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Y-Short Tandem Repeats (Y-STRs) in Fulanis and Yorubas of Ilorin, Kwara State and North Central of Nigeria

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Abstract

Introduction: Y-Short Tandem Repeats (Y-STRs) are used in evaluation of male genetic diversity and genealogical studies. Nigeria is comprised of over 250 ethnic groups. The Yorubas and Fulanis are arguably the second and fourth largest ethnic groups of Nigeria respectively. No previous study examined Y-STRs in Fulanis resident in any region of Nigeria, and no previous studies examined Y-STRs in Yorubas resident in North Central of Nigeria. Therefore, this study examined the genotyping data of Y-STRs in Fulanis and Yorubas resident in Ilorin, Kwara State and North Central of Nigeria. **Methods**: Samples of unrelated 25 Fulani males and 25 Yoruba males whose ethnicity were confirmed by three generations (paternal and maternal) were collected with informed consent. The samples were amplified using UniQ-Typer™ Y10-STR prototype genotyping kit, which was previously tested on South-African populations. The genotyping kit contains 10 Y-STR loci: *DYS385a/b, DYS449, DYS447, DYS481, DYS504, DYS518, DYS612, DYS626, DYS644* and *DYS710*; and genotyped subsequent to capillary electrophoresis. **Results**: Genotyping parameters showed no deviation from Hardy-Weinberg equilibrium expectation. Nine of the Ten Y-STR loci were polymorphic except *DYS626* with no alleles. Homozygosity, Expected Heterozygosity and gene diversity parameters showed lower genetic diversity amongst Fulanis compared to Yorubas except for *DYS449* and *DYS644*. **Conclusion**: The results provided further genotyping data of Y-STRs in Fulanis and Yorubas. Furthermore, the observed lower genetic diversity amongst Fulanis compared to Yorubas is possibly due to customs-prevalent marriages between immediate cousins amongst Fulanis. In contrast, Yoruba customs do not permit marriages between immediate cousins.

Keywords: Human genetics; Y-STRs; Population genetics; Gene diversity; Genealogy.

Introduction

Nigeria is located in West Africa and it is the most populous black nation in the world constituting one sixth of Africa's total population (Alaba *et al*., 2017). Nigeria is composed of over 250 ethnic groups with a population of over 140 million in 2006 (National Population Commission, Nigeria, 2006), and an estimated population of over 174 million in 2013 (Alaba *et al*., 2017). The Hausas, Yorubas, Igbos and Fulanis are arguably the first to fourth largest ethnic groups of Nigeria respectively (Mustapha, 2006; Okolie *et al*., 2018). The Fulanis are either nomadic herdsmen or settler Fulanis living in permanent settlements (Vicente *et al*., 2019); while the Yorubas have been their neigbouring farmers for hundreds of years (Mustapha, 2006).

Short Tandem Repeats (STRs) loci are highly variable diverse genetic markers which are widely used in forensic identification of individuals in civil and criminal investigations (Budowle *et al*., 2001; Fan and Chu, 2007). Y-STRs are informative for paternal familial relationships and are relevant to the investigations of disputed paternity cases and genealogical studies such as identification of

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surname, clan or geographic region-related profiles and male genetic diversity (Greenbaum *et al*., 2014).

Cultural and environmental factors such as religious practices, dietary practices and climate conditions caused differing genetic structuring, genetic stratifications and population genetic categorizations within historically-linked ethnic and regional populations (Torres *et al*., 2012; Haber *et al*., 2013). Nigeria is divisible into six distinct South-East, South-South, South-West, North-Central, North-East and North-West geo-political regions (Mustapha, 2006; Alaba *et al*., 2017; Okolie *et al*., 2018). The Hausas and Fulanis are located mainly in the North-West region of Nigeria (Nigeria Linguistic, 1979). However, the Fulanis in pursuit of their cattle rearing business are resident in other regions such as Ilorin, Kwara State in the North-Central region, where the traditional ruler is of Fulani origin (Ilorin, Encyclopeadia Britannica, 2019). The Yorubas are mainly located in the South-West and North-Central regions of Nigeria (Nigeria Linguistic, 1979), although they are scattered across different cities within and outside Nigeria. The Yorubas constitute the majority ethnic group in Ilorin, Kwara State, North-Central of Nigeria (Ilorin, Encyclopeadia Britannica, 2019).

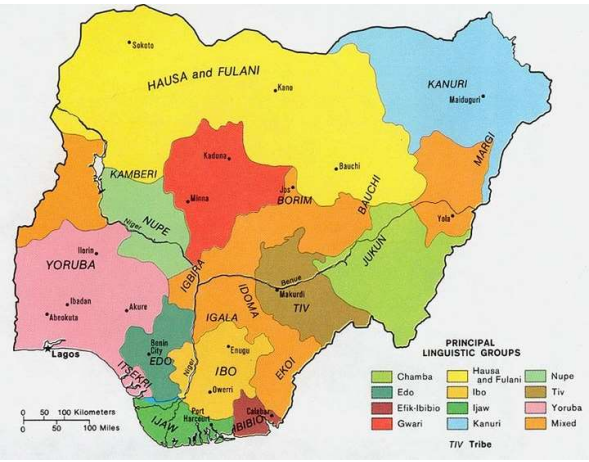

Figure 1. Geographical locations of linguistic groups of Nigeria (Nigeria Linguistic, 1979).

No previous study examined Y-STRs in Fulanis resident in any part of Nigeria. In addition, previous studies examined Y-STR haplotype frequencies and diversity in Hausas, Igbos and Yorubas resident in Lagos State, South West of Nigeria (Martineza *et al*., 2017), but not in Yorubas resident in Ilorin, Kwara State and North-Central of Nigeria. Similarly, Allele Frequencies and some population genetic parameters of evaluated Y-STRs (*DYS385a/b, DYS449, DYS447, DYS481, DYS504, DYS518, DYS644* and DYS710) were not reported in the previous studies on Yorubas resident in Lagos State, South West of Nigeria (Martineza *et al*., 2017). *DYS449, DYS518, DYS612* and *DYS626* are rapidly mutating Y-STRs (D'Amato and Kasu, 2017), out of which *DYS612* and *DYS626* were not evaluated in previous studies on Yorubas resident in Lagos State, South West of Nigeria (Martineza *et al*., 2017).

Therefore, this study evaluated Allele Frequencies, Allele Diversity, Homozygosity, Expected Heterozygosity, Observed Heterozygosity, Polymorphism Information Content, Haplotypes Frequencies and Haplotype Diversity of 10 Y-STR loci: *DYS385a/b, DYS449, DYS447, DYS481, DYS504, DYS518, DYS612, DYS626, DYS644* and *DYS710* in Fulanis and Yorubas resident in Ilorin, Kwara State and North Central of Nigeria.

Methods

Ethical approval

This research work was approved by the University of Ilorin Ethical Review Committee (UERC) with approval number; UERC/ASN/2018/1261. Experimental procedures were carried out in accordance with the National Ethics and Operational Guidelines for Research on Human Subjects, the Number code (1947); the World Medical Association Declaration of Helsinki (1964) and its amendments, the Helsinki Declaration of 1975, as revised in 2000 and the Council of International Organization of Medical Sciences (CIOMS) guidelines of 1993 as stated on the research policy of the UERC.

Determination of sample size and samples collection

Samples of twenty-five (25) adult unrelated males of both Fulani and Yoruba ethnic groups were collected amongst residents of Ilorin, Kwara State and North-Central of Nigeria, respectively using the purposive random sampling technique (Bacchetti *et al*., 2011; Haber *et al*., 2013; Akinlolu, 2016). The purposive technique or judgement sampling method is a non-probability technique which is employed in human invasive studies such

as DNA analyses of blood samples which are dependent solely on the number of individuals who chose to volunteer for the study (Bacchetti *et al.*, 2011; Haber *et al.*, 2013; Akinlolu, 2016). Hence, the total number of subjects (50) used in this study were based on the number of volunteers who agreed to donate their blood samples for DNA analyses as previously established (Bacchetti *et al.*, 2011; Haber *et al.*, 2013; Akinlolu, 2016).

Consent forms were distributed to the volunteers seeking their informed consent, and each subject signed the Consent Form to indicate given approval. Genealogies of each volunteer were traced to the third generation based on self-declaration. Only individuals whose parents, grandparents and great grandparents belong to the Fulani or Yoruba ethnic group were included in the study. The Age of Fulanis ranged from 20 - 80 years, while the Age of Yorubas ranged from 20 - 25 years.

DNA extraction

Genomic DNA was extracted from collected blood samples according to the manufacturer's instructions using ZYMO Quick-DNA™ Miniprep Plus Kit (D4068) (Essien *et al*., 2020). Genomic DNA extracted from two Yoruba samples were of poor quality and were not used for further Y-STRs analyses. Hence, 25 Fulani and 23 Yoruba samples were used for Y-STRs analyses.

PCR amplification, genotyping and bioinformatic analyses of Y-STR loci

PCR amplification was performed according to the manufacturer's instructions using UniQ-Typer™ Y10-STR prototype genotyping kit to amplify and detect the 10 Y-STR loci: *DYS385a/b, DYS449, DYS447, DYS481, DYS504, DYS518, DYS612, DYS626, DYS644* and *DYS710* included in the kit. The UniQ-Typer™ Y10-STR kit was developed by the University of Western Cape and Inqaba Biotechnical Industries (Pty) Limited. The UniQ-Typer™ prototype provides high discriminatory capabilities using Y-STR markers with increased discriminatory capacity (D'Amato and Kasu, 2017). Hence, the Y-STR markers evaluated in this study are unique and are further additions to previously studied Y-STRs.

Electrophoresis was performed on the Applied Biosystems® 3500 Genetic Analyzer using POP-4® polymer and Data Collection Software, Version 2.0. GeneMapper® ID 3.2.1 and GeneMapper® ID-X1.2/1.4 software were used for bioinformatics analyses. The UniQ- Typer™ Y10-STR prototype genotyping kit was provided free of charge by Inqaba Biotechnical Industries (Pty) Limited, Pretoria, South Africa. The corresponding UniQ-Typer™ Y10-STR Loci, Dye channel and Motif are as provided in Table 1.

Table 1. UniQ-Typer™ Y10-STR loci, dye channel and motif.

Serial Number	Locus	Dye channel	Repeat Motifs
1	DYS385a/b	Green	[GAAA]n
2	DYS447	Red	[TAATA]n[TAAAA]1[TAATA]m[TAAAA]1[TAATA]n
3	DYS449	Red	[TTTC]nN50[TTTC]n
4	DYS481	Red	[CTT]n]
5	DYS504	Yellow	TCCT]n N7[CCCT]3
6	DYS518	Blue	[AAAG]n [GGAG]1[AAAG]4 GAAGAG [AAAG]n
7	DYS612	Yellow	[CCT]5[CTT]1[TCT]4[CCT]1[TCT]n
8	DYS626	Yellow	[GAAA]nN24[GAAA]3N6[GAAA]5 [AAA]1[GAAA]2–3(GAAG)1(GAAA)3
9	DYS644	Green	[TTTTA]n…TTTA [TTTTA]n
10	DYS710	Blue	[AAAG]n [AG]n [AAAG]n[

Calculations of Allele Frequencies

Allele Frequency = Number of Allele repeat/2(n) (Motro *et al.*, 2002; Okolie *et al.*, 2018). Where n is population size.

Calculations of Homozygosity and Expected Heterozygosity

Homozygosity (H) = $\Sigma(P_i^2)$, where P_i is frequency of Allele (Mohammed *et al.*, 2015; Akinlolu *et al.*, 2021).

Expected Heterozygosity (H_E) = 1 – Homozygosity (Mohammed *et al.*, 2015; Akinlolu *et al.*, 2021).

Observed Heterozygosity (H_O) = $\Sigma H_n/N$.

Where H_n was number of heterozygote individual and N is the Total number of individuals in the population (Mohammed *et al.*, 2015; Akinlolu *et al.*, 2021).

Deviation from Hardy-Weinberg Equilibrium

Deviation from Hardy-Weinberg Equilibrium was determined using the formula:

$X^2 = \Sigma(O\text{-}E)^2/E$. Where O and E are the Observed and Expected number or Genotypes.

The calculated and X^2-Table at p = 0.05 and at 1 degree of freedom were compared to confirm deviation from Hardy-Weinberg proportions (Crow, 1999; Wigginton *et al.*, 2005; Mohammed *et al.*, 2015; Akinlolu *et al.*, 2021).

Calculations of Polymorphism Information Content (PIC)

PIC was calculated as PIC = $1 - \Sigma (P_i)^2$, Where P_i is Frequency of Allele (Mohammed *et al.*, 2015; Akinlolu *et al.*, 2021).

Calculations of F_{IS}, F_{ST}, F_{IT} and G_{ST}

F_{IS} = Variance of an Allele Frequencies within populations.

1 - Mean H_e/H_s

Mean H_e = Mean of Expected Heterozygosity for both Fulani and Yoruba subjects = 2 (multiplication of allele frequencies for Fulani) + 2 (multiplication of allele frequencies for Yoruba subjects)/ 2

$F_{ST} = 1\text{-}H_S/ H_T$

Where H_T is the proportion of the heterozygotes in the total population and H_S is the average proportion of heterozygotes in subpopulations.

F_{IT} = 1 - Mean H_E / H_T.

$G_{ST} = (H_T - H_S)/ H_T$ (Meirmans and Hedrick, 2011).

Calculations of Allele Diversity (AD), Haplotype Frequency (HF) and Haplotype Diversity (HD)

AD = $\frac{(n'-1)}{(n-1)}$ Where n' = the number of alleles expected following a bottle neck, and

n = original number of alleles (Akinlolu *et al.*, 2021).

n' = n- $\sum_{i=1}^{N}(1 - p_i)^{2N}$

HF = n/n-1 (1- $\sum p_i^2$), Where n = population size and p_i is Frequency of Allele.

HD = n/n-1 (1- $\sum X_i^2$), Where n = population size and X_i is haplotype frequency.

Statistical analyses

Computed data were statistically analyzed using the Statistical Package for the Social Science Software (SPSS Statistics - Version 23.0) developed by the International Business Machines Corporation (IBM). Data were presented as Mean±SD, with determination of level of significance at *P*-value less than or equals to 0.05.

Results

Absence of Alleles

No alleles were observed for *DYS626* in Fulani and Yoruba subjects. This could have possibly been due to absence of *DYS626* representation in Fulani and Yorubas, or no representation of *DYS626* in the tested population samples.

Partial Repeats (PR) and Variant Alleles (VA) of Y-STRs in Fulani and Yoruba Subjects

No partial repeats were observed for any of the 10 Y-STRs in Fulani and Yoruba subjects. In Fulanis, VA were only observed for *DYS644* (Alleles 20.4, 21.4, 22.4, 23.4 and 24.4) and *DYS710* (31.2, 32.2 and 34.2) (Tables 2 and 3). In Yorubas, VA were equally observed only for *DYS644* (Alleles 21.4 and 22.4)

and *DYS710* (28.2, 30.2, 31.2, 32.2, 33.2, 34.2, 35.1, 35.2, 36.2 ad 39.2) (Tables 4 and 5).

Population Genetic Parameters

The X^2-Table at p = 0.05 and 1 degree of freedom is 3.84. The X^2 values of evaluated the 10-Y-STRs were lesser than the X^2-table at 1 degree of freedom, indicating no deviation from Hardy-Weinberg proportions. The computed results of Alleles Frequencies (AF) of the evaluated 10 Y-STRs for Fulanis are as presented in Tables 2 and 3, while AF for Yorubas are as presented in Tables 4 and 5. The computed F_{IS} values for *DYS385a, DYS385b, DYS449, DYS447, DYS481, DYS504, DYS518, DYS612, DYS644* and *DYS710* were 0.0000. Computed values for F_{ST}, F_{IT} and G_{ST} of evaluated 10-YSTRs were 0.5000. The computed results of Allele Diversity, Haplotype Frequency, Haplotype Diversity, Homozygosity, Expected Heterozygosity and Polymorphism Information Content for the examined 10 Y-STRs in Fulani and Yoruba Subjects are as presented in Tables 6 and 7 respectively.

Table 2. Allele frequencies of *DYS385a, DYS385b, DYS447, DYS449* and *DYS481* in Fulani subjects.

Alleles	**DYS385a**	**DYS385b**	**DYS447**	**DYS449**	**DYS481**
11	0.0800	-	-	-	-
12	0.2800	-	-	-	-
13	0.6000	-	-	-	-
14	0.0400	0.1110	-	-	-
15	-	-	-	-	-
16	-	0.1110	-	-	-
17	-	0.5560	-	-	-
18	-	-	-	-	-
19	-	0.2220	-	-	-
20	-	-	-	-	-
21	-	-	-	-	-
22	-	-	-	-	0.0400
22.4	-	-	-	-	-
23	-	-	-	-	0.0400
24	-	-	0.6400	-	0.0400
24.4	-	-	-	-	-
25	-	-	0.0800	-	0.2000
26	-	-	0.2800	0.0480	-
27	-	-	-	0.1430	0.6400
28	-	-	-	0.0480	0.0400
29	-	-	-	0.0950	-
30	-	-	-	0.0480	-
31	-	-	-	0.2380	-
31.2	-	-	-	-	-
32	-	-	-	0.1430	-
32.2	-	-	-	-	-
33	-	-	-	0.0950	-
33.4	-	-	-	-	-
34	-	-	-	0.1430	-

Table 3. Allele frequencies of *DYS504*, *DYS518*, *DYS612*, *DYS644* and *DYS710* in Fulani subjects.

Alleles	**DYS504**	**DYS518**	**DYS612**	**DYS644**	**DYS710**
11	-	-	-	-	-
12	-	-	-	-	-
13	0.9200	-	-	-	-
14	-	-	-	-	-
15	0.0800	-	-	-	-
20.4	-	-	-	0.0714	-
21	-	-	-	-	-
21.4	-	-	-	0.3333	-
22	-	-	-	-	-
22.4	-	-	-	0.2917	-
23	-	-	-	-	-
23.3	-	-	-	0.0238	-
23.4	-	-	-	0.0476	-
24	-	-	-	-	-
24.4	-	-	-	0.0238	-
25	-	-	-	-	-
26	-	-	-	0.0476	-
27	-	-	-	-	-
31.2	-	-	-	-	0.8400
32	-	-	-	-	0.2800
32.2	-	-	-	-	0.0800
33	-	-	0.0400	-	-
34.2	-	-	-	-	0.0400
35	-	-	0.8400	-	-
36	-	-	0.0800	-	-
37	-	-	0.0400	-	-
38	-	0.0400	-	-	-
39	-	0.2400	-	-	-
40	-	0.7200	-	-	-

Table 4. Allele frequencies of *DYS385a, DYS385b*, *DYS447*, *DYS449* and *DYS481* in Yoruba subjects.

Alleles	**DYS385a**	**DYS385b**	**DYS447**	**DYS449**	**DYS481**
11	0.0420	-	-	-	-
12	0.0420	0.0500	-	-	-
13	0.0830	-	-	-	-
14	0.1500	0.2000	-	-	-
15	0.0420	-	-	-	-
16	0.4000	-	-	-	-
17	0.2500	0.2000	-	-	-
18	0.0830	0.5000	-	-	-
19	-	0.1000	-	-	-
20	-	0.1000	-	-	-
23	-	-	0.0417	-	-
24	-	-	0.1250	-	0.2080
25	-	-	0.3750	-	0.2500
26	-	-	0.1250	-	0.1670
27	-	-	0.1667	-	0.0830
28	-	-	0.1667	-	0.2080
28.2	-	-	-	-	-
29	-	-	-	0.1360	0.0830
30	-	-	-	0.5910	-
31.2	-	-	-	-	-
32	-	-	-	0.1360	-
32.2	-	-	-	-	-
33	-	-	-	-	-
33.2	-	-	-	-	-
33.4	-	-	-	0.1360	-

Table 5. Allele frequencies of *DYS504, DYS518, DYS612, DYS644* and *DYS710* in Yoruba subjects.

Alleles	**DYS504**	**DYS518**	**DYS612**	**DYS644**	**DYS710**
11	0.0420	-	-	-	-
12	0.0420	-	-	-	-
13	0.6250	-	-	-	-
14	0.2080	-	-	-	-
15	0.0830	-	-	-	-
16	-	-	-	0.0476	-
21.4	-	-	-	0.2500	-
22.4	-	-	-	0.9170	-
28.2	-	-	-	-	0.0417
30.2	-	-	-	-	0.0833
31	-	-	0.0830	-	-
31.2	-	-	-	-	0.1250
32	-	-	0.0420	-	-
32.2	-	-	-	-	0.1250
33	-	-	0.0420	-	-
33.2	-	-	-	-	0.2500
34	-	-	0.1250	-	-
34.2	-	-	-	-	0.1250
35	-	-	0.2920	-	-
35.1	-	-	-	-	0.0417
35.2	-	-	-	-	0.0417
36	-	0.0400	0.2500	-	0.0417
36.2	-	-	-	-	0.0833
37	-	0.1300	0.0830	-	-
38	-	0.2100	0.0830	-	-
39	-	0.1700	-	-	
39.2	-	-	-	-	0.0417
40	-	0.2100	-	-	-
41	-	0.2100	-	-	-
43	-	0.0400	-	-	-
44	-	0.0400	-	-	-

Table 6. Allele diversity (AD), Haplotype frequency (HF), Haplotype diversity (HD), Polymorphism information content (PIC), Homozygosity (H) and Expected Heterozygosity (H_E) of the Y-STRs in Fulani subjects.

Gene	AD	HF	HD	PIC	H	H_E
DYS385a	0.9500	0.5770	0.6950	0.5536	0.0180	0.9820
DYS385b	0.9970	0.6940	0.5830	0.6170	0.0430	0.9570
DYS447	0.9923	0.5267	0.7527	0.5056	0.0198	0.9802
DYS449	0.4711	0.6236	0.6400	0.5536	0.0180	0.9820
DYS481	0.5480	0.5670	0.7068	0.5440	0.0180	0.9820
DYS504	0.9850	0.1533	1.0172	0.1472	0.0341	0.9659
DYS518	0.9350	0.4400	0.8390	0.4224	0.0230	0.9770
DYS612	0.9070	0.2970	0.0920	0.2850	0.0290	0.9710
DYS644	0.4676	0.6570	0.0950	0.6300	0.0260	0.9740
DYS710	0.9892	0.2967	0.9500	0.2848	0.0286	0.9714

Table 7. Allele diversity (AD), Haplotype frequency (HF), Haplotype diversity (HD), Polymorphism information content (PIC), Homozygosity (H) and Expected Heterozygosity (H_E) of the Y-STRs in Yoruba subjects.

Gene	AD	HF	HD	PIC	H	H_E
DYS385a	0.9230	0.7900	0.3922	0.7570	0.0100	0.9900
DYS385b	0.9460	0.7210	0.5050	0.6850	0.0160	0.9840
DYS447	0.9741	0.8043	0.3683	0.7708	0.0096	0.9904
DYS449	0.4937	0.6164	0.6510	0.7570	0.0200	0.9800
DYS481	0.5973	0.8442	0.2998	0.8090	0.0080	0.9920
DYS504	0.9320	0.5800	0.6924	0.5560	0.0185	0.9815
DYS518	0.9394	0.8530	0.2840	0.8170	0.0080	0.9920
DYS612	0.9570	0.8470	0.7490	0.8120	0.0080	0.9920
DYS644	0.5700	0.0942	0.7490	0.0903	0.0380	0.9620
DYS710	0.9999	0.9076	0.1840	0.8698	0.0054	0.9946

Discussion

Cultural and environmental factors such as religious practices, dietary practices and climate conditions resulted in varied genetic structuring, genetic stratifications and population genetic classifications even within populations historically belonging to same ethnic and regional groups (Torres *et al*., 2012; Haber *et al*., 2013). Haber *et al*., 2013 analyzed SNPs and noted that religious cultural changes over two millennia facilitated admixture between culturally similar populations from the Levant, Arabian Peninsula, and Africa. These cultural changes resulted in the Levant populations now falling into two main groups: the first group having genetic affiliations with modern-day Europeans and Central Asians, while the second group has closer genetic affiliations with Middle Easterners and Africans. These observations emphasize the relevance of geo-political regions in population genetic studies. Hence, the genotyping Y-STRs data of Fulanis and Yorubas resident in Ilorin, Kwara State, and North-Central of Nigeria presented in this study are novel.

In this study, the F_{IS}, F_{ST}, F_{IT} and G_{ST} of 0.0000 and 0.5000 for all evaluated 10 Y-STRs implied little genetic differentiation and total lack of sub-structuring in the Fulani and Yoruba populations. Similarly, the X^2 values were lesser than the X^2-table at 1 degree of freedom, indicating that the population genetics data for all evaluated 10 Y-STRs did not deviate from Hardy-Weinberg proportions.

Homozygosity values were higher in Fulani subjects than in Yoruba subjects in 8 out of the evaluated 10 Y-STRs except *DYS449* (0.0180 for Fulanis and 0.0200 for Yorubas) and *DYS644* (0.0260 for Fulanis and 0.0380 for Yorubas) (Tables 6 and 7) indicating lower genetic diversity amongst the Fulani subjects compared with Yoruba subjects. In addition, Expected Heterozygsity (H_E) is a measure of genetic diversity and variation within populations, and it's computed value decreases with increased Inbreeding. H_E values were lower in Fulanis than Yorubas in 8 out of the evaluated 10 Y-STRs except *DYS449* (0.9820 for Fulanis and 0.9800 for Yorubas) and *DYS644* (0.9740 for Fulanis and 0.9620 for Yorubas) (Tables 6 and 7) indicating lower genetic diversity amongst the Fulani subjects compared with Yoruba subjects. The lower genetic diversity in Fulanis is probably due to differences in customs and norms between Fulanis and Yorubas, which permit Fulanis to marry their cousins who are of closer genetic matches, whereas the customs and norms of Yorubas do not permit them to marry their cousins or children of close relatives. Hence, the greater diversity amongst Yorubas than Fulanis.

Allele frequency (AF) or gene frequency describes the relative frequency of an allele at a genetic locus in a specific population. AF conforms with Hardy-Weinberg principle, which opined that in a large random mating population, and in the absence of mutation, migration, natural selection and random drift, the AF is unaltered from generation to generation. Gene diversity provides descriptive information on polymorphic loci proportion across the genome, and it is directly related to the evolutionary potential of the population and inbreeding. Similarly, the number of alleles (allelic richness) can help determine a population's long-term potential for adaptability and persistence (D'Amato and Kasu, 2017).

The highest value of Allele Diversity (AD) in Fulani subjects was 99.7% (*DYS385b*) while the lowest AD value was 46.8% (*DYS644*) (Table 6). For Yoruba subjects, the highest AD value was 99.9% (*DYS710*) while the lowest AD value was 49.4% (*DYS449*) (Table 7). The computed AD values were either approximately 0.5 or higher than 0.5, implying that the tested 10 Y-STRs are highly informative and effective polymorphic loci for the evaluations of gene diversity and evolutionary potentials of the tested populations (Ito *et al*., 2003). In addition, the AD values indicate that *DYS385b* and *DYS710* are the most effective polymorphic loci for the evaluations of gene diversity and evolutionary potentials for the Fulani and Yoruba populations respectively.

Haplotype Frequencies (HF) are used in the analyses of linkage disequilibrium, while Haplotype Diversity (HD) represents the uniqueness of a specific haplotype in a defined population (Ito *et al*., 2003). Haplotypes are, therefore, used for designating a phenotype to a genetic region, and for detecting associations (Ito *et al*., 2003).

The highest value of HF in Fulani subjects was 69.4% (*DYS385b*) while the lowest HF value was 15.3% (*DYS504*) (Table 6). For Yoruba subjects, the highest HF value was 99.9% (*DYS710*) while the

lowest HF value was 49.4% (*DYS449*) (Table 7). The highest value of HD in Fulani subjects was 101.7.7% (*DYS504*) while the lowest HD value was 9.5% (*DYS644*) (Table 6). For Yoruba subjects, the highest HD values were 74.9% (*DYS612* and *DYS644*) while the lowest HD value was 18.4% (*DYS710*) (Table 7). The computed AD values were either approximately 0.5 or higher than 0.5 (Ito *et al*., 2003), hence the Allele Frequencies (AF), AD, HF and HD values (Tables 6 and 7) for Fulani and Yoruba subjects indicate that the tested 10 Y-STRs are specific haplotypes for defining and designating these populations to the Nigerian genetic region.

The highest value of Polymorphism Information Content (PIC) was 63% (*DYS644*), while the lowest PIC value was 14.7% (*DYS504*) in Fulani subjects (Table 6). For Yoruba subjects, the highest PIC value was 86.9% (*DYS710*), while the lowest PIC value was 9% (*DYS644*) (Table 7). The PIC values indicate that the tested Y-STRs were highly polymorphic in Fulani and Yoruba subjects except *DYS644* locus which was less polymorphic compared to the other 9 evaluated loci.

Conclusion

This study provides Y-STRs genotyping data for the Fulanis and Yorubas resident in Ilorin, Kwara State, and North-Central of Nigeria, which can be included in forensic databases and for forensic analyses by relevant civil and security agencies. The obtained data on Allele Frequencies, Allele Diversity, Homozygosity, Expected Heterozygosity, Observed Heterozygosity, Polymorphism Information Content, Haplotypes Frequencies and Haplotype Diversity of 10 Y-STR loci in this study become quite relevant as it contributes to the provision of forensic databases for settler Fulanis (as against nomadic Fulanis), and their neighbouring Yorubas.

Limitations of the Study and Future Research Direction

This study is limited to genotyping data of Y-STRs, and does not include other Genome-wide association studies. Further Genome-wide association studies shall be carried out in future research studies in-order to provide further data on the genetic structures of Fulanis and Yorubas of Nigeria.

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