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Research Article

BSMI AND *TAQI* POLYMORPHISMS IN VITAMIN D RECEPTOR GENE OF TYPE 2 DIABETES MELLITUS PATIENTS FROM NORTH INDIA

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ABSTRACT

Objective: Polymorphisms in vitamin D receptor (VDR) genes are known to be linked with different metabolic diseases including Type 2 diabetes mellitus (T2DM) also. However, the association of these polymorphisms is not much explored for the Indian population. To determine the prevalence of *BsmI* and *TaqI* polymorphism in VDR gene of T2DM patients from North India.

Methods: Blood samples were obtained from 100 well-characterized T2DM patients and 100 healthy controls. Genomic DNA was isolated from blood samples and using polymerase chain reaction/restriction fragment length polymorphism based method, the presence of these polymorphisms was investigated in these samples. The data were statistically analyzed using SPSS 21.0 software.

Results: For *TaqI* polymorphism, both the wild type (TT) and heterozygous (TC) genotype showed a significant difference between patients and controls (p=0.023 and p<0.001, respectively). Whereas, the frequency of CC genotype was not significantly different among these groups (p=0.506). For *BsmI* polymorphism also, the frequency of wild type (GG) and heterozygous (GA) genotype was significantly different in patients and controls (p=0.027 and p=0.001), respectively. However, the frequency of AA genotype was not of statistical significance in patients (p=0.071).

Conclusions: The mutant alleles of *TaqI* and *BsmI* polymorphisms are known to be associated with different metabolic diseases, including diabetes too. In our study also, there is a significant difference between the frequency of wild type and heterozygous genotype for these polymorphisms. This suggests that *BsmI* and *TaqI* polymorphisms may be associated with T2DM patients.

Keywords: Type 2 diabetes mellitus, Polymorphism, Vitamin D receptor, Patient, Control, Restriction fragment length polymorphism.

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INTRODUCTION

Type 2 diabetes mellitus (T2DM) is one of the most prevalent lifestyle diseases, which is characterized by the high blood glucose levels resulting from defects in insulin action. It usually initiates with insulin resistance, a disorder in which the cells do not respond to insulin properly and increases the risks of many other diseases [1]. According to the International Diabetes Federation by 2035, worldwide the number of T2DM patients is estimated to exceed more than 600 million. India is known as a capital of diabetes, shelter to more than 63 million people suffering from diabetes, expected to increase to 100 million by 2030 [2]. This increase in the T2DM patient is matter of serious concern. Being a complex disease, T2DM is known to be caused by a large number of environmental and genetic factors too. The role of vitamin D in the pathogenesis and prevention of DM has sparked widespread interest. Apart from its classical role in Ca^{++} homeostasis, vitamin D also regulates insulin secretion from beta cells and its action on various target cells too [3-8]. All the vitamin D-mediated signaling is entirely dependent on its binding with the vitamin D receptors (VDR), which are present on the surface of the nuclear membrane. VDR, after binding with vitamin D, acts as active transcription factors, which controls the expression of approximately 200 genes including insulin too. Hence, variations/mutation in VDR gene is known to affect the insulin level, leading to diabetes [9-11].

Several polymorphisms in VDR gene have been reported to be associated with various metabolic diseases [12-15]. From last decade, these polymorphisms are also reported in different diabetic populations [16]. It has been hypothesized that VDR polymorphisms may influence both the risk of occurrence of diabetes and its prognosis too [17]. Out of all the reported VDR polymorphisms which are known to be associated with diabetes, four allelic variants have been commonly identified and described in great detail. These polymorphisms are rs731236 (*TaqI*), rs1544410 (*BsmI*), rs7975232 (*ApaI)*, and rs10735810 *(Fok1).* These four single nucleotide polymorphisms were identified using *TaqI, BsmI, ApaI,* and *FokI* restriction enzymes, respectively. The *TaqI* polymorphism is located at exon 9 (T65058C bp), codon 352. Although this is a synonymous change, it is reported to be associated with lower circulating levels of active vitamin D3 [18-20]. *BsmI* is present in intron 8 (63980 bp) at the 3' end, and being an intronic polymorphism, do not change the amino acid sequence of the encoded protein, but they may affect the expression of VDR gene by regulating the stability of mRNA [21]. Different research groups observed that both these polymorphisms, either independently or together, are associated with insulin resistance and increase in the fasting glucose levels [22,23]. In contrary, Ye *et al*., Malecki *et al*., and Cyganek *et al.* examined that there was no significant association of these polymorphisms with T2DM [24-26]. The status of association of these polymorphisms is also not very clear in context to the Indian population as there are very few reports available which highlight their association with diabetic phenotype in India [27]. Hence, the present work aims at investigating the association of the *TaqI* and *BsmI* polymorphism of VDR gene in T2DM patients from North India.

METHODS

Study population

A total of 100 T2DM patients and respective 100 controls were selected for the study. All the participants were recruited from All Indian Institute of Medical Sciences (AIIMS), New Delhi, India. These participants were between the ages of 35 and 55 years, non-smokers and belonged to the same ethnic group. T2DM patients were diagnosed on the basis of ADA Guidelines (2012). Individuals with fasting glucose ≥126 mg/dl and postprandial glucose ≥200 mg/dl were classified as diabetic. However, healthy controls with no metabolic disease were considered as controls. The present study was approved by the ethical committee of AIIMS,

New Delhi, India. The blood samples and clinical details were collected after taking the informed consent from all the participants.

Genomic DNA extraction

About 2 ml of the blood sample was collected in ethylenediamine tetra acetic acid coated BD Vacutainer and extraction of total genomic DNA was performed using the standard protocol of salting out method [28]. DNA extracted was stored at −80°C for further experiments.

Genotyping/polymerase chain reaction (PCR)-restriction fragment length polymorphism (RFLP)

To do genotyping by RFLP, a region of 745 and 155 bp carrying the restriction sites of *TaqI* and *BsmI,* was amplified by PCR. The specific PCR products were digested with *TaqI* and *BsmI* restriction enzyme. For amplification of VDR gene segments containing *TaqI* and *BsmI* restriction sites, the published primers were used (Table 1).

PCR amplification was carried out using the Biorad DNA Engine Thermal Cycler (PTC0200), the reaction mix was prepared using 50 ng of DNA, 10 pmol of both the forward (F) and reverse (R) primers (Sigma-Aldrich), 2 mM of dNTP's (Sigma-Aldrich), 0.5U *Taq* polymerase (Sigma-Aldrich), and nuclease-free water was used to make volume to 20 µl. PCR conditions were initial denaturation at 95°C for 5 minutes; 30 cycles of denaturation at 95°C for 1 minute; annealing at 68°C/63°C (*TaqI/BsmI)* for 1 minute; extension at 72°C for 1 minute followed by final extension at 72°C for 5 minutes. The PCR product of 745 and 155 bp was digested with 10 unit of each *TaqI* (65°C for 4 hrs, Thermo Scientific) and *BsmI* (37°C for 4 hrs, Thermo Scientific) restriction enzyme, respectively. These digested products were then resolved in 4% agarose gel stained with ethidium bromide using gel electrophoresis system at 100 V for 1-2 hrs. The gel was visualized under ultraviolet light using BioRad gel doc system.

As per the different genotypes for each polymorphism, the expected size of fragments obtained after digestion with *TaqI* and *BsmI* are mentioned in Table 1.

Statistical analysis

The statistical analysis was performed using a commercially available software program (SPSS 21.0, SPSS Inc., Chicago, Illinois, USA). The difference in allelic and genotypic frequencies was compared, using the Chi-square (χ^2) tests. Results were analyzed by calculating the p value and 95 confidence intervals. p values with <0.05 were considered to be statistical significant.

RESULTS

General characteristics of study population

The mean age of T2DM patients was 46.8±11.33 years, and it was observed to be 39.34±11.12 years for the control group. Among all the T2DM patients, the average fasting glucose level was found to be 158.25±48.85 mg/dl, whereas postprandial plasma glucose level was 235.57±86.0 mg/dl.

Distribution of *TaqI* and *BsmI* polymorphisms in VDR gene

For *TaqI* polymorphism, genotype frequencies were TT (36%), TC (54%), and CC (10%) in patients and TT (50%), TC (37%), and CC (13%) in controls. It indicated that out of 3 genotypes, the heterozygous genotype was the most common in patients. On the other hand, the wild type genotype was the most common type in control. In both the groups, the mutant profile was less prevalent (Table 2).

As a result of statistical analysis, the frequency of TT and TC genotype of *TaqI* polymorphism showed a significant difference between patients and controls (p=0.023 and p<0.001, respectively). Whereas the frequency of mutated profile (CC) was not significantly different among these two groups, with χ^2=0.442, p=0.506 (Table 2). After the comparison of the frequency of mutant allele (C), there was no significant difference observed between patients and controls (χ^2=1.100, p=0.294) (Table 3).

Analysis of different genotypes of *BsmI* revealed that frequency of genotypes was GG (20%), GA (56%), and AA (24%) in patients and GG (9%), GA (77%), and AA (14%) for controls. Here again, the heterozygous genotype was most common in both the groups, but its frequency was higher in controls. Unlike *TaqI,* the least common genotype in both groups was found to be wild type genotype (Table 4).

As similar to *TaqI* polymorphism, the frequency of wild type (GG) and heterozygous genotype (GA) of *BsmI* was also found to be significantly different in patients and controls (χ^2=4.88, p=0.027 and χ^2=10.945, p=0.001). However, the frequency of mutated profile (AA) was not different among these two groups of individuals (χ^2=3.249, p=0.071) (Table 4). Moreover, allelic frequency of mutant allele (A) was also found to be same in patients and controls (χ^2=0.020, p=0.887) (Table 5).

DISCUSSION

The importance of studying polymorphisms in the VDR gene initially emerges due to ethnic differences among different populations [18-20,31,32]. However, later it was also found to be associated with different metabolic diseases including diabetes [12-14,21-26]. As VDR gene is expressed in different types of tissues including pancreatic β-cells and adipocytes [33,34], which supports the idea that VDR polymorphisms possibly affects the insulin secretion and glucose metabolism [35,36].

In recent years, the relevance of VDR polymorphism has been investigated by a large number of studies in T2DM patients from different populations. The observations of different studies were not same. Most of the VDR gene polymorphism-related studies suggested a significant association between heterozygous and/or mutant genotype with different clinical parameters of diabetes such as glucose levels, obesity, and insulin level. For example, the study of *BsmI* polymorphism in T2DM patients done by Ortlepp *et al*. suggests a significant association of *BsmI* with fasting glucose levels of 1539 T2DM patients (p=0.018) [22]. Similarly, Oh *et al*. investigated *BsmI* polymorphisms and found a significant association with insulin levels of the 1545 T2DM patients, p<0.05 [36]. A study by Al-Daghri *et al*. found that *TaqI* and *BsmI* polymorphisms are significantly associated with T2DM n=627, p=0.033 [37]. On the similar lines, Ogunkolade *et al*. found a significant association of *TaqI* and insulin secretion in 143 Bangladeshi Asians (p<0.001) [32]. However, on the other hand, there are studies which contradict the same. For instance, the study by Bid *et al.,* 2009,

Table 1: Details of primer sequences and fragment lengths obtained after digestion of PCR products with *TaqI* and *BsmI* restriction enzymes

SNP	Position (bp)	SNP ID	Base change	Primer sequence	Annealing	Amplicon length (bp)	Genotype/RFLP product
TaqI	Exon 9 (65058)	rs731236	T/C	F5'CAGAGCATGGACAGGGAGCAA-3' R5'GCAACTCCTCATGGCTGAGGTCTC-3' [29]	68°C	745	TT/494, 251 CC/293, 251, 201 TC/494, 293, 251, 201
BsmI	Intron 8 (63980)	rs1544410	G/A	F-5'GTGTGCAGGCGATTCGTA -3' R5'TACCCTGCCCGCAAGAAA -3'[30]	63°C	155	GG/80, 70, AA/155, GA/155, 80, 70

PCR: Polymerase chain reaction, SNP: Single nucleotide polymorphisms, RFLP: Restriction fragment length polymorphism

Table 2: Distribution of *TaqI* polymorphism in T2DM patients and respective control

Genotype	Patients (N=100) %	Controls (N=100) %	χ^2	p value
TT (wild)	36 (36)	50 (50)	5.195	0.023*
TC (heterozygous mutant)	54 (54)	37 (37)	37.72	<0.001**
CC (mutant)	10 (10)	13 (13)	0.442	0.506

Statistical evaluation was made using the Chi-square test, *p<0.05, **p<0.01. T2DM: Type 2 diabetes mellitus

Table 3: Comparison of allelic frequencies of *TaqI* in T2DM patients and control

Allele	Patients (%)	Controls (%)	χ^2	p value
T	126 (63)	138 (69)	1.100	0.294
C	74 (37)	62 (31)		

Statistical evaluation was made using the Chi-square test. T2DM: Type 2 diabetes mellitus

Table 4: Distribution of *BsmI* polymorphism in T2DM patients and respective control

Genotype	Patients (N=100) %	Controls (N=100) %	χ^2	p value
GG (wild)	20 (20)	9 (9)	4.880	0.027*
GA (heterozygous mutant)	56 (56)	77 (77)	10.945	0.001**
AA (mutant)	24 (24)	14 (14)	3.249	0.071

Statistical evaluation was made using the Chi-square test, *p<0.05, **p<0.01. T2DM: Type 2 diabetes mellitus

Table 5: Comparison of allelic frequencies of *BsmI* in T2DM patients and control

Allele	Patients (%)	Controls (%)	χ^2	p value
G	96 (48)	92 (46)	0.020	0.887
A	104 (52)	108 (54)		

Statistical evaluation was made using the Chi-square test. T2DM: Type 2 diabetes mellitus

observed a non-significant association between any of common VDR polymorphisms (*FokI*, *BsmI*, and *TaqI)* and risk of T2DM [27]. Malecki *et al.* also studied VDR polymorphisms (*Fok1, ApaI, BsmI,* and *TaqI*) in Polish population and showed no association of these polymorphisms with T2DM [25]. Cyganek *et al.* did the same study in 267 T2DM patients of Poland, and there was no association found with the T2DM [26]. In 1998, Hitman *et al*. studied *ApaI, BsmI*, and *TaqI* in 164 T2DM patients and observed a non-significant association of *BsmI* and *TaqI* with T2DM [17].

In context to the Indian population, there is scarcity of the data which may support either of the view for VDR polymorphisms and its association with diabetes. Thus, in the current study, we have analyzed two common VDR gene polymorphisms; *TaqI* and *BsmI* in T2DM patients from North India. *TaqI* polymorphism is a silent substitution thus does not account for an amino acid change in VDR protein [32]. However, the wild type TT genotype of *TaqI* polymorphism is known to be associated with high copy number of VDR mRNA [17,32]. Hence, it may be hypothesized that the patients lacking wild genotype may have low copies of VDR gene transcripts which may probably affect level of VDR protein, and hence, the glucose metabolism too. In our study, the patient group had significantly a low number of wild type genotype TT, and it was found in only 36% of patients as compared to 50% of controls. The heterozygous TC genotype of *TaqI* polymorphism also shows a significant difference between T2DM patients and controls, further highlighting the possible role of mutant allele in determining the copy number of VDR gene transcript. The mutant profile (CC) of *TaqI* polymorphism was equally distributed in both the groups of individuals.

BsmI is an intronic polymorphism and proposed to affect the stability of VDR transcript [38]. It has also been demonstrated that an association exists between the *BsmI* polymorphisms of VDR gene and low insulin secretion in T2DM patients [17]. The study conducted by Speer *et al*. also showed that there is a link between heterozygous genotype of *BsmI* polymorphisms and T2DM in the Caucasian population [39]. In the similar context, we have also observed that the frequency of heterozygous GA genotype was significantly different among patients and controls (p=0.001). As similar to *TaqI*, we observed the significant difference between the frequency of wild type genotype between patients and controls, but surprisingly, the wild type genotype was higher in patients and heterozygous genotype was higher in controls. In addition, the mutant profile showed no difference between two groups of individuals as similar to *TaqI* data.

Comparison of frequency of mutant allele for both the polymorphisms indicated that there is no significant difference between patients and controls, however, to validate the same a large scale study design is required.

CONCLUSION

Both these polymorphisms are proposed to influence the transcription and/or stability of mRNA of VDR gene. Hence, based on our study and results from published literature, it can be proposed that *TaqI* and *BsmI* VDR polymorphisms may be associated with T2DM. Moreover, VDR signaling is also known to be important for insulin secretion and its action on the target cell. Hence, these polymorphisms may be suggested to be associated with altered insulin secretion and/or action, further contributing to the development of T2DM.

Although these two polymorphisms are not the only polymorphisms of VDR gene, known to be associated with T2DM, we propose to study the role of other VDR polymorphisms in these patients.

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