Influence of Interleukin-6 174G>C gene Polymorphism on Patients with Stable Coronary Artery Disease

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Abstract— **Background: Coronary artery disease is caused by plaque buildup in the arteries' walls that deliver blood to the heart.**

The study examined the correlation between the IL-6 gene promoter 174G>C polymorphism, blood IL-6 levels, and specific physiological parameters in Kurdish people from Iraq with stable coronary artery disease (CAD).

Methods: The investigation took place on a sample of 62 persons diagnosed with stable coronary artery disease (SCAD) and a control group of 31 individuals without CAD. The Sanger sequencing method was employed to detect IL-6 SNP genes, and the enzyme-linked immunoassay (ELISA) was used to measure serum IL-6 and A Cobas to evaluate serum biochemical variables.

Results: The prevalence of the wild homogeneous GG genotype was lower in stable CAD patients compared to non-CAD individuals with a major alteration, indicating its preventive role against the development of the disease. The presence of GC+CC genotypes has a more favorable effect on illness progression than the dominant GG genotype. Additionally, the C allele was found to be a risk factor for the disease. In the study, IL-6 showed strong positive associations with RBC count, HCT, Granulocyte count, WBC, PDW, ICAM1 levels, and OX-LDL. The stepwise multivariate regression analysis revealed that Ox-LDL was crucial in determining the serum IL-6 levels in individuals with stable CAD. Additionally, MDA had a minor impact on the relationship between total Ox-LDL and IL-6 levels, suggesting that there might be a partial mediation effect.

Conclusions: the results for IL-6 indicate that the CC genotype increases CAD risk, GG decreases this risk, and GC+CC genotypes decrease the risk of CAD progression.

Index Terms— **IL-6, SNP, stable coronary artery disease**.

I. Introduction

Coronary artery disease (CAD) is a medical illness characterized by insufficient delivery of blood and oxygen to the myocardium. It occurs due to blockage of the coronary arteries, leading to an imbalance between demand for and supply of oxygen(Shahjehan and Bhutta, 2023). cardiovascular disease (CVD) is responsible for 32% of deaths worldwide and ranks first as the cause of disease-related mortality in Iraq (Mohammad et al., 2021).

Interleukin-6 (IL-6) is now acknowledged as a cytokine that controls multiple processes, including the immediate response, inflammation, and hematopoiesis. The majority of tissues and nearly all immune system cells can produce it. IL-6 can transmit signals through receptors attached to cell membranes, or, distinctively among the IL-6 family of cytokines, it can transmit signals in a trans manner using a soluble form of its receptors (Tanaka et al., 2014). Although IL-6 possesses anti-inflammatory characteristics, it has an overall negative impact on the cardiovascular system. IL-6 levels tend to rise with age and are linked to increased mortality in individuals over 65 years old, regardless of whether the cause of death is cardiovascular or non-cardiovascular (Reiss et al., 2017). Increased levels of IL-6 have been observed in patients with coronary artery disease (CAD), suggesting that it may serve as an indicator of inflammation associated with cardiovascular risk (Zakai et al., 2007).

The IL6 gene in humans consists of five exons and four introns. The IL6 gene, which governs pathways of inflammation, is found at location 7p21 (Eze et al., 2016) . The functional impact of the SNP rs1800795 (174G>C) in the IL6 gene promoter has been proposed to result in an elevation of IL-6 levels (Jurečeková et al., 2018). In addition, the study demonstrated that individuals with the CC genotype for rs1800795 in the IL6 gene exhibited elevated levels of IL-6 and high-sensitivity C-reactive protein (hs-CRP), indicating an augmented inflammatory response (Rocha et al., 2021).

The current study aims to establish the correlation between the IL-6 gene polymorphism (rs1800795) and IL-6 serum levels and to examine how these factors relate to specific criteria in persons with stable CAD.

II. Material and Methods

A. Study participants

The investigation on stable coronary artery disease (CAD) was carried out at the Surgical Specialty Hospital Cardiac Centre in Erbil, Iraq, between January and June 2022. Ninety-three male participants with CAD disorders were recruited for this research out of a total of three hundred patients who underwent coronary angiography in the Department of Cardiology for diagnostic purposes. To maintain a uniform study population, individuals with cardiac issues, autoimmune disorders, kidney infections or acute liver malignancies, or any additional chronic medical conditions were not included in the research study. The study excluded patients who had unstable angina, such as both ST-elevation myocardial infarction (STEMI) and non-STEMI. The participant sample (Group I) comprised 62 patients, with a mean age of 53 years old, who exhibited stable coronary artery disease (CAD) characterized by stenosis of more than fifty percent (50%). The remaining 31

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subjects, which did not show any narrowing of the coronary arteries, were designated to be the non-CAD control subjects (Group II).

B. Blood collection

After fasting, 10 mL of blood was taken from the whole specimens, which were subsequently divided into two equal parts. The initial portion was gathered in an EDTA tube and subjected to molecular and hematological evaluations. The remaining part was added to gel tubes and then subjected to centrifugation to isolate the serum. The serum was subsequently stored at a temperature of -20 Celsius till it was needed for its next use.

C. Biochemical assay

Following the centrifugation of non-heparinized blood, the levels of serum IL-6 was assessed through a sandwich enzyme immunoassay approach (SL0372Hu-China) with a sensitivity of 1.2pg/mL. The variance coefficient for intra-assay and inter-assay was below 10% for all tests. A Cobasss e411: 1242-22, manufactured by Roche in Germany, was employed to evaluate serum biochemical variables.

D. Coronary Angiography

All patients had definitive coronary angiography to assess the degree and extent of coronary artery disease (CAD) using the right femoral route. Seasoned cardiologists examined coronary angiograms to determine the extent of coronary artery disease (CAD) without knowledge of the patient's medical background and biochemical findings. The degree of stenosis was classified with the coronary arteries disease Reporting and Data System (CAD-RADS) classification. (Cury et al., 2016). The study cohort was divided into two distinct cohorts: the initial cohort comprised sixty-two patients who had been diagnosed with CAD (CAD-RADS 3 or higher) and exhibited substantial narrowing of the coronary arteries (≥50%); the second cohort comprised thirty-one individuals who displayed no indication of CADss (CcAD-RADS 0), as confirmed by coronary angiography.

E. DNA extraction

Genomic material isolation The GeneAllss® ExgeneTM Genomic DNA Extraction for Clinics Cell SV small kit was utilized to isolate DNA from whole blood samples to get BNP gene polymorphisms. According to the instructions provided by GeneAll® (located in Songpa-gu, Seoul, KOREA), we used 50p-µL of the elution buffer for DNA extraction. Subsequently, the genomic extraction was subjected to freezing at a temperature of -20 °C prior to conducting a PCR test. The PCR (polymerase chain reaction) method was employed to amplify the fragment of target DNA for genotyping of the IL-6 gene rs1800795 loci. The amplification process known as PCR reaction uses specific primer sequences, conditions for reaction, and a designated apparatus. The resulting amplified DNA was subsequently identified using Sanger sequencing. An amplified process was conducted using a programmed thermal cycling PCR device. The forward primer: 5′-GCGATGGAGTCAGAGGAAAC -3′ and reverse primer: 5′-ATCTTTGTTGGAGGGTGAGG - 3′; The PCR cocktail was prepared using 50 µL reaction mixtures, consisting of 25µL of 2x PCR master mix (AMPLIQON, Denmark), 1.0 µL of each primer (10 pmol), and 1.5 µL of template genomic DNA. The final volume was adjusted to 50µLp using nuclease-free water. The PCR commenced with an initial denaturation phase at 94°C for a duration of 5 minutes, followed by 35 cycles at 94°C for 30 seconds, annealing at 60°C for 40 seconds, and extension at 72°C for 30 seconds. Lastly, a final extension phase was at 72°C for 5 minutes. After that, the total length of the PCR result, which was 408 bp, was confirmed by electrophoresis on a 1.5% agarose gel that was used.

F. Statistical analysis

The analysis of the data was performed using Graph Pad Prism version 9 and MedCalc version 18. All data were not normally distributed using the Shapiro-Wilk normality test and Kolmogorov-Smirnov normality test. Chi-square statistics were performed to analyze demographic characteristics. Spearman (r) correlation was used. The data were log-transformed, and stepwise multiple regressions were conducted to predict the relationships IL-6 and other variables; also, the Hardy - Weinberg equilibrium was estimated using the H-W calculator for two alleles. One-way ANOVA was performed to clarify the relationships between the genotype and physiological parameters.

III. RESULTS

A. Subject characteristics

Table 1 displays the clinical characteristics of ninety-three male participants, allowing for the distinction between those with and without CAD diagnoses. Those with CAD patients had significantly higher rates of advanced age, a greater body mass index (BMI), cigarette smoking, high blood pressure, and personal experiences of Type 2 diabetes mellitus and heart attacks, as well as family histories of hypertension and coronary artery diseases than did the non-CAD group.

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TABLE I
ANTHROPOMETRIC PARAMETERS IN CAD PATIENT AND NON-CAD CONTROL GROUP

Variable		CAD n=62 (%)	non-CAD n=31(%)	*p*-value
Mean ± SE of Age (years)		53 ±1.118	48±1.962	0.030
Smoking	Yes	17(27.4 %)	5 (16.12%)	0.027
	No	45(72.6%)	26 (83.87%)	
BMI (Kg/m^2)		29.37±0.596	26.31±0.468	0.000
SBP (mm Hg)		136.8±2.628	114.2±1.721	0.000
DBP (mm Hg)		84.94±2.058	77.53±1.118	0.010
Physical activity	Yes	20(32.25%)	11 (35.48%)	NS
	No	42(67.74%)	21 (64.51%)	
Fast food intake	Yes	22(35.48%)	11 (35.48%)	NS
	No	40(64.51%)	20 (64.51%)	
Soft drink	Yes	10 (16.12%)	6 (19.35%)	NS
	No	52 (83.87%)	25 (80.64%)	
Personal Diabetic	Yes	12(19.35%)	0 (0)	0.000
	No	50(80.64%)	31 (100%)	
Personal stork	Yes	3 (4.83%)	0 (0)	NS
	No	59(95.16 %)	31 (100%)	
Personal heart attack	Yes	12(19.35%)	0 (0)	0.000
	No	50(80.64%)	31 (100%)	
Family history of Diabetic	Yes	32(51.61%)	14 (45.16%)	NS
	No	30(48.38%)	17 (54.83%)	
Family history of hypertension	Yes	35(56.45%)	12 (38.70%)	0.001
	No	30(48.38%)	19 (61.29%)	
Family history of hyperlipidemia	Yes	14(22.58%)	9 (29%)	NS
	No	48(77.41%)	22 (70.96%)	
Family history of heart attack	Yes	13(20.96%)	5 (16.12%)	NS
	No	49(79.03%)	26 (83.87%)	
Family history of coronary artery	Yes	21(33.87%)	3 (9.6%)	0.000
	No	41(66.12%)	28 (90.32%)	

B. Simple Correlation analysis

In the current study, the correlation between IL-6 levels and various parameters in patients with CAD was investigated as in Table (2). The results, presented in this table indicate that IL-6 levels showed a no correlation with BMI (r=0.1460, p=0.162), age (r=0.0053, p=0.959), systolic blood pressure (r=0.104,p=0.3200) ,and diastolic blood pressure (r=0.068,p=0.511) .MPV(r=0.022,p=0.831).Whereas,RBC(r=0.222,p=0.032),Hb(r=0.193,p=0.062),HCT(r=0.213,p=0.039) , WBC (r=0.222, p=0.032), GRAN (r=0.219, p=0.034),PDWs (r=0.218,p=0.035), TAOC(r=0.115,p=0.271) , MDA (r=0.122,p=0.243), ICAM1 (r=0.217,p=0.036) , OX- LDL (r=0.305,p=0.002): have positively correlate with IL-6 levels. On the other hand each RDWs (r=-0.197,p=0.057), Lymphocyte count (r=-0.122, p=0.216), PLT(r=-0.118, p=0.258), PLT / LYM (r= -0.014,p=0.886),WBC/MPV (r=-0.197, p=0.057), Cholesterol (r=-0.042 ,p=0.682), HDL-C(r=-0.06, p=0.565), LDL-C(r= -0.0074, p=0.943) Cholesterol/HDL-C ratio (r=-0.07,p=0.502), TG/HDL-C ratio (r=-0.16,p=0.125), SOD (r=-0.214,p=0.039) GPX (r=-0.085,p=0.416), Urea (r= -0.023, p=0.823), Creatinine (r=-0.026, p=0.802), factors have negative correlation with IL-6 levels.

TABLE II
CORRELATION COEFFICIENT OF IL-6 WITH ANTHROPOMETRICS AND METABOLIC PARAMETERS OF THE STUDIED SUBJECTS

Parameter	r	p-value
Age	0.0053	0.959
BMI	0.146	0.162
Systolic	0.104	0.32
Diastolic	0.068	0.511
RBC	0.222	0.032
Hb	0.193	0.062
HCT	0.213	0.039
RDWs	-0.321	0.001
WBC	0.207	0.046
Lymphocyte	-0.122	0.216
GRAN	0.219	0.034
PLT	-0.118	0.258
MPV	0.022	0.831
PDWs	0.218	0.035
PLT/LYM	-0.014	0.886
WBC/ MPV	-0.197	0.057
Cholesterol	-0.042	0.682
TG	-0.183	0.078
HDL-C	-0.06	0.565
LDL-C	-0.0074	0.943
Cholesterol /HDL-C	-0.07	0.502
TG/HDL-C	-0.16	0.125
GPX	-0.085	0.416
SOD	-0.214	0.039
TAOC	0.115	0.271
MDA	0.122	0.243
ICAM1	0.217	0.036
OX-LDL	0.305	0.002
Urea	-0.023	0.823
Creatinine	-0.026	0.802

In the study, IL-6 showed strong positive associations between RBC number HCT, Granulocyte number WBC, PDW, ICAM1 levels, and OX-LDL. Notably, certain white blood cell differential counts, such as monocytes, neutrophils, and eosinophils, showed substantial relationships with the logarithm of IL-6, while lymphocytes or basophils did not demonstrate similar links. This discovery was rather surprising, considering it is well-established that lymphocytes are capable of generating IL-6 in laboratory conditions (Leng et al., 2005). Significant positive associations existed between CAM-1 and IL6, IL17, and TNF-α. This suggests that as the CAM-1 level found in the tissue fluid increases; it enhances the production of IL6, IL17, and TNF-α through cell adhesion and receptor binding. Consequently, this leads to higher expression levels in blood (Yang et al., 2019). IL-6 is a versatile cytokine produced by many different cell types, such as monocytes/macrophages, adipocytes, hematopoietic cells, and endothelial cells (Ataie-Kachoie et al., 2014). TheIL-6 regulates the synthesis of acute phase proteins and is elevated in the circulation during inflammatory conditions (Ataie-Kachoie et al., 2014). In addition, IL-6 has been found to influence the production of endothelium adhesion molecules and chemotactic proteins, such as Monocyte Chemo attractant Protein-1 (Wung et al., 2005). Furthermore, apart from conducting experiments, researchers have also identified iron independent effects of IL-6on the process of erythropoiesis in the setting of anemia caused by inflammation (Gardenghi et al., 2014). IL-6 exhibited a direct inhibitory effect on the proliferation of human TF-erythroleukemic cells in an in vitro environment, with the extent of inhibition depending on the dosage (McCranor et al.,

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2014). Heightened levels of oxidative stress play a crucial role in the progression of impaired vascular function, inflammation, blood clot formation, and the buildup of plaque in the arteries, ultimately leading to the emergence of vascular disease (Giugliano, 2000). High-sensitivity CRP (hs-CRP) and IL-6 are commonly used as inflammatory indicators in clinical research, and they have a major impact on the early stages of CAD (Luc et al., 2003). It is hypothesized that individuals diagnosed with multiple sclerosis may exhibit elevated levels of inflammation and oxidative stress. Antioxidant enzymes serve as the initial barrier towards ROS and result in a reduction in their levels of activity (Penckofer et al., 2002). The existing evidence indicates that inflammatory cytokines, including IL-6, have an impact on the synthesis and function of both eNOS and NADPH oxidase. Consequently, this Influence affects the levels of NO and superoxide, ultimately contributing to the occurrence of oxidative stress (Kofler et al., 2005, Karbach et al., 2014). The observed lack of connection between cholesterol and IL-6 implies that IL-6 may play an important part in modulating alterations in blood lipoprotein levels (Nakagomi et al., 2014). The reported impact on blood TC levels was also noted following the systemic administration of cytokines in animal models (Lewis et al., 2010).

C. Multiple regression analysis

The study used stepwise multiple regressions modeling (Table 3) to evaluate the variables influencing serum IL-6 levels in all individuals with coronary artery disease (CAD). Logarithmic transformation was applied to continuous variables deviating from a normal distribution. According to the stepwise multiple regression analysis, a number of independent variables had a substantial impact on serum IL-6 levels in individuals with stable coronary artery disease. In Model 1, there was a strong positive association between the total Ox-LDL and serum IL-6 levels, as indicated by a beta coefficient (β) of 0.998. The p-value was found to be less than 0.000, indicating a highly significant relationship indicating a highly significant association, which indicates that for every one-unit increase in total Ox-LDL, the IL-6 levels are expected to increase by 0.998 units. In Model 2, when a Family history of hyperlipidemia was introduced as an additional predictor, the beta coefficient for total Ox-LDL remained high at 0.989, and the p-value was still less than 0.000. This indicates that in the presence of a family history of hyperlipidemia, the effect of total Ox-LDL on IL-6 levels remains relatively unchanged and does not significantly modify the relationship between total Ox-LDL and IL-6 levels.

In Model 3, where MDA is introduced as an additional predictor, the beta coefficient for total Ox-LDL becomes 0.942, and the p-value is still less than 0.000 this indicates that after introducing both a Family history of hyperlipidemia and MDA, total Ox-LDL still significantly predicts serum IL-6 levels. The decrease in the beta coefficient from Model 2 to Model 3 may mean that MDA slightly modified the strength of the association between total Ox-LDL and IL-6 levels, potentially indicating a partial mediation effect.

TABLE III
SERUM IL-6 AS A DEPENDENT VARIABLE IN A WHOLE STUDY POPULATION USING STEPWISE MULTIPLE REGRESSION ANALYSIS ON

Model		B	beta	Partial correlation	95% CI		Adjusted R^2	P
					Lower	Upper		
1	OX-LDL	0.525	0.998	0.998	0.517	0.532	0.995	0.000
2	OX-LDL	0.52	0.989	0.997	0.512	0.529	0.995	0.000
	Family history of hyperlipidemia	0.04	0.017	0.216	0.002	0.078		
3	OX-LDL	0.496	0.942	0.972	0.47	0.521	0.996	0.000
	Family history of hyperlipidemia	0.043	0.019	0.236	0.06	0.081		
	MDA	0.096	0.048	0.213	0.04	0.191		

Furthermore, a multivariate stepwise regression model was utilized to determine clinical and anthropometric factors that were autonomously associated with IL-6. A multitude of anthropometric and biochemical factors were separately incorporated into the model. IOX-LDL, family history of hyperlipidemia, and MDA were found to have a direct association with IL-6. OX-LDL had been the main factor determining the serum IL-6 rate in individuals with stable CAD. Then MDA relatively influenced the relationship between total OX-LDL and IL-6 levels, suggesting a possible partial mediated impact. The initial indication of a potential relationship between OX-LDL and the development of atherosclerosis was provided by experimental studies demonstrating the detrimental effects of OX-LDL on endothelial cells (Hong et al., 2014). The condition of hypercholesterolemia is known to be linked with the generation of free radicals and lipoperoxides. Moreover, it is widely acknowledged that hypercholesterolemia can lead to phenotypic alterations in micro vascular cells (Simionescu, 2007). Furthermore, there exists a correlation between increased concentrations of is prostates in the bloodstream, which are byproducts of lipid peroxidation, and the occurrence of CAD and inflammation (Clejan et al., 2002), and high plasma levels of MDA-modified LDL-C are associated with plaque instability (Holvoet et al., 2008).

D. IL-6 genotype rs1800795

The IL-6 gene has been amplified, and the resulting amplicons were separated using gel electrophoresis, as depicted in Figure (1). Theo IL-6rs1800795 polymorphism was genotyped. The heterozygous and homozygous forms of IL-6 rs1800795 were identified as GC and CC, respectively, as shown in Figure (2). The GG genotype was regarded as a reference allele.

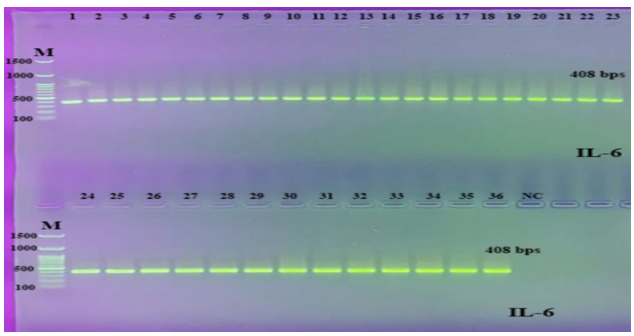

Fig. 1. Gel-electrophoresis of PCR product of the IL-6 gene. Lane M: DND ladder with 100 bp, Lane 1 to 36 positive for IL-6 gene at 408 bp,Lane NC: negative control.

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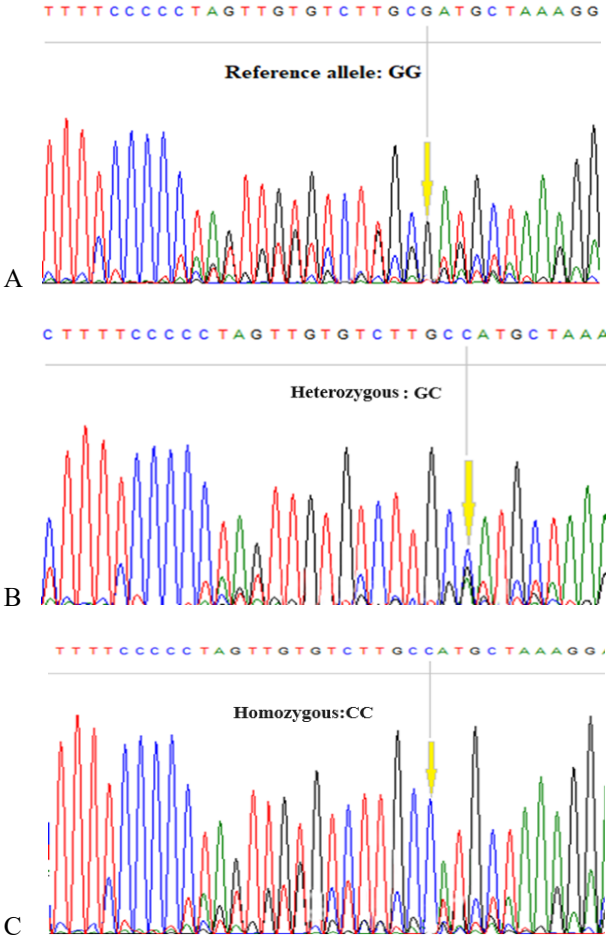


Fig. 2. Sequencing graph for the IL-6 gene rs1800795 (A) reference allele, homozygous genotype: GG; (B) heterozygous genotype: GC; (C) homozygous genotype: CC.

E. IL-6 rs1800795 genotype polymorphism with CAD

The higher producer and the intermediate CG genotype GG and CG had non-significant effects on the disease, respectively, p=0.87. Meanwhile, the low producer mutant genotype CC has almost a 10th fold effect on getting the disease, OR: 9.83, 95% CI: 2.2 to 21.0, P=0.03. The recessive GC+CC genotypes positively impact the disease progression than the dominant GG genotype, OR: 1.14, 95% CI: 0.43 to 2.96. The G allele has a protective effect with OR: 0.69, 95% CI: 0.33 to 1.40. The C allele, as shown in Table 4, was found to be a risk factor for the disease with an odds ratio (OR) of 1.46 and a 95% confidence interval (CI) ranging from 0.71 to 3.04.

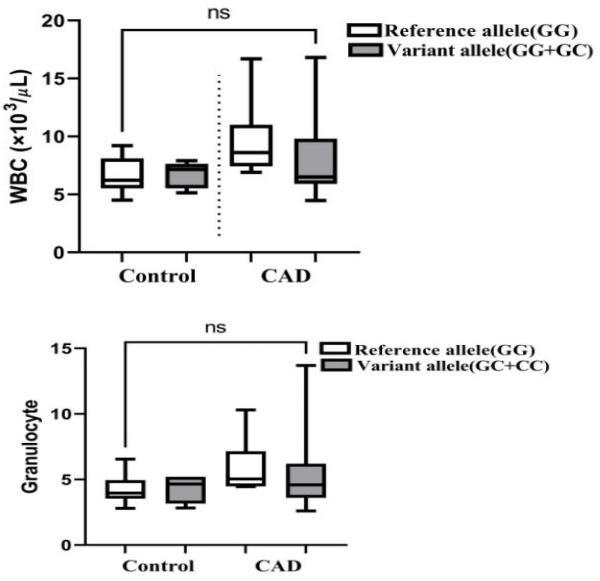
TABLE IV
THE FREQUENCY DISTRIBUTION OF GENOTYPE IL-6 RS1800795 BETWEEN CAD PATIENTS AND CONTROL0 IL-6 GENE WITH AN ODD RATIO

Genotypes	Patients N=62	Control N=31	OR	95% CI	*p*- value	x^2
GG	**26**	**14**	**0.88**	**0.34 to 2.30**	**0.46**	**0.087**
CG	**28**	**17**	**0.68**	**0.26 to 1.76**	**0.25**	**0.76**
CC	**8**	**0**	**9.83**	**2.2 to 21.0**	**0.03**	**4.32**
GG	**26**	**14**	**0.88**	**0.34 to 2.30**	**0.46**	**0.087**
GC+CC	**36**	**17**	**1.14**	**0.43 to 2.96**	**0.46**	**0.087**
G	**80**	**45**	**0.69**	**0.33 to 1.40**	**0.17**	**1.21**
C	**44**	**17**	**1.46**	**0.71 to 3.04**	**0.17**	**1.21**

The IL-6 rs1800795 genotype polymorphism was found to have a strong link between CAD risk factors. The GG genotype, which is less prevalent among stable people with CAD compared to non-CAD individuals, acts as a protective factor against developing the condition. GC+CC genotypes positively impact disease progression more than the dominant GG genotype, and the C allele was a risk factor for the disease. The study discovered that this genetic variation is linked to coronary artery disease (CAD). Specifically, depending on the genetic models employed, those who carry the -174G>C polymorphism had a heightened chance of developing CAD, ranging from 1.10 to 1.50 times higher. Elevated basal levels of IL-6 in the blood, which have both pro-inflammatory and pro-coagulant actions, be predictive of cardiovascular diseases (Vakili et al., 2011, Tuttolomondo et al., 2012, Wang et al., 2015). These results validate the association between those with the C allele of -174G>C and an increased risk of coronary artery disease (CAD). This data provides extensive support for the research conducted by Phulukdaree et al. (2013), which found that the occurrence of the IL-6 -174G>C; C allele affects the levels of IL-6 and raises the risk of coronary artery disease (CAD) among South African Indians.

F. The correlation between the IL-6 rs1800795 polymorphism and the risk factor linked with coronary artery disease (CAD)

The investigation was to examine the combined impact of the distribution of IL-6 rs1800795 alleles and specific risk factors of CAD, as shown in Figure 3. Interestingly, participants carrying the C allele (GC+CC genotype) displayed higher levels of WBC and granulocytes when compared to those with the G allele in the control group. However, it is essential to note that the observed differences were not statistically significant. The findings among participants with the CAD group's rs1800795 (GC+CC) genotype were equally intriguing. A non-significant rise in WBC/MPV, TG, and VLDL levels concerning the GG genotype controls.



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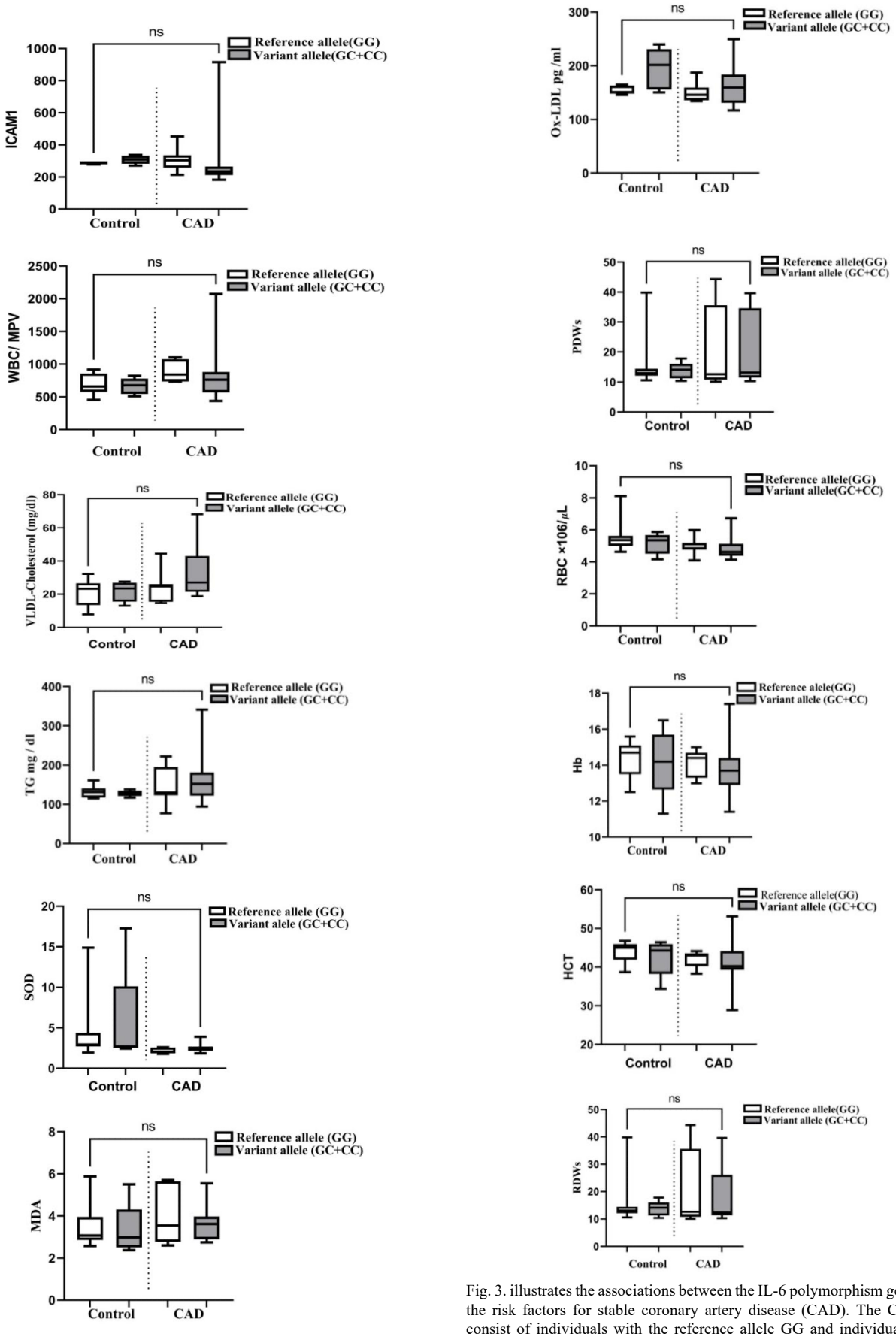

Fig. 3. illustrates the associations between the IL-6 polymorphism genotype and the risk factors for stable coronary artery disease (CAD). The CAD groups consist of individuals with the reference allele GG and individuals with the variant alleles GC and CC.

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Furthermore, the research also provides insight into the functioning of antioxidant enzymes. Within the CAD group, both the GG and GC+CC genotypes exhibited a significant reduction in SOD activity in comparison to the group of controls with the GG genotype. This suggests that oxidative stress may play a role in the progression of CAD. Furthermore, we observed a marginal elevation in levels of MDA in individuals with the GC+CC genotype compared to those with the GG genotypes in the control group, but this difference did not reach statistical significance. Another noteworthy finding was related to OX-LDL levels. Participants with the rs1800795 and GC+CC genotypes demonstrated higher OX-LDL concentrations than those with the GG genotype in the control group. However, similar to other observations, this difference was not statistically significant. The present study offers important knowledge of the correlation between the IL-6 rs1800795 polymorphism and other clinical markers in the CAD group. Although we discovered intriguing patterns and possible connections, we must acknowledge that the differences we noticed lacked statistical significance in our analysis. Participants in the CAD group have the rs1800795 GG genotype and those with the (GC+CC) genotype. There was a statistically insignificant reduction in red blood cell (RBC), hemoglobin (Hb), and hematocrit (HCT) levels when comparing the GG and (GC+CC) genotypes to the control group. Participants carrying the rs1800795 GG and (GC+CC) genotypes exhibited elevated levels of RDWs compared to those carrying the GG and (GC+CC) genotypes in the control group. Nevertheless, akin to other findings, this disparity did not yield a significantly different outcome.

Conclusion

In conclusion, our study highlights a significant association between Interleukin-6 promoter 174G>C gene polymorphisms and stable coronary artery disease in Kurdish men. Additionally, serum IL-6 levels were positively correlated with various physiological parameters.

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