



**International Journal of Biology, Pharmacy
and Allied Sciences (IJBPA)**
'A Bridge Between Laboratory and Reader'

www.ijbpas.com

STUDY OF THE ASSOCIATION BETWEEN THE RS12255372 (G/T) POLYMORPHISM AND ANTHROPOMETRIC PARAMETERS IN PATIENTS WITH TYPE 2 DIABETES

BAMBA ABOU^{1,2*}, DAGNOGO OLEFONGO^{1,3}, BAH GNOGBO ALEXIS², KOUAMAN
KOUAMÉ BOUATINI ANGELO¹, SORO MADOU¹, KONAN ANGE¹, BLA KOUAKOU
BRICE¹, YAPI HOUPHOUET FÉLIX¹ AND DJAMAN ALLICO JOSEPH^{1,2}

1: Laboratoire Biologie et Santé, ufr Biosciences, Université Félix Houphouët-Boigny, 22 BP 582

Abidjan 22, Côte d'Ivoire

2: Department of medical and basic biochemistry, institut Pasteur of Côte d'Ivoire, 01BP 490

Abidjan 01 Côte d'Ivoire

3: Department of Parasitology and Mycology, institut Pasteur of Côte d'Ivoire, 01 BP 490 Abidjan 01

Côte d'Ivoire

***Corresponding Author: Prof. Bamba Abou: E Mail: binobino2@yahoo.fr**

Received 16th April 2026; Revised 19th May 2026; Accepted 1st Aug. 2026; Available online 1st Nov. 2026

<https://doi.org/10.31032/IJBPA/2026/15.11.10789>

ABSTRACT

Type 2 diabetes (T2D) is a major public health concern resulting from interactions between environmental, anthropometric, and genetic factors. The *TCF7L2* gene plays a key role in genetic susceptibility to T2D, and the rs12255372 polymorphism has been associated with T2D risk in various populations. This study investigated the distribution of the rs12255372 (G/T) polymorphism and its associations with sociodemographic, anthropometric, familial, and behavioral factors.

A total of 150 subjects, including 80 diabetic patients and 70 non-diabetic controls, were enrolled. Sociodemographic and anthropometric data, family history, and physical activity were assessed. DNA was extracted from dried blood spots using the Chelex method. The polymorphism was investigated by allele-specific polymerase chain reaction, followed by agarose gel electrophoresis.

The mean age was 55 years, and 70.7% of participants were female. Overweight and obesity affected 67% of the population. Among diabetic patients, 50% reported a family history of diabetes, while 85% reported physical inactivity. Significant associations were observed between diabetic status and family history of diabetes and physical activity ($p < 0.05$). Fifteen subjects showed a positive G-allele profile, whereas no positive T-allele profile was detected. The G-allele profile was significantly associated with diabetic status and physical activity ($p < 0.05$).

Keywords: diabetes; *TCF7L2*; rs12255372; anthropometric parameters

INTRODUCTION

Type 2 diabetes mellitus (T2D) is a major global public health concern. Its prevalence continues to increase, particularly in low- and middle-income countries, driven by urbanization, physical inactivity, changes in dietary habits, and population aging. In sub-Saharan Africa, this increasing burden represents a growing challenge for healthcare systems, particularly because of difficulties related to diabetes screening, management, and prevention of diabetes-related complications (Hodé. & Dedjan, 2021).

T2D is a multifactorial disease resulting from the interaction of environmental, behavioral, and genetic factors. Genetic factors contribute substantially to individual susceptibility to the disease. Among the genes associated with T2D, *TCF7L2* (*Transcription Factor 7-Like 2*) is one of the most extensively studied genetic loci. This gene is involved in the regulation of glucose homeostasis and pancreatic β -cell function. Several variants of the *TCF7L2* gene have been associated with T2D risk, particularly

the single-nucleotide polymorphism (SNP) rs12255372 (G>T). Previous studies and meta-analyses have reported an association between this variant and susceptibility to T2D, although the magnitude and significance of this association may vary across populations (Murea *et al.*, 2012). Available data from African populations remain relatively limited, highlighting the need for further genetic studies in these populations (Martin *et al.*, 2019).

In addition, anthropometric parameters such as body weight, body mass index (BMI), and waist circumference are important indicators of body composition and metabolic risk in patients with diabetes. Investigating their relationship with genetic factors may contribute to a better understanding of the phenotypic heterogeneity observed among individuals with T2D (Lee & Yim, 2021).

In this context, investigating the rs12255372 (G>T) polymorphism of the *TCF7L2* gene in relation to anthropometric parameters is of particular interest in the Ivorian population, where available data remain limited. Such

research may contribute to a better characterization of genetic determinants associated with the phenotypic variations observed among patients with type 2 diabetes.

Therefore, the present study aimed to investigate the association between the rs12255372 (G>T) polymorphism of the *TCF7L2* gene and anthropometric parameters in patients with type 2 diabetes in Abidjan, Côte d'Ivoire. Specifically, the study aimed to describe the anthropometric characteristics of the study population, determine the genotype and allele frequencies of the rs12255372 polymorphism, and assess its association with anthropometric parameters.

I. MATERIALS AND METHODS

1. Study setting

Participants were recruited and blood samples were collected between February and April 2026 from the Diabetes, Endocrinology, and Internal Medicine departments of the Cocody University Hospital (CHU de Cocody), Abidjan, Côte d'Ivoire. Molecular biology analyses were performed at the Molecular Biology Units of the Institut Pasteur de Côte d'Ivoire.

2. Study design

This was an analytical cross-sectional case-control study designed to investigate the association between the *TCF7L2* rs12255372 (G/T) polymorphism and

anthropometric parameters in patients with type 2 diabetes mellitus (T2D) in Abidjan.

3. Study population

The target population consisted of adults aged 30–65 years living in Abidjan. The study included 80 patients with T2D diagnosed according to the American Diabetes Association (ADA) criteria (ADA, 1999b) and 70 normoglycemic control subjects. All participants were informed about the study objectives and provided written informed consent (Poulet, 2018).

4. Eligibility criteria

4.1. Inclusion criteria

Patients were eligible if they had a confirmed diagnosis of T2D for at least six months according to ADA criteria (Braillard & Santos, 2017), were aged 30–65 years, had lived in Abidjan for at least five years, and provided informed consent. Control participants were age- and sex-matched individuals without a history of diabetes or prediabetes, defined as fasting blood glucose <5.6 mmol/L and HbA1c <5.7%. Controls were also required to have lived in Abidjan for at least five years and to provide informed consent.

4.2. Exclusion criteria

Participants were excluded if they had type 1 or secondary diabetes, chronic conditions potentially affecting glucose metabolism (stage IV–V chronic kidney disease, decompensated cirrhosis, or active cancer), were pregnant or breastfeeding, were

receiving prolonged corticosteroid therapy, were unable or unwilling to provide informed consent, or had received a blood transfusion within the preceding three months, which could interfere with HbA1c assessment.

5. Sociodemographic and clinical data collection

Sociodemographic and clinical data were collected using a standardized questionnaire administered by trained investigators. Variables included age, sex, personal and family medical history, diabetes duration, diabetes-related complications, comorbidities such as hypertension, dyslipidemia and obesity, and current treatments. Lifestyle factors, including smoking, alcohol consumption, and physical activity, were also recorded.

6. Anthropometric measurements

Anthropometric measurements were performed by trained healthcare professionals according to a standardized protocol. Body weight was measured with participants wearing light clothing using a SECA electronic scale (Germany), with a precision of 0.5 kg. Height was measured in the standing position using a graduated stadiometer, with a precision of 1 cm. Body mass index (BMI) was calculated as body weight in kilograms divided by height in meters squared (kg/m^2).

7. Blood collection and dried blood spot preparation

After participant identification and informed consent, approximately 5 mL of venous blood was collected into an EDTA tube. The samples were gently mixed by inversion and identified using the corresponding sample code. Three dried blood spots (DBS) were prepared from each blood sample on Whatman filter paper. Each card was labeled with the corresponding sample code. The DBS cards were stored at room temperature and protected from insects and dust until DNA extraction (Kouassi, 2021).

8. DNA extraction

Genomic DNA was extracted from DBS samples using Chelex 100 resin. A 5% (w/v) Chelex 100 solution was prepared, and 180 μL was transferred into an Eppendorf tube and incubated at 100°C for 5 min. DBS fragments were then added, and the mixture was vortexed for 30 s before a second incubation at 100°C for 10 min. The samples were centrifuged at 12,000 rpm for 1 min 30 s. The supernatant was transferred to a new tube and centrifuged again under the same conditions. The resulting supernatant containing genomic DNA was either stored at -20°C or used immediately for PCR amplification (Simon et al. 2020).

9. Genotyping of the TCF7L2 rs12255372 polymorphism

The *TCF7L2* rs12255372 (G/T) polymorphism was investigated using allele-specific polymerase chain reaction (PCR). Two independent PCR reactions were

performed for each sample to detect the G and T alleles separately. Each reaction contained a common forward primer (CFw) combined with an allele-specific reverse primer.

The primer sequences were as follows:

Prime r	Sequence (5'-3')
CFw	CTGGAAACTAAGGCGTGAGGGA
Rev_ G	CAGAGGCCTGAGTAATTATCAGAATAT GATC
Rev_ T	CAGAGGCCTGAGTAATTATCAGAATAT GCTA

PCR amplification was performed using a PTC-100 thermocycler (MJ Research). The amplification protocol consisted of an initial denaturation at 95°C for 3 min, followed by 32 cycles of denaturation at 95°C for 1 min, annealing at 50°C for 1 min, and extension at 72°C for 1 min. A final extension step was performed at 72°C for 5 min.

10. Analysis of PCR products

PCR products were analyzed by electrophoresis on a 1.5% agarose gel prepared in Tris-acetate-EDTA (TAE) buffer. Ethidium bromide was used as the intercalating agent. Five microliters of each PCR product were loaded onto the gel, and electrophoresis was performed in 1× TAE buffer.

Following electrophoresis, DNA fragments were visualized under ultraviolet illumination. The presence of a 205-bp fragment in the G- or T-specific reaction was considered indicative of amplification of the corresponding allele.

11. Genotype determination

Genotypes were determined based on the results of the two allele-specific PCR reactions. Detection of a 205-bp product in the G-specific reaction and/or the T-specific reaction was used to identify the corresponding allele(s).

12. Statistical analysis

Associations between the *TCF7L2* rs12255372 (G/T) polymorphism and T2D were assessed by comparing genotype and allele distributions between patients with T2D and controls using Pearson's chi-square test or Fisher's exact test, as appropriate. The chi-square test was also used to assess Hardy–Weinberg equilibrium among control participants and to examine associations between the polymorphism and anthropometric parameters. Statistical analyses were based on contingency tables, and a *p*-value <0.05 was considered statistically significant.

13. Ethical considerations

The study was conducted in accordance with the principles of the Declaration of Helsinki (Poisson, 2002) and applicable good clinical practice guidelines. The study protocol was submitted to the National Ethics Committee for Health and Life Sciences Research (CNER) of Côte d'Ivoire, and the required administrative authorizations were obtained. All participants received clear information about the study and provided written informed consent. For participants who were

unable to read or write, consent was obtained by fingerprint in the presence of an independent witness.

III. RESULTS AND DISCUSSION

1. Sociodemographic and Anthropometric Characteristics

1.1. Age Distribution of the Study Population

The study population comprised 150 participants aged 32–80 years, with a mean age of 55 years. Participants aged 45–55 years accounted for the largest proportion of the study population, with 28.7% aged 45–55 years and 36.0% aged 55–65 years, representing 64.7% of the total sample. In contrast, 18.7% of participants were younger than 45 years, while only 2.0% were older than 75 years (**Figure 1**).

The concentration of participants between 45 and 65 years is consistent with the increasing occurrence of T2DM with age. Age is an established risk factor for T2DM, partly through progressive metabolic alterations and the accumulation of metabolic risk factors. Similar age distributions have been reported in West African populations, including by **Diop et al. (2013)**, who reported a predominance of T2DM among older adults.

The mean age of 55 years therefore places the study population within an age range commonly affected by T2DM. However, this distribution should be interpreted in light of the hospital-based recruitment, which may have favored the inclusion of individuals receiving care for diabetes or other metabolic risk factors.

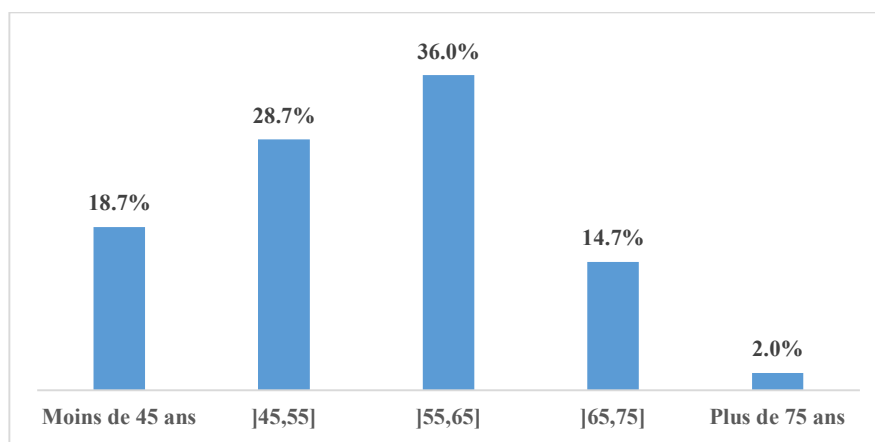


Figure 1: Age distribution of the study population

1.2. Sex Distribution of the Study Population

Among the 150 participants, 70.7% were women and 29.3% were men, corresponding

to approximately 106 women and 44 men, with a female-to-male ratio of approximately 2.4:1 (**Figure 2**). Among diabetic participants, women also predominated,

accounting for 62 cases (77.5%) compared with 18 men (22.5%). However, sex was not significantly associated with diabetes status ($p = 0.07165$).

The predominance of women is consistent with observations reported in some African populations, including those described by **Abir and Safia (2023)**. Several factors may contribute to this distribution, including obesity, metabolic changes associated with menopause, and a history of gestational

diabetes. Differences in healthcare-seeking behavior may also contribute to the observed sex distribution.

Nevertheless, the absence of a statistically significant association between sex and diabetes status suggests that the female predominance should be interpreted cautiously. It may partly reflect the composition of the study sample rather than a difference in diabetes risk between men and women.

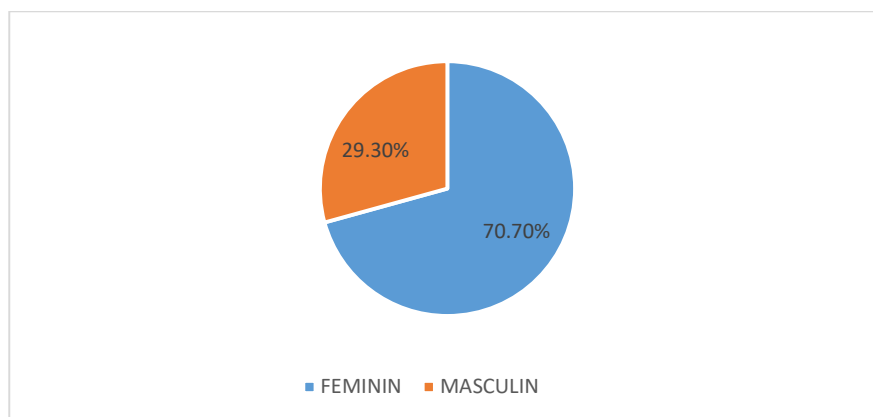


Figure 2: Sex distribution of the study population

1.3. Distribution According to Diabetes Status

Of the 150 participants, 80 (53.0%) had diabetes and 70 (47.0%) did not. This relatively balanced distribution likely reflects the study recruitment design rather than the prevalence of T2DM in the general population. Accordingly, the proportion of diabetic participants in this sample should not be interpreted as a population prevalence estimate. In African populations, the prevalence of T2DM in the general population is generally substantially lower

than that observed in the present sample, although estimates vary according to the population and setting (**Chevalier, 2022**). The observed distribution therefore primarily reflects the composition of the study groups.

1.4. Anthropometric Profile According to Body Mass Index

BMI classification showed that 67% of participants had excess body weight, including 39% who were overweight and 28% who were obese, whereas 33% had a normal BMI (**Table 1**). The high proportion

of overweight and obesity indicates a substantial burden of excess body weight in the study population. Excess weight is a well-established modifiable risk factor for metabolic disorders, including T2DM (Neeland *et al.*, 2024).

However, BMI was not significantly associated with diabetes status in this study ($p = 0.8965$) (Table 1). This finding indicates that BMI categories did not statistically distinguish diabetic from non-diabetic participants in the present sample

and does not contradict the established relationship between excess weight and T2DM risk. The lack of association may be related to the sample size, the high prevalence of excess weight in both groups, or population-specific characteristics. T2DM may also occur in African populations at relatively low BMI, potentially reflecting differences in the relative contributions of insulin deficiency and insulin resistance (ADA, 1999b; Neeland *et al.*, 2024).

Table 1: Classification of the study population according to BMI

BMI category	n	%
Normal weight	50	33 %
Overweight	58	39 %
Obesity	42	28 %
Total	150	100 %

1.5. Genetic Characterization of the rs12255372 (G/T) Polymorphism

The rs12255372 (G/T) polymorphism of the *TCF7L2* gene was investigated using allele-specific PCR followed by electrophoresis on a 2% agarose gel. Figure 4 presents the electrophoretic profiles obtained from 15 diabetic patients recruited in Abidjan.

Samples 8, 10, 11, 12, 14, and 15 showed clear and well-resolved bands, indicating efficient amplification of the target region.

In contrast, samples 1–7, 9, and 13 displayed weaker or more diffuse bands (Figure 4).

Variations in band intensity may result from differences in DNA quality or quantity, PCR efficiency, or experimental conditions. Band intensity alone should therefore not be used to determine allele presence or genotype. Genotype assignment should instead be based on the expected specific amplification pattern and appropriate experimental controls.

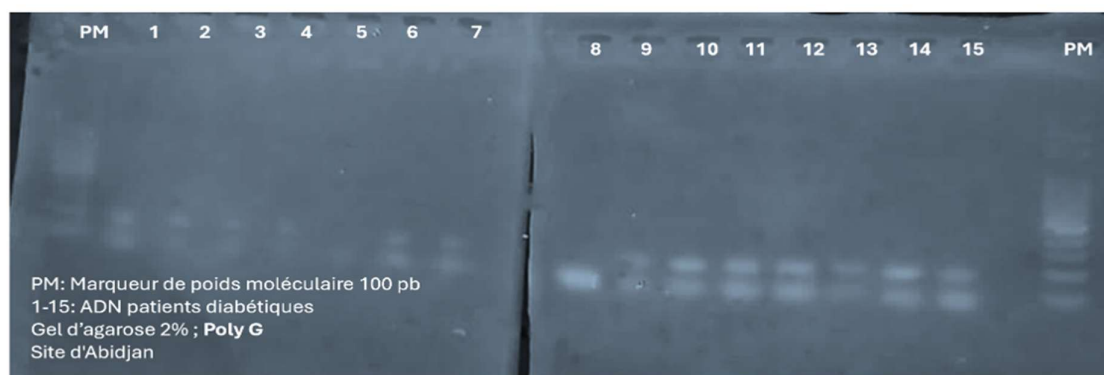


Figure 4: Positive genotyping results for the rs12255372 (G/T) polymorphism of the *TCF7L2* gene using allele-specific PCR

1.6. Distribution of the G/T Polymorphism in the Study Population

Among the 150 participants, 15 (10.0%) were positive for the G profile, whereas 135 (90.0%) were negative. No participant was positive for the T profile; all 150 participants (100.0%) were negative (**Table 2**).

The detection of the G profile in 10.0% of participants indicates its presence in the study population, whereas the absence of a positive T profile may reflect either a true absence or a frequency too low to be detected in this sample. Given the sample

size, the absence of a detected allele should not be interpreted as evidence that the allele is absent from the broader population.

It is also important to distinguish between PCR profile, genotype, and allele frequency. In the present analysis, the term “G profile” is retained according to the coding used in the available dataset. However, verification of the PCR protocol and primer nomenclature is recommended before manuscript submission to ensure an unambiguous interpretation of the rs12255372 genotype.

Table 2: Distribution of the G and T polymorphism profiles in the study population

Result	Poly G, n (%)	Poly T, n (%)
Negatif	135 (90.0)	150 (100.0)
Positif	15 (10.0)	0 (0.0)
Total général	150 (100.0)	150 (100.0)

2. Association of Anthropometric Parameters and Risk Factors with Diabetes Status and the G Profile

Associations between categorical variables were assessed using Pearson's chi-square (χ^2) test. The analysis compared diabetic and

non-diabetic participants and examined factors associated with the G profile.

2.1. Factors Associated with Diabetes Status

Physical activity was significantly associated with diabetes status ($p = 0.04391$). Among the 80 diabetic

participants, 68 (85.0%) reported no regular physical activity, whereas 12 (15.0%) reported participating in sports (**Table 3**). The high proportion of inactive participants among those with diabetes is consistent with the established role of physical activity in metabolic health and T2DM prevention. Reduced physical activity may contribute to metabolic disturbances and insulin resistance, as reported by **Thébaud et al. (2023)**.

However, because this was a cross-sectional study, the temporal relationship between physical inactivity and diabetes cannot be established. The observed association should therefore not be interpreted as evidence of causality. A strong association was also observed between parental history of diabetes and diabetes status ($p = 0.0005$).

Forty diabetic participants (50.0%) reported a diabetic parent. This finding is consistent with the recognized familial component of T2DM susceptibility. Familial aggregation may reflect both shared genetic factors and common environmental or behavioral exposures.

No significant association was observed between sex and diabetes status ($p = 0.071$), despite the predominance of women among diabetic participants. Similarly, parental history of hypertension was not associated with diabetes status ($p = 0.97$). BMI was also not significantly associated with diabetes status ($p = 0.89$). Among diabetic participants, 37.5% were overweight, 35.0% had normal weight, and 27.5% were obese (**Table 3**).

Table 3: Sociodemographic characteristics and risk factors associated with diabetes among the study participants

Variable	Category	Diabetic participants		P-Value
		n	%	
Sex	Female	62	77,5%	0,07165
	Male	18	22,5%	
Physical activity	No	68	85,0%	0,04391
	Yes	12	15,0%	
Smoking	No- Smoking	80	100,0%	N/A
	Smoking	0	0,0%	
Parental hypertension	No	47	58,8%	0,9735
	Yes	33	41,3%	
Parental diabetes	No	40	50,0%	0,0005547
	Yes	40	50,0%	
G profile	Négative	65	81,3%	0,00004531
	Positive	15	18,8%	
BMI	Obesity	22	27,5%	0,8965
	Normal weight	28	35,0%	
	Overweight	30	37,5%	

2.2. Association of the G Profile with Sociodemographic and Anthropometric Characteristics

Among the 150 participants, 15 (10.0%) were positive for the G profile. All 15 positive participants were diabetic, representing 18.8% of the 80 diabetic participants, whereas no positive participant was identified among the non-diabetic group. This distribution was significantly associated with diabetes status ($p = 0.000045$) (Table 4).

The strong statistical association indicates that, within this sample, the G profile was concentrated among diabetic participants. This finding is of interest given the established role of *TCF7L2* in T2DM susceptibility. *TCF7L2* participates in the Wnt/ β -catenin signaling pathway and has been implicated in pancreatic β -cell function and insulin secretion. Previous studies have associated *TCF7L2* variants primarily with impaired insulin secretion rather than isolated insulin resistance (Abdelkarim *et al.*, 2010; El Houch, 2022).

However, the present findings differ from those reported by Mulcare *et al.* (2004), where the T allele, rather than the G profile observed in the present dataset, was associated with T2DM. Such differences may reflect variations in allele frequencies across African populations, as well as differences in sample size, population

characteristics, study design, or genotyping methodology.

Interpretation should nevertheless remain cautious. The absence of a detected T profile prevents a balanced comparison of the different rs12255372 genotypes. The relatively small number of G-positive participants ($n = 15$) also limits statistical power and warrants confirmation in larger populations.

2.3. G Profile and Anthropometric Parameters

Among the 15 participants positive for the G profile, 46.7% had normal weight, 33.3% were overweight, and 20.0% were obese. No significant association was observed between BMI category and the G profile ($p = 0.5834$) (Table 4).

This finding indicates that, within the present sample, the G profile was not significantly associated with BMI category. This may be consistent with the proposed role of *TCF7L2* in pancreatic β -cell function and insulin secretion rather than a direct effect on adiposity (El Houch, 2022).

However, the absence of statistical significance should not be interpreted as evidence of an independent effect of the G profile on body weight. The small number of G-positive participants substantially limits the statistical power to detect differences between BMI categories.

These findings should therefore be regarded as exploratory and require validation in

larger populations. They are nevertheless consistent with evidence indicating that the genetic determinants of T2DM extend

beyond mechanisms directly related to obesity (Prasad & Groop, 2015).

Table 4: Sociodemographic and clinical characteristics of participants positive for the G profile

Variable	Category	G profile		P-Value
		n	%	
Sex	Female	11	73,3%	1
	Male	4	26,7%	
Physical activity	No	15	100,0%	0,04247
	Yes	0	0,0%	
Smoking	No- Smoking	15	100,0%	N/A
	Smoking	0	0,0%	
Parental hypertension	No	12	80,0%	0,09746
	Yes	3	20,0%	
Parental diabetes	No	9	60,0%	0,7835
	Yes	6	40,0%	
BMI	Obesity	3	20,0%	
	Normal weight	7	46,7%	
	Overweight	5	0,5834	

2.4. G Profile and Physical Activity

Physical activity was also significantly associated with the G profile ($p = 0.04247$). All 15 participants positive for the G profile reported no regular physical activity, whereas none reported participating in sports (Table 4). This finding is noteworthy because physical inactivity was also significantly associated with diabetes status ($p = 0.04391$). However, these results do not establish a gene–environment interaction. A larger study incorporating multivariable analyses and an interaction term would be required to determine whether physical activity modifies the association between the rs12255372 variant and T2DM. The observation remains relevant in light of the established role of physical activity in metabolic health and T2DM prevention (AlZahrani, 2025).

2.5. G Profile and Family History of Diabetes

Among G-positive participants, 40.0% reported a parental history of diabetes, whereas 60.0% did not. No significant association was observed between parental diabetes and the G profile ($p = 0.78$). This contrasts with the strong association observed between parental diabetes and diabetes status in the overall study population ($p = 0.0005$). Familial aggregation of T2DM is likely influenced by multiple genetic variants together with shared environmental and behavioral factors. Therefore, the absence of an association with the G profile does not exclude a genetic contribution to familial diabetes susceptibility; rather, it indicates that the specific profile investigated does not, by itself, explain the familial aggregation observed in this population.

2.6. G Profile, Sex, and Parental History of Hypertension

Among the 15 G-positive participants, 11 were women (73.3%) and four were men (26.7%). No association was observed between sex and the G profile ($p = 1.000$), suggesting that the female predominance among G-positive participants may largely reflect the sex distribution of the overall sample.

Similarly, no statistically significant association was observed between parental hypertension and the G profile ($p = 0.097$). Although this value was above the conventional 5% significance threshold, the small number of G-positive participants limits the interpretation of this result.

Larger studies will be necessary to determine whether the observed distribution represents a true association or sampling variability.

REFERENCES

- [1] Hodé A, Dedjan AH. Prévalence et facteurs associés à la dysfonction érectile chez les patients diabétiques du Centre National Hospitalier Universitaire-Hubert Koutoukou Maga (CNHU-HKM) Cotonou. *Annales d'Endocrinologie* 2021 ; 82 : 506. doi:10.1016/j.ando.2021.08.741.
- [2] Murea M, Ma L, Freedman BI. Genetic and environmental factors associated with type 2 diabetes and diabetic vascular complications. *Reviews in Diabetes Studies* 2012; 9 (1): 6-22. doi:10.1900/RDS.2012.9.6.
- [3] Martin AR, Teferra S, Möller M, Hoal EG, Daly MJ. The critical needs and challenges for genetic architecture studies in Africa. *Current Opinion in Genetics & Development* 2018; 53: 113-120. doi:10.1016/j.gde.2018.08.005.
- [4] Lee BJ, Yim MH. Comparison of anthropometric and body composition indices in the identification of metabolic risk factors. *Scientific Reports* 2021 ; 11 (1) : 9931. doi:10.1038/s41598-021-89422-x.
- [5] ADA E. Diagnostic et classification du diabète sucré : les nouveaux critères. *Diabetes & Metabolism* 1999 ; 25 : 72-83.
- [6] Poulet N. Information du patient et consentement éclairé en matière médicale. *Trayectorias Humanas Transcontinentales* 2018.
- [7] Braillard O, dos Santos Bragança A. Prise en charge thérapeutique du diabète de type 2. Hôpitaux Universitaires de Genève, Département de médecine communautaire, de premier recours et des urgences 2017 : 1-15.
- [8] Kouassi KC. Corrélation entre habitude alimentaire et prévalence de l'obésité : étude préliminaire chez 106 sujets adultes externes recrutés au CHU Campus de Lomé. *Sciences de la Vie, de la Terre et Agronomie* 2021 ; 8.
- [9] Simon N, Shallat J, Williams Wietzikoski C, Harrington WE. Optimization of Chelex 100 resin-based

- extraction of genomic DNA from dried blood spots. *Biology Methods and Protocols* 2020; 5 (1): bpaa009. doi:10.1093/biomethods/bpaa009.
- [10] Poisson D. Déclaration d'Helsinki. Quelles nouveautés ? *Laennec* 2002 ; 50 : 44-52.
- [11] Diop SN, Wade A, Lokrou A, Diédhiou D, Adoueni VK. Prise en charge du diabète de type 2 en pratique médicale courante en Afrique subsaharienne : résultats de l'étude AMAR-AFO au Sénégal et en Côte-d'Ivoire. *Médecine des Maladies Métaboliques* 2013 ; 7 : 363-367. doi:10.1016/S1957-2557(13)70603-5.
- [12] Abir T, Safia M. Estimation de la relation entre l'hérédité et le diabète de type II dans la région de Tébessa. *Université Echahid Chikh Larbi Tébessi, Tébessa* 2023 : 127 p.
- [13] Chevalier N. Diabète de type 2. *Société Française d'Endocrinologie* 2022.
- [14] Neeland IJ, Lim S, Tchernof A, Gastaldelli A, Rangaswami J, Ndumele CE, Powell-Wiley TM, Després JP. Metabolic syndrome. *Nature Reviews Disease Primers* 2024 ; 10 : 77. doi:10.1038/s41572-024-00563-5.
- [15] Thébaut JF, Namur A, Phirmis L, Attal D, Durlach V, Gautier JF, Chaumeil C, Roux B. Diabète et tabagisme : la Fédération française des diabétiques met en lumière ce facteur de risque méconnu. *Médecine des Maladies Métaboliques* 2023 ; 17 : 141-146.
- [16] Abdelkarim M, Caron S, Duhem C, Prawitt J, Dumont J, Bouchaert E, Briand O, Brozek J, Kuipers F, Fievet C. O37 Le récepteur nucléaire FXR régule la fonction et la différenciation adipocytaire en interférant avec la voie Wnt/ β -caténine et en induisant la voie de signalisation de PPAR γ . *Diabetes & Metabolism* 2010 ; 36 : A10.
- [17] El Houch S. Étude de la prédisposition génétique au diabète de type 2 (gène TCF7L2) et de la pharmacogénétique de la Metformine (gène SLC47A1) au sein d'une population marocaine. 2022.
- [18] Prasad RB, Groop L. Genetics of type 2 diabetes—pitfalls and possibilities. *Genes* 2015; 6 (1): 87-123. doi:10.3390/genes6010087.
- [19] Mulcare CA, Weale ME, Jones AL, Connell B, Zeitlyn D, Tarekegn A, Swallow DM, Bradman N, Thomas MG. The T allele of a single-nucleotide polymorphism 13.9 kb upstream of the lactase gene (LCT) (C-13.9kbT) does not predict or cause the lactase-persistence phenotype in Africans. *American Journal of Human Genetics* 2004; 74 (6): 1102-1110. doi:10.1086/421050.
- [20] AlZahrani EM. Profile of physical activity and sedentary lifestyle in health sciences students: prevalence and its association with academic performance. *Medicine* 2025 ; 104 (51):e46733.doi:10.1097/MD.00000000000046733.