

# Vitamin D Receptor Gene Polymorphisms (*TaqI*) in North Indian Population with Type 2 Diabetes

Nancy Taneja<sup>1</sup>, Priyadarshini<sup>2</sup> and Shalini Mani<sup>3</sup>

<sup>1,2,3</sup>Jaypee Institute of Information Technology, Noida  
E-mail: <sup>1</sup>nancytaneja@rocketmail.com, <sup>2</sup>mani.shalini@gmail.com

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**Abstract**—The numbers of diabetic patients is increasing rapidly worldwide and are expected to rise to 592 million by 2035. India is also predicted to become a capital of diabetes in 2020, which is a matter of serious concern. Vitamin D Deficiency is one of the new risk factors, known to cause Diabetes Mellitus (DM). Vitamin D after binding with vitamin D receptor (VDR) acts as active transcription factors which control the expression of Insulin. Hence variations in VDR gene may affect the level of insulin. The common VDR gene polymorphisms which are known to be associated with DM are *FokI*, *TaqI*, *BsmI* and *Apal*. Recent studies in different population such as Iranian, Polish, Syrian, Dravidian etc have revealed that these polymorphisms are associated with several metabolic diseases including diabetes. However, many other groups of researchers observed an opposite trend of association between VDR polymorphisms and DM. In case of Indian population, very few studies are reported which highlights the association between VDR polymorphism and diabetic phenotype. Hence, present work aims at studying the *TaqI* polymorphism in VDR gene of T2DM patients and control samples.

In this study, blood samples were obtained from 100 well characterized T2DM patients and 100 healthy age matched controls. VDR gene fragment containing *TaqI* (exon 9) region was amplified after isolation of total genomic DNA from these blood samples. Subsequently these PCR products were subjected to restriction digestion by using *TaqI* enzyme. Digested products were analyzed. Out of 100 patients and controls, TT (wild) was 37.5% for patients and 47.8% for controls; TC (heterozygous) was 56.25% for patients and 38.2% for controls; CC (mutant) was 6.25% for patients and 13.8% for control samples. After doing the Fisher's Exact test, no significant difference was observed with respect to *Taq I* polymorphisms between patients and controls ( $p=0.823$ ). In conclusion, our study suggests that there is no significant association of *TaqI* polymorphism with diabetic phenotype in our study population.