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Transcription Factor 7 Like 2 (TCF7L2) Expression Level Variation Contributes to VEGF Alteration in Diabetic Retinopathy

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Authors' contributions

This work was carried out in collaboration between both authors. Authors MHD and MM designed the study. Author MHD wrote the first draft of the manuscript. Authors MHD and MM managed the literature searches and corrected all grammatical errors. Both authors read and approved the final manuscript.

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ABSTRACT

Diabetic retinopathy (DR) is a multifactorial disease which causes blindness among people with Diabetes worldwide. It has complex pathophysiology linked to various genetic variations. TCF7L2 (Transcription factor 7 like 2) is among the most important candidate genes which play a major role in hyperglycemia and neovascularization. Neovascularization is a clinical symptom of DR associated with upregulation of vascular endothelial growth factor (VEGF) as established by numerous published articles. The purpose of this review is to highlight the role of TCF7L2 polymorphism in the development of DR via alteration in VEGF expression level. We used available published data to explain the association of TCF7L2 polymorphism with DR. We concluded that genetic studies reports revealed TCF7L2 polymorphism might be associated with DR development.

Keywords: DM; DR; NPDR; PDR; TCF7L2; Wnt; VEGF; polymorphism.

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ABBREVIATIONS

DM : Diabetes Mellitus
DR : Diabetic Retinopathy
NPDR : Non-proliferative DR
PDR : Proliferative DR
TCF7L2 : Transcription Factor 7 Like 2
VEGF : Vascular Endothelial Growth Factor

1. INTRODUCTION

Diabetes mellitus (DM) is a metabolic disorder characterized by chronic hyperglycemia leading to defect in insulin secretion or action which implicate in acute and chronic complications [1]. The complications usually manifest in the form of damage to the vascular system of the body and are less common in DM patients with controlled hyperglycemia [2]. Uncontrolled hyperglycemia causes impaired metabolism which may result in oxidative stress, increased lipolysis (breakdown of lipids), elevated ketone bodies and increased gluconeogenesis [3,4]. These factors affect the body tissues and subsequently, they can cause morphological and functional defects in organs such as the heart, kidneys, liver, and eye [5]. Diabetic Retinopathy (DR) is a diabetic complication which causes morphological damage to the eye leading to visual impairment and blindness [6]. DR clinically leads to retinal ischemia accompanied by hemorrhages, microaneurysms, hard exudates, cotton wool spots, intraretinal microvascular abnormalities and neovascularization [7–9]. The early stage of DR is characterized by vascular permeability; this condition is called non-proliferative diabetic retinopathy (NPDR) whereas progression of the NPDR results in abnormal growth of the retinal blood vessels leading to the neovascularization that is a major symptom in the advanced stage of DR, which is known as proliferative diabetic retinopathy (PDR) [10] (Fig. 1). Recent researches have shown abnormalities in the expression of glucagon-like peptide-1(GLP-1); an incretin hormone lead to hyperglycemia and vascular endothelial growth factor (VEGF), which subsequently lead to neovascularization that might be triggered as a result of variations in the gene of a transcription factor in the Wnt signaling pathway referred to as transcription factor 7 like 2 (*TCF7L2*) [11–15].

2. TRANSCRIPTION FACTOR 7 LIKE 2 (TCF7L2)

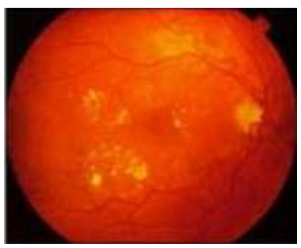
Transcription factor 7 like 2 (*TCF7L2*) also called transcription factor 4 (Tcf4) is a member of T-cell factor (Tcf)/Lymphoid enhancer factor (Lef) transcription factor family [16]. *TCF7L2* gene spans 17 exons on chromosome 10q25.3 which encodes for a transcription factor involved in the Wnt signaling pathway [16,17] (Fig. 2). Several single nucleotide polymorphisms (SNPs) including rs7903146 and rs12255372 in the intron region of the *TCF7L2* were identified and found to have an association with metabolic disorders including type 2 diabetes mellitus (T2DM) [18]. The rs7903146 is a nucleotide change from C to T at position 112998590 in the fourth intron of *TCF7L2*, whereas rs12255372 is a change in nucleotide at position 113049143 in the fifth intron from G to T (Fig. 3) [19,20].

Genome-wide association studies (GWAS) reported a relationship between a common micro-satellite region (DG10S478) in intron 3 of the TCF7L2 gene and T2DM [7,8]. In addition, several studies identified other polymorphisms of TCF7L2 gene associated to T2DM, amongst which are rs7903146 (C/T) and rs12255372 (G/T) [21].

3. ROLE OF *TCF7L2* POLYMORPHISMS IN UPREGULATION OF VEGF LINKED DR

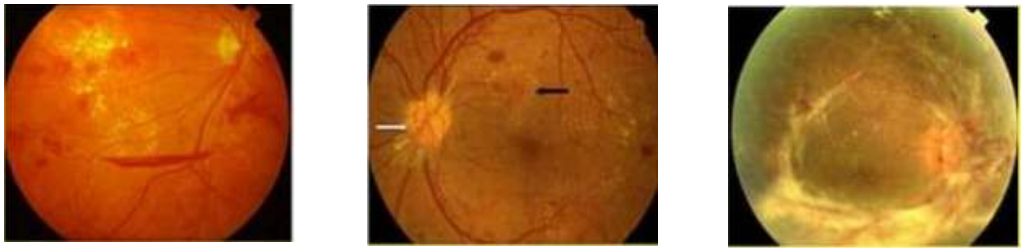
Genetic variation of rs7903146 (c.382-41435C>T) and rs12255372 (c.482+9017G>T) were successfully linked to T2DM in various ethnic groups [1,13,18-20,22–25]. But it is still not clear if *TCF7L2* genetic variant is related to DR [26,27].

Normal



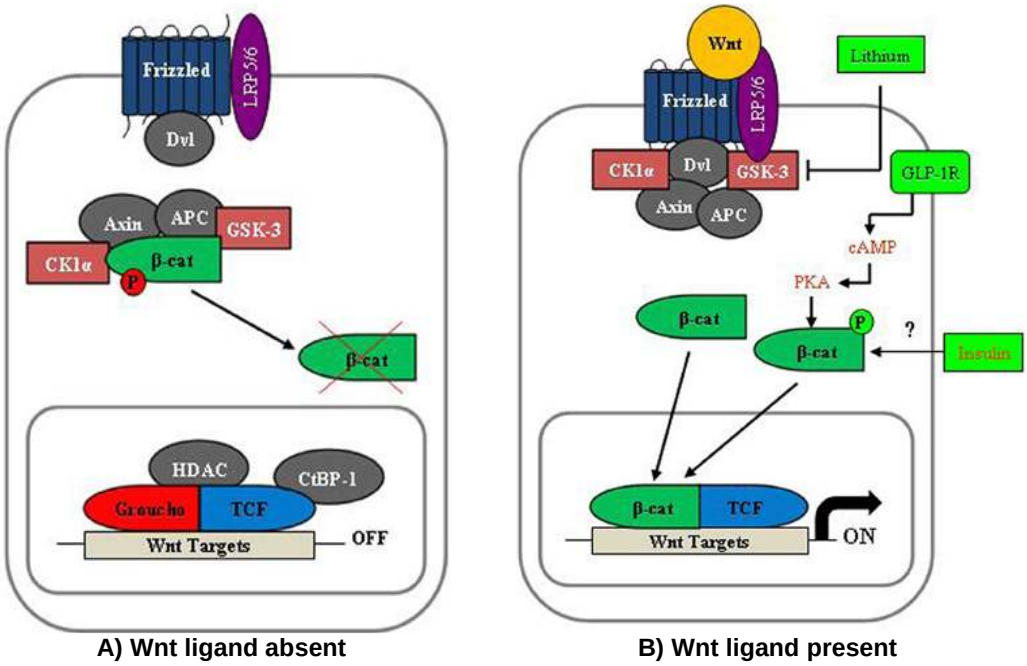
Background DR

Moderate NPDR



Severe NPDR **PDR neovascularization** **Fibrovascular membranes**

Fig. 1. Fundus images of DR progression. This progression develops from background DR (mild DR) a form of NPDR to Fibrovascular membrane a form of PDR, as the DR progresses new vessels are formed. The gradual loss of the red color and change in vein size occur with progression of DR. This image is adopted from El-bab et al. with modification [6]



A) Wnt ligand absent **B) Wnt ligand present**

Fig. 2. Canonical Wnt signaling pathway A) Shows β catenin regulation in the absence of Wnt ligands. The destruction complex containing CK 1α, axin, APC, and GSK-3 phosphorylates β catenin and mark it for proteasomal degradation B) Shows the β catenin stimulation in presence of Wnt ligands which prevents interaction between the destruction complex and β catenin and subsequently promote Wnt targeted gene expression. This image is adopted from Chiang et al. [12]

Although the exact mechanism of *TCF7L2* in DR development is not clearly established. However, polymorphisms in the *TCF7L2* might be associated with DR via Wnt targeted genes, several studies have reported the association of these genes with DR in different cohorts i.e. Chinese, Japanese, Indian and American population VEGF [15,28,29], ICAM-1 [30,31] and eNOS [28,32]. VEGF is a vasoactive factor and a mediator of vascular leakage; it is partly responsible for the collapse of the inner blood-retinal barrier. Which is upregulated in the retina in DR [29]. VEGF expression is increased in the neovascular membranes of diabetic patients with DR [33]. VEGF antagonists have been found useful in the treatment of DR [34]. The VEGF family is part of the platelet-derived growth factor (PDGF) supergene family members which consist of VEGFα, VEGFβ, VEGFγ, VEGFδ, VEGFε, and PlGF (placental growth factor)

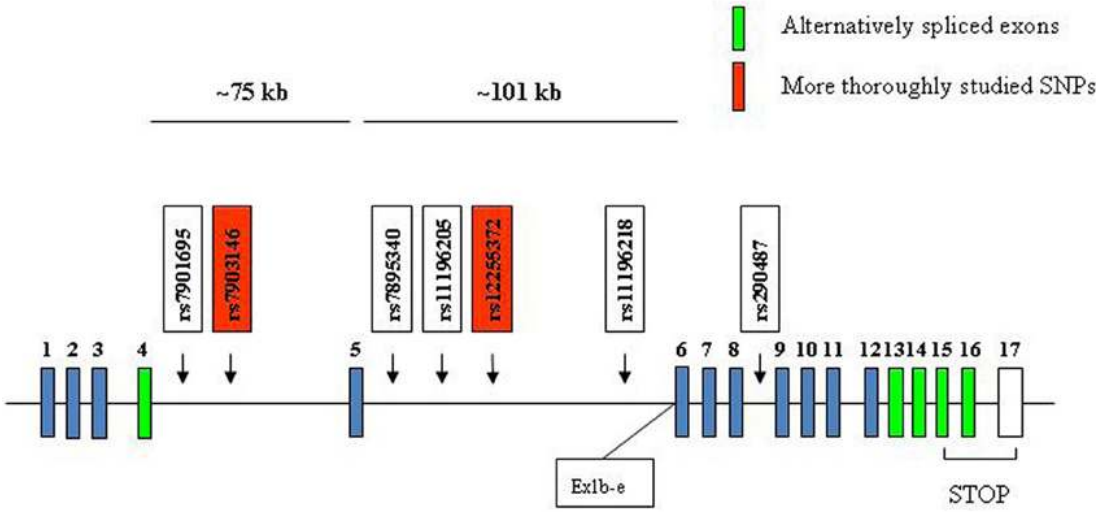


Fig. 3. *TCF7L2* gene structure. The *TCF7L2* is located on chromosome 10q25.3. The blue colored bar-shape are exons whereas the green colored bar-shape indicate exons that undergo alternative splicing, STOP is the region where transcription of TCF7L2 gene terminate, whereas The two single nucleotide polymorphisms (SNPs) in red are the most studied. This image is adopted from Ip et al. [22]

[6,35,36]. VEGFα has been studied extensively and reported to play a critical role in both vasculogenesis and neovascularization [37-42]. Investigation on PDR shows the relationship between *TCF7L2* and *VEGFα* [28].

The expression of *VEGFα* increases with increase in expression of *TCF7L2;* which might be as a result of rs7903146 (c.382-41435C>T), several studies have reported rs7903146 and rs12255372 (c.482+9017G>T) to be in linkage disequilibrium [19,34,35], thus showing that both rs7903146 and rs12255372 might play crucial role in the upregulation of VEGFα. There are two binding sites in the VEGFα promoter region linked to TCF7L2, which may implicate in increased expression of VEGFα transcription through TCF7L2 binding, therefore, genetic polymorphism may lead to elevated *TCF7L2 levels* which result in overexpression of *VEGFα*; related to derangement of retinal vessels and neovascularization [28]. We believe the mechanism revealing the association of TCF7L2 polymorphism to *VEGFα* is applicable to other genes expressed by TCF7L2 in the Wnt signaling pathway.

4. CONCLUSION

In addition to confirming the association of TCF7L2 gene variants to DM, TCF7L2 SNPs might play a role in the development of DM complications including DR via upregulation of VEGF. Studies are required to establish the relationship between TCF7L2 polymorphisms with other diseases associated with neovascularization such as Age-related macular degeneration, diabetic macular edema, and corneal neovascularization etc.

CONSENT

It is not applicable.

ETHICAL APPROVAL

It is not applicable.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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