Aim & Objectives
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Chronic Kidney Disease (CKD) is the second leading cause of non-communicable disease. Various metabolic disturbances such as acidosis, dyslipidemia and vitamin D deficiency are widely used as therapeutic targets to reduce the mortality and morbidity of CKD incidence. Patients with CKD often manifest a deregulated VDR level, weaker bone strength and osteoporosis and consequently undergo vitamin D therapy. Elucidation of working principles and molecular regulative mechanism of VDR may solve many problems among CKD patients. Moreover, knowledge of VDR structure has been a key in driving the design and development of a large number of VDR agonists/antagonists. Crystallographic studies have revealed that the binding site of VDR can accommodate a number of diverse molecular frameworks, exploiting various site of interaction. VDR deficiency is common problem among CKD patients, making VDR protein as an attractive target for the development of anti-osteoporotic drugs. The present study has two major scopes. Primarily, to understand the regulatory role of VDR SNPs an effort has been made to study the role of VDR polymorphism among CKD patients in South Indian population. Further, deleterious SNPs were identified form dbSNP database using in silico tools. The binding modes and selectivity for lead discovery, and optimization of VDR agonists are explored by combined molecular modeling approaches. Preliminary results from this study would pave way for the design of new drugs against VDR with reasonable computational cost.
The present study has following objectives:

- Study the association of VDR gene polymorphisms among CKD patients in South Indian population.
- Identification of potential deleterious VDR gene SNPs using Bioinformatics tools.
- Identification of SNPs involved in calcitriol drug response using molecular dynamics simulation calculations.
- Understand the agonist and antagonist mechanism of VDR analogs with the use of molecular docking, molecular dynamics simulation and binding free energy calculations.
- Insight into the structural basis from combined QM/MM study to determine the protein-ligand interaction energy with quantum chemical descriptors to rank the non-secosteroidal VDR agonists.
- Comparative QSAR analysis for VDR analogs by different semi-empirical and \textit{ab initio} charge model calculations.
- Identification of potent lead molecules against VDR using e – Pharmacophore mapping.