

FINGERPRINTS OF THE THUMB AND INDEX FINGER: THEIR PATTERN OF INHERITANCE AMONG THE URHOB0 ETHNIC GROUP IN DELTA STATE, NIGERIA

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ABSTRACT

Background: The heart of human science lies in the study of genetics, and for this reason, diseases, therapy, personality, security are all studied at the level of the genetic composition of humans. This study aimed at investigating if fingerprints are hereditary among families from the Urhobo ethnic group in Delta State. **Methods:** A total of 15 families and 45 unrelated individuals were recruited for this study. Fingerprints of the thumb and index finger were taken with an Hp G4010 fingerprint scanner. Chisquare was used to establish sex - associated differences, mood median test ascertained laterality of ridges while Heritability coefficient was used to calculate the certainty of inheritance among families. **Results:** We observed offspring having 80%; 66.7%;73.3%;60% and 73.3%;53.3%;73%;46.6% conformance for the related and unrelated group for R1D , R2D, L1D, L2D . The total H_0 for R1D and 2D was calculated as 0.278 (28%) while that for L1D and 2D was 0.123 (12%). Fingerprint patterns were not sexually influenced in the studied population ($p>0.05$). Parental combination of Ulnar loops (ULXUL) for the thumb and index fingers produced whorls in their offspring suggesting a possibility of epistasis. **Conclusion:** This study had established that fingerprints patterns on the thumb and index finger can be transmitted from parents to their F1 generation.

KEYWORDS: Fingerprints; Inheritance, Heritability Coefficient, Urhobo.

INTRODUCTION

Geneticists have recognized that offspring undoubtedly inherits traits which are genetic information shared from parents,^[1-3] with some degree of variations caused by exogenous intrusion and environmental influences.^[2-4] There are lots of theories on the patterns of inheritance, nevertheless, four have been comprehensively considered. They include; dominant-recessive, sex-linked, multifactorial and mitochondria inheritance.^[2,5-14] Some researchers reported phenotypic similarity and marker-gene segregation as the basic methods of establishing the heritability of traits.^[2] The former which is mainly used in developing countries involves a comparison of recognizable physical features of traits among families in dissimilar generations while the later approach encompasses marker genes being linked to the character under study in order to ascertain their connection to genes that influences the studied character.^[2]

Fingerprints have been described as the arrangement of epidermal ridges existing on the fingers and their uniqueness have been attributed to the minutiae which are reported as the most minute feature in dermatoglyphics.^[15-16] The issue is, something so minute

and presumed unique —are they also inherited trait? However, some scholars had documented that despite their uniqueness, stability and, pervasiveness, they can be considered as a multifactorial trait. According to Yang *et al.*,^[17] fingerprint is a compound pleiotropic trait which arises from the interaction of genes and influences from the environment. In a bid to correctly tackle challenges in a developing country like Nigeria were cases of parental determination have not been easy due to financial constraint, little attention and inadequate data on inheritance pattern among families, the study investigated heritability of fingerprints among the Urhobo ethnic group with consideration to the thumb and index finger.

MATERIALS AND METHODS

The study was cross sectional, observational and, comparative which involved 15 families that were related and 45 unrelated individuals. The related families comprised of a father, mother and, at least a child while the unrelated comprised of 15 men and women each respectively alongside 15 mixed males and females. In order not to assume inheritance because nothing of such is known about the studied population, we decided to have a comparative group. Slati *et al.* utilized this

approach in evaluating the inheritance of the fingerprint patterns among related and non-related Israelis families.^[18] All participants were Delta State descent and resided within the State. Preceding to the study, ethical clearance, was obtained from the University Ethics Committee, University of PortHarcourt, Rivers State, Nigeria. Fingerprints were taken with a Hp G4010 scanner.^[19] and participants were coded with serial number in a bid to maintain confidentiality. The thumb and index finger were represented as 1D and 2D for all participants. Ridges were obtained with the aid of an AUTOCAD version 2010. Descriptive statistics were

used to illustrate the frequency and distribution of patterns. Chisquare test ascertained sex associated differences of fingerprints, Mood median test was used to determine laterality of friction ridges in the studied population. Qualitative determination of heritability was family-based and therefore included parents (father & mother) and offspring without considering sex. The heritability coefficient (H_0) was calculated from the formula: $H_0 = C_0 - C_1 / 1 - C_0$, where H_0 was considered the coefficient estimate of heritability, C_0 as concordance among unrelated individuals and C_1 as estimated concordance among related individuals.^[20]

RESULT

Table 1: Qualitative fingerprint pattern and sex-associated differences.

Digit	Sex	Fingerprint pattern				Chi-Square Tests		
		A (%)	RL (%)	UL (%)	W (%)	df	X ²	P-value
R1D	Male	1(4.0)	-	16(64.0)	8(32.0)	2	3.113	0.211
	Female	1(5.0)	-	17(85.0)	2(10.0)			
	Total	2(4.4)	-	33(73.3)	10(22.2)			
R2D	Male	2(8.0)	2(8.0)	9(36.0)	12(48.0)	3	2.003	0.572
	Female	1(5.0)	2(10.0)	11(55.0)	6(30.0)			
	Total	3(6.7)	4(8.9)	20(44.4)	18(40.0)			
L1D	Male	1(12.0)	-	17(68.0)	5(20.0)	2	0.273	0.872
	Female	2(10.0)	-	15(75.0)	3(15.0)			
	Total	5(11.1)	-	32(71.1)	8(17.8)			
L2D	Male	3(12.0)	1(4.0)	10(40.0)	11(44.0)	3	0.31	0.818
	Female	2(10.0)	2(10.0)	9(45.0)	7(35.0)			
	Total	5(11.1)	3(6.7)	19(42.2)	18(40.0)			

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

Table 2: Quantitative fingerprint pattern and sex-associated differences.

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	12.00	13	12	8.50	(9,16)	1	0.018	0.894
	Female	13.50	10	10	7.50	(11,17)			
	Overall	13.00							
R2D	Male	10.00	13	12	9.00	(8,14)	1	0.040	0.841
	Female	11.00	11	9	7.25	(7,12)			
	Overall	11.00							
L1D	Male	14.00	12	13	10.00	(9,17)	1	0.218	0.641
	Female	12.50	11	9	8.25	(10,16)			
	Overall	13.00							
L2D	Male	12.00	17	8	12.00	(7,14)	1	0.799	0.371
	Female	12.00	11	9	10.00	(3,13)			
	Overall	12.00							

Note: R=Right, L= Left, 1D=Thumb, 2D=Index, N=distribution, CI=Confidence interval.

Qualitative estimation of heritability using finger ridge patterns- Inheritance prediction

Right fingerprint pattern: family & unrelated individuals

Table 3a: Inheritance of the combination patterns in parents for the thumb fingers (R1D) of the family group.

S/N	Parents		N	offspring outcomeL2 (R1D; Thumb)				Inference
				A	RL	UL	W	
1	A	A	0	0	0	0	0	Total inherited combinations: 12/15 = 80.0% possibility of inheritance
2	A	RL	0	0	0	0	0	
3	A	UL	1	0	0	1*	0	
4	A	W	0	0	0	0	0	
5	RL	RL	0	0	0	0	0	
6	RL	UL	0	0	0	0	0	
7	RL	W	0	0	0	0	0	
8	UL	UL	9	1†	0	6*	2†	
9	UL	W	4	0	0	3*	1*	
10	W	W	1	0	0	0	1*	
Total			15	1	0	10	4	

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

† Indicated that combination produced offspring without any of the combinations

Table 3b: Inheritance of the combination patterns in parents for the thumb fingers (R1D) of unrelated individuals.

S/N	Assumed parents		N	Assumed offspring outcome (R1D; Thumb)				Inference
				A	RL	UL	W	
1	A	A	0	0	0	0	0	Total inherited combinations: 11/15 = 73.33% possibility of unrelated
2	A	RL	0	0	0	0	0	
3	A	UL	2	0	0	1*	1†	
4	A	W	1	0	0	0	1*	
5	RL	RL	0	0	0	0	0	
6	RL	UL	0	0	0	0	0	
7	RL	W	0	0	0	0	0	
8	UL	UL	8	0	0	5*	3†	
9	UL	W	4	0	0	2*	2*	
10	W	W	0	0	0	0	0	
Total			15	0	0	8	7	

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

† Indicated that combination produced offspring without any of the combinations

Table 4a: Inheritance of the combination patterns in parents for the index fingers (R2D) of the family group.

S/N	Parents		N	offspring outcome (R2D; Index finger)				Inference
				A	RL	UL	W	
1	A	A	0	0	0	0	0	Total inherited combinations: 10/15 = 66.7% possibility of inheritance
2	A	RL	0	0	0	0	0	
3	A	UL	1	0	0	1*	0	
4	A	W	1	0	0	1†	0	
5	RL	RL	1	0	0	1†	0	
6	RL	UL	2	0	0	2*	0	
7	RL	W	0	0	0	0	0	
8	UL	UL	2	0	0	0	2†	
9	UL	W	6	0	0	2*	4*	
10	W	W	2	1†	0	0	1*	
Total			15	1	0	7	7	

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

† Indicated that combination produced offspring without any of the combinations

Table 4b: Inheritance of the combination patterns in parents for the index fingers(R2D) of unrelated individuals.

S/N	Assumed parents		N	Assumed offspring outcome				Inference
				(R2D; Index finger)				
				A	RL	UL	W	
1	A	A	0	0	0	0	0	Total inherited combinations: 8/15 = 53.33% possibility of unrelated
2	A	RL	2	0	1*	0	1†	
3	A	UL	1	0	0	1*	0	
4	A	W	1	0	1†	0	0	
5	RL	RL	0	0	0	0	0	
6	RL	UL	1	0	0	1*	0	
7	RL	W	2	1†	0	1†	0	
8	UL	UL	2	0	0	1*	1†	
9	UL	W	5	1†	0	3*	1*	
10	W	W	1	0	0	1†	0	
Total			15	2	2	8	3	

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

† Indicated that combination produced offspring without any of the combinations

Left fingerprint pattern: family & unrelated individuals

Table 5a: Inheritance of the combination patterns in parents for the thumb fingers (L1D) of the family group.

S/N	Parents		N	offspring outcome				Inference
				(L1D; Thumb)				
				A	RL	UL	W	
1	A	A	1	0	0	1†	0	Total inherited combinations: 11/15 = 73.33% possibility of inheritance
2	A	RL	0	0	0	0	0	
3	A	UL	2	0	0	1*	1†	
4	A	W	0	0	0	0	0	
5	RL	RL	0	0	0	0	0	
6	RL	UL	0	0	0	0	0	
7	RL	W	0	0	0	0	0	
8	UL	UL	8	0	0	7*	1†	
9	UL	W	3	0	0	2*	1*	
10	W	W	1	1†	0	0	0	
Total			15	1	0	11	3	

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

† Indicated that combination produced offspring without any of the combinations

Table 5b: Inheritance of the combination patterns in parents for the thumb fingers (L1D) of unrelated individuals.

S/N	Assumed parents		N	Assumed offspring outcome				Inference
				(L1D; Thumb)				
				A	RL	UL	W	
1	A	A	0	0	0	0	0	Total inherited combinations: 11/15 = 73.33% possibility of unrelated
2	A	RL	0	0	0	0	0	
3	A	UL	4	0	0	2*	2†	
4	A	W	0	0	0	0	0	
5	RL	RL	0	0	0	0	0	
6	RL	UL	0	0	0	0	0	
7	RL	W	0	0	0	0	0	
8	UL	UL	5	1†	0	3*	1†	
9	UL	W	6	0	0	5*	1*	
10	W	W	0	0	0	0	0	
Total			15	1	0	10	4	

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

† Indicated that combination produced offspring without any of the combinations

Table 6a: Inheritance of the combination patterns in parents for the index fingers (L2D) of the family group.

S/N	Parents		N	offspring outcome (L2D; Index finger)				Inference
				A	RL	UL	W	
				1	A	A	0	
2	A	RL	1	0	0	0	1†	
3	A	UL	1	0	0	1*	0	
4	A	W	3	0	0	1†	2*	
5	RL	RL	1	0	0	1†	0	
6	RL	UL	0	0	0	0	0	
7	RL	W	0	0	0	0	0	
8	UL	UL	4	0	0	2*	2†	
9	UL	W	4	0	0	0	4*	
10	W	W	1	0	0	1†	0	
Total			15	0	0	6	9	

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

† Indicated that combination produced offspring without any of the combinations

Table 6b: Inheritance of the combination patterns in parents for the index fingers (L2D) of unrelated individuals.

S/N	Assumed parents		N	Assumed offspring outcome (L2D; Index finger)				Inference
				A	RL	UL	W	
				1	A	A	0	
2	A	RL	0	0	0	0		
3	A	UL	2	0	0	0	2†	
4	A	W	2	1*	1†	0	0	
5	RL	RL	0	0	0	0	0	
6	RL	UL	0	0	0	0	0	
7	RL	W	1	1†	0	0	0	
8	UL	UL	3	0	1†	1*	1†	
9	UL	W	6	0	1†	4*	1*	
10	W	W	1	0	0	1†	0	
Total			15	2	3	6	4	

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

† Indicated that combination produced offspring without any of the combinations

Heritability Estimation

Using the formula; $H_0 = \frac{c_1 - \hat{c}_0}{1 - c_0}$, the heritability estimate for the individual fingers were obtained as presented in Table;

below;

Table 7: Estimated heritability [non-regression] for individual finger pattern.

Outcomes	Assessed	Offspring matched (Right)		$H_0 = \frac{c_1 - \hat{c}_0}{1 - c_0}$	Offspring matched (Left)		$H_0 = \frac{c_1 - \hat{c}_0}{1 - c_0}$
		Family (C_1)	Unrelated (C_0)		Family (C_1)	Unrelated (C_0)	
1D	15	12(0.80)	11(0.73)	0.259	11(0.73)	11(0.73)	0.000
2D	15	10(0.67)	8(0.53)	0.298	9(0.60)	7(0.47)	0.245
Total H_0				0.279			0.123

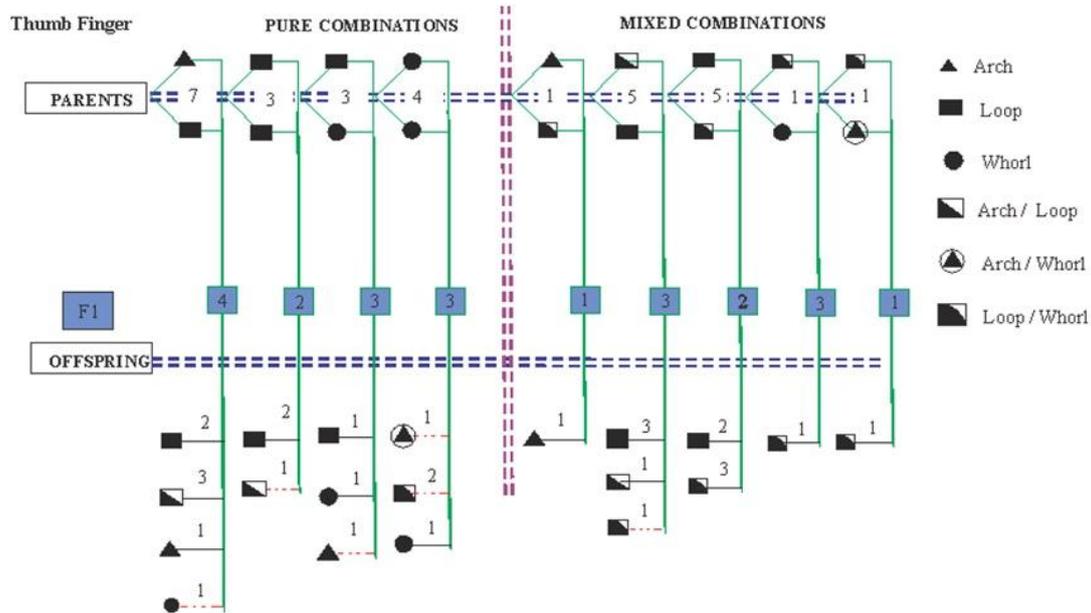


Fig. 1: Offspring inheritance patterns (conformance; black) and (outliners; red broken lines) for both thumb fingers.

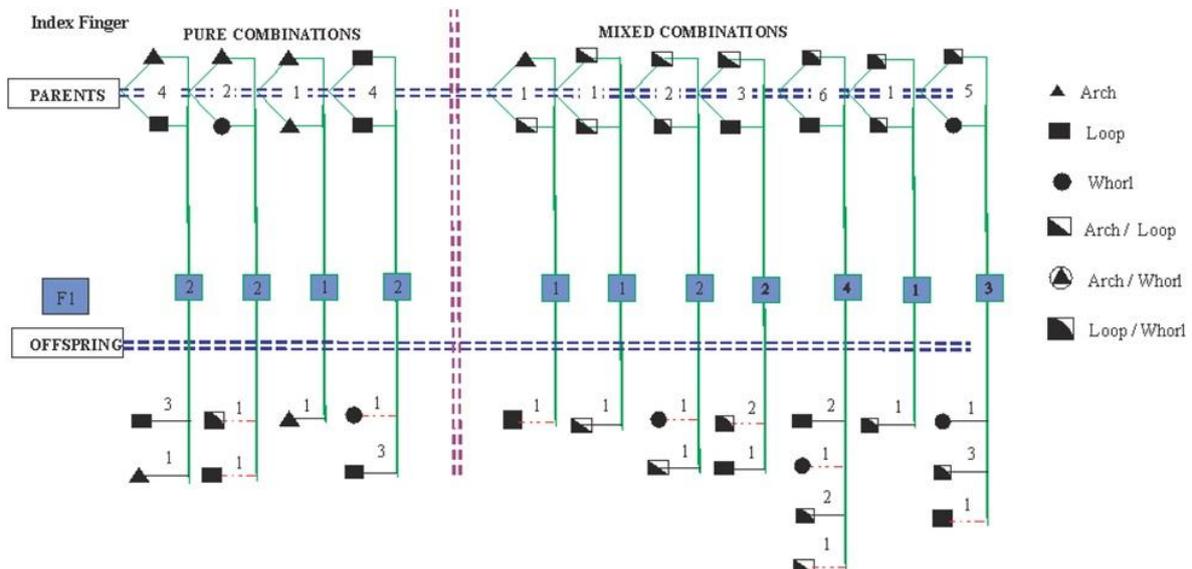


Fig. 2: Offspring inheritance patterns (conformance; black) and (outliners; red broken lines) for the Index fingers (right and left).

Table 1 showed that 4% males and 5% females had arch patterns on R1D. Ulnar loop and whorls were represented in 64%; 32% males as compared to 85%; 10% females. Further findings showed that 8% males each respectively and 5%; 10% females had the arches and radial loop on R2D. Ulnar loop and whorls were presented in 36%; 48% males and 55%; 30% females.

We also reported arches, ulnar loop and whorls in 12%, 68% and 20% males as compared to 10%, 75% and 15% in females (table 1). The left index finger (L2D) had arches and radial loop in 12%; 4% males and 10% females each respectively. Ulnar loop and whorls were noticed in 40%; 44% males as compared to 45%; 35% females. The thumb and index finger were not sexually influenced.

Table 2 showed the laterality of finger ridges using the mood median test. Findings showed that FRC were not sexually influenced at $p < 0.05$.

Table 3a&b illustrate the parental permutation on the right thumb (R1D) for both related and unrelated group. We observed offspring having 80% conformance (12 probable outcome of the 15 offspring print) and 73.3% conformance for the unrelated group for R1D. A conformance of 66.7% for the related group as against 53.3% for the unrelated group was observed for R2D (Table 4a&b). The parental combination on the left thumb and index finger (L1D; L2D) presented 73.3%; 60% conformance and 73%; 46.6% for the group that was not related (Table 5a&b ; 6a&b). The total H_0 for the

R1D and 2D was calculated as 0.278 (28%) while that for L1D and 2D was 0.123 (12%) (Table 7).

From the cross match, findings showed that ulnar loop and whorls were consistently presented in both the related and unrelated group for R1D, R2D, L1D, L2D (Table 3a-6b). Fig 1& 2 illustrate the pedigree for both thumb and index fingers. It shows parental combination of traits (upper boxes), number of traits that were expressed (middle blue boxes) and phenotypic expression among offspring (last boxes).

DISCUSSION

We observed that when traits of parents were combined, the trend of the offspring outcome was $UL > W > A > RL$. Ulnar loop was the predominant pattern observed in both the thumb and index fingers. This means that both parents may be homozygous dominant (DD) or heterozygous dominant for the trait (Dd). Findings conform to Slatis *et al.* and Ranjan *et al.*^[18,21] Slatis *et al.* in their study among the Israelis' discovered the ulnar loop as a trait that occurred on the thumbs of the F1 generation when seen on both parents.^[18] This study also discovered that radial loop was consistently absent in the family group but was seldom in the unrelated individual group. There is a probability that this trait is rarely inherited from parents, indicating that either parent could be heterozygous dominant (Dd) and the other homozygous recessive (dd) producing children with a 50% chance of having radial loop with the dominant gene being heterozygous. Nevertheless, this is an assumption explaining the occurrence of a recessive trait that is predominant Slatis *et al.*^[18] stated that individual genes may be responsible for the expression of fingerprints of only one or more fingers, and the genes may be dominant or semidominant.

This study also realized that for both the thumb and index finger (R1D; L1D; R2D; L2D) the females had more loops while the males had more whorls. Findings were consistent with Aadhyanth and Sudakshina who investigated dermatoglyphic patterns for the thumb and index finger among medical and paramedical students.^[22] They observed a higher frequency of loops among the females as compared to the whorls in males for both the thumb and index finger.^[22] Their study also conform with our study which revealed the thumb and index fingers having the utmost percentage of ulnar loop and whorls. However, findings were different from Ujaddughe *et al.* who investigated gender variation in fingerprint patterns among those from Esan origin. Findings from his study revealed that females had more arches while males had more loops.^[23]

Qualitatively we observed that fingerprints were hereditary, the percentage inheritance of these patterns represented parental combination and it was 60% and above for both thumb and index fingers. This is an indication that the thumb and index finger can be used in predicting heritability as earlier stated by Slatis *et al.* and

Muller-Ford.^[18,24] Muller-Ford in his study,^[24] reported that certain patterns on different fingers presented with heritability estimates ranging from 60% to 75%, which conforms with our study. However, further studies with a larger family size are recommended in order to actually established this fact we discovered from this study. The heritability coefficient was seen as 0.28 for the right digits and 0.12 for the left digits from this study. This was lower than that of Machado *et al.* who observed heritability estimate as 0.65 to 0.96 in monozygotic twins study.^[25] The differences could be as a result of sample size and ethnic variation which is one of the basic features of dermatoglyphics.

Parental combination of both parents having ulnar loop for both thumb and index finger produced whorls. There could be a possibility that the genotypes producing Ulnar loop may be epistatic to the whorl phenotype with an additive genetic effect. We observed a similar trend in radial loop on the right and left index fingers of parents. The outcome was ulnar loop. Apart from additive genetic effect that may be responsible, it has been documented that mutation of loop pattern could produce unlike phenotypic effects which depends on the second allele that is present.^[26]

CONCLUSION

This study had shown that there is a possibility of parents transmitting fingerprint patterns to their F1 generation. Hence study will provide a baseline for other genetic studies on this same or different ethnic group

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