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Single Nucleotide Polymorphism and Cardiovascular Disease: A Systematic Review

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Abstract

Cardiovascular diseases (CVDs) have been the leading cause of death globally in 2019, accounting for 32% of all deaths. Their improvement is driven by genetic elements, with single-nucleotide polymorphisms (SNPs) serving as key biological markers. This assessment aimed to discover the genetic elements of CVDs via population-specific SNPs to discover associations and determine destiny population health developments. This systematic assessment accompanied PRISMA recommendations and used the PICO framework. a seek of 10 databases was conducted for scholarly articles on SNPs associated with CVD, without a restriction on area, age, or sex. The Study found out a link between SNPs and CVD susceptibility across diverse populations. In Asian Indians, the rs1799983 variant becomes connected to a heightened STEMI threat, even as in Koreans, rs74457740 become associated with myocardial infarction (MI). inside the Uyghur population, rs17671591 and rs3761740 impacted lipid degrees in response to statin therapy. a gene-food regimen interaction becomes discovered in Iranians, where the rs1501299 and rs6450176 genotypes motivated the benefits of the DASH food regimen on blood strain and obesity. The findings highlight the vast impact of genetic ancestry and gene-surroundings interactions on CVD susceptibility. The assessment

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emphasizes the necessity of ancestry-knowledgeable precision remedy for powerful cardiovascular care.

Keywords: Cardiovascular diseases (CVDs); Nucleotide Polymorphisms (SNPs); population-specific; Systematic assessment; Coronary Artery disorder (CAD); Myocardial Infarction (MI)

1. Introduction:

Background: In 2019, over 17.9 million deaths, or 32% of all deaths, cardiovascular diseases (CVDs) were the leading cause of death worldwide, responsible for a significant number of fatalities each year. Heart attacks and strokes accounted for the majority of these deaths (85%), with more than 75% of them taking place in low- and middle-income nations. Furthermore, CVDs were responsible for 38% of the 17 million premature deaths linked to noncommunicable diseases that year (*1*).

Cardiovascular Disease (CVD): Cardiovascular disease is a group of diseases that affect the heart and blood circulation, leading to blockages that impair blood flow. This includes coronary artery disease, brain vascular disease, peripheral arterial disease, atherosclerosis, heart malformation, venous thromboembolism, and lung blockage that affect the heart and blood circulation, leading to blockages that impair blood flow. These blockages can be caused by the extra fat deposits, brain haemorrhages, or blood clots, frequently resulting in acute events such as heart blockage and strokes. (*2*).

CVD as a Noncommunicable Disease: Cardiovascular disease (CVD) is an example of a non-communicable disease (NCD) because it cannot be transmitted from person to person or through infectious vectors. Instead, its development is influenced by environmental, genetic, and behavioural factors, which are collectively referred to as risk factors (*1*). For example, Hypertension and diabetes are highly prevalent among Asian Indians, which leads to a higher prevalence of cardiovascular disease (CVD) (*3*). The risk factors include poor diets, insufficient physical activity, tobacco use, and alcohol consumption. These behaviours contribute to abnormal metabolic activity, increased blood glucose levels, and improper fat deposition in the bloodstream. (*4*). As a result, it's one of the serious global issues that causes mortality and morbidity; understanding CVDs as NCDs is crucial for developing strategies and overcoming this global burden.

Single Nucleotide Polymorphisms (SNPs): Single-nucleotide polymorphisms, or SNPs (called "snips"), represent the most common genetic variations among individuals, accounting for over 90% of the differences observed between unrelated people. A single-nucleotide polymorphism (SNP) occurs when there is a variation in a single nucleotide base in a DNA sequence, which consists of adenine (A), cytosine (C), guanine (G), or thymine (T), is replaced by another nucleotide. Snips is a rare incident that occurs in a single nucleotide in a base pair of a gene due to a point mutation, and it's also called a rare mutation, which happens in less

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than 1%. Most of the snips are present in non-coding genes, and very few in coding genes (*5)*. The important implication of SNPs in public health domains is their use as a key biological marker because of their prevalence and stability. They are used for the creation of genetic mapping, which is used in the study of multi-gene traits. In forensic science, snips are used as tools for identifying different biomolecules in a crime scene in addition to identifying individuals (*6*).

Aims & Objectives: The genetic aspects of cardiovascular diseases (CVDs) need to be explored from the perspective of single-nucleotide polymorphisms (SNPs). To achieve this, it's essential to identify population-specific SNPs that are associated with CVDs, as they can help determine future population health trends.

2. **Methodology**:

This systematic review is prepared using the Preferred Reporting Items for Systematic Review (PRISMA) guidelines. The PICO (Population, Intervention, Comparison, Outcome) is used for the preparation of the research question. Under the search strategy used, the key terms: 'SNPs associated with CVD', 'CVD risk factor & SNP', 'SNPs & CVD', and 'Relationship SNPs &

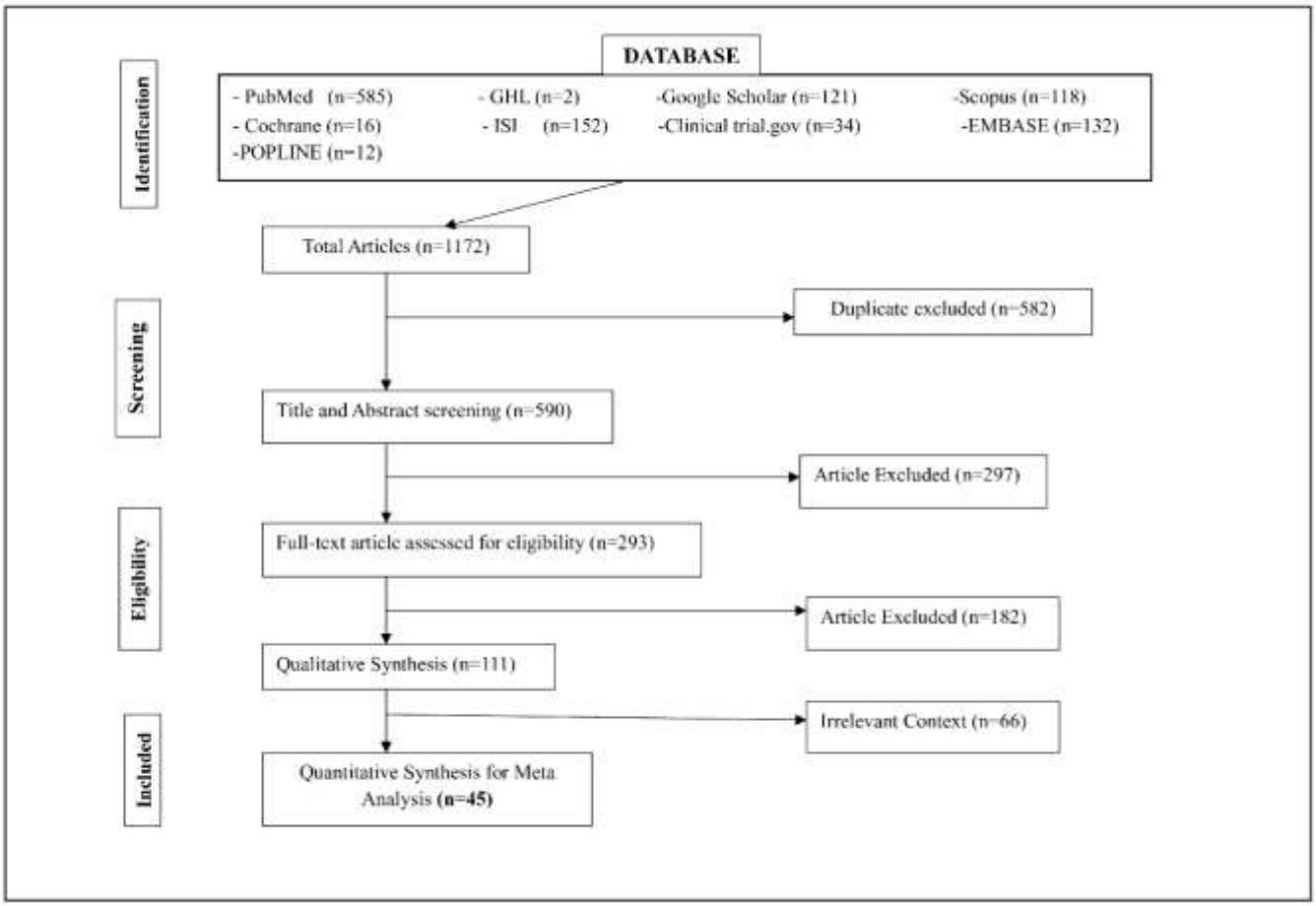

Figure 1: PRISMA flow diagram of studies' screening and selection

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CVD' were searched in the following 10 databases. After reviewing the articles, identify scholarly articles that have examined gene variants (SNPs) associated with cardiovascular disease (CVD), with no restriction on region, age, and sex, that are included for Quantitative assessment for meta-analysis. The Studies that have only presented abstracts, conference presentations, seminars, or have been published in non-indexed journals are excluded, along with articles that do not mention the specific SNPs responsible for direct cardiovascular disease (CVD) or CVD risk. The details of these steps are presented in the PRISMA flowchart below (**Fig.1)**

3. Results

Table 1 highlights that recent discoveries in cardiovascular genomics have opened many possible paths that link the single-nucleotide polymorphisms (SNPs) and the susceptibility to cardiovascular diseases (CVD) across ethnicity and geography. In a cross-sectional study of Asian Indian people, the *rs1799983* variant was considerably linked with an increased risk of ST-elevation myocardial infarction (STEMI); in contrast, *rs805305* showed a direct relationship with coronary artery disease (CAD) *(7)*. The *IL-8-rs4073* as strongly linked with the risk of CAD across all genetic diversity *(8)*. Another study in Asian populations shows a stronger influence on the risk. In a study of South Africa, the significant link of *rs28362286* in increasing CVD risk among older individuals, which shows the genetic vulnerability in aging populations (*9)*. Research from East Asia sheds light on the regional differences in CVD risk. The Korean Genome and Epidemiology Study (KoGESA large-scale cohort study conducted in Korea, was carried out by rs74457740, which is found in the MED13L gene, and was strongly linked to myocardial infarction (MI) along with other SNPs linked to HDL regulation (*10)*. The rs3761740 and rs17671591 influenced LDL-C and total cholesterol levels after statin administration with significant ethnic differences according to a study done in Han Chinese and Uyghur populations, highlighting pharmacogenomic diversity *(11)*. The study intertwined diet and genetic interaction in Iranian adults aged 20–70 the authors discovered that following the DASH diet was linked to lower blood pressure and less central obesity but only in those who carried particular genotypes (AA for rs6450176 and TT for rs1501299), indicating a link between diet and gene in the modulation of cardiovascular risk *(12)*.

Several studies have reported associations between single-nucleotide polymorphisms (SNPs) and specific vascular pathologies. A follow-up study discovered that among patients with pre-existing cardiovascular disease, the rs7566605 variant was more frequently linked to peripheral vascular and cerebrovascular disease in older individuals and was sex-specific (*13)*. In the context of Europe, SNPs like rs11061946 and rs11061973 further linked metabolic dysfunction with cardiovascular outcomes by increasing the risk of developing type 2 diabetes mellitus (T2DM) from impaired glucose tolerance (IGT) *(14)*. Another cross-sectional study was carried out in Japan. (2011) showed that people with the AA genotype of rs2805533 had higher triglyceride levels, belly circumference, and all-important metabolic indicators, including BMI, which are linked to an increased risk of cardiovascular disease (CVD) *(15)*. The clinical impact of pharmacogenetics, the rs1870377 SNP was found to be strongly associated with clopidogrel resistance in Arabian patients who had received percutaneous coronary intervention (PCI) *(16)*.

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The rs2231142 TT genotype was associated with a lower Framingham Risk Score for CVD, particularly among non-obese, hyperuricemic women, according to a 2024 cross-sectional study involving over 139,000 participants *(10)*. These finding highlights sex-specific genetic effects. CAD and stroke have a genetic basis, which has been continuously confirmed by regional and genome-wide association studies. For example, rs783396 and rs1804689 were linked to an increased risk of ischemic stroke (IS) in African American populations in a GWAS study *(17)*. A case-control study conducted by found that in the Belgian population, rs10757278 was associated with coronary heart disease, that linked to different pathogenic pathways compared to isolated cardiovascular disease *(18)* (**Table 1**).

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Table 1: Previous studies that enlighten the SNPs associated with cardiovascular disease (CVD)

SL NO.	AUTHOR (REFERENCE)	POPULATION	AGE GROUP	SAMPLE SIZE	Responsible SNPs	IMPACTS ON CVD	STUDY TYPE
1	*Shiraz Rizvi et al.,2025*	Asian Indian	Not Specified	148 CAD patients and 75 healthy controls	rs1799983, rs805305	rs1799983 polymorphism to heightened STEMI risk, and rs805305 is directly associated with CAD patients	Cross-sectional study
2	*Li et al.,2024*	Globally	Not Specified	14574 cases and 13001 controls	IL-8-rs4073	IL-8-rs4073 was strongly linked with a higher risk of CAD across all genetic models in the countries. Among them, IL-8-rs4073 conferred a substantially increased risk of CAD among Asians, including East, South, and West Asians.	Review
3	*Chalwe et al.,2024*	South Africa	Not Specified	61 elderly individuals	rs28362286	rs28362286 possible roles in the risk of CVDs	cross-sectional study
4	*Lee et al.,2025*	Korean	Not Specified	68,806 individuals	rs74457740	The study revealed the association of 7,877 SNPs in nine loci; among them six SNPs significantly related to both hypo- and hyper-HDL groups. Additionally, the study found that rs74457740, a SNP located in the MED13L gene locus, was significantly linked with an increased risk of MI.	Korean Genome and Epidemiology Study (KoGES)
5	*Z. Liu et al.,2024*	Chinese	Not Specified	Han Chinese (n=405) and Uyghur (n=373)	rs17671591, rs3761740	rs3761740 was correlated with the levels of TC, LDL-C, and non-HDL-C before and after oral statin in Uyghurs, but not with the blood lipid levels of the Han population. rs17671591 was linked with the level of LDL-C before and after oral statin, and also affected The changes in LDL-C after oral statins.	cross-sectional
6	*Mollahosseini et al.,2025*	Iranian	20–70 years	387 Adults	rs1501299, rs6450176	The results suggest that following the Dietary Approach to Stop Hypertension (DASH) diet may be related to lower blood pressure and central obesity indices only in individuals with the TT genotype of rs1501299 and the AA genotype of rs6450176.	cross-sectional
7	*Skelding et al.,2010*	White, Black, and Asian	Not Specified	947 Pre-existing CVD patients	rs7566605	Age and gender may influence the association of the rs7566605 with Peripheral Vascular Disease (PVD) and cerebrovascular disease in patients with pre-existing CVD.	Follow-up Study
8	*Siitonen et al.,2011*	European	Not Specified	540	rs10848554, rs11061937, rs1058322, and rs16928751	four SNPs (rs10848554, rs11061937, rs1058322, rs16928751) were associated with CVD risk. The individuals homozygous for the rare minor alleles of rs11061946 and rs11061973 had an increased risk of change from abnormal glucose tolerance (IGT) to Type 2 Diabetes Mellitus (T2DM).	Follow-up Study
9	*Oguro et al.,2011*	Japanese	Not Specified	1504	rs2805533	The subjects with the AA genotype of rs2805533 had a greater waist circumference, higher BMI, and higher triglyceride levels, influencing the CVD risk.	cross-sectional study
10	*Awaida et al.,2021*	Arabian	Not Specified	324 post percutaneous coronary interventions (PCI)	rs1870377	KDR rs1870377 SNP is robustly associated with clopidogrel resistance (CR). A variant in the rs1870377 SNP may have an impact on the serum levels of VEGFR2 and low-density lipoprotein.	Case-control study
11	*Lee et al.,2024*	Taiwanese	30–70 years	1,39,508	rs2231142	The ABCG2 rs2231142 TT genotype is related to a lower Framingham Risk Score for Cardiovascular Disease (FRS-CVD), particularly in non-obese hyperuricemic female individuals	cross-sectional study

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12	*Lappalainen et al.,2010*	European	Not Specified	6214 men	rs9939609	rs9939609 may subsidize to the progress of CVD in men with an abnormal glucose metabolism.	Mixed method
13	*Carty et al.,2012*	Europe, America, and Africa	Not Specified	European Americans (EA) N=26 276, African-Americans (AA) N=8970, and American Indians (AI) N=3570	rs783396 and rs1804689	rs783396 and rs1804689 were associated with increased IS ischemic stroke (IS) hazard in the African American cohort.	GWAS study
14	*Lemmens et al.,2009*	European	Not Specified	926 patients with CAD from the CAREGENE study, in 648 patients with CVD from the Leuven Stroke Genetics Study (LSGS) and the Belgian Stroke Study (BSS), and 828 unrelated controls	rs10757278	rs10757278 is allied with coronary heart disease in the Belgian population, but not with isolated CVD. These discoveries propose different infective mechanisms in CAD versus CVD	Case-control study
15	*Y Iwamoto et al.,2011*	Japanese	Not Specified	357 hypertensive patients	Ser49Gly, Glu27Gln, and Trp64Arg	These three SNPs might be danger factors for CVD in hypertensive patients.	Follow-up cohort study
16	*Amrita et al.,2020*	Asian Indian	Not Specified	cases (n=265) and controls (n=258)	rs1501299	Based on observed results, the present study reveals that the rs1501299 variation in the AdipoQ gene is among the genetic factors predisposing the population of Punjab to CVD.	case-control study of menopausal women with CVD
17	*Yang et al.,2021*	European	Not Specified	4,953	rs632793 and rs41300100	rs632793 and rs41300100 were autonomously related with higher serum NT-proBNP levels, which is a biomarker of CVD.	cross-sectional study
18	*Manichaikul et al.,2018*	Caucasian, African, American, Hispanic, Chinese-American	Not Specified	7,806	rs10846744	rs10846744 is significantly associated with Lp-PLA2 activity, atherosclerosis, and CVD events	cross-sectional study
19	*Bouchard et al.,2009*	American	Not Specified	962 obese individuals	rs1055419	Significant associations between rs1055419 (variants of OSBPL11) and diastolic blood pressure. The results suggest that the OSBPL11 gene is involved in cholesterol and glucose metabolism in obese individuals.	cross-sectional study
20	*Al-Shammari et al.,2017*	Arabian	Not Specified	T2D (320 patients), CVD (250 patients) or both (60 patients) and 516 healthy controls	rs2237892, rs151290 and rs2237895	SNPs rs151290 and rs2237895 are linked with CVD in this population, but present no association with T2D.	Case-control study
21	*Buraczynska et al.,2014*	European	Not Specified	920 patients with diabetes and 834 healthy controls	rs11614913	The study findings suggest that rs11614913 is associated with an increased risk of CVD in type 2 diabetes patients.	Case-control study

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22	*Ley et al.,2013*	Malaysian	Not Specified	141 patients with high LDLc levels	rs12720762	SNP rs12720762 in the APOB gene is associated with the significant risk of Familial hypercholesterolemia (FH).	Case-control study
23	*Ramkaran et al.,2016*	African Indian	Not Specified	568 (204 CAD patients and 364 control)	rs1467568 and rs7895833	rs1467568 and rs7895833 SNP variant alleles occurred more frequently in SA Indians than in SA blacks, but no difference was found between CAD patients and controls	case-control study
24	*Aka et al.,2021*	Bangladesh	Not Specified	250 T2DM cases and 246 healthy controls	rs5219	The study finds that the rs5219 polymorphism is correlated with the risk of T2DM-related CVD.	Case-control study
25	*Wang et al.,2022*	European	Not Specified	800 individuals	rs415235	37 SNPs revealed associations with CVD, among them, rs415235 is highly associated.	cross-sectional study
26	*Melton et al.,2010*	American Indians	Not Specified	Not Specified	rs7875153	The rs7875153 genetic variation may be related with Heart Rate (HR).	cross-sectional study
27	*Van Schie et al.,2010*	European	male (18-45), female (18-55)	421 young patients with a first event of acute coronary heart disease (CHD) or ischemic stroke (IS), and 409 healthy control participants	rs1063857	The study established that the association between rs1063857 and CVD risk	Case-control study
28	*Aghasizadeh et al.,2021*	Iranian	Not Specified	9700 participants without cardiovascular disease (CVD)	rs1748195, rs11207997, and rs10789117	The findings of this study suggest that rs1748195, rs11207997, and rs10789117 are related to CVD risk	Follow-up Study
29	*Fantino et al.,2021*	American	Not Specified	725 genetically confirmed familial hypercholesterolemia (FH) patients	rs17609940	After correction for confounding cardiovascular risk factors, the relation between the rs17609940 and incident Major adverse cardiovascular events (MACE) remained strongly significant.	follow-up study
30	*Devi et al.,2022*	Asian Indian	Not Specified	A total of 191 subjects were involved in this study, including 100 CVD cases and 91 controls, with ages ranging from 18 to 65 years from the state of Haryana (India)	rs2237892	The present association study of the KCNQ1 gene variant rs2237892 (C/ T) with cardiovascular diseases found a link between this polymorphism and CVD susceptibility in the Indian population	cross-sectional study
31	*Key et al.,2022*	American	Not Specified	124 Latinx adults	rs4680	The rs4680 genotype is associated with depressive symptoms in Latinx adults, which may increase CVD risk	randomized controlled trial
32	*Paquatte et al.,2020*	American	Not Specified	725 CVD patients	rs964184	The rs964184 plays a role in forming Myocardial Infarction (MI) even after correction for common CVD risk factors.	cross-sectional study
33	*Fojas et al.,2025*	European	Not Specified	12,872 UK Biobank data	rs268, rs11542065,	The rs547644955 variant had major significance for both T2D and CVC.	Retrospective study

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					rs116403115, rs118204057, rs118204061, rs144466625, and rs547644955		
34	*Verbeek et al.,2019*	European	39 -79 years	25,639 individuals	rs3135506, rs662799, and rs328	The 3-SNP have an role to triglyceride (TG) gene risk score (GRS) and a metabolic risk score (MetRS) are significantly associated with increased plasma TG concentrations and an increased risk of CVD.	follow-up study
35	*Liang L, et al.,2019*	Chinese	Not Specified	232 Myocardial infarction (MI) cases and 661 control subjects	rs3825807	rs3825807 contributes to Myocardial infarction (MI) susceptibility in the Chinese Han population	Case-control study
36	*Zhao et al.,2019*	Chinese	Not Specified	2,742 subjects in a	rs833061, rs3025010, and rs699947	rs3025010 may play a key role in the pathogenesis of hypertension	cross-sectional population study
37	*Aghabozorg Afjeh SS et al.,2014*	Iranian	Not Specified	200 subjects with 100 cases and 100 controls	rs3184504	Our study demonstrated that there was no direct association between the rs3184504 C>T variant and with risk of CAD in the Iranian population, whereas there is a significant association between this variant with increased blood LDL and diastolic blood pressure.	Case-control study
38	*Shanker et al.,2014*	Asian Indians	Not Specified	500 CAD patients (cases) and 500 controls	rs10757274 and rs599839	rs10757274 and rs599839 GRS showed a 2.5-fold higher risk of CAD in Asian Indians	Case-control study
39	*Kodaman et al.,2017*	African	Not Specified	1,032	rs1649292, rs63111160, rs404890, rs1420101, rs28550932, rs10738554, and rs9880989	The most significant result among all univariate and multivariate tests performed in this study was the heterogeneity of correlation between PAI-1 and mean arterial pressure at rs10738554	exome-wide study
40	*Shalia et al.,2015*	Asian Indians	Not Specified	48 Acute myocardial infarction (AMI) patients and 48 healthy controls	rs9978223	The study identified an SNP rs9978223 on the IFNGR2 gene, associated with increased risk in AMI patients from India	Not Specified
41	*Kaur et al.,2023*	Asian Indians	Not Specified	CAD cases (n=206) and controls (n=206)	rs2274907 and rs2274908	The present case-control research found that both the SNPs at the ITLN1 locus were significantly associated with the occurrence of CAD in the people of Punjab.	Case-control study
42	*S.U. Shahid et al.,2016*	South Asian	Not Specified	650 subjects (430 CAD cases and 220 controls)	rs4341 and rs1799983	The SNPs were not solely associated with CAD but were associated with BP in Pakistani subjects under study and may be causing CAD by modulating BP	Case-control study
43	*Leonard et al.,2018*	European	Not Specified	Patients with systemic lupus erythematosus (n=1045)	rs17581834 and rs799454	IL19 risk allele was associated with stroke/MI in SLE and RA, not in the general population, which indicates a common gene pathway of CVD pathogenesis in inflammatory rheumatic diseases.	Case-control study

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44	*Abudureyimu et al.,2021*	Chinese	Not Specified	914 subjects with 493 CHD patients and 421 healthy controls	rs1122608, rs2230806, rs12563308, and rs662799	rs662799 GG allele is related with higher triglyceride and might act as a risk factor for CHD; SMARCA4rs1122608 TT allele and APOA5 rs662799 AA allele are associated with elevated high-density lipoprotein cholesterol levels, and might play a protective role in the development of CHD	Case-control study
45	*Vangjeli et al.,2021*	European	Not Specified	5092	rs2285666	The A allele of the rs2285666 SNP (HR = 0.3, p = 0.04) was strongly linked with the risk of cardiovascular death in female subjects. These results complement those findings in other studies of SNPs in the ACE2 gene with cardiovascular disease risk.	MORGAM project

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4. Discussion:

A population-specific meta-analysis of single-nucleotide polymorphisms (SNPs) associated with cardiovascular disease (CVD) risk, based on the previous scholarly articles, reveals distinct genetic influences across different ancestral groups.

Population-wise overview of cardiovascular-related SNPs

A summary of the 45 studies arranged by the population under investigation can be found below. It emphasizes the following for each group: Key loci/SNPs that have been reported frequently or have a significant impact on the main pathophysiologic pathway that is implicated (lipids, endothelial function, inflammation, glucose/obesity, drug response etc.)

Various SNPs have shown robust associations with CVD risk factors. Such as, the *NOS3* rs1799983 polymorphism theatres a crucial role in ST-elevation myocardial infarction (STEMI), while rs805305 was directly associated with coronary artery disease (CAD) *(7)*. In the same way, the rs10757274 and rs599839 variants were linked with a 2.5-fold increased risk of CAD in Indians, specifically highlighting the impact of the 9p21 loci (*19*). Other studies noted that the roles of *IFNGR2* rs9978223 and *ITLN1* rs2274907/08, respectively, in forming inflammation and lipid metabolism in myocardial infarction and CAD cases *(20, 21).* The *ADIPOQ* rs1501299 as a key variant among menopausal women predisposed to CVD *(22) (***Table 2**).

East Asian population; most of the polymorphisms are related to metabolic pathways, which lead to CVD risk factors. The PCSK9-related SNPs, rs17671591 and rs3761740, significantly impact the statin therapy on lipid levels, particularly in the Uyghur population *(23)*. Additionally, the ADAMTS7 rs3825807 as a risk variant for myocardial infarction in the Han Chinese population *(24)*, while the role of VEGFA rs3025010 in the hypertension pathway *(25)*. The character of *ABCG2* rs2231142 in a decreased Framingham risk score in Taiwanese females, as shown the protective role of certain variants in context-specific environments *(10)*. Furthermore, the *rs2805533* as influencing the abdominal obesity and triglyceride levels, which are key markers to predict CVD in Japanese populations *(15)* (**Table 3**).

European Caucasian populations, a comprehensive set of SNPs has been identified with implications for metabolic, lipid, and inflammatory pathogenesis. The four SNPs (rs10848554, rs11061937, rs1058322, rs16928751) that are helps to development the Type 2 diabetes and subsequent CVD risk *(14)*. The *ACE2* rs2285666 is a protective variant in women *(26)*, while the inflammatory *IL19* rs17581834 as a hazardous factor in autoimmune diseases that affect the cardiovascular system *(27)*. Additionally, the *TG-GRS* identified using rs3135506, rs662799, and rs328 showed a substantial suggestion with plasma triglyceride levels and CVD risk, showing a polygenic effect *(28)* (**Table 4**).

African and South African Indian cohorts; studies demonstrate the ancestry-specific SNP effects. The heterogeneous correlation between PAI-1 levels and mean arterial pressure at rs10738554 among Africans, suggesting population-specific regulatory mechanisms *(29)*. The higher frequencies observed of *VISFATIN*-related SNPs (rs1467568 and rs7895833) in South

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African Indians compared to Blacks, though there is no direct CAD association *(30)*, also the *APOL1* rs28362286 may elevate CVD risk in old-age South Africans *(9)* (**Table 5**).

Middle Eastern groups, gene-diet and pharmacogenetic interactions have become essential. The *ADIPOQ* rs1501299 and *FADS1* rs6450176 as changes in blood pressure and central obesity in applying the DASH diet, which shows the potential for personalized nutrition approaches *(12)*, and the *KDR* rs1870377 variant was associated with clopidogrel resistance and altered lower-density lipoprotein (LDL) levels in Arabian patients' post-percutaneous coronary intervention, highlighting its importance with how patients respond to medication *(16)*. Further, the lipid-related SNPs—rs1748195, rs11207997, and rs10789117—to increased CVD risk in a large Iranian cohort *(31)* (**Table 6**).

Multi-ethnic & Global GWAS / meta-analyses:

In multi-ethnic cohort perspectives, IL-8 rs4073 is a universally significant danger factor for CAD, which has a specific effect on Asian Indians *(8),* For the analysing three cohorts i.e. America, Europe, and Africa, find rs783396 and rs1804689 to be significantly linked with ischemic stroke (IS) in American people who lived in Africa, which shows the importance of ethnicity-specific analysis in stroke mechanism *(17)*. The rs10846744 to be strongly influenced by the Lp-PLA2 function and atherosclerotic risk from several ethnic groups, reinforcing inflammation as a key trans-ethnic mechanism *(32)*.

Table 2: **South-Asian ancestry (Asian Indian, Bangladeshi, Pakistani) specific SNPs related to CVD risk Factors.**

Authors (Reference)	Recurrent / high-impact SNPs	Genes/pathway	Cardiovascular impact
Shiraz Rizvi et al.,2025	**rs1799983**, **rs4341**	*NOS3* (endothelial nitric-oxide synthase)	STEMI, BP modulation → increased CAD risk
Mollahosseini et al.,2025	**rs1501299**	*ADIPOQ* (adiponectin)	CVD predisposition in menopausal women; DASH-diet interaction on BP/central obesity (Iran + India)
Amrita et al.,2020	**rs2237892**	*KCNQ1* (β-cell K^+ channel)	CAD in Indians; CVD risk independent of T2D in Arabs
Shanker et al.,2014	**rs10757274 / rs10757278**	9p21 locus (*CDKN2A/B* region)	2–2.5-fold increased CAD risk (India, Belgium)
Shalia et al.,2015, Kaur et al.,2023, S.U. Shahid et al.,2016, and Aka et al.,2021	**rs9978223**, **rs2274907/08**, **rs268**	Immune (IFNGR2, ITLN1) & lipid genes	AMI susceptibility; CAD in Punjab; T2D + CVD comorbidity

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Table 3: **East-Asian ancestry (Chinese, Korean, Japanese, Taiwanese, Uyghur) specific SNPs related to CVD risk Factors.**

Authors (Reference)	Recurrent SNPs	Gene/function	Cardiovascular impact
Lee et al.,2025	**rs74457740**	*MED13L* (lipid & cardiac transcription)	3.5× increased MI risk in KoGES cohort
Z. Liu et al.,2024	**rs17671591 / rs3761740**	*PCSK9* region	Determines LDL-C response to statins; ethnic heterogeneity between Han vs Uyghur
Liang L, et al.,2019	**rs3825807**	*ADAMTS7*	MI susceptibility (Han)
Zhao et al.,2019	**rs3025010**, **rs833061**	*VEGFA*	Hypertension, triglyceride levels
Abudureyimu et al.,2021	**rs2231142 (TT)**	*ABCG2* urate transporter	**Protective:** Decreased Framingham CVD score in non-obese hyperuricemic women
Oguro et al.,2011, and Y Iwamoto et al.,2011	**Ser49Gly / Glu27Gln / Trp64Arg**	*β2-adrenergic receptor*	Risk modifiers in hypertensive Japanese patients

Table 4: **European ancestry specific SNPs related to CVD risk Factors**.

Authors (Reference)	High-priority SNPs / scores	Biology	Cardiovascular impact
Verbeek et al.,2019, and Fojas et al.,2025	**FTO rs9939609**, **TG-GRS (rs3135506 + rs662799 + rs328)**	Obesity / triglyceride regulation	Progression to CVD and Increased plasma TG
Siitonen et al.,2011, Lappalainen et al.,2010, and Buraczynska et al.,2014	**rs10848554 etc. (four-SNP cluster)**	Glucose metabolism	Transition from IGT → T2D → CVD
Leonard et al.,2018	**rs17581834 (IL19)**	Immune signalling	Stroke/MI in SLE & RA patients
Van Schie et al.,2010,	**rs964184**, **rs17609940**	Lipid packaging genes (*APOA5*, *APOE* modulators)	MI and major adverse CV events, even after classical-risk adjustment
Vangjeli et al.,2021	**rs2285666 (ACE2)**	RAS / endothelial	Lower cardiovascular mortality in females (protective)

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Table 5: **African & African-descent populations (Sub-Saharan, African-Americans, South-African Indians) specific SNPs related to CVD risk Factors**.

AUTHOR (REFERENCE)	SNPs	Gene/pathway	Cardiovascular impact
Chalwe et al.,2024	**rs28362286**	*APOL1* variant context	Increased CVD risk in elderly South Africans
Kodaman et al.,2017	**rs10738554**	PAI-1 regulation	Ethnic heterogeneity in arterial pressure correlations
Skelding et al.,2010	**rs7566605**	*INSIG2* (lipogenesis)	Age/sex-modulated risk of peripheral & cerebrovascular disease
Ramkaran et al.,2016	**rs1467568 / rs7895833**	*VISFATIN* locus	Higher allele frequency in SA Indians vs SA Blacks; no clear CAD difference

Table 6: **Middle-Eastern ancestry (Iranian, Arabian) specific SNPs related to CVD risk Factors.**

Authors (Reference)	SNPs	Gene/interaction	Cardiovascular impact
Mollahosseini et al.,2025	**rs1501299, rs6450176 + DASH diet**	*ADIPOQ / FADS1*	Genotype-specific BP & obesity benefit from DASH (gene–diet interaction)
Awaida et al.,2021	**rs1870377**	*KDR* (VEGFR-2)	Clopidogrel resistance; altered VEGFR-2 & LDL levels
Aghasizadeh et al.,2021	**rs1748195 / rs11207997 / rs10789117**	Lipid metabolism	CVD prediction in a large prospective Iranian cohort

5. Conclusion:

This population-wise analysis emphasizes how genetic ancestry, environmental context, and gene-lifestyle interactions significantly impact on how SNPs affect cardiovascular disease (CVD). While some key variants like PCSK9 rs17671591 in Uyghurs or APOL1 rs28362286 in South Africans show ancestry-specific affects others like IL-8 rs4073 variant is associated with the risk of coronary artery disease (CAD) across various genetic models in different countries, particularly among AsiansNOS3 rs1799983 ADIPOQ rs1501299, and the 9p21 region are recurrent across multiple populations. These genetic indicators are key pathways affecting lipid metabolism, endothelial function, inflammation, and drug response. The potential of individualized approaches to CVD prevention and treatment is highlighted by significant gene–environment and gene–drug interactions, particularly in Middle Eastern and East Asian populations. This study conclude that the population specific SNPs are directly linked with CVD risk factors which needs for ancestry-informed precision medicine, that guarantees fair and efficient cardiovascular treatment for a wide range of international populations.

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Limitation: This review gives treasured insights into genetic scenario of CVD from SNPs point of view; but numerous limitations must be noted. The literature has changed into limited to English-language research published within the beyond decade, potentially with the exception of great findings from non-English sources. Case reports were also excluded, as many concerned patients with pre-existing or newly evolved cardiac conditions, which conflicted with the evaluation's inclusion standards. variations in observe layout (case control vs. cross-sectional study) and inconsistent follow-up periods similarly restrict the comparison of findings and the capacity to conclude long-term results.

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