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## **VDR, CYP24A1 and KL Gene Variations Significantly Associated with CKD Pathogenesis: A Comparative Genetic Study**

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**KEYWORDS** Chronic Kidney Disease. Single Nucleotide Polymorphism. Amplification-Refractory Mutation System-Polymerase Chain Reaction

**ABSTRACT** Allelic variation and genomic instability of the VDR, KL and CYP24A1 variations are influencing the pathogenesis of chronic kidney disease (CKD) in the computational analysis. To correlate this observation this study aimed to screen the population frequencies of the following alleles in the Indian populations. The *VDR gene*: rs121909800, rs121909797; *CYP24A1 gene*: rs387907322, rs114368325, and *KL gene*: rs9536314, rs649964 in CKD patient's genotyping was done from blood sample DNA using the ARMS-PCR method and significant results were statistically validated through MDR analysis. In this study, 120 CKD cases and 120 control subjects were included. The allele distribution and genotype of the rs121909800 variant were significantly associated with CKD patients (Variant Allele Frequency or VAF = 11.67) (*p-value*: 0.03), versus control subjects (VAF=4.17), respectively. The *CYP24A1* polymorphic variants rs387907322 and rs114368325 are significantly associated with CKD patients. The disease association was confirmed through Multifactor Dimensionality Reduction (MDR) analysis. Hence, the researchers concluded that the associated genes with specific variants may be considered a potential marker for the early diagnosis of CKD.