

Inheritance of fingerprints among the Urhobo people of Nigeria: implication in forensic genetics

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ABSTRACT

Introduction: Several scholars had proposed the possibility of parentage determination using physically expressive diallelic morphogenetic traits of their offspring and, have provided a clue of the possibility that certain traits could be predominant in a population, yet exist as recessive traits. Nevertheless, arguments about the heritability of “variant expressive” triallelic traits such as the fingerprints in humans have been on for years, with only assumptive explanations. This study investigated the inheritance of fingerprints among the Urhobo people residing in Delta State, Nigeria. **Materials and Methods:** The study, which was comparative and, family-based was comprised of 60 families and 180 unrelated individuals. Prints were taken with an Hp G4010 scanner, Chisquare test evaluated sex-associated differences, Mood median test ascertained laterality of ridges, Heritability coefficient and One-way analysis of variance determined qualitatively and quantitatively the certainty of inheritance of fingerprint patterns. **Results:** A conformance for the family and unrelated group for R1D-5D was calculated as 90%, 68%, 87%, 81%, 90% and, 57%, 47%, 60%, 60%, 80% while for L1D-5D a conformance of 80%, 67%, 85%, 90%, 87% and, 53%, 63%, 67%, 77%, 73% was obtained. We observed an HO of 57% and, 46% for the digits of the right and left hands. The left little finger (L5D) was sexually dimorphic among the family group ($X^2=10.233$; $P=0.006$). **Conclusion:** We observed that the same patterns combined for parents produced a different phenotype in some offspring, suggesting a possibility of epistatic and, hypostatic influence of genes.

Keywords: fingerprint, genes, heritability coefficient, Urhobo, Nigeria

INTRODUCTION

Phenotypes are observable traits, determined by a gene or sets of genes, alongside environmental effects upon these genes. Several genes are transmitted in a Mendelian or non-Mendelian pattern and, they include polygenes, co-dominance, sex-linked, lethal and, epistatic genes [1-2]. Among humans, about 99.9 % of the bases in the whole genome are surprisingly alike; the residual minute 0.1 % actually defines the uniqueness of a person, and it is inherited by offspring, thus, forming the basis for population diversity [3]. Several scholars had pointed out phenotypic similarity and, marker-gene segregation as basic methods in studying the heritability of traits [4]. However, the

most used is phenotypic similarity among families, which happens to be the most accessible proof about heritability. Over the years, we have often seen children who looked just like their parents or relatives when the latter were younger and, suddenly, we could tell that they are related because of several similar morphogenetic (physical) traits, such as facial features, hair color, and body marks. This happens as a result of the shared genetic blueprints every child receives [5-6]. Nevertheless, how about a trait so minute and assumed unique as the fingerprint?

Fingerprints which have been described as the array of epidermal ridges present on the fingers and alleged as the panacea for individualization were discovered by the scientist Jan Purkinje in the

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year 1823 . He stated that they were individualistic and in 1941, Walker established uniqueness and heritability [7-8]. Fingerprints have being considered a multifactorial trait by Yang et al., Machado et al. and, Vij; with an earliest proof of heritability been documented by Slatis et al. [9-12]. Subsequently to Slatis et al. [12], several studies had made it clear that finger ridge count is one of the anthropometric features that can be passed from one generation to another [13-17].

The understanding of inheritance of traits goes beyond determining parentage or evaluating uniqueness. Morphogenetic trait inheritance and expressivity are very much associated with population genetics. The manner traits are inherited, and, the characteristics of the allele expressed by a particular population could be a significant factor in explaining the evolutionary trend of a population and, how close to extinction it is [18-19]. However, the major obstacle to the investigation of the heritability of finger dermatoglyphics using phenotypic similarity is the fact that researchers have continued to use a single pattern of classification and representation, thus, limiting its application to its genetic implication [20-23]. Hence this study investigated inheritance of fingerprints qualitatively and quantitatively among the Urhobo people of Nigeria. A research as this one will provide a breakthrough in the field of medical genetics especially in a developing country like Nigeria.

MATERIAL AND METHODS

The study was cross-sectional, analytical, observational and, comparative. We utilized a comparative study because there is no detailed documentation on the inheritance of fingerprints of the Urhobo people of Nigeria. Slatis et al. used this approach in studying those of the Israelis'[12]. The Urhobo ethnic group is one of the major ethnic groups in Delta State, Nigeria with a population of 1,882,828 [24-25] and, they dwell in almost all local governments within the State. The population for this study which comprised, of 60 families and, 180 unrelated individuals were obtained from the State under study. Each family comprised of a mother, father and, at least a child while the unrelated group was made up of 60men, 60women, and, 60mixed

men and women. The family size was considered from the projected estimated formula = $P_o \times [1 + (r / 100)]^t$ and, Cochran method for sample size ($SS = z^2 \times p \times q / d^2$) [24,26]. Ethical approval was obtained from the Research and, Ethics Committee of the Faculty of Basic Medical Sciences, Delta State University, Abraka, Delta State, Nigeria. (DELSU / CHS/ ANA /18/06). All participants were healthy and, without deformities of the hands. Participants were instructed to place their palms on a Hewlett placard G4010 Photo scanner connected to a Hp laptop through a USB cord [27]. Fingerprints were acquired in a tranquil and, closed position for a clearer and, well defined imprint. The scanner was powered by a 500 solar power inverter connected to a 12volts rechargeable battery [28]. Digits were numbered as follows; 1D (thumb), 2D (index finger), 3D (middle finger), 4D (ring finger) and, 5D (little finger) for both hands. They were classified as arches, radial loop, ulnar loop, and, whorls (29). The scanned prints were coded for fathers, mothers and, offspring for all of the investigated families . The basic dermatoglyphics landmarks which are the triradius, core and radiants were used to differentiate fingerprint patterns into arches, radial loop, ulnar loop and, whorls. The ridge counts were obtained with the aid of AUTOCAD version 2010 [27]. The data collected were recorded and, analyzed with the aid of the International Business Machine (IBM) Statistical Package for the Social Sciences (SPSS) version 23. A p-value of <0.05 was evaluated significant. Obtained data were presented using descriptive statistics (deviation and mean), Chi-square ascertained an association between categorical variables while Mood median test determined laterality of ridges. We also used one-way analysis of variance to test for an association of ridge counts of parents and offspring. Qualitatively heritability was calculated for both the related and unrelated groups and it was done by dividing the number of combination outcome to total offspring' prints. Heritability coefficient; $H_o = \frac{c_1 - c_0}{1 - c_0}$ which was adopted from Muller-Ford, [30] was subsequently calculated for fingerprint patterns.

RESULTS

The percentages of males and, females with ulnar loop were 56.4% and, 50% for R1D (Table 1). Whorls were represented in 36.2% males and, 32.6% females while the arches were seen in 7.4% males and, 17.4% females. For R2D, ulnar loop (UL), whorls (WLs), arches (ARs) and, radial loop (RL) were represented in 50%, 28.7%, 14.9% and, 6.4% males while they occurred in 52.3%, 24.4%, 15.1% and, 8.1% females. Radial loop in R3D and R4D were observed in 2.1% males and, 1.2% females. We discovered ulnar loop, whorls and, arch patterns in 90.4%, 7.4%, 2.1% males and 81.4%, 11.6%, 7.0% females (Table 1). The distribution was without sexual preference for all digits (R1D- 5D); R1D (χ^2 [df=2]= 4.18, P=0.12), R2D (χ^2 [df=3]=0.55, P=0.90), R3D (χ^2 [df=3]= 2.70, P= 0.44), R4D (χ^2 [df=3]=6.33, P= 0.10) , R5D (χ^2 [df=2]= 3.63, P=0.163)

The authors observed the percentages of UL, WLs and ARs in L1D for males as 64.9%, 18.1%, 17.0% and 58.1%, 16.3%, 25.6% for females. Furthermore, radial loop (RL) was seen in 1.1% males as compared to 8.1% females (Table 2). The study also recorded 53.2%; 56.4% UL, 31.9%; 41.5% WLs ;14.9%; 2.1% ARs in males and, 62.8%; 55.8% UL, 24.4%; 38.4% WLs, 12.8%; 5.8% ARs in females for L3D and, 4D. Table 2 also presented UL, WLs, ARs in 90.4%, 6.4%, 3.2% males while the females had 72.1%, 16.3% and, 11.6% for LD5. The distribution was not sexually influenced for L1D-4D); L1D (χ^2 [df=2] = 1.98, P=0.372), L2D (χ^2 [df=3] =5.73, P=0.13), L3D (χ^2 [df=2] = 1.75, P= 0.42), L4D (χ^2 [df=2] =1.68,P= 0.43) but L5D was sexually dimorphic (χ^2 [df=2]= 10.23, P=0.01),

In Tables 3 and 4, findings showed that the distribution of FRCs for RL1D to R5D and, L1D to L5D were not sexually inclined(P>0.05).

Table 5 presented the parental combination on the thumb (R1D). The offspring presented a 90% conformance (54 possible outcomes of the 60 offspring print) and 57% conformance in the related and, unrelated group. A conformance of 68%, 87%, 82%, 90% and, 57%, 47%, 60%, 60%, 80% were also recorded for the family and, isolated group for R2D ,3D,4D and,5D (Table SM 6-9)

The authors analysed the conformance for the left digits in Table SM 10-14. Findings revealed 80% (41 feasible outcomes of the 60 offspring count) and, 53% conformance for the family and mixed group for L1D. The authors also obtained 67%, 85%, 90%, 87% conformance for the related group while 63%, 67%,77% and 73% were recorded for the unrelated group. The H0 obtained for R1D, 2D,3D,4D and, 5D were 0.77, 0.40, 0.68, 0.53, 0.50 while those of the left digits were 0.57, 0.11, 0.55, 0.57, 0.52 (Table SM 15). It was further observed from Table SM 15 that the total H0 for the right digits were 0.57(57%) while that of the left was 0.46 (46%)

Table SM 16 revealed a non- significant association between the right digits ridge counts (R1D-5D; R-AFRC) (P=0.141, 0.326, 0.148, 0.245, 0.077; 0.096) and the left digits ridge counts (L1D-5D; L-AFRC) (P=0.454, 0.560, 0.196, 0.087, 0.190) for parents and, the offspring. The distribution of the TFRc was also not statistically significant (P=0.174).

Table SM 17 illustrated selected families among the 60 investigated families, that had same patterns bilaterally. Family 12 had the sequence WUUWU on all right digits, family 25 had UUUUU on all left digits, family 26 and 50 had UAUUU and UWUUW on all right digits.

Figure 1 and Figure SM 2-5 presented the pedigree for both the thumb, index, middle, ring and, little fingers. It showed parental permutation of traits (upper boxes), those that were expressed from the combinations (middle blue boxes) and phenotypic distribution among offspring (last boxes).

DISCUSSION

Findings from this study showed that the UL for all digits was the most predominant pattern expressed among offspring. This was not startling, because it has earlier been affirmed by Slatis et al. that the UL was the most genetically determined pattern with several genes producing divergence from this pattern [12]. He proposed the dominant and, semi dominant genes acting independently or showing epistatic for fingerprint patterns. However, from this study, it could be ascertained that a dominant allele for UL may always be present in either parent producing at least an offspring with the phenotypic expression. This was buttressed by

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Juberg et al. who investigated the inheritance of these prints among the American Caucasians' and, they discovered that the offspring from their study had the utmost proportion of ulnar loop [31]. They affirmed that a single gene had effects on fingerprint patterns amid the Louisianians. Further findings from this study showed that, the combination outcome of radial loop was observed only on the index finger, the arches more on the left thumb while whorls were expressed alongside ulnar loop for all digits. Nevertheless, not all families exhibited these trends depicting incomplete penetrance with variable expressivity in the studied population. These findings were consistent with Slatis et al. and, Juberg et al. [12, 31]. According to Nagy and, Pap, each finger may be influenced by the same genetic factors but are not affected in the same way [32].

In assessing the possibility of inheritance of fingerprints, qualitatively we observed a range of conformance for the related families as 68% to 90% for the right digits (R1D-5D) while those of the left varies between 67% to 90%. Some digits had a very high heritability estimate indicating that offspring inheritance were in a predictable fashion. However, our findings were not that different from those of Muller ford (65-96%); Sengupta and, Karmakar (59% and 77%); and, Machado et al. (60-75%) [30, 33-34]. We observed a coefficient of 0.57(57%) and 0.46(46%) for the right digits and left digits. The authors accept from this study that, hereditary of fingerprints can be ascertained qualitatively. The authors observed that the FRC and TFRC from this study among parents and offspring can be used to establish heritability of fingerprints as earlier stated by Machado et al., Meenakshi et al., Bhasin, Medland et al. and, Cheng et al. [10, 14-17].

Some families from this study had the sequence WUUWU,UUUUU ,UAUUU and UWUW bilaterally. These patterns within these families had 100% penetrance for the respective digits. The authors also observed symmetry of patterns and sex- associated dissimilarity in the studied population. The results from this study showed that arches were common on all the digits of the females with an exception to L3D. Radial loop was prominent on the index fingers (R2D, L2D) of the females, whorls were dominant on the males for 1D,2D and, 3D for both right and left digits while ulnar loop was

pronounced on the males for 1D, 4D, and 5D. Findings were consistent with Abue et al. and, Ekanem et al. studies in Cross River and, Akwa Ibom States, Nigeria [35-36]. Abue et al. observed that the ulnar loop was frequently distributed among males as compared to their counterparts while Ekanem et al. highlighted the arches as the common pattern seen in females in contrast to whorls in men [35-36]. Contrary to the above, Eboh (2012) observed the arches more in males and, the whorls being frequent in females amongst the Anioma people of Nigeria [37]. The authors also observed that L5D was the only finger that was sexually influenced in the studied population ($P=0.006$). Sexual dimorphism has been associated with traits that are transmitted in an autosomal inheritance pattern by previous scholars [38-39] and, due to the fact that fingerprint have been acknowledged as a multifactorial trait, the result of our findings can be ascertained valid.

Nevertheless, we are recommending that more studies should be carried out on the inheritance of fingerprints among Nigerians' and perhaps Sub-Saharan Africans'. The authors critically studied the combination patterns of parents and, their possible outcome for all digits. Findings revealed the whorls were the outcome of some offspring from the permutation of ulnar loop (ULx UL) for all digits among parents while for all left digits, a combination of whorls (WL x WL) produced some offspring with ulnar loop, indicating a possibility of epistatic and hypostatic effects of genes

CONCLUSION

Findings from this study showed that fingerprints of parents were randomly distributed among their offspring demonstrating the possibility of heritability of these patterns. The combination of some patterns of parents produced different phenotypic expression in some offspring suggestive of epistasis.

CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

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RESUMO

Herança de impressões digitais do povo Urhobo da Nigéria:

implicações na genética forense

Introdução: Vários estudos propuseram a possibilidade de determinação de parentesco usando traços morfogenéticos dialélicos fisicamente expressivos de seus descendentes e forneceram uma pista da possibilidade de que certos traços podem ser predominantes em uma população, mas existem como traços recessivos. No entanto, os argumentos sobre a herdabilidade de traços dialélicos “expressivos variantes”, como as impressões digitais em humanos, existem há anos, com apenas explicações presumidas. **Objetivo:** Este estudo investigou a herança de impressões digitais entre o povo Urhobo que reside no Estado do Delta, Nigéria. **Materiais e métodos:** O estudo, de caráter comparativo e de base familiar, compreendeu 60 famílias e 180 indivíduos não aparentados. As impressões foram feitas com um scanner Hp G4010, o teste do Qui-quadrado avaliou as diferenças associadas ao sexo, o teste da mediana do humor verificou a lateralidade das cristas, o coeficiente de herdabilidade e a análise de variância unilateral determinou qualitativa e quantitativamente a certeza da herança dos padrões de impressão digital. **Resultados:** A conformidade para a família e o grupo não relacionado para R1D-5D foi calculada como 90%, 68%, 87%, 81%, 90% e, 57%, 47%, 60%, 60%, 80% enquanto para L1D -5D obteve-se uma conformidade de 80%, 67%, 85%, 90%, 87% e 53%, 63%, 67%, 77%, 73%. Observamos HO de 57% e 46% para os dígitos da mão direita e esquerda. O dedo mínimo esquerdo (L5D) era sexualmente dimórfico entre o grupo familiar ($X^2 = 10,233$; $P = 0,006$). **Conclusão:** Observamos que os mesmos padrões combinados para os pais produziram um fenótipo diferente em alguns filhos, sugerindo a possibilidade de influência epistática e hipostática dos genes.

Palavras-chave: impressão digital, genes, coeficiente de heritabilidade, Urhobo, Nigéria

TABLES AND FIGURES

Table 1: Finger friction ridge patterns on the right hand and test of association

Digit	Sex	Fingerprint pattern				Chi-Square Tests		
		A (%)	RL (%)	UL (%)	W (%)	Df	X ²	P-value
R1D	Male	7(7.4)	-	53(56.4)	34(36.2)	2	4.184	0.123
	Female	15(17.4)	-	43(50.0)	28(32.6)			
	Total	22(12.2)	-	96(53.3)	62(34.4)			
R2D	Male	14(14.9)	6(6.4)	47(50.0)	27(28.7)	3	0.553	0.907
	Female	13(15.1)	7(8.1)	45(52.3)	21(24.4)			
	Total	27(15.0)	13(7.2)	92(51.1)	48(26.7)			
R3D	Male	5(5.3)	2(2.1)	65(69.1)	22(23.4)	3	2.695	0.441
	Female	7(8.1)	-	62(72.1)	17(19.8)			
	Total	12(6.7)	2(1.1)	127(70.6)	39(21.7)			
R4D	Male	-	-	57(60.6)	37(39.4)	3	6.330	0.097
	Female	4(4.7)	1(1.2)	44(51.2)	37(43.0)			
	Total	4(2.2)	1(0.6)	101(56.1)	74(41.1)			
R5D	Male	2(2.1)	-	85(90.4)	7(7.4)	2	3.633	0.163
	Female	6(7.0)	-	70(81.4)	10(11.6)			
	Total	8(4.4)	-	155(86.1)	17(9.4)			

Note: Df=Degree of freedom; X²=Chi-square; A=Arch, RL=Radial Loop, UL=Radial Loop, W=Whorl

Table 2: Finger friction ridge patterns on the left hand and test of association

Digit	Sex	Fingerprint pattern				Chi-Square Tests		
		A (%)	RL (%)	UL (%)	W (%)	Df	X ²	P-value
L1D	Male	16(17.0)	-	61(64.9)	17(18.1)	2	1.976	0.372
	Female	22(25.6)	-	50(58.1)	14(16.3)			
	Total	38(21.1)	-	111(61.7)	31(17.2)			
L2D	Male	16(17.0)	1(1.1)	42(44.7)	35(37.2)	3	5.728	0.126
	Female	14(16.3)	7(8.1)	39(45.3)	26(30.2)			
	Total	30(16.7)	8(4.4)	81(45.0)	61(33.9)			
L3D	Male	14(14.9)	-	50(53.2)	30(31.9)	2	1.750	0.417
	Female	11(12.8)	-	54(62.8)	21(24.4)			
	Total	25(13.9)	-	104(57.8)	51(28.3)			
L4D	Male	2(2.1)	-	53(56.4)	39(41.5)	2	1.681	0.431
	Female	5(5.8)	-	48(55.8)	33(38.4)			
	Total	7(3.9)	-	101(56.1)	72(40.0)			
L5D	Male	3(3.2)	-	85(90.4)	6(6.4)	2	10.233	0.006
	Female	10(11.6)	-	62(72.1)	14(16.3)			
	Total	13(7.2)	-	147(81.7)	20(11.1)			

Note: Df=Degree of freedom; X²=Chi-square; A=Arch, RL=Radial Loop, UL=Radial Loop, W=Whorl

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Table 3: Mood's median test of the distributional difference in the right FRC

Finger	Sex	Summary statistics and distribution					Mood's Median Test		
		Median	N ≤Overall Median	N >Overall Median	Q3 – Q1	95% (median CI)	DF	Chi- Square	P- Value
R1D	Male	14.00	45	49	7.25	(11,16)	1	0.826	0.363
	Female	12.50	44	42	8.00	(10,14)			
	Overall	13.00							
R2D	Male	10.00	48	46	8.25	(8,13)	1	0.106	0.745
	Female	10.00	46	40	7.00	(9,12)			
	Overall	10.00							
R3D	Male	12.00	45	49	8.25	(11,14)	1	0.826	0.363
	Female	11.00	47	39	6.25	(10,13)			
	Overall	11.00							
R4D	Male	16.00	53	41	7.00	(15,18)	1	1.752	0.186
	Female	17.00	40	46	7.00	(15,18)			
	Overall	16.00							
R5D	Male	12.00	49	45	8.00	(11,15)	1	0.195	0.659
	Female	13.00	42	44	7.00	(11,14)			
	Overall	12.00							
TR	Male	65.50	46	48	29.00	(59,70)	1	0.372	0.542
	Female	63.00	46	40	25.50	(54,68)			
	Overall	64.00							

Note: R=Right, 1D=Thumb, 2D=Index, 3D=Middle, 4D=Ring, 5D=little, N=distribution, TR=Total right, CI=Confidence interval

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Table 4: Mood's median test of the distributional difference in the left FRC

Finger	Sex	Median	Summary statistics and distribution				Mood's Median Test		
			N ≤Overall Median	N>Overall Median	Q3 – Q1	95% (median CI)	DF	Chi- Square	P-Value
L1D	Male	13.50	42	52	10.00	(11,16)	1	3.256	0.071
	Female	11.50	50	36	9.25	(10,13)			
	Overall	12.00							
L2D	Male	9.00	49	45	11.50	(9,12)	1	0.017	0.897
	Female	10.00	44	42	5.50	(9,11)			
	Overall	10.00							
L3D	Male	12.00	56	38	8.00	(11,13)	1	0.125	0.724
	Female	12.00	49	37	6.00	(10,13)			
	Overall	12.00							
L4D	Male	15.00	48	46	6.00	(15,16)	1	0.020	0.887
	Female	15.50	43	43	9.25	(13,17)			
	Overall	15.00							
L5D	Male	13.00	46	48	7.00	(11,13)	1	1.528	0.216
	Female	12.00	50	36	5.00	(11,13)			
	Overall	12.00							
TL	Male	61.50	44	50	39.25	(52,68)	1	1.105	0.293
	Female	60.00	47	39	28.25	(52,65)			
	Overall	60.00							
TFRC	Male	128.50	46	48	69.00	(112,141)	1	0.372	0.542
	Female	119.50	46	40	51.75	(102,133)			
	Overall	122.00							

Note: L=Left, 1D=Thumb, 2D=Index, 3D=Middle, 4D=Ring, 5D=little, N=distribution, TL=Total left, TFRC=Total finger ridge count, CI=Confidence interval

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Table 5: Combination patterns and outcome for the right thumb fingers (R1D)

S/N	Parents		N	Offspring outcome (related) (R1D; Thumb)				Inference	N	Assumed offspring outcome (unrelated) (R1D; Thumb)				Inference
				A	RL	UL	W			A	RL	UL	W	
1	A	A	0	0	0	0	0		0	0	0	0		
2	A	RL	0	0	0	0	0		0	0	0	0		
3	A	UL	15	1*	0	13*	1†		2	0	0	0	2†	
4	A	W	2	2*	0	0	0	Total inherited combinations: 54/60= 90.00% possibility of inheritance	10	2*	2†	4†	2*	
5	RL	RL	0	0	0	0	0		0	0	0	0	0	Total inherited combinations: 34/60 = 56.67% possibility of unrelated
6	RL	UL	0	0	0	0	0		0	0	0	0	0	
7	RL	W	0	0	0	0	0		0	0	0	0	0	
8	UL	UL	17	1†	0	13*	3†		32	6†	0	22*	4†	
9	UL	W	14	1†	0	7*	6*		10	2†	0	8*	0	
10	W	W	12	0	0	0	12*		6	6†	0	0	0	
Total			60	5	0	33	22		60	16	2	24	8	

Note: *indicates that combination produced offspring with one- or all of the combinations

† Indicated that combination produced offspring without any of the combinations. A-arches, RL-radial loop, UL-ulnar loop, W-whorls

Table 6 : Combination patterns and outcome for the right index fingers (R2D)

S/N	Parents		N	offspring outcome (related) (R2D; Index finger)				Inference	N	Assumed offspring outcome (unrelated) (R2D; Index finger)				Inference
				A	RL	UL	W			A	RL	UL	W	
1	A	A	5	3*	0	2†	0		0	0	0	0		
2	A	RL	2	0	0	2†	0		0	0	0	0		
3	A	UL	6	1*	0	5*	0		2	0	0	0	2†	
4	A	W	4	0	0	4†	0	Total inherited combinations: 41 / 60= 68.33% possibility of inheritance	0	0	0	0	0	
5	RL	RL	1	0	0	1†	0		0	0	0	0	0	Total inherited combinations: 28/60 = 46.67% possibility of unrelated
6	RL	UL	4	0	2*	2*	0		2	2†	0	0	0	
7	RL	W	1	0	0	1†	0		0	0	0	0	0	
8	UL	UL	17	0	0	12*	5†		10	0	0	6*	4†	
9	UL	W	14	0	0	10*	4*		36	14†	4†	10*	8*	
10	W	W	6	1†	2†	0	3*		10	0	0	6†	4*	
Total			60	5	4	39	12		60	16	4	22	18	

Table 7: Combination patterns and for the middle fingers (R3D)

S/N	Parents		N	offspring outcome(related) (R3D; Middle finger)				Inference	N	Assumed offspring outcome (unrelated) (R3D; Middle finger)				Inference
				A	RL	UL	W			A	RL	UL	W	
1	A	A	0	0	0	0	0	0	0	0	0	0		
2	A	RL	0	0	0	0	0	0	0	0	0	0		
3	A	UL	5	2*	0	3*	0	0	0	0	0	0		
4	A	W	5	0	0	1†	4*	Total inherited combinations: 52 / 60= 86.67% possibility of inheritance	2	0	0	2†	0	Total inherited combinations: 36/60 = 60.00% possibility of unrelated
5	RL	RL	0	0	0	0	0	0	0	0	0	0		
6	RL	UL	0	0	0	0	0	4	0	0	2*	2†		
7	RL	W	1	0	0	1†	0	0	0	0	0	0		
8	UL	UL	25	0	1†	21*	3†	36	12†	0	16*	8†		
9	UL	W	22	0	0	22*	0	18	0	0	16*	2*		
10	W	W	2	0	0	2†	0	0	0	0	0	0		
Total			60	2	1	50	7	60	12	0	36	12		

Table 8: Combination patterns and outcome the right ring fingers (R4D)

S/N	Parents		N	offspring outcome (R4D; Ring finger)				Inference	N	Assumed offspring outcome (unrelated) (R4D; Ring finger)				Inference
				A	RL	UL	W			A	RL	UL	W	
1	A	A	0	0	0	0	0	0	0	0	0	0		
2	A	RL	0	0	0	0	0	0	0	0	0	0		
3	A	UL	1	0	0	0	1†	0	0	0	0	0		
4	A	W	2	0	0	2†	0	Total inherited combinations: 49 / 60= 81.67% possibility of inheritance	2	0	0	0	2*	Total inherited combinations: 36/60 = 60.00% possibility of unrelated
5	RL	RL	0	0	0	0	0	0	0	0	0	0		
6	RL	UL	0	0	0	0	0	0	0	0	0	0		
7	RL	W	0	0	0	0	0	0	0	0	0	0		
8	UL	UL	15	0	1†	11*	3†	30	0	0	16*	14†		
9	UL	W	35	1†	0	18*	16*	28	10†	0	16*	2*		
10	W	W	7	0	0	4†	3*	0	0	0	0	0		
Total			60	1	1	35	23	60	10	0	32	18		

Table 9: Combination patterns and outcome for the right little finger (R5D)

S/N	Parents	N	offspring outcome(related) (R5D; Little finger)				Inference	N	Assumed offspring outcome(unrelated) (R5D; Little finger)				Inference
			A	RL	UL	W			A	RL	UL	W	
1	A A	0	0	0	0	0	0	0	0	0	0		
2	A RL	0	0	0	0	0	0	0	0	0	0		
3	A UL	4	0	0	4*	0	2	0	0	2*	0		
4	A W	2	0	0	2†	0	0	0	0	0	0	Total inherited combinations: 54/60= 90.00% possibility of inheritance	
5	RL RL	0	0	0	0	0	0	0	0	0	0		
6	RL UL	0	0	0	0	0	0	0	0	0	0		
7	RL W	0	0	0	0	0	0	0	0	0	0		
8	UL UL	44	2†	0	40*	2†	54	10†	0	42*	2†		Total inherited combinations: 48/60 =80.00 % possibility of unrelated
9	UL W	10	0	0	7*	3*	4	0	0	2*	2*		
10	W W	0	0	0	0	0	0	0	0	0	0		
Total		60	2	0	53	5	60	10	0	46	4		

Table 10: Combination patterns and outcome for the left thumb fingers (L1D)

S/N	Parents	N	offspring outcome(related) (L1D; Thumb)				Inference	N	Assumed offspring outcome (unrelated) (L1D; Thumb)				Inference
			A	RL	UL	W			A	RL	UL	W	
1	A A	1	0	0	1†	0	0	0	0	0	0		
2	A RL	0	0	0	0	0	0	0	0	0	0		
3	A UL	22	10*	0	10*	2†	10	0	0	8*	2†		
4	A W	0	0	0	0	0	12	2*	0	8†	2*	Total inherited combinations: 48/60 = 80.00% possibility of inheritance	
5	RL RL	0	0	0	0	0	0	0	0	0	0		
6	RL UL	0	0	0	0	0	0	0	0	0	0		
7	RL W	0	0	0	0	0	0	0	0	0	0		
8	UL UL	21	1†	0	19*	1†	18	14†	0	4*	0		Total inherited combinations: 32/60 = 53.33% possibility of unrelated
9	UL W	8	1†	0	5*	2*	18	2†	0	16*	0		
10	W W	8	2†	0	4†	2*	2	2†	0	0	0		
Total		60	14	0	39	7	60	20	0	36	4		

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Table 11: Combination patterns and outcome for the left index fingers (L2D)

S/N	Parents	N	offspring outcome(related) (L2D; Index finger)				Inference	N	Assumed offspring outcome(unrelated) (L2D; Index finger)				Inference
			A	RL	UL	W			A	RL	UL	W	
1	A A	2	2*	0	0	0	Total inherited combinations: 40/60 = 66.67% possibility of inheritance	0	0	0	0	Total inherited combinations: 38/60 = 63.33% possibility of unrelated	
2	A RL	2	1*	0	0	1†		2	2†	0	0		0
3	A UL	12	1*	0	8*	3†		6	2*	0	0		4†
4	A W	6	0	0	3†	3*		16	0	0	14†		2*
5	RL RL	1	0	0	1†	0		0	0	0	0		0
6	RL UL	0	0	0	0	0		6	0	2*	2*		2†
7	RL W	2	0	0	0	2*		0	0	0	0		0
8	UL UL	14	0	1†	8*	5†		10	0	0	10*		0
9	UL W	15	2†	0	3*	10*		20	0	0	12*		8*
10	W W	6	0	0	4†	2*		0	0	0	0		0
Total		60	6	1	27	26	60	4	2	38	16		

Table 12: Combination patterns and outcome for the left middle fingers (L3D)

S/N	Parents	N	offspring outcome(related) (L3D; Middle finger)				Inference	N	Assumed offspring outcome(unrelated) (L3D; Middle finger)				Inference
			A	RL	UL	W			A	RL	UL	W	
1	A A	2	0	0	2†	0	Total inherited combinations: 51/60 = 85.00% possibility of inheritance	0	0	0	0	Total inherited combinations: 40/60 = 66.67% possibility of unrelated	
2	A RL	0	0	0	0	0		0	0	0	0		
3	A UL	13	1*	0	12*	0		0	0	0	0		
4	A W	6	0	0	2†	4*		2	0	0	2†		0
5	RL RL	0	0	0	0	0		0	0	0	0		0
6	RL UL	0	0	0	0	0		0	0	0	0		0
7	RL W	0	0	0	0	0		0	0	0	0		0
8	UL UL	16	1†	0	13*	2†		42	12†	0	26*		4†
9	UL W	17	0	0	11*	6*		16	2†	0	10*		4*
10	W W	6	0	0	2†	4*		0	0	0	0		0
Total		60	2	0	42	16	60	14	0	38	8		

Inheritance of fingerprints among Nigerians

Table 13: Combination patterns and outcome for the left ring fingers (L4D)

S/N	Parents		N	offspring outcome (L4D; Ring finger)				Inference	N	Assumed offspring outcome(unrelated) (L4D; Ring finger)				Inference	
				A	RL	UL	W			A	RL	UL	W		
1	A	A	0	0	0	0	0	0	0	0	0	0			
2	A	RL	0	0	0	0	0	0	0	0	0	0			
3	A	UL	0	0	0	0	0	0	0	0	0	0			
4	A	W	6	0	0	0	6*	Total inherited combinations: 54/60 = 90.00% possibility of inheritance	2	0	0	0	2*	Total inherited combinations: 46/60 = 76.67% possibility of unrelated	
5	RL	RL	0	0	0	0	0		0	0	0	0			
6	RL	UL	0	0	0	0	0		0	0	0	0			
7	RL	W	0	0	0	0	0		0	0	0	0			
8	UL	UL	21	0	0	20*	1†		18	0	0	16*	2†		
9	UL	W	25	0	0	12*	13*		40	12†	0	24*	4		
10	W	W	8	1†	0	2†	5*		0	0	0	0	0		
Total			60	1	0	34	25		60	12	0	40	8		

Table 14: Combination patterns and outcome for the left little finger (L5D)

S/N	Parents		N	offspring outcome (L5D; Little finger)				Inference	N	Assumed offspring outcome(unrelated) (L5D; Little finger)				Inference	
				A	RL	UL	W			A	RL	UL	W		
1	A	A	0	0	0	0	0	0	0	0	0	0			
2	A	RL	0	0	0	0	0	0	0	0	0	0			
3	A	UL	8	2*	0	6*	0	Total inherited combinations: 52/60 = 86.67% possibility of inheritance	2	0	0	2*	0	Total inherited combinations: 44/60 = 73.33% possibility of unrelated	
4	A	W	0	0	0	0	0		0	0	0	0			
5	RL	RL	0	0	0	0	0		0	0	0	0			
6	RL	UL	0	0	0	0	0		0	0	0	0			
7	RL	W	0	0	0	0	0		0	0	0	0			
8	UL	UL	37	0	0	34*	3†		46	0	0	40*	6†		
9	UL	W	13	3†	0	10*	0		12	10†	0	2*	0		
10	W	W	2	0	0	2†	0		0	0	0	0	0		
Total			60	5	0	52	3		60	10	0	44	6		

Table 15: Estimated heritability of finger patterns

Outcomes	Offspring matched (Right)		$H_0 = \frac{C_1 - C_0}{1 - C_0}$	Offspring matched (Left)		$H_0 = \frac{C_1 - C_0}{1 - C_0}$
	Family (C ₁)	Unrelated (C ₀)		Family (C ₁)	Unrelated (C ₀)	
1D	54(0.90)	34(0.57)	0.77	48(0.80)	32(0.53)	0.57
2D	41(0.68)	28(0.47)	0.40	40(0.67)	38(0.63)	0.11
3D	52(0.87)	36(0.60)	0.68	51(0.85)	40(0.67)	0.55
4D	49(0.81)	36(0.60)	0.53	54(0.90)	46(0.77)	0.57
5D	54(0.90)	48(0.80)	0.50	52(0.87)	44(0.73)	0.52
Total H ₀			0.57			0.46

Note: 1D=Thumb, 2D=Index, 3D=Middle, 4D=Ring, 5D=little, O=Offspring, F=father, M=Mother, D=Digit.

Table 16: Distribution of finger ridge counts of fathers', mothers' and offspring'

Variables	Right digits				Left digits			
	Father	Mother	Offspring	p-value	Father	Mother	Offspring	p-value
AFRC	59.95±23.57	55.25±22.09	63.97±20.00	0.096	55.65±24.24	53.68±25.02	60.30±21.92	0.296
THUMB	12.75±6.68	10.42±7.07	12.05±5.97	0.141	12.00±6.56	9.75±7.37	11.25±6.61	0.454
INDEX	9.58±6.32	9.13±5.48	10.67±5.41	0.326	8.50±6.64	9.12±5.60	10.87±5.86	0.560
MIDDLE	11.33±6.23	9.98±4.92	11.80±4.46	0.148	9.70±6.63	10.38±6.45	11.63±4.42	0.196
RING	14.55±6.22	14.40±6.19	16.07±5.57	0.245	14.03±5.89	13.92±6.94	15.02±5.48	0.087
LITTLE	11.73±5.51	11.32±5.44	13.38±4.76	0.077	11.42±4.80	10.52±5.39	11.53±4.28	0.190
TFRC	115.60±47.00	108.93±46.16	124.27±41.13	0.174				

Table 17: Selected family fingerprint sequence illustrating penetrance

Family	Right digits (LRMIT)	Left digits (TIMRL)
12	WUJWU	UUWU(F), AUJW(M), URUWA(O)
25	WUJUU(F), UUUUU(M),WUJWU(O)	UUUUU
26	UAUUU	UUUUU(F), UUAUU(M), AUUU(O)
50	UWJWU	UUWU(F), AUJW(M), URUWA(O)

A-arches, R-radial loop, U-ulnar loop, W-Whorls, F-father, M-mother, O-offspring

Inheritance of fingerprints among Nigerians

Figure 1. Inheritance patterns (conformance; black) and (outliners; red broken lines) for both thumb fingers among family group.

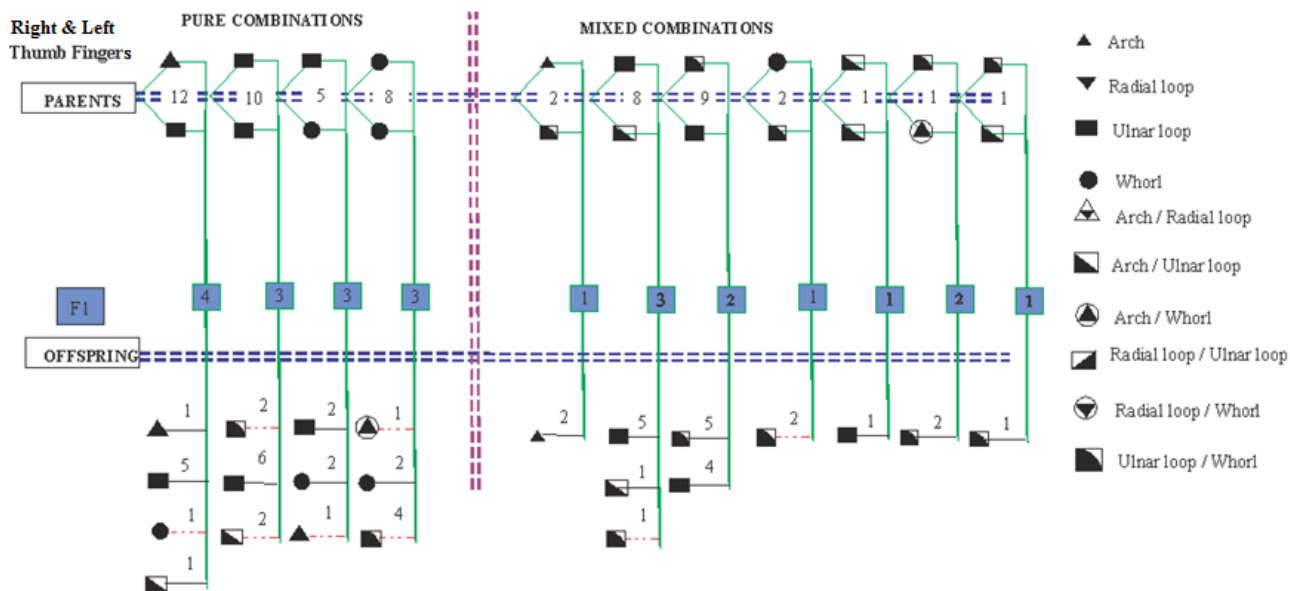
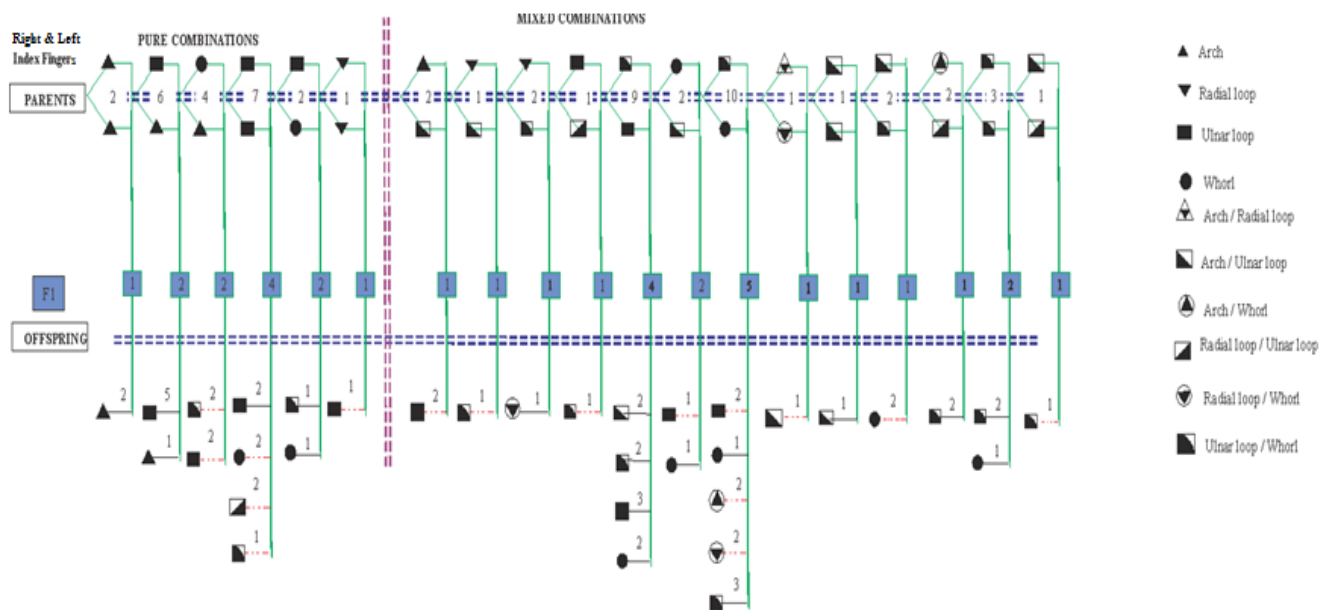


Figure 2. Inheritance of the combination patterns in parents and outcome in offspring for both index fingers



Inheritance of fingerprints among Nigerians

Figure 3. Inheritance of the combination patterns in parents' and outcome in offspring' for both middle fingers among family group

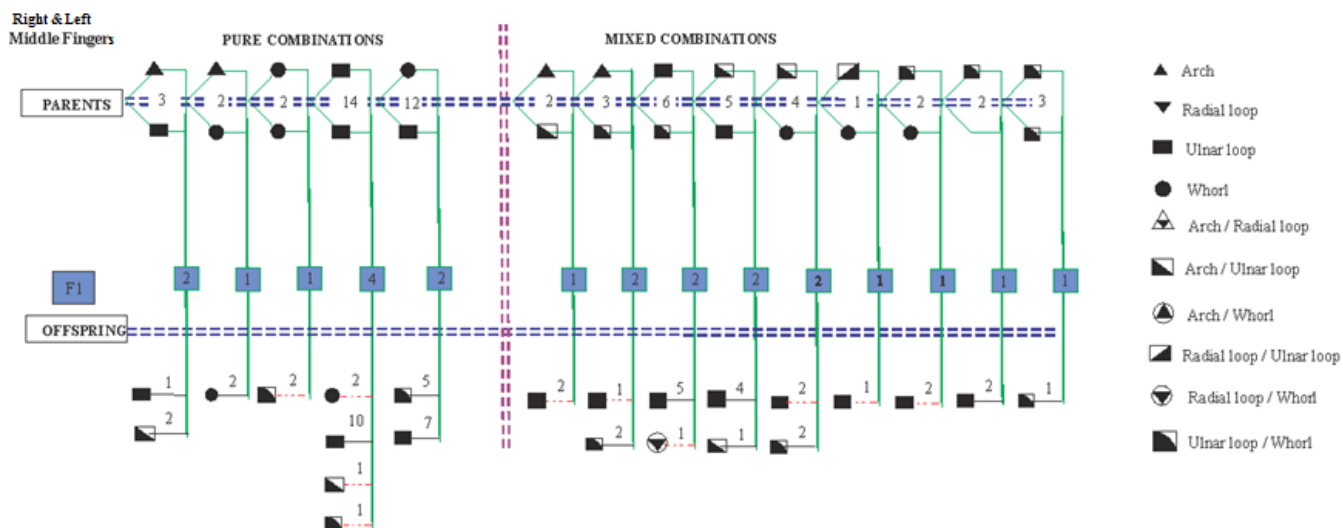
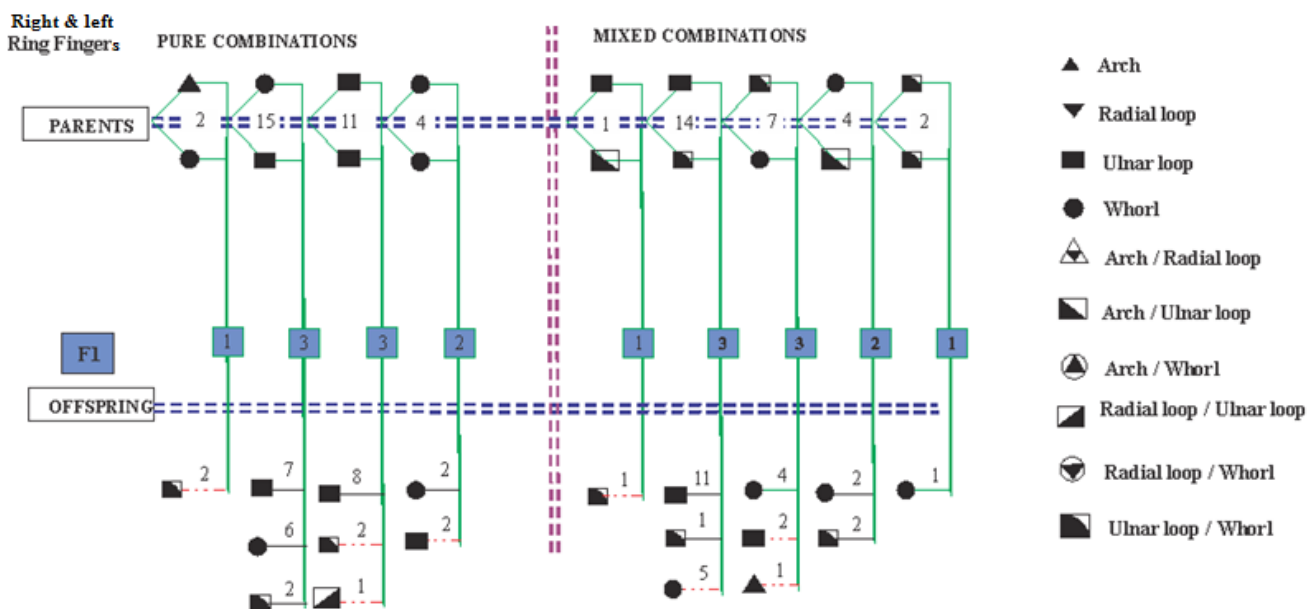


Figure 4. Inheritance patterns (conformance; black) and (outliners; red broken lines) for both ring fingers among family group



Inheritance of fingerprints among Nigerians

Fig 5. Inheritance patterns (conformance; black) and (outliners; red broken lines) for both ring fingers among family group

