***Original Research Article***

# STUDY OF GENETIC DRIFTS IN SOME FAT MASS AND OBESITY ASSOCIATED GENE VARIATIANTS IN TYPE 2 DIABETICS IN SOME ETHINIC GROUPS RESIDING IN DELTA STATE, NIGERIA.

## ABSTRACT

***Aim:****Detailing and distribution of some predominant FTO genes among subjects with diabetes mellitus selected from Igbo, Ika, Ijaw and Isoko tribes of Delta state, Nigeria.*

***Study Design:*** *Case-control, observational study.*

***Place and Duration of Study:*** *Federal Medical Center, Asaba, Delta State and Safety Molecular Pathology Laboratory Enugu, Nigeria, between March 2020 and Febuary 2022.*

***Methodology****: Four (4) variants of FTO (Fat Mass and Obesity Associated) gene allele were investigated using a total of 100 subjects, comprising 20 diabetic subjects each from Igbo, Ika, Ijaw and Isoko ethnic groups in Delta State, Nigeria and 20 non-diabetic subjects (5 each from the four tribes). Venous blood was collected for the assay of FBS, Hb1ac and molecular assay of FTO genes. Results obtained were statistically analysed.*

***Result:****The genotypes identified in the subjects were AA, GA, GG, AC, CC, TT, and AT. AA (Ijaw 17, Urhobo 18, Ika 18, Igbo 19) and GG (Ijaw 17, Urhobo 18, Ika 19, Igbo 18) had highest level of occurrence in all tribes. Recombinant genotype and recessive allele had higher number of subjects as compared to the originating genotypes. Hardy- Weinberg statistics demonstrated significant genetic deviations in rs2388405(AA -0.12 $x^2$ =0.0002, GA 0.12 $x^2$=0.002) rs201041270(GG-0.12 $x^2$ =0.0002, GA 2.12 $x^2$=0.002),and rs8050136 (CC -0.34 $x^2$ =0.001, AC 2.32, $x^2$=0.05) proving a chance of finding new SNP in the studied population with a probability of 2.25 as seen in the odd ratio of T allele in Igbo tribe.*

*Keywords: Obesity, Diabetes, Ethinic groups, Gene, Genetic drifts, Fat Mass*

## 1.0 INTRODUCTION

Diabetes, as defined by the World Health Organization, is a condition characterized by persistent hyperglycemia caused by insulin insufficiency or insulin resistance [1]. Diabetes mellitus (DM) is a major cause of mortality and disability globally, this raises concerns about the financial burden it places on both people and society as a whole [2]. Endocrinology and Metabolism Society of Nigeria (EMSON) reported in 2022 that over 10 million Nigerians are living with diabetes and warned that if preventive measures are not applied, the numbers are expected to double by 2030 [3].An obesity sensitivity gene, whose intron 1 region has multiple SNPs that are strongly associated with Body Mass Index, energy metabolism and anthropometric indices has been identified, the gene is known as the fat mass and obesity-associated (*FTO*) gene [4]. The FTO gene exists in different genetic forms known as variants of FTO polymorphisms. According to [5]*FTO* rs9939609 SNP is significantly associated with obesity, With the AA genotype carriers having a 2.02 increased risk of developing obesity.Research conducted by [6]existing relationshipbetween biochemical parameters of T2D, namely insulin, glucose, and HOMA with genotypes of rs8050136 polymorphism Insulin Resistance levels, BMI, waist and hips circumference.

Results obtained from genetic risk score (GRS) calculated for two FTO single-nucleotide polymorphisms (SNPs) rs8050136 and rs2388405 demonstrated that the two SNPs were significantly related to increased BMI and obesity (Surendran, *et al.,* 2019) [7].Understanding the genetic make-up of FTO gene, its various variants, distribution and how it affects and influences manifestation of diabetes can assist with early intervention measures, improvement of diabetes clinical diagnostic processes, and grant insight on developing targeted treatment options for patients with diabetes.Reports of results obtained from various studies for FTO gene variants association with obesity and diabetes varies with population and continents. This research will give insight of FTO gene presence and distribution in various ethnic tribes residing in Delta state region of Nigeria.

## 2.0MATERIALS AND METHODS

### 2.1 Study Area

This research was carried out in Delta State, Nigeria.Samples were collected from subjects attending clinic at Federal Medical Centre, Asaba and General Hospitals in Agbor & Bomadi Delta State, Nigeria. Participants ware people from Ijaw, Urhobo, Ikah and Igbo ethinic groups residing in Delta State.Nigeria's Delta State capital, Asaba, is located on a terrace of the lower Niger River, with geographical co-ordinates of 6°11′52.23″N6°43′42.48″E. Asaba serves as a link between western, eastern, and northern Nigeria through the Asaba Niger Bridge, which connects East and West, and the Niger River in the north.

Figure 1: **Map of Delta state Nigeria, showing Ethnic and Local Government Area** (Dele, 2021).

### 2.2 Research Design

This is a case-control, observational study involving the identification of FTO gene allele variants and to evaluate HbA1c, Fasting blood sugar, Insulin, Lipid Profile (Total cholesterol, Triglycerides, HDL-cholesterol, LDL-cholesterol), C-peptide, Ferretin, Interleukin 6, Adiponectin and HOMA-IR in obese/T2D subjects from selected ethnic groups in Delta State.

Through questionnaire the bio-data and medical history of the subjects were obtained. Some other parameters like weight, height and waist circumference was obtained using a calibrated weighing scale, and a measuring tape.

### 2.3 Sample Size

Sample size for this study was determined using the Cochrane formula:

N = $\frac{Z^2pq}{d^2}$ (Cochrane, 1977)

N = the desired sample size

Z = The Standard Normal deviate usually set at 1.962 corresponding to the 95% Confidence level

p = The SNPs Prevalence rates. (Minor Alleles Frequency of SNPs set at >0.02) (Adeyemo et al. 2010)

q = 1- p

d = degree of accuracy desired set at 0.05

Minimum Size – 30

By adding 10% of non-respondent = 33

Therefore, total sample size was 33. However, this study used 100 subjects, with 20 subjects selected from each of the four ethnic groups in Delta State, and 20 control subjects

## 2.4 Sampling Method:

A multistage sampling technique was used to choose the subjects. First, the participants were divided into two groups: new cases (those diagnosed with diabetes mellitus within a year of diagnosis) and old cases (those diagnosed with the disease for one year or more). Then they were placed in three clusters (21-40, 41-60, 61 & above years of age). Next, a similar number of research participants were selected at random from each grouping.

## 2.5 Selection Criteria

### 2.5.1 Inclusion Criteria

Individuals who are of the selected tribes in Delta State aged at least 30 years diagnosed with T2D for at least one year.

Controls: Five (5) individuals from each of the selected tribes Ika, Urhobo, Ijaw, Igbo with no history of diabetes, and are non-obese and having a fasting blood glucose of less than 6.5mmol/l. The cluster groups was considered also.

### 2.5.2 Exclusion Criteria

1. Individuals not from the selected tribes.
2. Critically ill subjects.
3. Pregnant female participants.

## 2.6 Sample Collection:

From each subject, venous blood was collected using standard veni-puncture technique then, 2ml was dispensed into fluoride-oxalate bottle for the assay of FBS and Hb1ac another 3ml was dispensed into lithium heparin bottle for molecular assay of FTO genes.

After allowing the sample in the plain tube to retract, it was centrifuged. The analysis was performed within one week of collection at the Federal Medical Centre, Asaba. The first EDTA tube was transported in cold box to Safety Molecular Pathology Laboratory Services located at 44 Rangers Avenue, Enugu for DNA extraction and genotyping (Sequencing). The second EDTA tube for Glycated hemoglobin was for stored at 2-8$^0$C and analysis was done within two days of sample collection.

### 2.6.1 Fasting Blood Sugar (FBS):

FBS was performed using glucose oxidase method with kit from Randox Laboratories, UK.

Principle: After enzymatic oxidation in the presence of glucose oxidase, glucose is measured. Under the catalysis of peroxidases, the generated hydrogen peroxide combines with phenol and 4-aminophenazone to create a red-violet quinoneimine dye as an indicator.

### 2.6.2 Glycosylated Haemoglobin (HbA1c)

Quantitative determination of glycosylated Haemoglobin in blood was done using the modified Ion Exchange Resin method with kit from INTECO Diagnostics, UK (Trivelli *et al*., 1971).

## 2.7 Genetic Analysis

### *2.7.1 Genomic DNA Extraction*

Genomic DNA extractions of the samples was performed using Geneaid DNA Mini Kit (Blood/Cultured Cell).

## 2.8 Genotyping of SNPs

Genotyping of SNPs of the *FTO* gene was performed with the Illumina next-generation sequencing (NGS) using NextSeq 2000 Sequencing System. The NanoDrop ND-1000 UV/VIS spectrophotometer was used to measure the concentration and purity of the isolated DNA.(Appendix I).

## 2.8 Statistical Analysis

The whole data was categorised based on Age, duration of Type-2 diabetes, and sex. These were the requirements to set data into sub-classes. Utilizing GraphPad Prism, version 8.0.2 (California, USA), the obtained data were analyzed. The standard deviation (SD) of the mean was used to express the quantitative variables.

The research population's variance in genotype and allele distribution was assessed using the **Hardy Weinberg** equilibrium statistical test. To ascertain the significant differences, chances of finding SNPs and associated hazards of the genotypic and allelic frequencies of the FTO gene variations in Type 2 diabetic (T2D) and non-diabetic participants, respectively, chi-square and odds ratio (OR) analyses were conducted, allelic frequencies were determined by gene counting.

Furthermore, using general linear regression and Pearson's correlation, the relationship between the FTO gene variations and metabolic indices, lipid profile, and T2D and obesity was established. Using Pearson’s correlation, General linear regression (GLR) or simply linear regression (LR). The student's statistical t-test was used for the comparison. The level of statistical significance was fixed at. $P \le 0.05$

## 3.0 RESULTS AND DISCUSION

### 3.1 Results

Table 1: **Mean±SD of Metabolic and Immunologic Parameters of Subjects with FTO gene variations with Varying Duration of T2D against Control Subjects**

| Parameters | Control | 1-5 yrs | 6 -10 yrs | 11 -15 yrs | 16 -20 | Fvalue | pvalue | Remark |
|---|---|---|---|---|---|---|---|---|
| FBS (mmol/L) | 4.92±0.65$^{a}$ | 8.11±3.41$^{b}$ | 8.27±2.88$^{b}$ | 8.32±3.56$^{b}$ | 7.35±3.37$^{a}$ | 5.168 | 0.0008 | S |
| HbA1c (%) | 6.57±0.99$^{a}$ | 8.84±1.86$^{b}$ | 8.85±1.39$^{b}$ | 9.59±2.08$^{b}$ | 9.46±1.95$^{b}$ | 9.027 | <0.0001 | S |

**Table 2: Distribution of FTO Genotypes of Diabetic Subjects according to Tribes**

| | AA | GA | GG | AC | CC | TT | AT |
|---|---|---|---|---|---|---|---|
| Ijaw | 17 | 3 | 17 | 5 | 15 | 14 | 3 |
| Urhobo | 18 | 2 | 18 | 5 | 15 | 14 | 3 |
| Ika | 18 | 2 | 19 | 5 | 15 | 16 | 3 |
| Igbo | 19 | 1 | 18 | 2 | 18 | 17 | 2 |
| p-value | 0.992 | 0.682 | 0.990 | 0.662 | 0.934 | 0.931 | 0.273 |
| $\square^{2}$-value | 100.00 | 1.500 | 0.111 | 1.588 | 0.429 | 0.443 | 0.965 |

Table 3: **Hardy-Weinberg Statistical Test of FTO gene Variants of FTO gene in T2D subjects and control**

| FTO gene Variant | rs2388405 | rs201041270 |
|---|---|---|

| Genotype | AA | GA | GG | GG | GA | AA |
|---|---|---|---|---|---|---|
| No, Obs | 92 | 8 | 0 | 92 | 8 | 0 |
| Freq, Allele | 0.97 | - | 0.03 | 0.97 | - | 0.03 |
| Freq, Exp | 0.94 | 0.06 | 0.0009 | 0.94 | 0.06 | 0.0009 |
| No, Exp | 92.12 | 5.88 | 0.09 | 92.12 | 5.88 | 0.09 |
| Deviation | -0.12 | 0.12 | -0.09 | -0.12 | 2.12 | -0.09 |
| $X^2$ | 0.0002 | 0.002 | 0.99 | 0.0002 | 0.002 | 0.99 |

Key: A|G=wild (Dominant), G|A=Polymorphic, $X^2$ =chi-square, Exp=Expected, Obs=Observations

Table 4: **Hardy-Weinberg Statistical Test of some FTO gene Variants in T2D subjects and control**

| **FTO gene Variant** | **rs9939609** | | | **rs8050136** | | |
|---|---|---|---|---|---|---|
| Genotype | TT | AT | AA | CC | AC | AA |
| No, Obs | 77 | 14 | 9 | 81 | 18 | 1 |
| Freq, Allele | 0.85 | - | 0.15 | 0.91 | - | 0.09 |
| Freq, exp | 0.72 | 0.26 | 0.02 | 0.83 | 0.16 | 0.008 |
| No, Exp | 70.6 | 25.48 | 1.96 | 81.34 | 15.68 | 0.8 |
| Deviation | 6.4 | -11.48 | 7.04 | -0.34 | 2.32 | 0.2 |
| $X^2$ | 0.5 | 0.26 | 0.25 | 0.001 | 0.5 | 0.6 |

T|C=wild (Dominant), A|A=Polymorphic, $X^2$ =chi-square, Exp=Expected, Obs=Observations

Table 5: **Genotype and allele distribution of rs2388405 Variant of FTO gene in Obese and T2D subjectsand control**

| **Tribes** | **Ijaw** | | **$X^2$** | **P** | **OR** | **Urobo** | | **$X^2$** | **P** | **OR** | **Ikah** | | **$X^2$** | **P** | **OR** | **Igbo** | | **$X^2$** | **P** | **OR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | |
| AA | 17 (89.5%) | 5 (100%) | - | - | - | 18 (94.7%) | 5 (100%) | - | - | - | 18 (90%) | 5 (100%) | - | - | - | 19 (95%) | 5 (100%) | - | - | - |
| GA | 3 (10.5%) | 0 (0.0%) | | | | 2 (5.2%) | 0 (0.0%) | | | | 2 (10%) | 0 (0.0%) | | | | 1 (5%) | 0 (0.0%) | | | |
| GG | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | |
| AA | 17 (89.5%) | 5 (100%) | 0.57 | 0.45 | 0.00 | 18 (94.7%) | 5 (100%) | 0.27 | 0.60 | 0.00 | 18 (90%) | 5 (100%) | 0.27 | 0.60 | 0.00 | 19 (95%) | 5 (100%) | 0.27 | 0.60 | 0.00 |
| GA + GG | 3 (10.5%) | 0 (0.0%) | | | | 2(5.2%) | 0 (0.0%) | | | | 2 (10%) | 0 (0.0%) | | | | 1 (5%) | 0 (0.0%) | | | |
| AA+GA | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - |
| GG | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | |
| A | 36 (94.7%) | 10 (100%) | 0.55 | 0.45 | 0.00 | 37 (94.7%) | 10 (100%) | 0.26 | 0.60 | 0.00 | 38 (95%) | 10 (100%) | 0.52 | 0.47 | 0.00 | 39 (97.5%) | 10 (100%) | 0.26 | 0.61 | 0.00 |
| G | 2 (5.2%) | 0 (0.0%) | | | | 1 (5.2%) | 0 (0.0%) | | | | 2 (5%) | 0 (0.0%) | | | | 1 (2.5%) | 0 (0.0%) | | | |

A=wild (Dominant), G=Polymorphic, T2D=Type 2 Diabetes, ND = Non- Diabetes (control), $X^2$ =chi-square, p= chi-square -pvalue, OR= Odd Ratio

Table 6: **Genotype and allele distribution of rs201041270 Variant of FTO gene in T2D subjects and control**

| | **Ijaw** | | **$X^2$** | **P** | **OR** | **Urobo** | | **$X^2$** | **P** | **OR** | **Ikah** | | **$X^2$** | **P** | **OR** | **Igbo** | | **$X^2$** | **P** | **OR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | |
| GG | 17 (89.5%) | 5 (100%) | - | - | - | 18 (94.7%) | 5 (100%) | - | - | - | 19 (95%) | 5 (100%) | - | - | - | 18 (90%) | 5 (100%) | - | - | - |
| GA | 2 (10.5%) | 0 (0.0%) | | | | 1 (5.2%) | 0 (0.0%) | | | | 1 (5%) | 0 (0.0%) | | | | 2 (10%) | 0 (0.0%) | | | |
| AA | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | |
| GG | 17 (89.5%) | 5 (100%) | 0.57 | 0.45 | 0.00 | 18 (94.7%) | 5 (100%) | 0.27 | 0.60 | 0.00 | 19 (95%) | 5 (100%) | 0.27 | 0.60 | 0.00 | 18 (90%) | 5 (100%) | 0.110 | 0.73 | 0.00 |
| GA + AA | 3 (10.5%) | 0 (0.0%) | | | | 2 (5.2%) | 0 (0.0%) | | | | 1 (5%) | 0 (0.0%) | | | | 2 (10%) | 0 (0.0%) | | | |
| GG+GA | 20(100%) | 5 (100%) | - | >0.99 | - | 20(100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - |
| AA | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | |
| G | 36 (94.7%) | 10 (100%) | 0.54 | 0.45 | 0.00 | 37 (94.7%) | 10 (100%) | 0.26 | 0.60 | 0.00 | 39 (97.5%) | 10 (100%) | 0.25 | 0.61 | 0.00 | 38 (95%) | 10 (100%) | 0.52 | 0.47 | 0.00 |
| A | 2 (5.2%) | 0 (0.0%) | | | | 1 (5.2%) | 0 (0.0%) | | | | 1 (2.5%) | 0 (0.0%) | | | | 2 (5%) | 0 (0.0%) | | | |

G=wild (Dominant), A=Polymorphic, T2D=Type 2 Diabetes, ND = Non- Diabetes (control), $X^2$ =chi-square, p= chi-square -pvalue, OR= Odd Ratio

Table 7: **Genotype and allele distribution of rs9939609 Variant of FTO gene in T2D subjects and control**

| **Tribes** | **Ijaw** | | **$X^2$** | **P** | **OR** | **Urobo** | | **$X^2$** | **P** | **OR** | **Ikah** | | **$X^2$** | **P** | **OR** | **Igbo** | | **$X^2$** | **P** | **OR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | |
| TT | 14 (73.7%) | 4 (80%) | 0.58 | 0.74 | - | 14 (73.7%) | 4 (80%) | 1.09 | 0.57 | | 16 (80%) | 4 (80%) | 1.87 | 0.39 | - | 17 (85%) | 4 (80%) | 1.63 | 0.44 | - |
| AT | 3 (15.8%) | 1 (20%) | | | | 3 (10.5%) | 1 (20%) | | | | 3 (15%) | 0 (0.0%) | | | | 2 (10%) | 0 (0.0%) | | | |
| AA | 3 (10.5%) | 0 (0.0%) | | | | 3 (15.8%) | 0 (0.0%) | | | | 1 (5%) | 1 (20%) | | | | 1 (5%) | 1 (20%) | | | |
| TT | 14 (73.7%) | 4 (80%) | 0.08 | 0.77 | 0.70 | 14 (73.7%) | 4 (80%) | 0.08 | 0.77 | 0.70 | 16 (80%) | 4 (80%) | 0.00 | >0.99 | 1.0 | 17 (85%) | 4 (80%) | 0.07 | 0.78 | 1.41 |
| AT + AA | 6 (26.3%) | 1 (20%) | | | | 6 (26.3%) | 1 (20%) | | | | 4 (20%) | 1 (20%) | | | | 3 (15%) | 1 (20%) | | | |
| TT+AT | 17 (94.7%) | 5 (100%) | 0.57 | 0.45 | 0.00 | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - |
| AA | 3 (10.5%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | |
| T | 31 (81.6%) | 9 (90%) | 0.40 | 0.52 | 0.49 | 30 (78.9%) | 9 (90%) | 0.63 | 0.42 | 0.41 | 35 (87.5%) | 8 (80%) | 0.37 | 0.54 | 1.75 | 36 (90%) | 8 (80%) | 0.75 | 0.38 | 2.25 |
| A | 7 (18.4%) | 1 (10%) | | | | 8 (21.1%) | 1 (10%) | | | | 5 (12.5%) | 2 (20%) | | | | 4 (10%) | 2 (20%) | | | |

A=wild (Dominant), T=Polymorphic, T2D=Type 2 Diabetes, ND = Non- Diabetes (control), $X^2$ =chi-square, p= chi-square -pvalue, OR= Odd Ratio

Table 8: **Genotype and allele distribution of rs8050136 Variant of FTO gene in T2D subjects and control**

| **Tribes** | **Ijaw** | | **$X^2$** | **P** | **OR** | **Urobo** | | **$X^2$** | **P** | **OR** | **Ikah** | | **$X^2$** | **P** | **OR** | **Igbo** | | **$X^2$** | **P** | **OR** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Genotype | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | | | | T2D n=20 | ND n=5 | | | | T2D n=20 | ND n=5 | | |
| CC | 15 (78.9%) | 4 (80%) | - | - | - | 15 (78.9%) | 5 (100%) | - | - | - | 15 (75%) | 5 (100%) | - | - | - | 18 (90%) | 4 (80%) | - | - | - |
| AC | 5 (21.1% | 1 (20%) | | | | 5 (21.1% | 0 (0.0%) | | | | 5 (25%) | 0 (0.0%) | | | | 2 (10%) | 1 (20%) | | | |
| AA | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | |
| CC | 15 (78.9%) | 4 (80%) | **0.002** | 0.95 | 0.93 | 15 (78.9%) | 5 (100%) | 1.26 | 0.26 | 0.00 | 15 (75%) | 5 (100%) | 1.56 | 0.21 | 0.00 | 18 (90%) | 4 (80%) | 0.37 | 0.53 | 2.25 |
| AC + AA | 5 (21.1% | 1 (20%) | | | | 5 (21.1% | 0 (0.0%) | | | | 5 (25%) | 0 (0.0%) | | | | 2 (10%) | 1 (20%) | | | |
| CC+AC | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - | 20 (100%) | 5 (100%) | - | >0.99 | - |
| AA | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | | 0 (0.0%) | 0 (0.0%) | | | |
| C | 34 (89.5%) | 9(90%) | **0.002** | 0.96 | 0.94 | 34 (89.5%) | 10 (100%) | 1.14 | 0.28 | 0.00 | 35 (87.5%) | 10 (100%) | 1.38 | 0.23 | 0.00 | 38 (95%) | 9 (90%) | 0.35 | 0.55 | 2.11 |
| A | 4 (10.5%) | 1 (10%) | | | | 4 (10.5%) | 0 (0.0%) | | | | 5 (12.5%) | 0 (0.0%) | | | | 2 (5%) | 1 (10%) | | | |

C=wild (Dominant), A=Polymorphic, T2D=Type 2 Diabetes, ND = Non- Diabetes (control), $X^2$ =chi-square, p= chi-square -pvalue, OR= Odd Ratio

## 3.2 Discussion

This study involved the detailing and distribution of some predominant FTO genes among subjects with diabetes mellitus. The four (4) variants of FTO allele investigated were rs8050136, rs2388405, rs9939609 and rs201041270. The genotypes identified in the subjects were AA, GA, GG, AC, CC, TT, AT. The distribution of these FTO genotypes of diabetic subjects according to tribes showed that, genotype AA and GG had highest level of occurrence in all tribes while genotype GA had the lowest level of occurrence in all tribes. This finding agrees with the work of[8], which has reported a similar observation. Further, comparison of the frequencies of these genotypes among the four tribes showed that they were not statistically different among the different tribes.

The results obtained in this study demonstrated significant genetic deviations in rs2388405, rs201041270, rs9939609 and rs8050136 FTO gene variants. This indicates that there were disturbing factors that caused the genetic deviations [9]. This finding may be due to cross-breeding that may have occurred in previous generations, considering the multi-ethnic nature of the geographical population of the study area. This finding agrees with the work of [10], which reported a similar finding among Brazillian population.

The result of this study indicates that there were tendencies of SNPs in the study population. That is, there are possible instances of recombination of the alleles of the genes in the different tribes in the study population.In this study, rs2388405 Genotype AA had the highest number of occurrences for T2D in all tribes. Its Recombinant genotype AA+GA also had the highest number of occurrences.In rs201041270 Genotype GG had the highest number of occurrences for T2D in all tribes.Recombinant genotype GG+GA had the highest number of subjects as compared to the originating genotypes, with the recessive allele G having the highest number of subjects. Also, thers9939609 Genotype TT had the highest number of occurrences for T2D in all tribes with varying number of occurrence, with TT+AT had the highest number of possible occurrence in all tribes. Allele T had the highest number of subjects in Igbo tribe. For rs8050136, Genotype CC had the highest number of occurrences for T2D in all tribes with varying number of occurrenceits Recombinant genotype CC+AC had the highest number of subjects. This finding agrees with the reserach of [11], which reported similar finding in some ethnic groups in the Niger Delta region of Nigeria. This finding may be due to SNP that occurs in the genes of members of a population[12].

This study evaluated some metabolic and immunological parameters in the study subjects. Results for fasting blood sugar (FBS) levels in the diabetic subjects from the different ethnic groups was significantly higher than that of the control subjects. Similarly, they have significantly higher levels of HbA1c in diabetic subjects than control subjects. This could be due to the dysregulation of the glucose which characterizes the diabetic condition [13].

## 4.0 CONCLUSIONS

The findings from this investigation showed that genotype AA and GG has the highest level of occurrence in all tribes for the studied population, while according to the genotype and allele distribution of the four variants of FTO gene in T2Dsubjects these genotypes had the highest number of occurrences in all tribes. Genotype AA in rs2388405, Genotype GG in rs201041270, Genotype TT In rs9939609, and Genotype CC in rs8050136. Statistically significant genetic drifts in the studied population exists, which has caused a deviation from expected frequencies in Hardy-Weinberg statistics. This correlates with higher numbers observed in recombinant genotypes rs2388405, rs201041270, rs9939609 and rs8050136, than the originating genotypes as well as notable odd ratios. However, the Odd Ratio (OR) found in this study showed that the chances of finding a new SNP in the studied groups is slim as the highest odd ratio found was 2.25 in Igbo tribe.

## CONSENT

All authors declare that written informed consent was obtained from the patient (or other approved parties) for publication of this case report and accompanying images.

## ETHICAL APPROVAL

Ethical approval was sought and obtained from the Ethical Committee of Federal Medical Centre, Asaba, Delta State, Nigeria. Informed consent of the participants involved was also obtained using the consent form.

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