

Review Article

Links between vitamin D receptor gene polymorphisms and coronary artery disease: a review of evidence

M. Maruf-Ur-Rahman^{1*}, M. Rafiqul Islam², Wazeda Begum³, M. Shafiqul Islam⁴, Hosne Ara⁵

¹Department of Biochemistry, Dhaka National Medical College, Dhaka, Bangladesh

²Department of Biochemistry and Molecular Biology, Jagannath University, Dhaka, Bangladesh

³Department of Dermatology and Venereology, Dhaka National Medical College, Dhaka, Bangladesh

⁴Department of Biochemistry and Molecular Biology, Ibn Sina Diagnostic Lab and Consultation Centre, Jatrabari, Dhaka, Bangladesh

⁵Department of Molecular Biology, Central Dogma Lab, Invent Technologies Ltd., Dhaka, Bangladesh

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*Correspondence:

Dr. M. Maruf-Ur-Rahman,

E-mail: marufbd80@gmail.com

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ABSTRACT

Vitamin D receptor (VDR) serves as a nuclear receptor, playing a significant role in mediating the physiological effects of vitamin D through the regulation of gene expression. Polymorphisms in the VDR gene have the potential impact on receptor activity through modifications in gene transcription, mRNA stability and protein function. Within the extensive array of single-nucleotide polymorphisms (SNPs) identified in the VDR gene, which exceeds 470, four specific variants have captured significant scientific attention: FokI (rs2228570), ApaI (rs7975232), BsmI (rs1544410) and TaqI (rs731236). The examination of these polymorphisms has been conducted within the framework of various diseases, such as malignancies, diabetes mellitus, myocardial infarction and coronary artery disease (CAD). Numerous studies indicate a possible links between these genetic variants and an increased risk of developing CAD; however, discrepancies in findings across various populations and research methodologies persist. This review will thoroughly overview the existing literature regarding the links between VDR polymorphisms and CAD.

Keywords: Coronary artery disease, Single-nucleotide polymorphisms, Vitamin D receptor, Vitamin D receptor gene

INTRODUCTION

Coronary artery disease (CAD) is the most common form of cardiovascular disease and remains a leading cause of global morbidity and mortality.¹⁻³ The condition predominantly stems from thrombotic blockage in the coronary arteries, usually initiated by the rupture of atherosclerotic plaques and the ensuing activation of the coagulation cascade.⁴ CAD is a complex condition shaped by a combination of genetic factors and environmental influences.⁵ Traditional risk factors, including poor diet, obesity, diabetes mellitus, hypertension, dyslipidemia, systemic inflammation, tobacco use and excessive alcohol consumption, are recognized contributors to cardiovascular health. However, they are believed to

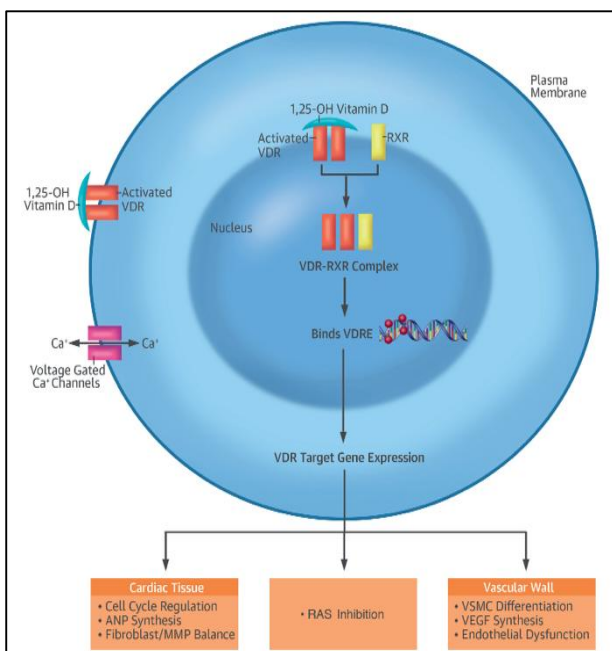
account for merely half of an individual's total cardiovascular risk.^{6,7} The residual risk is believed to be predominantly influenced by genetic factors.⁸

Polymorphisms in various genes that play a role in pathways associated with coagulation, regulation of blood pressure and metabolic processes concerning glucose, lipids and homocysteine.⁷ The vitamin D receptor (VDR) gene stands out among the many genes being studied, presenting itself as a noteworthy candidate in relation to cardiovascular disease. Its potential influence on vascular health and inflammatory responses adds to its significance in this field of research.⁹ The VDR, a member of the nuclear receptor superfamily, is integral to regulating the expression of numerous genes containing vitamin D

response elements (VDREs) within their promoter regions. It exhibits high affinity and specificity for its active ligand, 1,25-dihydroxyvitamin D ($1,25(\text{OH})_2\text{D}$). Upon ligand binding, VDR typically forms a heterodimer with the retinoid X receptor (RXR), enabling the complex to bind to VDREs and modulate transcriptional activity related to cell growth, differentiation and physiological function.¹⁰

Notably, the presence of VDR in cardiac myocytes and vascular endothelium has highlighted its potential role in cardiovascular homeostasis.¹¹ Structurally, VDR comprises three major domains: an N-terminal dual zinc finger DNA binding domain, a C-terminal ligand-binding activity domain and, an extensive and unstructured region that links the two functional domains of this protein together. These features collectively support VDR's ability to interact with specific DNA sequences and recruit coactivators or corepressors, thus regulating gene expression in a context-dependent manner.¹²

The biological effects of vitamin D primarily occur through its interaction with the VDR, a widely expressed nuclear receptor that plays crucial regulatory roles in numerous tissues. Upon activation by its high-affinity ligand, 1,25-dihydroxyvitamin D ($1,25(\text{OH})_2\text{D}$), VDR embarks on two principal modes of action. The classical genomic pathway features the nuclear VDR creating a heterodimer with the retinoid X receptor (RXR).



(VDR:Vitamin D receptor; 1,25-OH vitamin D:1,25-dihydroxyvitamin D; ANP:Atrial natriuretic peptide; Ca^{2+} : Calcium cation; MMP:Matrix metalloproteinases; RAS:Renin-angiotensin system; RXR:Retinoid-X receptor; VDRE:Vitamin D response elements; VEGF:Vascular endothelial growth factor; VSMC:Vascular smooth muscle cell).

Figure 1: Potential effects of vitamin D via VDR on cardiovascular system.¹³

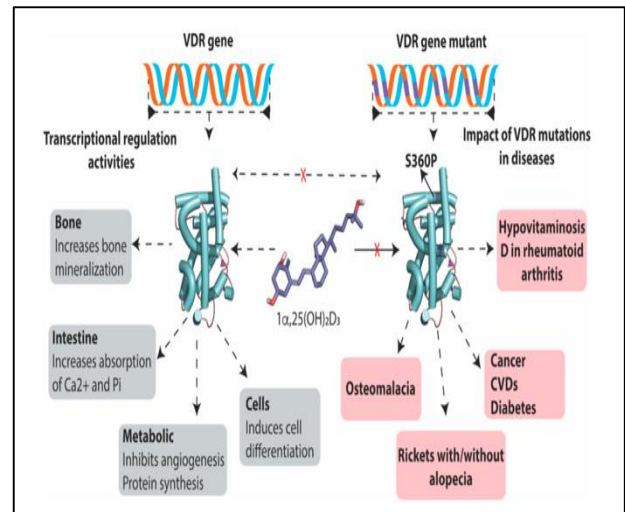


Figure 2: Transcriptional regulation activities of VDR gene & consequences of VDR gene mutation.²¹

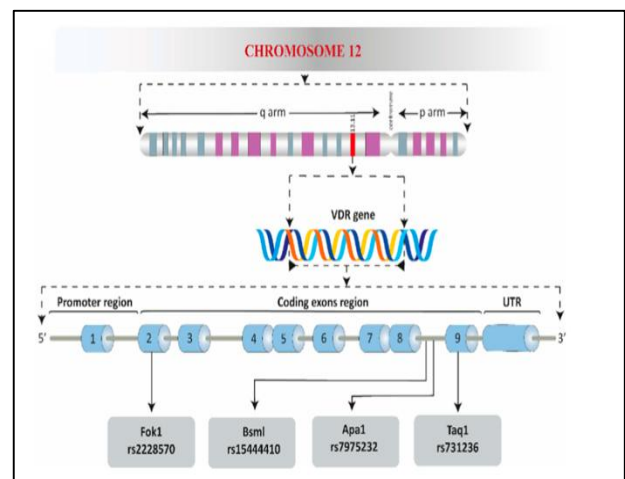


Figure 3: Structure of human VDR showing promoter region, coding exons region, three prime untranslated region (UTR) and the well-known polymorphic sites.²¹

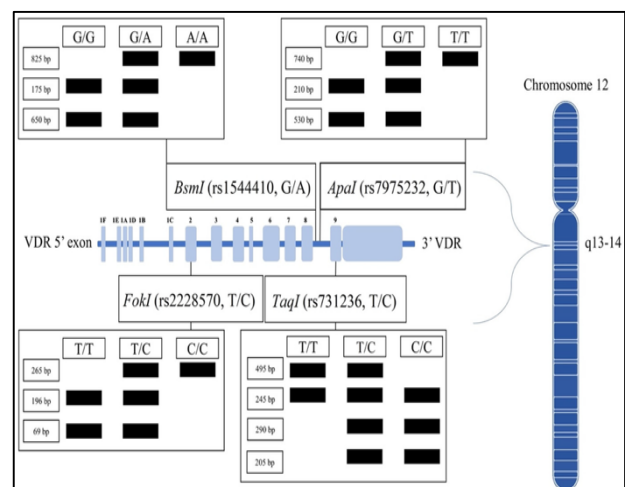


Figure 4: Common polymorphisms in VDR genes and its PCR-RFLP based genotyping.³⁸

This complex subsequently attaches to vitamin D response elements (VDREs) located in the promoter regions of target genes, influencing their transcriptional activity. This pathway plays a crucial role in a wide range of cellular functions, encompassing calcium homeostasis, immune modulation and cardiovascular regulation. In contrast, the swift, non-genomic signalling pathway is facilitated by membrane-associated VDRs, initiating prompt intracellular signalling cascades in reaction to external stimuli, without relying on direct gene transcription.¹⁴ Genetic polymorphisms in the VDR gene have the potential to alter its transcriptional efficiency and mRNA stability, thereby influencing VDR function and modulating the downstream physiological actions of vitamin D. Among the many single nucleotide polymorphisms (SNPs) identified in the VDR gene, several have drawn considerable scientific interest due to their possible clinical implications. Notably, rs2228570 (FokI), located in exon 2, affects the translation initiation codon, potentially altering the structure and activity of the VDR protein. In addition, rs1544410 (BsmI) and rs7975232 (ApaI) both situated in intron 8-as well as rs731236 (TaqI) in exon 9, have been widely studied for their associations with various diseases and their regulatory roles in gene expression.¹⁵

Polymorphic variations in the VDR gene have emerged as important genetic determinants implicated in a wide spectrum of pathological conditions. These variants have been associated with increased susceptibility to prostate cancer, inflammatory bowel disease, osteopenia and tuberculosis, as well as neurodegenerative disorders such as Parkinson's disease.^{16,17}

Additionally, links have been identified between VDR polymorphisms and metabolic disorders, including diabetes mellitus and cardiovascular diseases, highlighting their potential relevance in both inflammatory and systemic chronic diseases.¹⁸⁻²⁰ A recent meta-analysis has

demonstrated a significant inverse association between serum levels of 25-hydroxyvitamin D and the risk of cardiovascular disease, emphasizing the potential cardioprotective role of maintaining sufficient vitamin D status.²² The VDR is pivotal in mediating the genomic actions of 1,25-dihydroxyvitamin D across various tissues.²³ Genetically, the VDR gene is located on chromosome 12q12-14 and comprises at least five promoter regions, eight protein-coding exons and six untranslated exons, all subject to alternative splicing.²³⁻²⁵

To date, over 470 single-nucleotide polymorphisms (SNPs) have been identified within the VDR gene. Among these, FokI (rs2228570), ApaI (rs7975232), BsmI (rs1544410) and TaqI (rs731236) are the most widely studied due to their potential clinical relevance. These polymorphisms have been associated with the pathogenesis of several diseases, including cancer, type 2 diabetes, Parkinson's disease, myocardial infarction and CAD.²³⁻²⁷

SEARCH STRATEGY OF LITERATURE

We conducted a thorough search of databases including PubMed and Scopus to identify all relevant studies examining the relationship between VDR gene polymorphisms and the risk of coronary artery disease (CAD). The search terms included: "coronary artery disease" or "CAD" or "coronary syndrome" or "ischemic heart disease" or "myocardial infarction" or "MI" or "atherosclerosis" or "arteriosclerosis" or "coronary stenosis" or "coronary disease" or "CHD" and "VDR" or "vitamin D receptor" and "single nucleotide polymorphism" or "SNP" or "polymorphisms" or "mutation". In addition, the references to review articles underwent meticulous scrutiny to uncover any potential publications that may have eluded detection during the initial search. Only studies involving humans and publications in the English language were assessed.

Table 1: Characteristics of the studies included in the meta-analysis.¹⁹

First author (ref.)	Year	Country	Ethnicity	Sex	Case/control	Case/control age, years	Genotype method	Polymorphism	Quality score
Ortlepp et al ⁴⁶	2001	Germany	Caucasia	M/F	217/273	61.5±9.9/61.5±9.9	PCR-RFLP	BsmI	7
Ortlepp et al ⁴⁷	2003	Germany	Caucasia	M/F	2,087/775	59.8±7.1/56-5±11.2	PCR-RFLP	BsmI	7
Pan et al ⁴¹	2009	China	Asian	M/F	152/212	59.2±11.3/58.6±11.1	PCR-RFLP	ApaI, FokI	8
Abu el Maaty et al ⁴⁹	2016	Egypt	Caucasia	M	137/58	35-50/35-50	PCR-RFLP	TaqI, ApaI	8
He et al ⁴³	2015	China	Asian	M/F	215/67	62.1±9.4/59.6±13.3	PCR-RFLP	Tru91, ApaI, TaqI, FokI	9

NR: not reported; PCR: Polymerase chain reaction; RFLP: Restriction fragment length polymorphism. Age is reported as mean ± standard deviation or range.

DISCUSSION

The gene responsible for the VDR, located on chromosome 12q12–q14, is crucial in governing the biological processes influenced by vitamin D.²⁸ When calcitriol, the hormonally active form of vitamin D, is activated, VDR forms a heterodimer with the retinoid X receptor (RXR). The heterodimeric complex subsequently engages with vitamin D response elements (VDREs) found in the promoter regions of target genes.²⁹ This binding process engages a range of coactivators and corepressors, effectively influencing gene expression related to cellular proliferation, differentiation, immune response and calcium homeostasis.²⁸⁻³⁰

The VDR is extensively expressed in various human tissues and is believed to modulate nearly 3% of the human genome, affecting the transcription of over 900 genes implicated in a broad spectrum of physiological functions.^{31,32} The VDR gene, responsible for encoding this nuclear receptor, is mapped to chromosomal region 12q13.1 and spans over 100 kilobases.^{16,33} It features multiple promoter regions at least five identified to date alongside eight protein-coding exons and six or more untranslated exons. These structural elements are subject to alternative splicing, adding layers of complexity to the regulation of VDR expression and activity.³⁴

The VDR, a member of the steroid/thyroid hormone receptor superfamily, plays an important role in the pathogenesis of CAD, principally via influencing atherosclerotic plaque development.³⁵ A growing body of research has investigated the potential link between VDR gene polymorphisms and susceptibility to a variety of disorders, including asthma, rheumatoid arthritis, osteoarthritis, type 1 diabetes, urolithiasis, Parkinson's disease, metabolic syndrome and multiple sclerosis.³⁶

In recent years, growing attention has been directed toward the role of vitamin D and its receptor gene (VDR) polymorphisms in the pathogenesis of CAD. Among the numerous single nucleotide polymorphisms (SNPs) identified in the VDR gene over 30 to date FokI (rs2228570), ApaI (rs7975232), BsmI (rs1544410) and TaqI (rs731236) have emerged as the most extensively studied due to their potential clinical relevance. These SNPs have garnered interest for their possible contribution to individual susceptibility to a range of physiological and pathological conditions, including cardiovascular diseases, malignancies and metabolic disorders such as diabetes.³⁷

Damir et al, investigated three commonly studied polymorphisms in the VDR gene FokI (rs2228570), BsmI (rs1544410) and TaqI (rs731236) in a cohort of patients with CAD following acute myocardial infarction. Their analysis revealed a potential association between the BsmI and TaqI variants and the presence of CAD in this population. Conversely, no significant relationship was observed between the FokI polymorphism and CAD risk

in the studied group.³⁹ Pan et al, found no significant link between the FokI polymorphism and CAD in a study on a Chinese population.^{40,41} These findings are consistent with ours. An Iranian meta-analysis found no relationship between FokI and CAD, supporting this finding.¹⁹ He et al, found that the G/G genotype of the FokI polymorphism may protect against CAD in a Chinese population.⁴¹ A recent meta-analysis by Chinese researchers suggests that the FokI variant's G allele may protect against CAD development.⁴² Despite these findings, the research remains divided on the impact of VDR gene variants on CAD risk. Pan et al, found no link between the BsmI polymorphism and CAD in the Chinese population, while Van Schooten et al, identified BsmI as a risk factor for CAD in Dutch individuals.^{40,43} Ortlepp and colleagues discovered a substantial connection between BsmI polymorphism and CAD in German patients with type II diabetes, indicating that ethnicity and comorbidities may influence genetic correlations.⁴⁴

Nonetheless, larger cohort research found no connection between the BsmI polymorphism with the occurrence or severity of CAD.⁴⁵ However, this study has methodological flaws, including the lack of a proper control group and deviation from the Hardy-Weinberg equilibrium, which could jeopardize the credibility of its conclusions. In contrast, a French study found a link between the minor alleles of BsmI and TaqI polymorphisms and an elevated risk of CAD in people with type II diabetes.⁴⁶ Two meta-analyses were conducted to further analyze these connections; however, their findings are conflicting. An Iranian meta-analysis revealed no significant link between TaqI and BsmI polymorphisms and CAD.¹⁹ In contrast, a more extensive meta-analysis by Chinese researchers discovered an elevated risk of CAD related with these SNPs, particularly in Caucasian populations.⁴² These disparities between studies may be due to variances in ethnic backgrounds, sample sizes and the clinical severity of CAD among participants.

Abu el Maaty et al, proposed that the FokI polymorphism within the VDR gene may serve as a genetic indicator of susceptibility to CAD.⁴⁷ Supporting this notion, findings from a multinational cohort study indicated that the minor allele of the BsmI variant was significantly associated with increased CAD risk, particularly in individuals diagnosed with type 2 diabetes.⁴⁶ Similarly, a study conducted by Soad M. Eweida et al, in an Egyptian population reported a robust correlation between several VDR gene polymorphisms and heightened cardiovascular disease (CVD) risk, independent of diabetic status.⁴⁸ Collectively, these results highlight the potential of VDR genetic variants as predictive markers for identifying individuals with an elevated inherited predisposition to cardiovascular diseases.

A systematic review and meta-analysis conducted by Samira Tabaei et al, demonstrated that all genetic inheritance models of the FokI single nucleotide polymorphism (SNP) were significantly associated with an

elevated risk of CAD.⁴⁹ In the case of the ApaI SNP, all models except the recessive model also showed a significant association with increased CAD risk. Importantly, the analysis revealed that both FokI and ApaI polymorphisms were linked to greater CAD susceptibility in Asian and European populations across multiple genetic models. These results suggest that FokI and ApaI variants may serve as genetic risk factors for CAD, with a particularly notable impact observed among Asian individuals.

CONCLUSION

A noteworthy number of molecular and epidemiological studies has been undertaken worldwide to evaluate the potential link between VDR gene polymorphisms and the risk of CAD. Nevertheless, the results have frequently shown variability, with certain studies affirming a notable connection, while others indicate a lack of correlation. Such discrepancies can stem from various factors, including restricted sample sizes, inadequate statistical power or differences in methodology across studies. Addressing these inconsistencies and drawing more definitive conclusions necessitates comprehensive systematic reviews and meta-analyses. Such efforts can synthesize the available evidence and tackle the limitations present in individual studies. Moreover, it is essential for future studies to expand their focus by exploring more VDR polymorphisms and incorporating environmental and lifestyle elements that could influence genetic vulnerability to CAD. Adopting multifactorial approaches is essential for developing a deeper and more precise comprehension of the relationship between VDR gene polymorphisms and CAD.

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