, and SM.SH substantially contributed to the conception, design, acquisition, and analysis of the work. All authors involved in drafting the work or reviewing the manuscript, and final approval of the version to be published, and agreed to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

**Conflict of Interest:** None declared.

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