Vitamin D Receptor Interactions and Genetic Variants in the Context of Type 2 Diabetes Mellitus

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Introduction

About 90% of diabetic patients around the world have type 2 diabetes mellitus according to the World Health Organization. A significant proportion of the health care system resources worldwide are devoted to cover diagnosis, treatment and management of type 2 diabetes [1]. Moreover, it is associated with morbidity like blindness, renal failure and mortality. Type 2 diabetes is a progressive chronic disease which is marked by the inability of tissues like liver and skeletal muscles to respond to the hormone insulin which is secreted by the pancreas. Several risk factors like genetics, environmental factors and obesity contribute to the development of type 2 diabetes. Studies on genes which predispose to type 2 diabetes have been conducted by various researchers among different ethnic populations. Genome wide association studies have led to the identification of many single nucleotide polymorphisms in certain genes and linked them to type 2 diabetes [2,3]. Recently, genes involved in vitamin D metabolism have gained interest because of the association between vitamin D deficiency and type 2 diabetes. High vitamin D levels were significantly associated with reduced risk for type 2 diabetes among Australian adult men and [4]. Vitamin D deficiency results in reduced insulin secretion in humans and rats, and its supplementation improves glucose tolerance [5]. One major study has suggested that vitamin D supplementation could lead to a significant reduction in mortality [6]. In addition, vitamin D is required for absorption of dietary calcium. Calcium is essential for insulin-mediated processes in insulin-responsive tissues. Calcium repletion normalizes glucose tolerance and secretion of insulin in vitamin D-depleted rats and hypocalcemia in nondiabetics reduces insulin secretion [4].

Vitamin D and Vitamin D Receptor Interactions

Vitamin D deficiency has become an insidious epidemic among all age groups in many parts of the world. Recent discoveries have documented a protective role for vitamin D in the case of several chronic morbidities like osteoporosis, cancer, diabetes, and cardio-vascular diseases [7]. Maintaining a good vitamin D status requires adequate exposure to UV or sufficient intake from diet and supplements. Biomarkers of vitamin D status are also affected by season and geographic latitude [8]. However, variability is also attributable to genetic factors which can affect by as high as 53% [9]. Elucidations about the role of common genetic variants variability is also attributable to genetic factors which can affect by as high as 53% [9]. Elucidations about the role of common genetic variants.

Findings from a research study indicated that VDR polymorphism in exon 9 (Taq I) and intron 8 (Bsm I) were significantly associated with type 2 diabetes among Caucasian Americans from European origin [14,10]. Moreover, the metabolic parameters which characterize type 2 diabetes including dyslipidemia, hypertriglyceridemia, and low HDL levels were correlated with the reported VDR polymorphism. The results were in concordance with another research conducted in Saudi Arabia [15]. Other researchers failed to demonstrate a similar link among Indians, Turkish and Polish Populations [3,16]. This discrepancy in findings from different studies is attributed in fact to the differences in population genetics. Examining population-based genetic association between VDR variants and type 2 diabetes could of extreme importance for a specific population that has a high prevalence of both type 2 diabetes and VTD deficiency like that of the United Arab Emirates [17]. Such studies could direct future strategies for prevention and treatment of type 2 diabetes by designing new more relevant population-based interventions which can specifically and effectively target “high risk individuals”.

Conclusion

Genetics plays a complex role in the pathogenesis of both vitamin
D deficiency and type 2 diabetes. Genome wide studies have led to the identification of several genetic variants which are associated with certain diseases like type 2 diabetes mellitus. These variants are often population-based determinants which could predispose a particular ethnicity to a certain disease, hence significantly increasing its prevalence. The VDR primarily acts as a transcription factor—controlling the amounts of certain proteins that are produced from the DNA in the genetic code. The proteins produced by the DNA that the VDR targets are responsible for processes from inflammation to lipid storage and calcium regulation, and deficiencies in vitamin D are associated with many diseases, particularly type 2 diabetes. The VDR also has several non-DNA-related actions, but these are generally much less well understood than the genomic effects. Studies which aim to characterize the interaction of the VDR and its ligand would be informative. Model membranes which mimic the composition of sphingolipid- and cholesterol-rich microdomains act as a model of ‘normal’ VDR-membrane interactions. Examining the interaction of vitamin D with such models could help identify the factors that modulate these interactions and develop a better understanding of the mechanisms of VDR-related pathogenesis in several disorders including type 2 diabetes.

The DNA sequences of the human genome have revealed that many genes are polymorphic. In coding or non-coding regions of a specific gene, there may be either a single base pair substitution of one nucleotide for another or a variable number of repeats of a short, repetitive DNA sequences. These variations may influence the rate of gene transcription, the stability of the messenger RNA or the quantity and activity of the resulting protein. Thus the susceptibility or severity of a number of disorders will be influenced by possession of specific alleles of polymorphic genes. The polymorphic many genes that have received a great deal of research interest such as PPARG2, TCF7L2, and alleles of polymorphic genes. The polymorphic many genes that have of a number of disorders will be influenced by possession of specific gene transcription, the stability of the messenger RNA or the quantity repetitive DNA sequences. These variations may influence the rate of a specific gene, there may be either a single base pair substitution of 4.

References

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