http://ijmpes.com
doi:10.34172/ijmpes.6299
Open Access
Original Article
APMI Press
Aras Part Medical International Press
A scientific publishing imprint of PMC Pharmaceutique France
Int J Med Parasitol Epidemiol Sci 2026;7(Suppl 1):S70-S75
eISSN 2766-6492
International Journal of Medical Parasitology & Epidemiology Sciences

Evaluation of Serum and Salivary Visfatin Levels in Type 2 Diabetics with Investigation of the Relationship of SNP (rs11977021) to Susceptibility of Diabetes in the Iraqi Population

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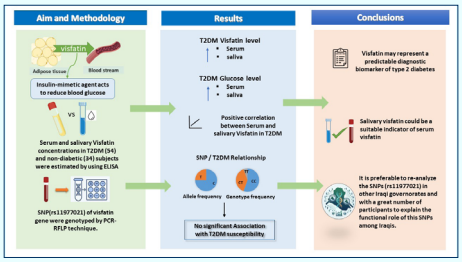
Abstract

Introduction: Type 2 diabetes and its associated issues are considered a health complaint in Iraq and the world. Recently, scientific efforts have been directed towards measuring many vital parameters in saliva because of its ease of obtaining, which serves in repeatable tests. Visfatin, which is secreted from the adipose tissue, especially the central adipose, has many roles, the most important of which is simulating the action of insulin in the type 2 diabetic patients.

Methods: 54 cases of type 2 diabetic (T2DM) group and 34 non-diabetic (ND) healthy group participated in this study for the period from December 2021 to February 2022 in Baghdad - Iraq. Serum and salivary Visfatin concentrations of both groups were estimated by using an Enzyme linked Immuno-sorbent- ELISA kit, Single nucleotide polymorphisms -SNPs (rs11977021-Visfatin gene) were genotyped using the Restriction fragment length polymorphism- RFLP technique.



Results: signified that the concentration of visfatin in serum and saliva in the T2DM group exhibited a medium positive significant correlation, but there was no relationship of single nucleotide polymorphism with the susceptibility to type 2 diabetes in Iraqis.

Conclusion: saliva may serve as a substitute to serum in evaluating the concentration of visfatin, in addition visfatin can be considered as a useful indicator in the diagnosis or prediction of the manifestation of type 2 diabetes. Moreover, it is preferable to re-analyze the SNPs (rs11977021) in other Iraqi governorates and with a great number of participants to explain the functional role of this SNPs among Iraqis.

Keywords: Type 2 diabetes –T2DM, Serum, Saliva, Visfatin, Single nucleotide polymorphisms –SNPs

Received: July 31, 2026, **Revised:** August 13, 2026, **Accepted:** August 15, 2026, **ePublished:** September 10, 2026

Introduction

Type 2 diabetes has gained its clinical importance from being a complex metabolic disease worldwide (1). It is characterized by a decrease in insulin production or the presence of insulin resistance or both (2). Pursuant to the World Health Organization, the rate of type 2 diabetes among Iraqis is estimated at (8.5% to 13.9%), meaning that there are 1.4 million patients with type 2 diabetes (3). Type 2 diabetes is developed depending on both heredity and environment (4). Decreased physical activity related with a raise in in body mass index are risk indicators for type 2 diabetes development (5). Blood is the approved vital fluid to diagnose and monitor several diseases and ailments (6). Saliva represents one of the vital fluids in the body that contains a lot of components that cross to the salivary glands from the blood Therefore, it can serve as an alternative to serum (7). Acute and chronic elevation in the level of blood glucose cause many damages to the composition and physiological role of tissues and organs in the body (8). The secretion of insulin from the pancreas occurs in consequence of high blood glucose, allowing glucose to enter the cells, and at the same time inhibiting the process of glycogenolysis in the liver and muscles (9). Visfatin is an adipocyte-released produced by adipose tissue that mimics the action of insulin, but does not connect to the insulin receptor. Its secretion increases in patients with type 2 diabetes (10). Genetic variations of single nucleotides, according to their locations in genes, affect the process of gene expression and thus the level of protein production (11). The location of single nucleotide polymorphism- SNP (rs11977021) is in the promoter region of the gene of visfatin, and may affect

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the gene transcription process (12). Also it is related with the levels of plasma visfatin, obesity, hypertension, and hypertriglyceridemia in obese children (13). The current study designed to find the relationship of visfatin levels between serum and saliva of type 2 diabetes, and to find the relationship of SNP (rs11977021) to the susceptibility of type 2 diabetes in the city of Baghdad.

Materials and Methods

Study groups

Samples of blood and saliva, height, weight, age and sex were collected from 88 subjects (54 Type 2 diabetes -T2DM group), (34 Non-diabetic -ND - group) who attended to the laboratory of the consulting clinic at Baghdad Teaching Hospital in Iraq from December 2021 to February 2022. Both groups, their ages ranged between 40 and 55 for both sexes. For both groups, cases with systemic or oral disease were excluded, subjects partially or completely dependent on insulin were excluded, and a body mass index (BMI) over 27 was excluded for the ND group.

Collection of blood

For both study groups, 5ml of fasting blood samples were collected in the morning (8-11 am). Three milliliter for the purpose of obtaining the serum (centrifuging for 20 min at 1000 × g), the serum was stored in Eppendorf tubes at -20°C until the tests are conducted, and 2 ml of venous blood for DNA extraction by K3 EDTA tubes.

Collection of saliva

Unstimulated fasting saliva was collected by the drolling method (14). Before collecting saliva, the mouth was rinsed with 10 ml of distilled water for 30 seconds to get rid of residual cells and moisturize the mouth, followed by a ten-minute rest. Then collect 4 ml of saliva, collection time from 8 am to 11 am, after fasting for a period of 8 hours at least (15). After collection is complete, saliva is centrifuged immediately for 15 minutes at 3000 rpm. In The Eppendorf tubes, the supernatant is kept at -20 °C until the desired assay is performed.

Measurements

An estimation of the serum fasting blood glucose concentration for both groups was obtained from the records of the consulting clinic lab in Baghdad Teaching Hospital - Iraq. Fasting salivary glucose concentration was estimated according to Jouda et al. (2016) (16). Which adopted the principle of oxidase - peroxidase method by using Randox assay kit. Visvatin concentrations were measured in serum and saliva samples for both T2DM and ND group by ELISA kit –Elabscience -USA.

Genotyping of Visfatin gene polymorphism

The Single Nucleotide polymorphisms (rs11977021) were genotyped by PCR-RFLP technique. Frozen blood samples of both groups were left at room temperature to thaw, for DNA extraction using Promega- USA extraction kit. (Relia Prep™ Blood g DNA Mini-prep System-Promega- USA). The selection of genotyping technique was referenced to Hashim & Al-Shuhaib (2019) (17). The design of the primers of PCR was as stated in the procedure of Hashim et al. (2015) (18). The DNA fragment of the polymorphism (rs11977021) was amplified by PCR using the primers presented in Table (1).

Reaction conditions such as thermal cycles, contents of the PCR mixture were optimized to obtain high quality PCR products. Twenty microliters (20µl) PCR reaction was conducted, 0.1µl of (Acu I) restriction endonuclease was used to digest the PCR products over night. The digestion produces were segregated by using 2% agarose gel. Ethidium bromide was used for staining. Agarose gel (2%) was prepared according to the method of Samboork and Russell (2001) (19), (100-1000) bp DNA ladder was used to identify the size of the resulting RFLP products. A horizontal electrophoresis device was used at 100 volts and 50 mA for one hour. The Agarose gel template was then photographed and analyzed in order to obtain results.

Statistical analysis

By using G*Power version 3.1.9.4, power analysis of the study was obtained depending on the level of salivary visfatin of the results of Srinivasan et al, (α error probability (0.01), 99% test power (1-β), and effect size of d = 2.4895). The sample size of each group is 10 participants. To compensate for the losses in samples, the study included 88 saliva and serum samples (34 healthy subjects and 54 patients with type 2 diabetes).

All statistical calculation was accomplished by the using of SPSS software Version 23. The results were conveyed as mean ± SE (95% confidence interval -CI). By Kolmogorov–Smirnov tests of homogeneity, all data were examined. For normally distributed data, student T-test was utilized to compare between the means of healthy and patients. While, Mann-Whitney test have been used for the non-normally distributed data. Correlation was done using Spearman correlation. To determine differences between visfatin concentrations for the three genotypes, Kruskal-Wallis analysis was utilized for data that were not normally distributed. Chi-square and Hardy-Weinberg equilibrium test were used to assess the distribution of alleles and genotypes between the two study groups, according to sole et al. (2006) (20).

Results

The results related to the glucose parameters in Table 2 indicated a significant elevation (p = 0.000) in the percentage of HbA1c analysis in the T2DM group

Table 1. Primers used to amplify target DNA sequences

Primer of	Sequence (5'->3')	Length	Amplicon
(rs11977021)		bp	Length bp
Forward	ATGGGCCCCCTCACTTGATT	20	307
reverse complement	GTTGCAGGTAGGTGAGTTCCA	21	

(8.10 ± 0.17 %) compared to ND group (5.02 ± 5.02%). As well, there is a high significant elevation (p = 0.000) in the fasting serum glucose concentration between T2DM group (223.09 ± 12.37 mg/dl) and the ND group (90.23 ± 0. 75 mg/dl). Moreover, there is a significant difference (P = 0.000) for fasting glucose concentration in saliva between T2DM group (18.81 ± 0.53 mg/dl) and the ND group (6.82 ± 0.19 mg/dl).

The results related to the concentration of visfatin was illustrated in Table 2 that appeared a significant increasing (P < 0.05) in the fasting serum visfatin concentration between T2DM group (14.19 ± 0.61ng/ml) ND group (2.19 ± 0.20 ng/ml). Moreover, the results presented a significant increasing (P = 0.02) in the concentration of fasting salivary visfatin between T2DM group (0.99 ± 0.08ng/ml) and ND (control) group (0.69 ± 0.09 ng /ml).

Figure 1 demonstrated a strong positive significant correlation (r = 0.844; p = 0.000) between fasting serum glucose and HbA1c.

In comparison between salivary and serum visfatin, Figure 2 revealed a medium positive significant correlation (r = 0.528, p = 0.000) in fasting visfatin concentration between serum and saliva in the T2DM group.

The results related to the genotyping of the (rs11977021) in visfatin Gene by PCR-RFLP technique are shown in Figure 3. The size of the DNA segment 307bp represents the (C) allele, and the two DNA segments of size (56 and 242) bp represent the (T) allele. Accordingly, the size of the DNA segment 307bp represents the genotype (C/C), 242bp represents the genotype (T/T), and finally the DNA segments of size (242 and 307) bp represent the genotype (C/T).

From Table 3, the odds ratio analysis has no significant difference (p > 0.05) between (C) and (T) alleles, nor between (C/C), (C/T) and (T/T) genotypes for single nucleotide polymorphisms.

In addition, the H-WE test, signify no difference (p > 0.05) which means that the study group was within the Hardy-Weinberg equilibrium (P ≥ 0.05). Moreover, the difference was not significant (p = 0.999) between the concentrations, in the results presented in Table 4 regarding the comparison of visfatin concentrations among carriers of genotypes (C/C, C/T, T/T).

Table 2. Comparison of Serum and saliva parameters between T2DM and ND groups

Parameters	ND N = 34	T2DM N = 54	P-value
Age (year)	44.5294 ± .22828	50.2963 ± .65055	*0.000
HbA1c (%)	5.0285 ± 5.0285	8.1093 ± 0.17581	*0.000
FG serum (mg/dl)	90.2353 ± . 75886	223.0963 ± 12.37370	*0.000
FG saliva(mg/dl)	6.8265 ± .19746	18.8148 ± 0.53466	*0.000
Serum Fasting visfatin (ng/ml)	2.1919 ± .20249	14.1986 ± 0.61510	*0.000
Saliva Fasting visfatin (ng/ml)	0.6968 ± .09231	0.9983 ± 0.08212	*0.023
Total		**88**	

T2DM: type 2 Diabetic's millets, ND: non- diabetics (control group)
Data were expressed with mean and ± SE,
*P-value ≤ 0.05 (Mann-Whitney Test), **p-value ≤ 0.05 (T-test),

Discussion

High blood glucose levels is the diagnostic feature of diabetes of all kinds (21). The finding of this study demonstrated that the levels of serum and salivary glucose were highly significant in the T2DM group, which is consistent with several studies that were conducted to demonstrate the benefit of saliva, due to its ease of collection and painlessness, as in examining the salivary glucose levels in patients with type 2 diabetes (22-24).

However, no correlation was observed in glucose level between serum and saliva in the type 2 diabetes (T2DM) group. Wang et al. (2017) reported no correlation in glucose level between serum and unstimulated whole saliva (25); alternatively, a significant direct correlation of glucose level between serum and saliva collected from the parotid gland, despite many studies showing a correlation in the levels of glucose between serum and saliva in the type 2 diabetic group and healthy group (22,26,27).

On the other hand, other studies reported an association between serum and saliva glucose level in the type 2 diabetes group only (24, 28). There are various factors that affect the composition of saliva collected in the mouth, unlike saliva that is collected directly from the salivary gland, whose composition is not affected by the biological conditions of the mouth (24). Increasing of glucose concentration in saliva may be due to a change in the permeability of the basement membrane of the parotid glands in patients with type 2 diabetes (29).

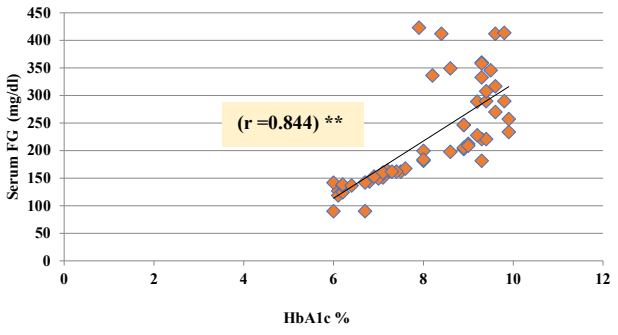

Figure 1. Correlation between serum FG and HbA1c in T2DM group.
FG: Fasting glucose, r: correlation coefficient (Spearman's rho Test)
** Significance at p = 0.01 level

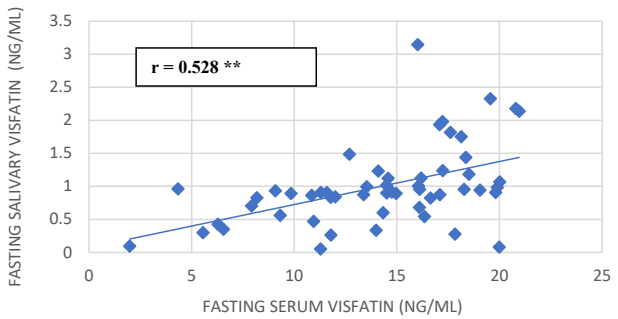

Figure 2. Correlation between Serum and Saliva Fasting Visfatin in T2DM group.
R: correlation coefficient (Spearman's rho Test)
** Significance at p = 0.01 level

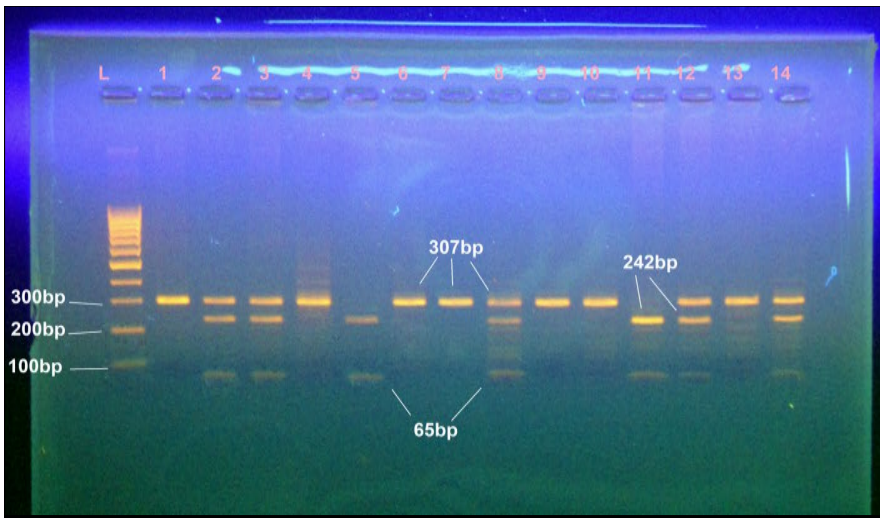

Figure 3. Genotyping of (rs11977021-Visfatin gene) by PCR-RFLP.
lane L: DNA ladder100-1000 bp, lanes 5 and 11 T/T genotype; lanes 1,4,6,7,9,10 and 13 C/C genotype; lanes 2,3,8,12 and 14 C/T genotype,100V., 50A.-1h., 2%Agarose.

Table 3. The distribution of alleles and genotypes in the SNP (rs11977021- visfatin gene).

Model	Genotype	ND	T2DM	OR (95% CI)	P-value
Codominant	C/C	20 (58.8%)	30 (55.6%)	1.00	
	C/T	11 (32.4%)	21 (38.9%)	1.27 (0.51-3.20)	0.74
	T/T	3 (8.8%)	3 (5.6%)	0.67 (0.12-3.64)	
Dominant	C/C	20 (58.8%)	30 (55.6%)	1.00	0.76
	C/T-T/T	14 (41.2%)	24 (44.4%)	1.14 (0.48-2.72)	
Recessive	C/C-C/T	31 (91.2%)	51 (94.4%)	1.00	0.56
	T/T	3 (8.8%)	3 (5.6%)	0.61 (0.12-3.20)	
Overdominant	C/C-T/T	23 (67.7%)	33 (61.1%)	1.00	0.53
	C/T	11 (32.4%)	21 (38.9%)	1.33 (0.54-3.28)	
		ND	T2DM	OR (95% CI)	P-value
Allele		Count	Proportion	Count	Proportion
C		51	0.75	81	0.75
T		17	0.25	27	0.25
SNP(rs11977021- Visfatin gene) exact test for Hardy-Weinberg equilibrium (n=88)					
		CC	CT	TT	C	T	P-value
All subjects		50	32	6	132	44	0.78
ND		20	11	3	51	17	0.39
T2DM		30	21	3	81	27	1

T2DM: type 2 diabetics millets group, ND: non-diabetics (control group), OR: Odds ratio

SNP: single nucleotide polymorphism.

Table 4. Comparison of serum visfatin concentration among carriers of genotypes of SNP (rs11977021)

Genotype of rs11977021	N	Fasting Serum Visfatin (ng/ml)	Mean Rank	P-value
CC	30	14.2346±.83377	27.77	
CT	21	14.1152±.98493	27.19	0.999
TT	3	14.422±3.4218	27.00	
T2DM (n)	54			

Data are expressed as mean±SE, and mean Rank by Kruskal Wallis test, p≤0.05, n=number

The study demonstrated a moderate direct correlation between HbA1c and serum glucose in the type 2 diabetes group, consistent with previous studies (30) (31). While HbA1c was not correlated with glucose levels in saliva, unlike what was stated in the study by López et al. (2003) (32) and Abhikshyeet et al. (2012) (27). Results indicating that glycated hemoglobin does not correlate with glucose in saliva may reflect the fact that glycated hemoglobin indicates glucose levels in the body during the last three months prior to the test, which may not be related to daily changes in glucose levels in other body fluids (30).

The current results exposed a highly significant

difference in the levels of serum and salivar visfatin in the T2DM group in comparing to the control group, as reported in other previous studies (33-35). In comparison between serum and salivary visfatin, our results revealed a significant positive correlation between them in the T2DM group, which is consistent with what was found in other previous studies (34, 35). Visfatin has a strong relation with high weight gain in patients with type 2 diabetes (36). In addition, high blood glucose levels may affect the visfatin signaling pathway in the target cells; thus the production of visfatin is increased as compensation (37).

From the odds ratio analysis, the results presented no significant variance in the distribution between the (C) and (T) alleles, nor between (C/C), (C/T), and (T/T) genotypes. Despite the presence of the SNP (rs11977021) upstream of the promoter of the vsfatin gene, which may affect the transcription step of the gene (12). Despite this, no significant difference was shown in the current results for the concentrations of visfatin among the three genotypes, which perhaps indicates that there is no effect of the SNP (rs11977021) on visfatin expression and production. This is inconsistent with the study of Ooi et al. (2016)(12), which indicated the role of (rs11977021) in promoting transcription and thus increasing the levels of visfatin in obese children.

A few previous studies on SNP (rs11977021), showed a strong association with total and LDL cholesterol (38). Another study showed that obese (C/C) carriers had high levels of proinsulin in obese subjects (39), while Taiwanese (C/C) carriers showed a high predisposition to oral squamous cell carcinoma (40). All of these findings regarding SNP (rs11977021) may indicate that it has a key role in type 2 diabetes (41-44). Therefore, there may be a need to repeat this study in other circumstances that include more tests that may explain and confirm the current results, possibly with a larger number of participants.

Conclusion

Fasting serum and saliva visfatin may represent a predictable diagnostic biomarker of type 2 diabetes. Salivary visfatin could be a suitable indicator of serum visfatin, since the strong correlation between serum and salivary visfatin. In regard to SNP (rs11977021), it has no association with visfatin level. It is preferable to re-analyze the SNPs (rs11977021) in other Iraqi governorates and with a great number of participants to explain the functional role of this SNPs among Iraqis.

Acknowledgments

The authors would like to thank all patients and persons who participate in this study.

Authors' Contribution

Conceptualization: Zainab Hadi Kamil, Belqis Hamed Rabie, Aizhar Hamzih Hasan
Data Curation: Zainab Hadi Kamil, Belqis Hamed Rabie, Aizhar Hamzih Hasan
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Validation: Zainab Hadi Kamil
Visualization: Belqis Hamed Rabie
Writing–Original Draft: Belqis Hamed Rabie
Writing–Review & Editing: Zainab Hadi Kamil, Belqis Hamed Rabie

Competing Interests

None.

Ethical Approval

After reviewing the research plan, research subject information, and approval form, the Ethics Committee in the Department of Biology/ College of Science / University of Babylon / Iraq approved according to document number z220101 on 17/1/2022. Oral consent was taken from the contributors (two study groups) before sampling was taken from them.

Funding

This research received no external funding.

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