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Investigation the role of PCSk9 and IL-6 genes polymorphism in patients with CVD

Eman Redha Omran

Medical Biotechnology Department, College of Biotechnology, Al-Qasim Green University, Babylon, 51013, Iraq. E-mail: imanreda@biotech.uoqasim.edu.iq

Abbas Abed Sharhan

*Corresponding author. Medical Biotechnology Department, College of Biotechnology, Al-Qasim Green University, Babylon, 51013, Iraq. E-mail: abbas_sharhan@biotech.uoqasim.edu.iq

Nktel Faiz Nassir Al-Saad

Medical Biotechnology Department, College of Biotechnology, Al-Qasim Green University, Babylon, 51013, Iraq. E-mail: nktel@biotech.uogasim.edu.iq

Abstract

Objective

Cardiovascular diseases are one of the most important causes of death worldwide. Research has shown that genetic and inflammatory factors play an important role in their occurrence. The aim of this study was to investigate the association of PCSK9 and IL-6 gene polymorphisms with cardiovascular diseases and to evaluate the status of lipid profile and inflammatory markers in affected patients.

Materials and methods

In this case-control study, 90 blood samples were collected from the Shahid Al-Mehrab Medical Center for Cardiac Diseases and Surgery at Marjan Teaching Hospital. The time period of this study was October 2023 to March 2024. Of these, 60 samples were from patients with cardiovascular diseases aged 30 to 70 years and 30 samples were from healthy individuals. Lipid profile including total cholesterol, triglycerides, LDL, VLDL and HDL were measured. Serum levels of PCSK9 and IL-6 and PCSK9 rs505151 and IL-6 −174G/C polymorphisms were also examined.

Results

The results showed that patients with cardiovascular diseases had a significant increase in total cholesterol, triglycerides, LDL and VLDL and a significant decrease in HDL compared to the healthy group. Serum PCSK9 levels were significantly higher in patients. This could play a role

in lipid metabolism disorders, vascular inflammation and the development of atherosclerosis. Examination of the PCSK9 rs505151 polymorphism showed that the protective GG genotype was less observed in patients and the AG and AA genotypes and the A allele were more observed in patients. In contrast, there was no significant difference in the genotypic distribution of the IL-6 −174G/C polymorphism between the two groups. However, serum IL-6 levels were significantly increased in patients.

Conclusions

The findings of this study suggest that PCSK9 gene polymorphisms may be associated with an increased risk of cardiovascular disease, while IL-6 acts more as an inflammatory marker than a direct genetic risk factor. These results may be useful in identifying individuals at risk and designing effective prevention and treatment strategies.

Keywords: cardiovascular disease, gene polymorphism, IL-6, lipoprotein, PCSK9

Paper Type: Research Paper.

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Introduction

Cardiovascular diseases are the most common cause of death worldwide, affecting millions of people annually (Vaduganathan et al., 2022). This group of diseases includes a wide range of heart and blood vessel disorders. The most important of them are coronary artery disease, stroke, peripheral vascular disease, congenital heart defects, rheumatic heart disease, and thromboembolic disorders such as pulmonary embolism and deep vein thrombosis. Among these diseases, coronary artery disease is the most common and deadly type. It accounts for a significant share of deaths from cardiovascular diseases (Vaduganathan et al., 2022). Several factors contribute to the development and progression of cardiovascular diseases. Some of these factors include lipid metabolism disorders, chronic inflammation, genetic factors, and unhealthy lifestyle.

Dyslipidemia is one of the most important risk factors for these diseases. It is associated with increased total cholesterol, low-density lipoprotein (LDL), and triglycerides, and decreased high-density lipoprotein (HDL) (Kalwick & Roth et al., 2025). These lipid changes contribute to the accumulation of fat in the vascular wall and the development of atherosclerosis. The PCSK9 protein is one of the main regulators of lipid metabolism. This regulator binds to the LDL receptor on the surface of liver cells, causing its degradation, resulting in increased LDL levels in the blood (Seidah et al., 2014). Increased PCSK9 activity can lead to lipid imbalance, progression of atherosclerosis, and increased risk of cardiovascular disease. For this reason, PCSK9 has been proposed as an important therapeutic target for the control of hypercholesterolemia, and its inhibitors have shown promising results in reducing LDL (Chaudhary et al., 2017). In addition to lipid disorders, inflammation plays a key role in the initiation and progression of cardiovascular diseases. Interleukin-6 (IL-6) is one of the most important inflammatory cytokines that plays a role in immune responses and the regulation of inflammatory processes in the body. Increased levels of IL-6 are associated with damage to the vascular wall, increased inflammation, and accelerated atherosclerosis (Favalli, 2020; Alhassan et al., 2022). Studies have also shown that IL-6 can affect lipid metabolism and increase the risk of cardiovascular diseases by increasing triglycerides and decreasing HDL (Favalli, 2020; Alhassan et al., 2022). It is important to investigate the genetic factors associated with these pathways, as genetic polymorphisms can affect the expression or function of proteins such as PCSK9 and IL-6, altering the susceptibility of individuals to cardiovascular disease. On the other hand, conventional biochemical methods alone are unable to accurately detect molecular and genetic differences and do not allow for the differentiation of different pathogenic factors (Ahsani et al., 2010; Mohammadabadi et al., 2004; Khabiri et al., 2025). In contrast, genomic techniques such as polymerase chain reaction (PCR) and DNA sequencing are rapid, accurate, and reliable tools for examining genetic alterations (Mohammadabadi et al., 2011; Shahdadnejad et al., 2016) and allow for direct identification of these alterations from clinical samples (Khabiri et al., 2023; Mohammadabadi et al., 2024; Mohammadabadi et al., 2025). Considering the simultaneous role of lipid disorders, inflammation, and genetic factors in the occurrence of cardiovascular diseases, the aim of this study was to investigate the association between polymorphisms of the PCSK9 and IL-6 genes to better understand the mechanisms of the disease, identify individuals at risk, and design more effective prevention and treatment strategies.

Materials and methods

Study design and population: This case-control study was conducted to investigate the biochemical and genetic associations of PCSK9 and IL-6 with cardiovascular diseases (CVD). A

total of 90 subjects participated in this study. Of these subjects, 60 were patients with cardiovascular disease associated with lipid disorders and 30 were apparently healthy controls. The age range of the participants was between 30 and 70 years. The control group was age-matched to the patients to minimize age-related confounding effects. Patients were recruited from the Shahid Al-Mehrab Medical Center for Cardiac Diseases and Surgery at Marjan Teaching Hospital between October 2024 and March 2025. The control group had no documented history of cardiovascular disease, dyslipidemia, inflammatory disorders, or chronic systemic diseases. Written informed consent was obtained from all participants before entering the study, and the research protocol was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki.

Sample collection: Venous blood samples (approximately 5 mL) were collected from all participants under sterile conditions. The blood samples were divided into two parts. The first part was collected in plain tubes for serum separation and biochemical tests. The second part was collected in EDTA-containing tubes for genomic DNA extraction. Serum samples were separated by centrifugation at 3000 rpm for 10 minutes and stored at -20°C until the tests were performed.

Biochemical analyses: Serum lipid profiles including total cholesterol (TC), triglycerides (TG), high-density lipoprotein cholesterol (HDL-C), low-density lipoprotein cholesterol (LDL-C), and very-low-density lipoprotein cholesterol (VLDL-C) were measured in all participants. These measurements were performed using commercial enzymatic-colorimetric kits from Biolabo (France) and according to the manufacturer's instructions. Optical absorbance was read with a spectrophotometer. Lipid concentrations were also calculated based on standard calibration curves. Serum PCSK9 and interleukin-6 (IL-6) concentrations were measured using ELISA kits from BT Lab (China). All experiments were performed in duplicate to ensure analytical precision. Optical density was read with a microplate reader. Concentrations were calculated based on standard curves prepared for each test.

DNA extraction and quality assessment: Genomic DNA was extracted from whole blood samples using the FavorPrep Genomic DNA Mini Kit (Favorgen, Taiwan) according to the manufacturer's protocol for fresh and frozen samples. The quantity and purity of the extracted DNA were assessed using a NanoDrop spectrophotometer by measuring the absorbance ratio at 260/280 nm. Samples with acceptable purity ratios were used for further molecular analyses.

Primer design and PCR amplification: Specific primers were designed to amplify regions containing polymorphisms of PCSK9 (rs505151) and IL-6 (rs1800795). Primer sequences were designed using the Primer-BLAST tool in the NCBI database and checked for specificity by BLAST analysis against the human genome. Primer selection criteria included appropriate melting temperature, primer length, GC percentage, and amplicon size (Table 1). PCR

amplification was performed using Promega PCR Master Mix (USA) in a final volume of 25 µL. PCR conditions included an initial denaturation step followed by 35 cycles of amplification. After optimization, the annealing temperature for both PCSK9 and IL-6 reactions was set to 58°C. The amplified PCR products were confirmed by agarose gel electrophoresis.

Table 1. Characteristics of primers used to amplify target genes in this study

Gene	Primer sequence (5'-3')	Tm (°C)
PCSK9 (rs505151)	F- GGGATGGGGCAGGCTATG R- CAGAGTGAGTGAGTTCCAGGC	58
IL-6 (rs1800795)	F- CAATACATGCCAATGTGCTGAGTCACTA R- AGAATGATCCTCAGTCATCTCCAGTCCT	58

Genotyping by PCR-RFLP: Genotyping of PCSK9 (rs505151) and IL-6 (rs1800795) polymorphisms was performed using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). Enzymatic digestion was performed using MboII enzyme for PCSK9 and FaeI enzyme for IL-6 (SibEnzyme, Russia) according to the manufacturer's recommendations. Each digestion reaction consisted of 5 µL of PCR product, 4 µL of appropriate enzyme buffer, 1 µL of restriction enzyme, and nuclease-free water to a final volume of 15 µL. The digested products were separated by agarose gel electrophoresis and visualized under ultraviolet light. Genotypic patterns were determined based on the size of the fragments obtained.

Statistical analysis: Statistical analyses were performed using SPSS version 23 software. Data were reported as mean ± standard deviation for continuous variables and as frequency and percentage for qualitative variables. Independent t-test was used to compare biochemical indices between patients and controls. Genotype and allele frequencies were compared using odds ratio (OR) and 95% confidence interval (CI). A P value of less than 0.05 was considered statistically significant.

Results and discussion

Changes in serum lipid profile in cardiovascular diseases: The results of this study showed that patients with cardiovascular diseases (CVD) had significant changes in blood lipid indices compared to apparently healthy individuals. As shown in Table 1, the levels of total cholesterol (TC), triglyceride (TG), low-density lipoprotein cholesterol (LDL-C), and very low-density lipoprotein cholesterol (VLDL-C) in patients were significantly higher than those in the control group. On the other hand, the level of high-density lipoprotein cholesterol (HDL-C) was significantly reduced. These findings are consistent with the known role of dyslipidemia as one of the main factors in the initiation and progression of atherosclerosis and cardiovascular diseases. When LDL-C and VLDL-C are increased, cholesterol accumulates in the vascular wall, foam

cells form, atherosclerotic plaques grow, and ultimately vascular occlusion occurs. At the same time, a decrease in HDL-C impairs reverse cholesterol transport and reduces its protective anti-inflammatory and antioxidant effects. Epidemiological studies and large clinical trials have shown that an increase in LDL-C and TG, accompanied by a decrease in HDL-C, significantly increases the risk of cardiovascular events. Therefore, the lipid abnormalities observed in this study provide further evidence to support the key role of metabolic abnormalities in the pathophysiology of cardiovascular diseases.

Table 1. Mean ± SD of lipid profile for patients and control

Parameter	Ch	TG	HDL	LDL	VLDL
Cases	174.10 ± 4.50	201.33 ±3.55	29.18 ± 1.44	186.76 ±5.54	40.27 ±1.91
Control	136.0 ±3.63	121.46 ± 4.44	41.22 ± 2.39	88.95 ±4.58	24.292 ± 0.88
T-test	5.137	2.670	3.219	5.467	2.302
P- Value	<0.0001	0.0096	0.0026	<0.0001	0.0247

Increased serum PCSK9 levels and clinical implications: As shown in Table 2, one of the important findings of this study was a significant increase in serum PCSK9 levels in patients with CVD compared with controls ($P < 0.0001$). This result is consistent with the growing evidence that PCSK9, in addition to its classical role in lipid metabolism, also plays an important role in the pathogenesis of cardiovascular diseases. PCSK9 reduces the clearance of LDL from the circulation by binding to LDL receptors on the surface of hepatocytes and directing them to the lysosomal degradation pathway. As a result, plasma LDL-C levels increase. Increased circulating PCSK9 is therefore directly associated with an increased risk of atherosclerosis. However, emerging evidence suggests that PCSK9 also plays a role in the progression of cardiovascular diseases through LDL-independent pathways. A meta-analysis by Vlachopoulos et al. (2016) showed that for every one standard deviation increase in baseline PCSK9 levels, the risk of future cardiovascular events significantly increased, even independently of LDL-C levels. Clinical and laboratory studies have shown that high levels of PCSK9 are associated with increased plaque necrotic core size, endothelial dysfunction, and increased vascular inflammation (Ragusa et al., 2025). PCSK9 can increase the expression of adhesion molecules such as ICAM-1 and VCAM-1, as well as inflammatory cytokines such as IL-6 (Tang et al., 2017). Thus, it can facilitate leukocyte recruitment to the vascular wall. The increase in PCSK9 observed in the patients in this study is likely a reflection of worsening dyslipidemia and increased vascular inflammation (Zhao et al., 2023). These findings reinforce the clinical importance of PCSK9 inhibitors. Randomized

trials and multiple meta-analyses have shown that these drugs, in addition to significantly reducing LDL-C, also significantly reduce the incidence of major cardiovascular events (Seidah et al., 2014). Although the cross-sectional design of the present study limits the possibility of proving a causal relationship, the results obtained suggest PCSK9 as a valuable biomarker and potential therapeutic target in cardiovascular diseases.

Table 2. Concentration of (PCSK9) pg/mL for CVD patients and controls

	Group	N0.	Mean	Std. Deviation	Std. Error Mean	T- value	*P*-value
PCSK9 (pg/mL)	Case	60	660.29	126.9063581	23.169825	t=6.507, df=88	<0.0001
	Control	30	460.85	148.8485332	19.216263		

Association of the rs505151 polymorphism of the PCSK9 gene with cardiovascular disease: Genotypic analysis showed that the rs505151 polymorphism of the PCSK9 gene is significantly associated with the risk of cardiovascular disease (Table 3 and Figure 1). The GG genotype (722 bp) was significantly less common in patients with CVD than in the control group, which may indicate the protective role of this genotype. In contrast, the AG (722 bp+470 bp+252 bp) and AA (470 bp+252 bp) genotypes were more prevalent in patients. Also, the allele frequency analysis showed that the A allele was more common in the patient group and the G allele was less common. These results indicate that the AA genotype and the A allele may increase the risk of cardiovascular disease. The present findings are consistent with previous studies that have shown that some PCSK9 polymorphisms are associated with increased PCSK9 expression, increased LDL-C, and increased risk of atherosclerosis (Al-Anbari et al., 2022; Chuan et al., 2019; Mushtaq Hashim Al-Bderee et al., 2023). Coggi et al. (2025) also reported that a reduced frequency of the G allele is associated with increased circulating PCSK9 levels, impaired endothelial function, and increased susceptibility to coronary artery disease. Mechanistically, genetic variations in PCSK9 can affect protein expression or its binding to the LDL receptor. Thus, they can regulate both lipid metabolism and inflammatory pathways. Overall, the genotypic and allelic distributions observed in this study support the growing evidence that genetic variations in PCSK9 contribute to cardiovascular disease risk through lipid-dependent and -independent mechanisms.

Increased serum IL-6 levels and inflammatory burden in CVD: As shown in Table 4, the results of this study showed that serum interleukin-6 (IL-6) levels were significantly higher in patients with CVD than in controls (P = 0.0072). IL-6 is a key proinflammatory cytokine that plays an important role in immune activation, endothelial dysfunction, and the progression of atherosclerotic plaques. Several studies have shown that increased circulating IL-6 is predictive

of coronary artery disease (Rai et al., 2021). This increase is strongly associated with disease severity, plaque instability, and thrombosis (Zahraa *et al.,* 2022 and Ridker *et al.,* 2018).

Table 3. Association of PCSK9 (rs505151) genotypes and allele frequencies with cardiovascular disease (CVD)

Genotype	Control	Case	OR (95% CI)	*P*-value
AA	16	40	-	
GG	8	4	0.2 (0.0529, 0.7586)	0.0312
AG	6	16	1.0384 (0.354, 3.213)	
		Allele Frequency		
A	38	96	-	
G	22	24	0.432 (0.861,0.217)	0.0156

*(*P*<0.05), OR: odd ratio, CI: confidence interval

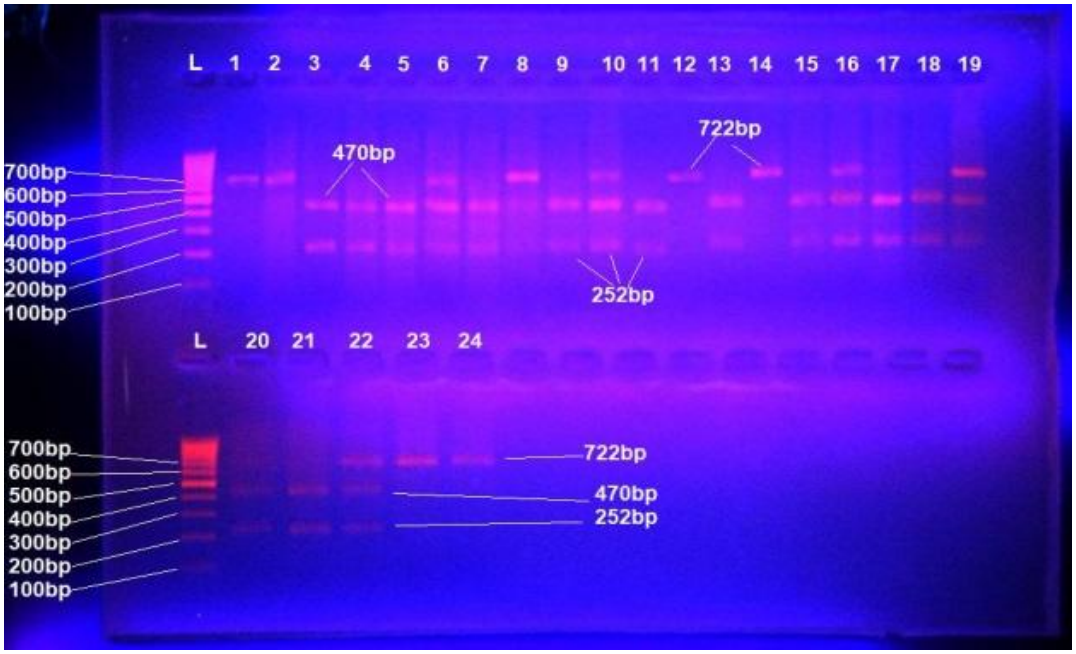

Figure 1. Genotyping of rs505151 polymorphism by PCR-RFLP. Lane L is 100bp DNA ladder. Lanes 1, 2, 8, 12, 14, 23 and 24 are GG genotype (722 bp). Lanes 6, 10, 16, 19 and 22 are AG genotype (722 bp+470 bp+252 bp). Lanes 3, 4, 5, 7, 11, 13, 15, 17, 18, 20 and 21 are AA genotype (470 bp+252 bp)

Meta-analyses have also confirmed that IL-6 levels are significantly higher in patients with ischemic heart disease. This level contributes to increased cardiovascular risk through inflammatory and metabolic pathways. In addition to its inflammatory role, IL-6 also affects lipid

metabolism. It can increase hepatic triglyceride synthesis, stimulate VLDL secretion, and reduce HDL-C levels (Kaptoge *et al.,* 2012; Luay et al., 2021; Nadhim, 2020). These dual inflammatory-metabolic effects may partly explain the strong association between increased IL-6 and dyslipidemia in CVD patients. Therefore, the increased IL-6 observed in this study reinforces its role as a marker of systemic inflammation and cardiovascular injury.

Table 4. Concentration of (IL-6) pg/mL for CVD patients and controls

IL-6 (pg/mL)	Group	N0.	Mean	Std. Deviation	Std. Error Mean	T- value	*P*-value
	Case	60	460.16666	154.8923	19.99651	t=2.752, df=88	0.0072
	Control	30	367.333333	137.03635	25.019301		

No association of IL-6 gene rs1800795 polymorphism with CVD: In contrast, genotyping results of IL-6 gene rs1800795 polymorphism (174G/C−) showed no significant difference in genotype distribution or allele frequency between patients and controls (Table 5 and Figure 2). This finding suggests that this specific genetic variant does not play a determining role in cardiovascular disease susceptibility in the study population. Previous studies in this area have reported conflicting results. While some studies have suggested a weak association, many other studies have not found a significant association between this polymorphism and the risk of coronary artery disease (Hou et al., 2015; Al-Saad et al., 2020). These discrepancies could be due to racial differences, environmental factors, sample size, and the multigenic and complex nature of inflammatory pathways in CVD. Therefore, although IL-6 protein levels are increased in patients, this increase appears to be influenced more by environmental factors and non-genetic settings than by this specific gene variant.

Table 5. Association of IL-6 (SNP1800795) genotypes and allele frequencies with cardiovascular disease (CVD)

Model	Control	Case	OR (95% CI)	*P*-value
GG	22	43	-	0.48
GC	8	15	1.52 (0.44-5.26)	
CC	0	2	2.8 (0.13-60.9)	
		Allele frequency		
G	52	101	-	0.31
C	8	19	2 (0.63-6.31)	

*(P<0.05), OR: odd ratio, CI: confidence interval

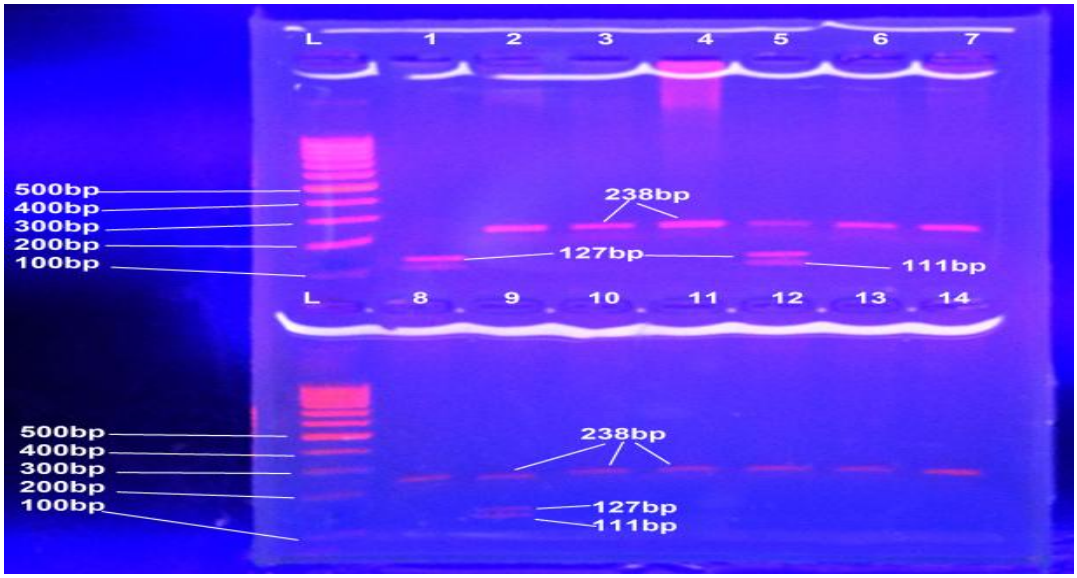

Figure 2. Genotyping of rs1800795 polymorphism by PCR_RFLP. Lane L is 100bp DNA ladder. Lane 1 is CC genotype (127 bp+111 bp). Lanes 5 and 9 are GC genotype (238 bp+127 bp+111 bp). Other lanes are GG genotype (238 bp)

Overall, the findings of this study emphasize the complex interaction between metabolic disorders, systemic inflammation, and genetic factors in the onset and progression of cardiovascular disease. Patients with CVD had marked dyslipidemia, elevated serum levels of PCSK9 and IL-6, and a different genetic distribution of the PCSK9 gene. These results indicate that PCSK9 plays a pivotal role in connecting the lipid and inflammatory pathways. While the genetic role of IL-6 appears to be limited in this population. These findings may provide a basis for the development of targeted diagnostic and therapeutic approaches in cardiovascular disease.

Conclusion: The results of this case-control study provide strong evidence for the interrelated role of lipid disorders, systemic inflammation, and genetic alterations in the pathogenesis of cardiovascular diseases. Patients with CVD had significant changes in their lipid profile. This was characterized by increased total cholesterol, triglycerides, LDL-C, and VLDL-C, and decreased HDL-C. This confirms the pivotal role of lipid metabolism disorders in cardiovascular pathology. One of the prominent findings of this study was a significant increase in serum PCSK9 levels in patients compared to healthy individuals. This result indicates that PCSK9 plays a role in increasing the risk of cardiovascular diseases through different pathways. Through lipid pathways such as regulation of LDL receptors, cholesterol homeostasis, and through lipid-independent pathways such as exacerbation of vascular inflammation and endothelial dysfunction. The significant association of the rs505151 polymorphism of the PCSK9 gene with CVD also emphasizes the importance of the genetic background of this protein. In such a way that the decrease in the frequency of the GG genotype and the increase in the A allele in

patients may indicate the protective role of the G allele and the risk role of the A allele in the study population. Also, the significant increase in serum IL-6 levels in patients highlights the role of systemic inflammation in the progression of cardiovascular diseases. IL-6 is associated with endothelial activation, plaque instability, and adverse metabolic effects. However, the lack of a significant association between the rs1800795 polymorphism of the IL-6 gene and the risk of CVD suggests that this particular genetic variant does not play a major role in disease susceptibility in this population. Environmental, epigenetic, or regulatory factors are likely to play a more prominent role in the increase in IL-6 levels. Taken together, the results of this study suggest that cardiovascular diseases are the result of a complex interaction between metabolic, inflammatory, and genetic factors. PCSK9 is proposed as a key factor in connecting these pathways. It can be considered as a valuable biomarker and therapeutic target. These findings provide a deeper understanding of the mechanisms underlying CVD and could provide a basis for the development of targeted diagnostic and therapeutic strategies. Based on the results obtained, the following should be considered for clinical applications and future research.

Measuring serum PCSK9 levels in combination with routine lipid profile assessments. This could help improve cardiovascular risk prediction, especially in individuals with dyslipidemia or a family history of heart disease.

Investigating PCSK9 gene polymorphisms, especially rs505151, in the context of personalized medicine. This could identify individuals with a higher genetic predisposition to CVD and provide more appropriate preventive and therapeutic strategies for them.

Conducting larger, multicenter, and more ethnically diverse studies. This could be useful to confirm the present findings and examine population differences. Because these longitudinal studies are essential to investigate causal relationships between PCSK9, IL-6, genetic variants, and cardiovascular outcomes.

Focusing on investigating gene-environment interactions, epigenetic regulation, and combined models of lipid, inflammatory, and genetic markers. This could pave the way for early diagnosis, effective prevention, and personalized treatment of cardiovascular diseases.

Author contributions

ERO: Conceptualization, methodology, software, validation, formal analysis, investigation, resources, and data curation. AAS and NFA: Writing-original draft preparation, writing-review, visualization, and funding acquisition.

Data availability statement

Data are available from the authors upon reasonable request.

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Ethical considerations

This research has been approved by the Ethical Approval Committee of College of Education (Reference No., 318, 7/4/2024) at the Al-Qasim Green University, Iraq. Moreover, the study was carried out with integrity, with no fabrication, falsification, plagiarism, or any scientific misconduct.

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Conflict of interest

The authors declare that they have no conflict of interest.

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بررسی نقش پلی‌مورفیسم ژن‌های PCSK9 و IL-6 در بیماران مبتلا به بیماری‌های قلبی-عروقی

ایمان رضا عمران

گروه زیست‌فناوری پزشکی، دانشکده زیست‌فناوری، دانشگاه سبز القاسم، بابل ۵۱۰۱۳، عراق. ایمیل: imanreda@biotech.uoqasim.edu.iq

عباس عبد شَرْحان

*نویسنده مسئول. گروه زیست‌فناوری پزشکی، دانشکده زیست‌فناوری، دانشگاه سبز القاسم، بابل ۵۱۰۱۳، عراق. ایمیل: abbas_sharhan@biotech.uoqasim.edu.iq

نکتل فایز نصیر السعد

گروه زیست‌فناوری پزشکی، دانشکده زیست‌فناوری، دانشگاه سبز القاسم، بابل ۵۱۰۱۳، عراق. ایمیل: nktel@biotech.uogasim.edu.iq

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چکیده

هدف: بیماری‌های قلبی-عروقی یکی از مهم‌ترین علل مرگ‌ومیر در سراسر جهان به شمار می‌روند. پژوهش‌ها نشان داده‌اند که عوامل ژنتیکی و التهابی نقش مهمی در بروز این بیماری‌ها ایفا می‌کنند. هدف از این مطالعه بررسی ارتباط پلی‌مورفیسم ژن‌های PCSK9 و IL-6 با بیماری‌های قلبی-عروقی و همچنین ارزیابی وضعیت پروفایل لیپیدی و شاخص‌های التهابی در بیماران مبتلا بود.

مواد و روش‌ها: در این مطالعه مورد-شاهدی، ۹۰ نمونه خون از مرکز پزشکی و جراحی بیماری‌های قلبی شهید المحراب در بیمارستان آموزشی مرجان جمع‌آوری شد. این مطالعه در بازه زمانی اکتبر ۲۰۲۳ تا مارس ۲۰۲۴ انجام گردید. از این تعداد، ۶۰ نمونه مربوط به بیماران مبتلا به بیماری‌های قلبی-عروقی در محدوده سنی ۳۰ تا ۷۰ سال و ۳۰ نمونه مربوط به افراد سالم بود. پروفایل لیپیدی شامل کلسترول تام، تری‌گلیسرید، LDL، VLDL و HDL اندازه‌گیری شد. همچنین سطوح سرمی PCSK9 و IL-6 و پلی‌مورفیسم‌های PCSK9 rs505151 و IL-6−174G/C مورد بررسی قرار گرفتند.

نتایج: نتایج نشان داد که در بیماران مبتلا به بیماری‌های قلبی-عروقی، میزان کلسترول تام، تری‌گلیسرید، LDL و VLDL به‌طور معنی‌داری افزایش و سطح HDL به‌طور معنی‌داری کاهش یافته بود. سطح سرمی PCSK9 در بیماران به‌طور قابل توجهی بالاتر بود که می‌تواند در اختلالات متابولیسم لیپیدها، التهاب عروقی و پیشرفت آترواسکلروز نقش داشته باشد. بررسی پلی‌مورفیسم PCSK9 rs505151 نشان داد که ژنوتیپ محافظتی GG در بیماران کمتر مشاهده شد، در حالی که ژنوتیپ‌های AG و AA و آلل A در بیماران شیوع بیشتری داشتند. در مقابل، تفاوت معنی‌داری در توزیع ژنوتیپی پلی‌مورفیسم IL-6 −174G/C بین دو گروه مشاهده نشد؛ با این حال، سطح سرمی IL-6 در بیماران به‌طور معنی‌داری افزایش یافته بود.

نتیجه‌گیری: یافته‌های این مطالعه نشان می‌دهد که پلی‌مورفیسم‌های ژن PCSK9 می‌توانند با افزایش خطر ابتلا به بیماری‌های قلبی-عروقی مرتبط باشند، در حالی که IL-6 بیشتر به‌عنوان یک نشانگر التهابی عمل می‌کند تا یک عامل خطر ژنتیکی مستقیم. این نتایج می‌تواند در شناسایی افراد در معرض خطر و طراحی راهبردهای مؤثر پیشگیری و درمان مفید باشد.

کلمات کلیدی: بیماری قلبی-عروقی، پلی‌مورفیسم ژنی، لیپوپروتئین، IL-6، PCSK9

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