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Introduction: Coronary artery disease (CAD) is a complex, multifactorial disease. CAD is a cause of morbidity and mortality worldwide. Different studies from different countries have established the genetic association between CAD and vitamin D receptor gene polymorphism. Vitamin D receptor (*VDR*) binds with active form of vitamin D and play crucial role in regulating the transcription of many genes and has significant impact on the morphology, proliferation, and growth of cardiac cells. Genetic variation in *VDR* gene such as intronic and exonic polymorphism may results in altered structure and function of vitamin D receptor which disturb the binding of vitamin D that may cause adverse effect in CAD. The study objective included, analyzing serum vitamin D levels and the association of intronic and exonic polymorphism in coronary artery disease patients and controls in order to examine its role towards the susceptibility of disease condition

Materials & Methods: The study included 1016 Blood samples, 516 from coronary artery disease patients collected (National Institute of Cardiovascular Diseases (NICVD), Pakistan) that were compared with 500 age and gender matched healthy controls. Genomic DNA was extracted by standard phenol chloroform method. Amplification of targeted sequence was carried out through allele specific polymerase chain reaction (AS-PCR). The PCR products were examined by agarose gel electrophoresis. The genetic variations were confirmed by Sanger sequencing the and serum Vitamin D levels were assessed by using Enzyme Linked Immunosorbent Assay (ELISA) for the quantification analysis between diseased and healthy subjects.

Result & Discussion: The presenting research has focused primarily on human subjects, but

the implications of current findings extend far beyond human species. The observed allelic variants for *intronic* and *exonic* polymorphism resulted successful amplification in amplified PCR products confirmed by Sanger sequence. The sequence analyses confirmed both match and variant mismatches. The high frequency for heterozygous variation has been observed in CAD patients showed significant association with exonic variation *TaqI* Polymorphism ($P < 0.001$). However, no association was found with intronic variation *BsmI* Polymorphism ($P>0.05$) between cases and controls. Serum vitamin D levels showed significantly lower levels in CAD patients compared to controls ($P<0.001$). Haplotype analysis on both SNPs showed the possible risk with multiple haplotypes combination. The Linkage disequilibrium (LD) plot of SNPs was found in linkage for *intronic* and *exonic* polymorphisms in *VDR* gene. The results obtained might aid in disease surveillance and monitoring in an integrated manner to gain a better understanding of disease dynamics and to develop effective prevention and control strategies

Conclusion: This study may represent a potential insight to consider clinical approach for better therapeutic intervention and management of the disease. The One Health framework beckons not only to consider the genetic threads within human species but also to acknowledge the shared vulnerabilities arising from our environment.

Keywords:

Coronary artery disease (CAD), Allele specific polymerase chain reaction (AS-PCR), Vitamin D Receptor (VDR), Linkage disequilibrium (LD).