Original Article

Association of Vitamin D Receptor Gene Single Nucleotide Polymorphism (TaqI) with COPD

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Abstract

Background: Vitamin D receptor gene (VDR) polymorphism and its association with various diseases have been previously investigated. But the association of vitamin D receptor gene polymorphism with COPD has not been investigated yet. **Objective:** To assess the association between vitamin D receptor gene polymorphism (TaqI) and COPD. **Methods:** This cross-sectional study was carried out in the Department of Physiology, Bangabandhu Sheikh Mujib Medical University (BSMMU), Dhaka, from March 2019 to February 2020. For this study, 15 (fifteen) pulmonologists diagnosed COPD patients with age 40 to 80 years (post-bronchodilator FEV1/FVC <0.70 and FEV1 <80% predicted) and 15 (fifteen) apparently healthy age-matched individuals (for comparison), were selected. The single nucleotide polymorphism of the vitamin D receptor gene (TaqI) of all subjects was assessed byPCR-RFLPs. Data were expressed as mean \pm SD and percentage. Statistical analysis was done by independent sample 't' test and chi-square test. In the interpretation of the results, \leq 0.05 level of probability (p) was accepted as significant. **Results:** The frequency distribution of the TaqI VDR SNP was 0% (TT), 0% (Tt), 100% (tt) and 0% (TT), 0% (Tt), 100% (tt) COPD patients and healthy subjects, respectively. There was no association between TaqI VDR SNP with COPD. **Conclusion:** The present study reveals that TaqI of VDR SNP is not associated with COPD.

Keywords: Vitamin D receptor gene, Single nucleotide polymorphism, TaqI

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Introduction

Chronic obstructive pulmonary disease (COPD) is a common, preventable, and treatable disease characterized by persistent respiratory symptoms and airflow limitation due to airway and or alveolar abnormalities usually caused by significant exposure to noxious particles or gases. It is a complex disease associated with the multifactorial background of long-term exposure to noxious gases and particles, combined withvarious host factors, including genetics, airway hyper-responsiveness and poor lung growth during child hood1. It has been found that different genes are associated with COPD. Among them, alphal- antitrypsin (AAT) deficiency is one of the most common genetic causes of COPD. This enzyme deficiency occurs due to Taq-1 polymorphism of AAT, Z-isoform of AAT, and mutation of serpin family A member 1 (SERPINA1). In addition, Single nucleotide polymorphism (SNP) of matrix metalloproteinase 9 (MMP9), the promoter region of tumour necrosis factor-alpha (TNFα) gene and SERPINA3 were also associated with COPD²⁻⁶.

As COPD is a chronic inflammatory respiratory ailment, so, immunomodulation would be one of its

factor⁷⁻⁹. major causative Recently immunomodulatory role of vitamin D has been researchers 10-14. by the explored immunomodulatory characteristic has been found in several studies that it acts via vitamin D receptor (VDR), which alters genomic signaling system 12,15-¹⁹. So, the main regulator of vitamin D signaling is the VDR²⁰, which is present in numerous tissues, including kidney, heart, muscle, breast, colon, prostate, brain, and immune cells, that makes itself a natural target of modulation in disease pathogenesis, including a variety of the cancers²¹, metabolic syndrome^{22,23}, renal transplant²⁴ and dermal disorders²⁵. In addition, polymorphisms of the VDR gene have been found to be associated with immune-mediated diseases characterized by an imbalance in the development of the helper T- cell 9, such as in Crohn's disease²⁶ and tuberculosis²⁷. VDR gene is located on 12q13.11 possessing 11 exons with a length of 5.6 kb²⁸. This VDR gene has more than 470 single nucleotide polymorphisms (SNPs), a number of which modulate the uptake of 1,25(OH)₂ D₃²⁹. Among them, the common SNPs found on the research are the ApaI³⁰, BsmI³¹, TaqI³² and FokI³³.

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These SNPs have been found to be associated with the efficacy of antiresorptive treatments in postmenopausal women (with BsmI)34, essential hypertension (with FokI)35, metabolic syndrome (with FokI)²³, prostate cancer (with ApaI)³⁶, Leprosy (with FokI and ApaI)¹³, lumbar spine pathogenesis (with BsmI, ApaI and TaqI)37 and multiple familial sclerosis (with TaqI)³⁸. Moreover, in the perspective of respiratory ailments, both FokI and ApaI VDR SNPs were associated with asthma^{11,39-40} and FokI VDR SNP was found to be associated with tuberculosis^{41,42}. In addition, ApaI was associated with osteoporosis⁴³ and FokI along with BsmI were associated with skeletal muscle strength in COPD patients⁴⁴. To the best of our knowledge, different diseases were associated with VDR polymorphism. However, as far as we searched, no study was available on the association of VDR SNP with COPD. Therefore, this study aimed to investigate the association of one common VDR SNP (TaqI) with COPD.

Materials & Methods

Data collection: This cross-sectional study was conducted from March 2019 to February 2020 in the Department of Physiology, Bangabandhu Sheikh Mujib Medical University (BSMMU), after getting protocol approval from the Institutional Review Board (IRB) of BSMMU. For this study, 15 male (age 40 to 80 years) COPD patients (Study group) were diagnosed by a Pulmonologist with spirometric evidence of COPD (presence of a postbronchodilator FEV1/FVC < 0.70 and FEV1 < 80% predicted) and enrolled by purposive sampling from Out-Patients Department (OPD) of the National Institute of the Diseases of Chest and Hospital (NIDCH). For comparison, 15 age, BMI and smoking status matched apparently healthy males (Comparison group) were selected by personal contacts. Written informed consent was taken from all the participants after detailing the study

procedure. With all aseptic precautions, 5 ml of venous blood was drawn from the ante-cubital vein.

DNA extraction: DNA extraction was done by ReliaPrepTM Blood gDNA isolation kit (Promega, Wisconsin, USA) and assayed for purity and concentration by spectrophotometry (absorbance at 260 nm and 280 nm).

TaqI polymorphism: PCR amplification of the VDR gene was done in 25 μl reaction mixtures containing primers for TaqI polymorphism45. The PCR amplification conditions were initial denaturation at 95°C for 5 minutes, followed by 35 cycles at 94oC for 30 sec, 52°C for 1 min, 72°C for 1 min and final extension at 72°C for 5 minutes. The primers for TaqI polymorphism were 5′-CTAGGTCTGGATCCTAAATGCA-3′ and 5′-TTAGGTTGGACAGGAGAGAGAGAA-3′ 45.

The PCR product (628 bp) was digested with a 1.0-unit TaqI restriction enzyme (New England Biolabs Inc, USA) in a heat block at 25°C for 20 minutes. The products of restriction enzyme cleavage were analyzed on 1% agarose gels and were visualized under UV light after staining with ethidium bromide (Figure 1, Table I). TaqI VDR SNP resulted in fragments of 628 bp, 433 bp and 201 bp. Thus, for TaqI, tt resulted in two fragments of 433 bp and 201 bp.

Statistical analysis: The data were expressed as mean with standard deviation (mean \pm SD) and frequency distribution in percentage. The data were statistically analyzed by SPSS statistical package, version 22.0 (IBM, SPSS Inc., Chicago, IL) using the Chi-square test. Allelic frequencies of VDR gene polymorphisms were determined by Hardy-Weinberg equilibrium. In the interpretation of the results, \leq 0.05 level of probability (p) was accepted as significant.

Table-I: Primer sequence and PCR conditions for genotyping of TaqI VDR

Location	Locus	Alleles	PCR primer	PCR product (bp)	Restriction enzyme	RFLP products (bp)
Exon 9	rs731236	T/C	F: CTAGGTCTGGATCCTAAATGCA R: TTAGGTTGGACAGGAGAGAGAA *Initial denaturation: 95 °C for 5 min; 35 cycles: 94 °C for 30 s, 52 °C for 1 min, and 72 °C for 1 min; and final extension: 72 °C for 5 min	628	TaqI	628 433 201

PCR-Polymerase chain reaction; RFLP-Restriction fragment length polymorphism; bp-Base p.

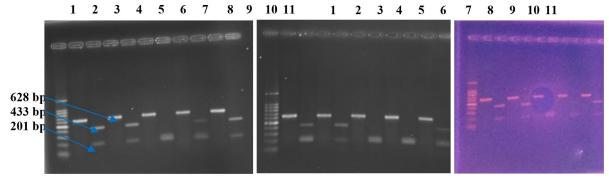


Figure-1: Restriction fragment length polymorphism digestion of TaqI in 1% agarose gel stained with ethidium bromide with 100 bp ladder in the first Lane, in lanes 2, 4, 6, 8, 10 shows PCR products; in lanes 3, 5, 7, 9, 11 shows digested products in gel picture. TaqI digestion – tt/433, 201 (minor homozygous).

Results

The baseline characteristics of all our study subjects are presented in Table II. The distribution of TaqI VDR genotype and allele frequency is shown in Table III. Frequency distribution of the TaqI VDR SNP was 0% (TT), 0% (Tt), 100% (tt) and 0% (TT), 0% (Tt), 100% (tt) COPD patients and healthy subjects, respectively. There was no statistical association between TaqI VDR SNP with COPD.

Data were expressed as mean \pm SD; Figures in parentheses indicate ranges; Statistical analysis was done by Independent sample t-test; N= Total number of subjects; n= number of subjects in each group; Pack year= (number of cigarettes smoked per day/20) X no. of years smoked; FEV1= Forced expiratory volume in the first second; FVC = Forced vital capacity; ns= non-significant; ***= statistically significant (p<0.001).

Table-II: Baseline characteristics of COPD patients and healthy subjects (N=30)

Characteristics	COPD patients (n=15)	Healthy subjects (n=15)	p-value
Age (years)	60.46 ± 6.31 (40 - 80)	56.00 ± 7.80 (40 - 80)	0.096 ^{ns}
Body mass index (BMI) (kg/m²)	22.76 ± 4.26 $(16.90 - 33.70)$	21.96± 2.30 (18.80 - 25.91)	0.531 ^{ns}
Duration of smoking (pack year)	$14.07 \pm 5.41 \\ (4 - 30)$	17.16 ± 5.17 $(4 - 30)$	0.121 ^{ns}
FEV1/FVC (%)	57.60 ± 10.61 (39 - 68)	80.60 ± 6.38 (72 - 92)	0.000***
FEV1(% of predicted value)	44.88 ± 10.98 (28.30 - 63.60)	83.26 ± 10.51 (70 - 100)	0.000***

Table-III: Genotype and allele distribution of TaqI VDR SNP in study subjects (N=30)

SNP	COPD patients (n=15)		Healthy subjects (n=15)		OR (95%CI)	χ² value (p value)
	no	%	no	%		
TaqI						
TT	0	0	0	0	-	-
Tt	0	0	0	0	-	-
tt	15	100	15	100	- -	-
T	0	0	0	0	-	-
t	30	100	30	100	-	-

VDR=Vitamin D receptor; SNP=Single Nucleotide polymorphism; OR=odds ratio; CI=confidence interval.

Discussion

It is well known that the VDR gene is located on chromosome 12q13.11^{28,46} encoding the VDR protein by exon II to IX. Among the four common VDR SNPs, TaqI is located in exon 9^{10,47-49} codon 352 near the 3′ UTR. However, it has been reported

that exon VII to IX involves the binding of VDR to vitamin D⁴⁷. In addition, it has also been observed that variations in the 3′ UTR sequence often affect mRNA stability and the efficiency of protein translation³² and altered protein levels^{13,50-51}. The TaqI polymorphism in which a T nucleotide has

been substituted with a C. Since VDR is a transcriptional regulating factor for a large number of target genes, its altered expression can influence various aspects of cellular function⁵². Therefore, this TaqI polymorphism may affect the activity of VDR and subsequent downstream effects of vitamin D, including its immune-modulatory role⁵³. Moreover, it has been observed that the vitamin D-VDR signalling pathway is related to some regulatory proteins, such as Smad3⁵⁴, β-catenin⁵⁵, NF- kB⁵⁵ and cyclin D3⁵⁶. Among them, as a transcription factor⁵⁶, NF-kB binds to specific DNA sequences in different gene promoters to regulate the transcription of a wide range of genes, including those involved in immune and inflammatory responses⁵⁷⁻⁵⁹.

These genes produce pro-inflammatory cytokines IL-1 and TNF- α^{55} along with chemokines IL-6, IL-8, IL-12⁵⁷⁻⁵⁸. TaqI VDR SNP is associated with gastric carcinoma, colorectal carcinoma, Crohn's disease, metabolic syndrome, obesity, breast cancer and new onset diabetes at transplant^{52,60}. From the perspective of respiratory ailments, it was found that TaqI VDR SNP was associated with tuberculosis in Asian populations⁶¹. Very recently it has been found that this VDR SNP is associated with COVID-1962. However, in our study, neither the genotype nor the allele of TaqI VDR single nucleotide polymorphism was associated with COPD. Similarly, in India, as well as in Greece, China, Chile and American study, there was found no association between asthma and TagI VDR SNP⁶⁻⁶⁶. It may be explained as respiratory diseases showing similarity of genetic involvement.

Limitation & Recommendation:

There were a few limitations in our study. First, the intake of vitamin D and environmental exposure to ultraviolet radiation of our study population could not be assessed. Second, as a genetic association study, the results were based on a small number of samples. For further research, a similar type of study should be done, including information on vitamin D intake and environmental exposure to ultraviolet radiation in a large number of COPD patients.

Conclusion

The results of the present study elucidate that TaqI VDR SNP is not associated with COPD.

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