VITAMIN D RECEPTOR GENE *APAI* AND *TAQI* POLYMORPHISM IN PATIENTS WITH TYPE II *DIABETES MELLITUS* USING PCR-RFLP METHOD IN KURDISTAN REGION

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ABSTRACT

Background: Type 2 diabetes mellitus that characterized by insulin resistance and it is a risk of many diseases the impact of genetic factors on diabetes is well documented. Vitamin D receptor (VDR) gene polymorphisms have been linked to T2DM. In this study, we analyzed the relation between TaqI and ApaI VDR gene polymorphisms and T2DM subjects by using the PCR-RFLP method in Kurdish patients.

Material and Methods: Forty patients with T2DM and 30 uninflected individuals were included in this study. Genomic DNA was amplified using PCR and VDR gene was analyzed by the PCR-RFLP method. The ApaI product G allele yielded fragments of 528 and 217 bp; T allele, 745 bp, and TaqI T allele yielded fragments of 494 and 251 bp; C allele, 293, 251, and 201 bp.

Results: Forty patients with T2DM and 30 uninflected individuals have been studied, both patients and the control group were age-matched, (43.59%) of patients have had a family history of type2 Diabetes. The allele and genotype frequencies of the VDR TaqI (g.60058 T>C) gene and VDR ApaI (g.59979 G>T) gene polymorphisms were investigated. In VDR TaqI (T>C) gene polymorphism genotypes are expressed as TT in normal wild-type homozygote, TC in the heterozygote, and CC in the homozygote mutant polymorphic genotype. There were statistically significant differences between patients withT2DM and controls regarding the distribution of TaqI genotypes and alleles ($p< 0.0001$) and no significant difference regarding ApaI alleles (P=0.5532).

Conclusion: Current study findings demonstrated no associations between ApaI polymorphism and Kurdish T2DM patients and only associations between VDR TaqI gene polymorphism, it can be assumed that VDR and its exon 9 polymorphism are crucial in the pathogenesis of T2DM.

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Keywords: *ApaI VDR, Gene* Polymorphisms, *TaqI*, T2DM, VDR.

Two major forms of vitamin D which are called calciferol exist one of them that is largely ingested is called vitamin D2 and another one is called vitamin D3. These two forms of vitamin D are activated enzymatically by hydroxylation reactions. The first activation occurs in the liver forming 25-

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hydroxyvitamin D that is mediated by 25-hydroxylase and the second is mediated by 1 α-hydroxylase in the kidney forming calcitriol (1,25 dihydroxy vitamin D) which is a final activated product1. The most important contemporary medical problem is Type 2 diabetes mellitus (T2DM) characterized by insulin resistance and it is at risk of many diseases such as cardiovascular disease, kidney failure, blindness, neuropathy, and peripheral circulatory disease2. Resistance of insulin action and the defect of its secretion leads to many metabolic defects such as disturbance in protein, carbohydrate, and lipid metabolism. Both environmental factors and genetics influence T2DM and T1DM development[1,3].

There is an important role of vitamin D in insulin release and normal glucose tolerance. It plays this role through its impact on binding to a specific intracellular receptor called vitamin D receptor (VDR). Vitamin D induces glucose tolerance by complex of Vitamin D and VDR which induce insulin secretion from pancreatic β-cells. The gene that is responsible for VDR is located at the 12q13 chromosome and in this region there are many polymorphisms the most crucial ones are ApaI, TaqI, and BsmI. These genes are among those which influence T2DM development1. Angel et al (2018) reported that FokI, BsmI, TaqI, and ApaI are the most prevalent VDR single nucleotide polymorphisms (SNPs)4.

Insulin secretion can be affected by genetic polymorphism of VDR gene enhancing insulin resistance which may in turn influence vitamin D metabolism from synthesis, transportation, and their active forms. It was concluded that single nucleotide polymorphisms (SNP) in the VDR gene modulate insulin secretion, glucose intolerance, and sensitivity5.

The gene product that mediates vitamin D action is called vitamin D binding protein (DBP). Cholecalciferol enters the bloodstream through binding to DBP. Fatma and Abdul (2019) reported that VDR gene genotype BsmI polymorphism found in intron 8is related to the onset of type 2 diabetes mellitus and TaqI polymorphism with obesity and early onset T2DM[5].

The normal functioning of pancreatic beta cells regulate by vitamin D and the deficiency of this vitamin has been reported to be associated with T2DM various polymorphisms of the VDR gene have been identified as a risk factor for T2DM and the most often studied VDR polymorphisms (single nucleotide polymorphisms [SNPs]) are FokI (T/C; rs2228570), BsmI (A/G; rs1544410), ApaI (A/C; rs7975232), and TaqI (C/T; rs731236)[6].

Our study aimed to use the PCR-RFLP technique in the Kurdistan Region of Iraq to detect and identify the VDR gene ApaI and TaqI polymorphism and its relationship to type 2 diabetes mellitus.

MATERIALS AND METHODS

Forty patients with T2DM (19 females and 21 males), and 30 uninflected individuals, were investigated in the present study. Twelve females and eighteen males mean age ∓SD. (55.2 ± 5.39), while in the case of the family history (43.59%%) type2 Diabetes was positive and (56.40%) negative. The samples enrolled in this study were

obtained from Layla Qassim Diabetic Center in Erbil City. The study was approved by the biology department and carried out in the science college's biology department at the University of Salahaddin Erbil (SUE). Patients were diagnosed in accordance to American Diabetes Association (ADA) and World Health Organization (WHO) standards, and everyone involved in the present study was made aware of it.

Two to four milliliters of human venous blood samples were drawn and placed in sterile EDTA tubes using a sterile syringe. The DNA was extracted from patient whole blood samples via a DNA extraction kit (Promega-USA) and kept at -20 0C until use.Primers for each SNP were used in the PCR (polymerase chain reaction) technique to amplify genomic DNA, and the PCR-RFLP method was used to analyze the VDR gene. By using primers a 745-bp fragment was amplified; Forward: 5′-CAGAGCATGGACAGGGAGCAAG-3′ and Reverse:5′-ACTCCTCATGGCTGAGGTCTCA-3′2-7.

The PCR conditions program was performed at 950C for 5 min (initial denaturation), 35 cycles consisting of 940C for 25 s, 640C for 30 s primer nailing and 720C for 45 s, and 720C for 5 min (final extension). PCR products (5 µl) of the VDR gene were digested in a 20-µl reaction volume for 5 hr with 1.5 U of ApaI restriction enzyme (Promega-USA) at 370C and TaqI R.E at 650C. The products of restriction enzyme digestion were analyzed on 2% agarose gel electrophoresis and staining with Ethidium bromide after that visualized under UV light. In the presence of the T-allele, there was no restriction enzyme cleavage site and a product of 740 bp was obtained. In subjects carrying ‘G-allele’, the cleavage products of 529 and 215 bp were detected. Allele ‘T’ was associated with the presence of 495bp and 245bp cleavage products while allele ‘C’ was assigned in the presence of 290, 245, and 210-bp fragments respectively. The ApaI product G allele yielded fragments of 528 and 217 bp; T allele, 745 bp, and TaqI T allele yielded fragments of 494 and 251 bp; C allele, 293, 251, and 201 bp2.

STATISTICAL ANALYSIS:

The Statistical Package for Social Science SPSS version(24), Graphpad prism version 6, and , computer software and were used for analyzing our data in the current study. The significance of the association between T2DM and Controls data was assessed by using the Chi-square ($\chi 2$) test for association between two groups. Both genotype and allelic odds ratio and 95% confidence interval were calculated to determine the association of VDR gene ApaI and TaqI gene polymorphisms with T2DM. A p-value of less than 5% ($p<0.05$) was set to be statistically significant.

RESULTS

In the present study forty patients with T2DM (19 females, mean age ∓SD of age 55±3 years, and 21 males, mean age ∓SD of age 57±4 years). Patients diagnosed in accordance with the American Diabetes Association (ADA) and World Health Organization’s (WHO) criteria8 and 30 uninflected individuals (free from any ailments), were investigated in this study. Twelve females and eighteen males mean age ∓SD. (55.2 ± 5.39), while in the case of family history (43.59%) type2 Diabetes was positive and (56.40%) negative. In this

prospective study, both patients and the control group were age-matched.

Table 1: Parameters of the demographic for patients with Type 2 diabetes mellitus and control Subjects

Variations	Patients	Control Subjects
Subjects (n)	40	30
Gender (M/F)	21/19	18/12
Age (Years)	56±3.5	55.2 ± 5.39

M: Male, F: Female

The allele and genotypes frequencies of the VDR TaqI (g.60058 T>C) (in exon 9) and VDR ApaI (g.59979 G>T) (in intron 8) genes polymorphisms were investigated and compared between 40 patients (T2DM) and 30 healthy control persons, as illustrated in Table 2 and 3, respectively.

Table 2: Genotype/allele frequency of VDR TaqI (T>C) gene polymorphism in patients with T2DM and healthy control group

Genotypes/Allele	Frequency of Healthy Controls (N= 30) and (%)	Frequency of T2DM Patients (N= 40) and (%)	OR	(95% CI)	P-Value
g.60058 T>C					
TT (Wild type)	20 (66.67%)	4 (10 %)	0.08	0.01911 to 0.3349	0.0002
TC (Heterozygous)	4 (13.33%)	21 (52.50 %)	2.1	0.5033 to 8.762	0.3032
CC (Mutant)	6 (20%)	15 (37.50 %)	12.5	2.986 to 52.32	0.0002
T – Allele	44 (73.33%)	29 (36.25 %)	0.2068	0.09947 to 0.4298	< 0.0001
C – Allele	16 (26.67%)	51 (63.75 %)	4.836	2.327 to 10.05	< 0.0001

T2DM: Type 2 diabetes mellitus, OR: Odds Ratio, CI: Confidence Interval

Table 3: Genotype/allele frequency of VDR ApaI (G>T) gene polymorphism in patients with T2DM and healthy control group

Genotypes/Allele	Frequency of Healthy Controls (N= 30) and (%)	Frequency of T2DM Patients (N= 40) and (%)	OR	(95% CI)	P-Value
g.59979 G>T					
GG (Wild type)	12 (40.0 %)	18 (45.0 %)	1.35	0.4233 to 4.306	0.5532
GT (Heterozygous)	9 (30.0 %)	12 (30.0 %)	0.7407	0.2323 to 2.362	0.6116
TT (Mutant)	9 (30.0 %)	10 (25.0 %)	1.2	0.3443 to 4.182	0.7746
G – Allele	33 (55.0 %)	48 (60.0 %)	1.227	0.6233 to 2.416	0.5532
T – Allele	27 (45.0 %)	31 (40.0 %)	0.8148	0.4138 to 1.604	0.5532

T2DM: Type 2 diabetes mellitus, OR: Odds Ratio, CI: Confidence Interval.

In VDR TaqI (T>C) gene polymorphism genotypes expressed as TT in normal wild-type homozygote, TC in the heterozygote, and CC in the homozygote mutant polymorphic genotype. In the normal TT genotype, two bands of 494 bp and 251 bp were produced. In heterozygote TC genotype, four bands of 494 bp, 293 bp, 251, and 201 bp were indicated, in homozygote CC genotype (mutant) three bands of 293 bp, 251 bp, and 201 bp were produced (Figure 1).

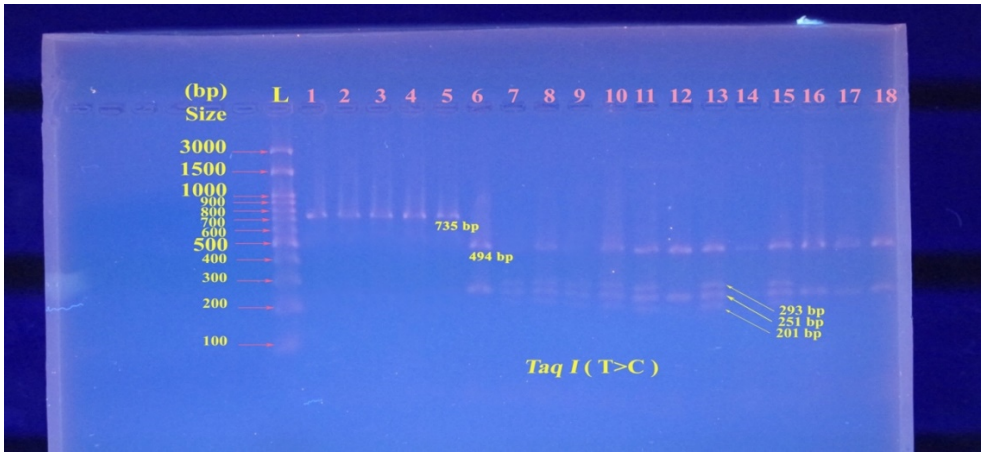

Figure 1: Agarose gel electrophoresis (2%) illustrating PCR-RFLP products obtained in Type 2 diabetes mellitus (T2DM) patient cases of the genotyping VDR *TaqI* (g.60058 T>C) (in exon 9) gene polymorphism. Lanes 1-5: undigested PCR products. Lanes 6, 12, 14, 16, 17, and 18 represented 494 and 251 bp amplified bands of the polymorphisms of the VDR TaqI gene for the (TT) genotype (homozygous, wild type). Lanes 8, 10, 11, 13, and 15 revealed 494, 293, 251, and 201 bp amplified bands of the polymorphisms of the VDR *TaqI* gene for the (TC) genotype (heterozygous). Lanes 7 and 9 exhibited 293, 251, and 201 bp amplified bands of the polymorphisms of the VDR *TaqI* gene for the (CC) genotype (homozygous, mutant). Lane L indicated known standard sizes of (100 – 3000 bp) DNA Ladder.

Moreover, genotypes expressed in VDR ApaI (G>T) gene polymorphism as GG in normal wild-type homozygote, GT in the heterozygote, and TT in the homozygote mutant polymorphic genotype. In the normal GG genotype, two bands of 528 bp and 217 bp were obtained. In the heterozygote GT genotype, three bands of 745 bp, 528 bp, and 217 bp were yielded; in the homozygote TT genotype (mutant) only one band of 745 bp was detected (Figure 2).

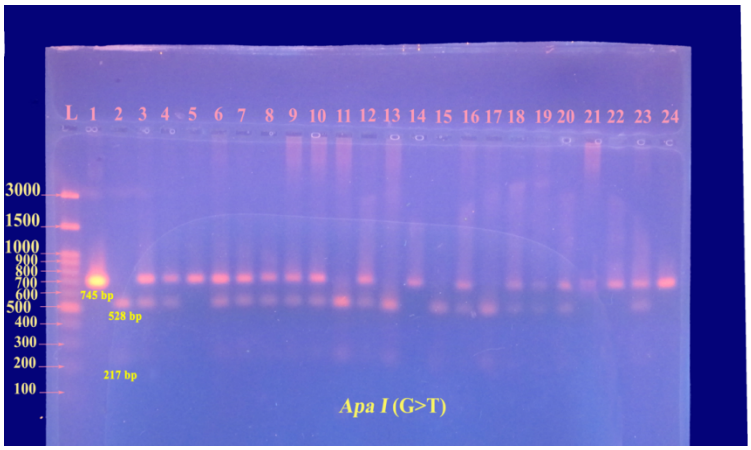

Figure 2: Agarose gel electrophoresis (2%) representing PCR-RFLP products obtained in Type 2 diabetes mellitus (T2DM) patient cases of the genotyping VDR ApaI (g.59979 G>T) (in intron 8) gene polymorphism. Lanes 1: undigested PCR product. Lanes 2, 11, 13, 5, and 17 showed 528 and 217 bp amplified bands of the polymorphisms of the VDR *ApaI* gene for the (GG) genotype (homozygous, wild type). Lanes 3, 6, 7, 8, 9, 10, 12, 16, 18, 19, 20, and 23 observed 745, 528, and 217 bp amplified bands of the polymorphisms of VDR ApaI gene for (GT) genotype (heterozygous). Lanes 5, 14, 21, 22, and 24 demonstrated a 745 bp amplified band of the polymorphisms of the VDR ApaI gene for the (TT) genotype (homozygous, mutant). Lane L indicated known standard sizes of (100 – 3000 bp) DNA Ladder.

There were 40 patients of the 40 patients, had a family history of T2DM and comprised the prevalence of 18 (45%) GG (not polymorphic, wild-type), 12 (30%) GT (heterozygous), and 10 (25%) TT (homozygous, polymorphic) genotypes of ApaI, while they had the prevalence of 4 (10%) TT (not polymorphic, wild-type), 21 (52.50%) TC (heterozygous) and 15 (37.50%) CC (homozygous, polymorphic) genotypes of TaqI polymorphisms. As a result, the assessment of the polymorphisms within g.60058T>C exon 9 of the VDR gene by TaqI restriction digestion illustrated significant differences. Tables 2 and 3 demonstrated that in T2DM cases and the healthy group a significant difference was observed in the VDR gene g.59979TT (homozygous mutant) and g.60058CC (homozygous mutant) genotypes, respectively. Similarly, it was also revealed that association of T2DM to VDR g.59979T and g.60058C alleles was significant, in comparison with healthy controls.

Table (2) illustrates the frequency of the genotypes, odds ratio (OR), 95 % confidence intervals (CI), and a p-value of VDR TaqI (T>C) gene polymorphism in both T2DM patients and healthy control. Those patients with (CC) genotypes (mutant) were 12.5- fold significantly higher (P= 0.0002) to develop T2DM and those with (TC) and (TT) genotypes were 2.1- fold and 0.08- fold not significantly higher (P= 0.3032 and P= 0.0002) to develop T2DM, respectively. Additionally, those patients carrying the C allele of the VDR gene g.59979 polymorphic site show greater susceptibility to developing T2DM cases by 4.836- fold (OR 4.836; 95% CI, 2.327 to 10.05; P-value < 0.0001) as compared with wild type TT genotype (Table 2).

Table 3 observed the frequency of the genotypes, odd ratio (OR), 95 % confidence intervals (CI), and a p-value of VDR ApaI (G>T) gene polymorphism in both T2DM patients and healthy control. Those patients with (TT) mutant genotypes were 1.2- fold not significantly higher (P= 0.7746) protected to develop T2DM. Besides, the T-allele of VDR gene g.60068 polymorphic site is not significantly positively associated with T2DM by 0.8148 fold (95% CI, 0.4138 to 1.604, P= 0.5532) and was not a risk factor for T2DM (Table 3).

DISCUSSION

A receptor of vitamin D has an impact on the progression of Type 2 Diabetes Mellitus and on insulin action besides inflammatory complications, such as nephropathy. It noted that many factors related to the immune serve crucial roles in the pathogenesis and etiology of Type 2 Diabetes Mellitus[9,10].

As displayed in Table (1) the results represented that 43.59% of Type2 Diabetes Mellitus individuals had a positive family history of Patel diabetes, whereas 56.40% were negative; these results coincide with the results of the study done by Geetha et al., (2017) who found that 68.8% of the Type 2 Diabetes Mellitus participants in his study had a family history of diabetes[11]. Other studies observed similar findings which showed a positive family of diabetes (66.2% and 67% respectively)[12].

American Diabetes Association (ADA) and World Health Organization (WHO) confirmed that the chief risk factor for diabetes is a family history and added that

patients who had a family history of diabetes are 2-6 times more likely to develop T2DM compared to patients without a family history[13]. Vitamin D participates in glucose metabolism and insulin release as well as it is related to the incidence of T2DM. Vitamin D receptor gene polymorphism cause insulin resistance due to it is effect on insulin secretion. In early 1990, some VDR variants have been investigated such as; ApaI, BsmI, EcoRV, TaqI, Tru9I, FokI, and CDX2, and recently, one of them has not been found associated with T2DM that has restriction fragment length polymorphism for ApaI[14].

In current study, we researched the correlation of VDR TaqI (g.60058 T>C) (in exon 9) and VDR ApaI (g.59979 G>T) (in intron 8) genes polymorphisms in type2 diabetic patients and healthy groups.

Most studies have described several polymorphisms in the VDR gene, such as BsmI and ApaI which are positioned in intron 8 and TaqI in exon 9. Chronic diseases caused by inflammation, infection, and autoimmunity such as Graves' disease, prostate cancer, Hashimoto's thyroiditis, and Type 1 and T2D have been related to these VDR genes4. VDR polymorphisms are linked with deficiency of vitamin D and have been found that this deficiency predisposes to T2DM so the relation between T2DM onset and VDR polymorphisms gene has focused on it by several studies14. According to the results in a table (2) and table (3), the genotype of TaqI(T>C) gene polymorphisms represented that there were significant differences between a patient with T2DM and healthy group were founded and in the control group the TT genotype of Taq1 was more frequent than T2DM group. Furthermore, the TC allele and CC allele were more frequent in the T2DM group. Whereas the results were not approved any significant differences between the T2DM group and control group in both ApaI genotypes of VDR, other studies also showed a similar finding[1,2,15,16]. Hence, it may that copy numbers of VDR mRNA have been decreased in our patients and increased levels of insulin secretion may be associated with the TT genotype.

The results obtained for VDR TaqI in table (2) found that patient with (CC) genotypes (mutant) was significantly higher (P= 0.0002) to develop T2DM and those patients carrying the C allele of VDR gene g.59979 polymorphic site shows a greater susceptibility to develop T2DM cases by 4.836- fold as compared with wild type TT genotype, whereas those with (TC) did not confirm any difference (P= 0.3032). Another study in the Iranian population found that TaqI genotype between T2DM patients and control group confirmed a major difference and, in their result, showed that TT genotype is decreased in T2DM patients' group so that he indicated that a major difference between the Taq1 evaluated genotype of exon 9 within the VDR gene between the diabetic group and controls7. Ma et al., (2020) observed that T2D patients had a higher significance of TaqI heterozygous mutant, and he clarified that insufficient or deficient vitamin D levels and homozygous or heterozygotes mutants of TaqI polymorphism predispose to T2D development, and he concluded that variants of VDR polymorphisms and deficiency of vitamin D are greatly

associated with the susceptibility to T2DM[18].

In his research, Al-Hazmi (2019) examined and looked at VDR. Based on VDR genotypes, his findings revealed important differences in TaqI polymorphism in the two groups (those with T2DM and controls). He furthermore looked into the fact that the TT allele was more common in the control group, whereas the TT genotype was significantly more prevalent in the T2DM group than in the controls[19].

We indicated that it is crucial to combine genotype and serum vitamin D levels for TaqI polymorphism with the onset of T2DM. Likewise, in our study, we observed that VDR ApaI (G>T) gene polymorphism in both T2DM patients and healthy control, and the T-allele of VDR gene g.60068 polymorphic is not significantly positively associated with T2DM and it is not a risk factor for T2DM (Table 3). In agreement with our result, the study done by Dilmec and his colleagues (2010) used Apa1 to asses VDR polymorphisms in type 2 diabetic patients and they did not find any correlation between them[2].

Rivera-Leon et al (2015) revealed no association between ApaI polymorphisms and T2D ($p > 0.05$)19. Besides, other studies did not succeed to show the link between VDR polymorphism Apa1 and type 2 diabetes[1,2].

Sikander (2017) found that differences in ApaI allele distributions between T2DM subjects and control groups were statistically not significant, and he added that type 2 diabetes mellitus might progressed as a result of the interface between acquired or environmental and genetic factors[14]. A cohort from a multinational study found that the main reason for inducing type 2 diabetes is stress, therefore may environmental factors impact the effects of polymorphisms[16].

Our findings also exhibited that genotypes expressed in VDR ApaI (G>T) gene polymorphism as GG in normal wild-type homozygote, GT in the heterozygote, while TT in homozygote mutant polymorphic genotype. In the normal GG genotype, two bands of 528 bp and 217 bp were obtained. In the heterozygote GT genotype, three bands of 745 bp, 528 bp, and 217 bp were yielded; in the homozygote TT genotype (mutant) only one band of 745 bp was detected (Figure2).

Sikander (2017) confirmed that the ApaI genotype indicates heterozygosity after the presence of three fragments (217, 528, and 745 bp) when digested with a restriction enzyme[14].

Dilmec et al., (2010) reported that no major difference in the frequencies of g.59979GNT alleles and genotypes and they indicated that in T2DM the VDR gene g.59979T allele was not related with compared to healthy individua[l2].

Because insulin is produced by pancreatic β-cells and induced by vitamin D supplementation either directly by linking to VDR in β-cells or indirectly by stimulation of release of calcium from these cells and it is also impaired glucose tolerance and improves insulin resistance in T2DM patients[1].

Due to the VDR's role as a key regulator of the endocrine system and the onset of autoimmune illness, numerous genetic variants have been found in this gene,

making it an intriguing candidate for genetic investigations[20,21].

Conclusions: We concluded that a correlation was approved between TaqI genotypes and patients with T2DM but there is no association between ApaI and T2DM among Kurdish patients in Erbil City. In conclusion, VDR and it is polymorphism in exon 9 play a vital role in the pathogenesis of T2DM.

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پوختە

باکگراوند: نەخۆشی شەکرەی جۆری 2 کە بە بەرگری لە ئەنسۆلین دیاری دەکرێت و مەترسی زۆری نەخۆشییە و کاریگەری فاکتەری بۆماوەیی لەسەر شەکرە بە باشی دۆکیومێنت کراوە. پۆلی مۆرفیزمی جینی ڤیتامین دی VDR بە T2DM بەستراوەتەوە. لەم توێژینەوەیەدا بە بەکارهێنانی شێوازی PCR-RFLP لە نەخۆشانی کورد پەیوەندی نێوان پۆلیمۆرفیزمی جینی TaqI وVDR ApaI و بابەتی T2DM مان شیکردەوە.

مادەکان و شێوازەکان: چل نەخۆشی شەکرەی جۆری تی 2 دی ئێم (T2DM) و 30 کەسی تەندروست لەم توێژینەوەیەدا بوون . دی ئێن ئەی جینۆمیکی گهورە کراو بە بەکارهێنانی PCR ئهنزیمی پهلمهری دی ئێن ئەی وة جینی VDR بە شێوازی PCR-RFLP لێکۆلراو ولێکدرایەوە. بەرهەمی ApaI ئەلیلی جی G پارچەی ٥٢٨ و٢١٧ بی پی bp بەرهەم هێنا، T تی ئەلێل، 745 بی پی، وە T *TaqI* تی ئەلێل پارچەی 494 و251 بی پی بەرهەم هێنا، C سی ئەلێل، 293، 251، و201 بی پی.

ئەنجامەکان: چل نەخۆش بە نەخۆشی تی 2 دی ئێم T2DM و30 کەسی تەندروست خوێندرانەوە، هەردوو نەخۆش و گروپی کۆنترۆل هاوچەشن بوون، 43.59٪ نەخۆشەکان مێژووی خێزانی نەخۆشی شەکرەی جۆری 2 یان هەبووە. لێکۆڵینەوە لە فرەمۆرفیزمی جینی ڤی دی ئار تاقی VDR TaqI g.60058 T>C وTaqI VDR ApaI g.59979 G>T کرا. لە جینی پۆلی مۆرفیزمی جینی VDR TaqI T>Cبە شێوەی TT لە جۆری ئاسایی هۆمۆزیگۆتی کێوی، TC لە هیترۆزیگۆتدا دەریدەبڕێن، لە کاتێکدا سی سی CC لە جینۆتایپی فرە مۆرفیکی مۆتێنت هۆمۆزیگۆت. لە ڕووی ئامارەوە جیاوازی بەرچاو هەبوو لە نێوان ئەو نەخۆشانەی کە نەخۆشییەکانی تی 2 دی ئێم و کۆنترۆڵیان هەیە سەبارەت بە دابەشکردنی جینوتایپای TaqI و ئەلێلەکان p< 0.0001 و هیچ جیاوازییەکی گرنگ سەبارەت بە ئەلێلەکانی ApaI P=0.5532 نەبوو.

ئەنجام: لە ئەنجامەکانماندا بۆمان دەرکەوت کە تەنها لە نێوان پۆلیمۆرفیزمی جینی VDR TaqI و نەخۆشانی کوردستان لەگەڵ T2DM هەیە و هیچ پەیوەندیەکی تایبەت بە پۆلیمۆرفیزمیAPAI نیە، وە دەتوانرێت ئەوە دەربخرێت کە ڤی دی ئار (VDR) و ئەوە فرە مۆریزمە لە ئیکسۆن 9 ڕۆڵێکی گرنگ دەگێڕێت لە نەخۆشیزاکەی تی 2 دی ئێم (T2DM).

الخلاصة

تعدد الأشكال في مستقبلات فيتامين د ل جينات Apai و Taqi في مرضى السكري من النوع الثاني باستخدام طريقة PCR-RFLP في إقليم كردستان

الخلفية والأهداف: داء السكري من النوع 2 الذي يتميز بمقاومة الأنسولين وهو خطر من العديد من الأمراض وتأثير العوامل الوراثية على مرض السكري موثق جيدا. تم ربط تعدد الأشكال الجينية لمستقبلات فيتامين (د) ب . T2DM في هذه الدراسة ، قمنا بتحليل العلاقة بين تعدد الأشكال الجينية TaqI و VDR ApaI ومواضيع T2DM باستخدام طريقة PCR-RFLPفي المرضى الأكراد.

المواد والأساليب: تم تضمين أربعين مريضا يعانون من T2DM و 30 فردا سليما في هذه الدراسة. تم تضخيم الحمض النووي الجيني باستخدام PCR وتم تحليل جين VDR بواسطة طريقة . PCR-RFLP أنتج أليل G المنتج ApaI شظايا من 528 و217 بقيس بير. الأليل T، 745 بقيس بير، وأليل TaqI T أنتجت شظايا من 494 و 251 بقيس بير C. الأليل، 293، 251، و201 بقيس بير.

النتائج: تمت دراسة أربعين مريضا يعانون من T2DM و30 فردا سليما ، وكان كل من المرضى والمجموعة الضابطة متطابقين في العمر، (43.59٪) من المرضى لديهم تاريخ عائلي من مرض السكري من النوع 2. تم التحقيق في ترددات الأليل والنمط الجيني لجين VDR TaqI (g.60058 T>C) وتعدد الأشكال الجينية. VDR ApaI (g.59979 G>T) في VDR TaqI (T>C) الأنماط الجينية متعددة الأشكال الجينية المعبر عنها باسم TT في النوع البري العادي homozygote، TC في heterozygote ، في حين CC في النمط الوراثي متعدد الأشكال المتحور متماثل الزيجوت. توجد فروق ذات دلالة إحصائية بين المرضى الذين يعانون من T2DM وضوابط تتعلق بتوزيع الأنماط الجينية والأليلات TaqI (p< 0.0001)ولا توجد فروق ذات دلالة إحصائية فيما يتعلق بأليلات ApaI (P=0.5532).

الاستنتاج: في نتائجنا، وجدنا أن هناك ارتباطات فقط بين تعدد الأشكال الجينية VDR TaqI ومرضى كردستان الذين يعانون من T2DM ولا توجد ارتباطات فيما يتعلق بتعدد الأشكال ApaI، يمكن استنتاج أن VDR وتعدد الأشكال في exon 9 يلعبان دورا مهما في التسبب في T2DM.