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RESEARCH ARTICLE
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Linkage Group and Segregation Analyses of Fingerprint and Foot Patterns in the Yoruba, Igbo and Ibibio Populations of Nigeria

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ABSTRACT

The study of the highly heritable human fingerprint patterns has been applied in personal identification, crime detection, disease diagnosis and analysis of population characteristics. Results of several studies on the mode of inheritance and the number of loci involved in fingerprint determination have been discordant. In this study, fingerprint patterns and foot patterns were obtained from a total of 127 individuals from the Yoruba, Igbo and Ibibio ethnic populations of Nigeria. Frequency of occurrence, patterns of segregation and linkage analysis on fingerprint patterns and foot types were analyzed within the ethnic groups and combined groups. The study showed the ulna loop to be the most prevalent print pattern type while accidental whorl was least observed among the ethnic groups evaluated. The traits were linked in 4 groups in the Yoruba ethnic group, 4 linkage groups in the Igbo ethnic group and 3 linkage groups in Ibibio. The linkage map for fingerprints pattern and foot types revealed 4 linkage groups when data from all ethnic groups were pooled together, the largest spanning 323.9 cM. Segregation of most of the print pattern evaluation showed segregation of the traits mainly in a 1:1 and 1:3 expected ratios at 5% level of significance. This information provides an insight into the genetics of fingerprint patterns and foot types in these ethnic groups, a precursor to understanding the forensics and genetic structure of the Nigerian populations based on the studied traits.

Keywords: Forensic, Dermatoglyphics, Ridge count, Accidental whorl, Arch, Inheritance pattern

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INTRODUCTION

Dermatoglyphics deals with the study of the forms of epidermal ridge on the skin of the palms, soles, toes and fingers. Epidermal ridge pattern and distribution are not only unique from one finger to another, but also from person to person (Sudha et al., 2021; Sharma et al., 2018; Lakshmana et al., 2017). As a result, no two individuals have the same fingerprint pattern, including identical twins (Tao et al., 2012; Jain et al., 2002). Dermatoglyphics is a well-researched field in human identification and population studies because of its underlying biological and genetic features (Deshpande et al., 2024; Rastogi et al., 2023; Venurkar et al., 2022; Kapoor and Badiye 2015; Gutierez et al., 2012). Fingerprint patterns/ridges are formed between 12th – 19th week of gestation and are permanent throughout life except there is an environmental assault (Vashisht et al., 2021; Kahn et al., 2008; Godfrey et al., 1993).

The evidence that fingerprint patterns tend to run in families is very strong and well established. The mode of inheritance and population genetics of fingerprint patterns have been continuously examined from as far back as 1892. However, the inheritance pattern of the fingerprint characteristics has been undefined or at best contradictory. Slatis et al. (1976) proposed seven different genes for inherited patterns. A multi-allelic major gene mode of inheritance of fingerprints patterns and the distribution of

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interdigital patterns have also been defined (Meenakshi et al., 2006; Bhasin 2007; Cheng et al., 2009). Sengupta and Karmakar (2004) attributed the inability to detect clear Mendelian mode of inheritance for dermatoglyphics traits in pedigree studies to either low inheritance or a large number of contributing genes. Devi et al. (2023) presented data that suggested that the inheritance of fingerprints followed strong father to daughter, and mother to son patterns respectively.

The human foot is a multifaceted structure consisting of several bones, joints, muscles, tendons and ligaments which support, move and give balance to the body. The foot is anatomically divided into three parts; hindfoot, midfoot and forefoot with five phalanges (Xiao et al., 2012). There is presently no consensus method for the classification of foot types (Chuckpaiwong et al., 2009; Razeghi and Batt 2002). The different methods employed for establishing foot types are generally subjective and based on visual observation (Simmons et al., 2004). The trait may be determined by more than one gene, or by a combination of genetics and the environment. Different and conflicting models have been suggested including a simple two-allele model with sex influence, without sex influence, and an additive inheritance with sex influence (Mukherjee and Rao 1976; Papadopoulos and Damon 1973; Kaplan 1964; Romanus 1952). Adekoya et al. (2020) maintains that toe-pattern traits may be controlled by multiple genes and therefore have additive effects in the progeny expression. A clear inheritance pattern allowing for pleiotropy, epigenetics and environmental factors might be more easily determined if the segregation pattern of the fingerprint traits and relative toe length patterns are first established.

Few characters indeed have sufficiently high penetrance and wide distributions to provide samples large enough to facilitate rigorous testing for loose linkage. Fingerprint patterns and relative toe-length possess these attributes (Kaplan 1964). The earliest attempt to map fingerprint patterns with a specific chromosome is by Anderson et al. (1979) who demonstrated the linkage of arch patterns to the *haptoglobin* locus. A relatively recent attempt to map fingerprint characteristics to specific chromosomes or linkage groups found significant genomic linkage to chromosome 5 (5q14.1) predominantly driven by multivariate ridge count analyses from the ring, index, and middle fingers, and chromosome 1 (1q42.2) for univariate ridge count on all ten fingers (Medland et al., 2007).

Although genetic linkage and chromosome mapping in humans have been largely explored (Nadeau et al., 2000; Dixon 1993; Lander and Botstein 1986; McKusick 1971), basic linkage determination is crucial to understanding discrimination of genes implicated in polygenic traits. These traits exhibit significant differences between different ethnic populations of the world studied so far including Nigeria (Akpan et al., 2019; Paul et al., 2023). Given the complexity of the genetics of the traits and their ability to show marked differences between populations, a systematic observation of the occurrence of the traits in the Nigerian populations is necessary. Hence, this study aimed to assess the frequency and distribution of the different fingerprint patterns in the Yoruba, Igbo and Ibibio ethnic groups; compute the association, genetic linkage and segregation patterns of the different fingerprint and toe patterns in the Nigerian population groups.

MATERIALS & METHODS

The study populations consist of individuals of all ages of Yoruba, Igbo and Ibibio ethnic groups. Fifty individuals were sampled from each of the three ethnic groups making a total of 150 subjects. The Yoruba and Igbo populations were sampled in Lagos (6° 27' 55.5192'' N, 3° 24' 23.2128'' E) while the Ibibio was collected in Lagos and Eket, Akwa Ibom (4° 38' 48.12'' N, 7° 56' 34.439'' E). Fingerprints were collected according to the widely accepted rolled print protocol of Cummins and Midlo (1961) using an already prepared form designed to collect other data including the foot types, age, sex and tribe of participants (Fig. 1). The fingerprints were observed using a hand lens (where necessary) and classified. Classification of fingerprint patterns and ridge count was carried out according to established standards (Growns et al., 2022; Chen et al., 2022; Busey et al., 2021; Hawthorne, 2009). The fingers were represented as Right Thumb Finger (RTF), Right Middle Finger (RMF), Right Index Finger (RIF), Right Ring Finger (RRF), Right Little Finger (RLF), Left Thumb Finger (LTF), Left Middle Finger (LMF), Left Index Finger (LIF), Left Ring Finger (LRF), Left Little Finger (LLF).

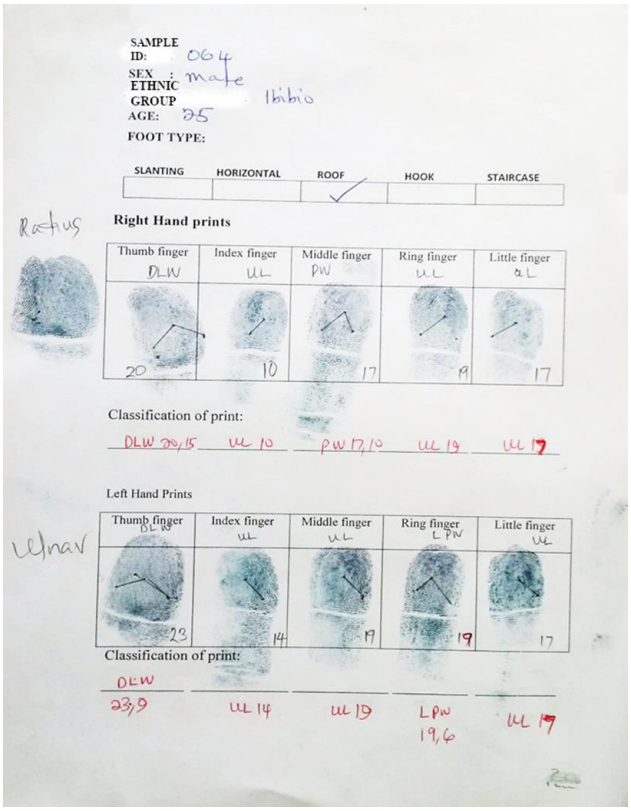

Fig. 1: Form used for collection of data for the study.

The foot types were categorized into five according to News.Com.Au. (2013) with slight modification to remove any idea of ancestry and rather treat them as traits. Thus, the feet were classified as either slanting, horizontal, roof,

hook, or staircase type. Fingerprint pattern and foot types were then coded and entered into Excel 2016 MS Package. Each pattern-finger association was treated as a trait to yield 40 traits (10 fingers by four pattern types).

The 40 traits are Right Thumb Arch (RTA), Right Thumb Whorl (RTW), Right Thumb Ulnar Loop (RTU), Right Thumb Radial Loop (RTR), Right Index Arch (RIA), Right Index Whorl (RIU), Right Index Ulnar Loop (RIU), Right Index Radial Loop (RIR), Right Middle Arch (RMA), Right Middle Whorl (RMW), Right Middle Ulnar Loop (RMU), Right Middle Radial Loop (RMR), Right Ring Arch (RRA), Right Ring Whorl (RRW), Right Ring Ulnar Loop (RRU), Right Ring Radial Loop (RRL), Right Little Arch (RLA), Right Little Whorl (RLW), Right Little Ulnar Loop (RLU), and Right Little Radial Loop (RLR) from the right hand. And Left Thumb Arch (LTA), Left Thumb Whorl (LTW), Left Thumb Ulnar Loop (LTU), Left Thumb Radial Loop (LTR), Left Index Arch (LIA), Left Index Whorl (LIU), Left Index Ulnar Loop (LIU), Left Index Radial Loop (LIR), Left Middle Arch (LMA), Left Middle Whorl (LMW), Left Middle Ulnar Loop (LMU), Left Middle Radial Loop (LMR), Left Ring Arch (LRA), Left Ring Whorl (LRW), Left Ring Ulnar Loop (LRU), Left Ring Radial Loop (LRL), Left Little Arch (LLA), Left Little Whorl (LLW), Left Little Ulnar Loop (LLU), and Left Little Radial Loop (LLR) from the left hand. The foot types were slanting (FTSL), horizontal (FTHL), roof (FTRF), hook (FTHK) and staircase (FTSC) foot types.

Using IBM SPSS version 25, the data were analyzed for count, percentage and frequency of occurrence of the patterns in each of the populations and gender, as well as the mean and standard deviation. Statistical differences were taken at $P<0.05$ using chi-square and ANOVA for each of the population and gender.

To examine the association and therefore transmission of the trait, a correlation analysis was performed followed by a linkage analysis. For the linkage analysis, each pattern type was assumed to be dominant in a mutually exclusive way to other pattern type occurrence on the same finger/foot type. This accumulated to 40 dominant finger pattern-position and five-foot pattern types.

The pattern type on a finger was coded '1' for presence and '0' for absence. Segregation of each pattern type was checked using χ^2 goodness of fit test to check the expected 1:1, 1:3 and 3:1 ratio. MapDisto v1.1 was used to construct a linkage map of all pattern types (Lorieux 2012). The Kosambi mapping function was used to convert recombination frequencies to centiMorgans (Kosambi 1944). To assign patterns to linkage groups, a step-wise reduction of LOD score of 3 with maximum recombination of 0.3 was used. A dendrogram of the relationship between the three ethnic groups was constructed using SPSS.

RESULTS

The distribution of the samples of 127 individuals from the three ethnic groups included 72 males and 55 females. Forty-one of the individuals were of Yoruba ethnicity, 42 were Igbo and 44 were Ibibio. The ages of the individuals ranged from 6-40 years. A total of 1270 fingerprint patterns by finger were examined and 127-foot types recorded for the individuals in the study. For the fingerprint patterns, arches constituted 6.61% of the observed prints, loops 48.98% and whorls 44.41% in the pooled population (Table 1). The highest occurring sub pattern was the ulnar loop which constituted 44.65% of the pooled samples whereas only one accidental whorl (0.08%) was observed in the 1270 patterns observed. Females had a significantly different and higher number of arch patterns (12.63%) compared to the males (2.23%) (Table 1).

The percentage of ulnar loop among the Yoruba was the highest observed (56.83%) of all fingerprint patterns in all ethnic populations and the combined loop pattern had a frequency of 63.17% (Tables 2a and 2b). The Igbo and Ibibio populations had the ulnar loop as the most prevalent fingerprint sub patterns with frequencies of 38.57 and 39.09%, respectively. Whereas the Igbo population had the whorl as the major pattern (52.86%), the Ibibio had an almost equal number of loops (43.64%) and whorls (48.18%) as the major patterns in their population (Tables 2a and 2b).

The distribution of all fingerprint patterns for the 10 fingers is presented in Table 3. The ulnar loop had the highest occurrence and this was prominent on the little fingers of both left and Left hands. The percentage occurrences were 64.6% on the Left little finger and 61.4% left little finger. The accidental whorl pattern had the least distribution, found only in the left ring finger with a 0.8% occurrence.

The means and standard deviations of ridge counts were also obtained for all fingers across gender. The ridge count was consistently greater in males than females on all ten fingers (Fig. 2). Overall, males had a mean total finger ridge count (TFRC) of 161.00±36.52 while females had 130.65±47.14. In both sexes, the ring finger had the highest number of ridges in both hands.

Table 1: Count and frequencies of the different fingerprint pattern in the pooled population

Fingerprint Pattern	Male			Female			Total				
	Count	%	Freq	Count	%	Freq	Count	%	Freq	Count	%
Plain Arch	4	0.56	0.006	49	8.91	0.089	53	4.17	0.042	84	6.61
Tented Arch	12	1.67	0.017	19	3.45	0.035	31	2.44	0.024		
Radial Loop	30	4.17	0.042	25	4.55	0.045	55	4.33	0.043	622	48.98
Ulnar Loop	305	42.36	0.424	262	47.64	0.476	567	44.65	0.446		
Plain Whorl	202	28.06	0.281	103	18.73	0.187	305	24.02	0.24	564	44.41
Double Loop Whorl	87	12.08	0.121	28	5.09	0.051	115	9.06	0.091		
Central Pocket Whorl	68	9.44	0.094	59	10.73	0.107	127	10.00	0.1		
Lateral Pocket Whorl	12	1.67	0.017	4	0.73	0.007	16	1.26	0.013		
Accidental Whorl	0	0	0	1	0.18	0.002	1	0.08	0.001		
	720			550			1270			1270	

Count: Number of fingers observed with pattern type, %: Percentages based on counts, Freq: Frequencies of each fingerprint pattern in the population.

Table 2a: Count and frequencies of the major fingerprint pattern in each of the three populations

		Yoruba (n = 410)			Igbo (n = 420)			Ibibio (n = 440)			Total (1270)		
Fingerprint Pattern		Count	%	Freq	Count	%	Freq	Count	%	Freq	Count	%	Freq
ARCH	Plain Arch	10	2.44	0.024	18	4.29	0.043	25	5.68	0.057	53	4.17	0.042
	Tented Arch	11	2.68	0.027	9	2.14	0.021	11	2.50	0.025	31	2.44	0.024
LOOP	Radial Loop	26	6.34	0.063	9	2.14	0.021	20	4.55	0.045	55	4.33	0.043
	Ulnar Loop	233	56.83	0.568	162	38.57	0.386	172	39.09	0.391	567	44.65	0.446
WHORL	Plain Whorl	62	15.12	0.151	134	31.90	0.319	109	24.77	0.248	305	24.02	0.24
	Double Loop Whorl	28	6.83	0.068	46	10.95	0.110	41	9.32	0.093	115	9.06	0.091
	Central Pocket Whorl	35	8.54	0.085	35	8.33	0.083	57	12.95	0.130	127	10.00	0.1
	Lateral Pocket Whorl	5	1.22	0.012	6	1.43	0.014	5	1.14	0.011	16	1.26	0.013
	Accidental Whorl	0	0	0	1	0.24	0.002	0	0	0	1	0.08	0.001

Count: Number of fingers observed with pattern type, %: Percentages based on counts, Freq: Frequencies of each fingerprint pattern in the population.

Table 2b: Summary of count and frequencies of the major fingerprint patterns in the three populations

	Yoruba (n = 410)			Igbo (n = 420)			Ibibio (n = 440)		
Fingerprint Pattern	Count	%	Freq	Count	%	Freq	Count	%	Freq
Arch	21	5.12	0.051	27	6.429	0.064	36	8.182	0.082
Loop	259	63.17	0.632	171	40.71	0.407	192	43.64	0.436
Whorl	130	31.71	0.317	222	52.86	0.529	212	48.18	0.482

%: Percentages based on counts, Freq: Frequencies of each fingerprint pattern in the population.

Table 3: Percentage occurrence of fingerprint pattern in each of the ten fingers in the pooled population

	Left Hand Fingers					Left Hand Fingers				
Fingerprint Pattern	Thumb	Index	Middle	Ring	Little	Thumb	Index	Middle	Ring	Little
Plain arch	4.7	7.1	7.1	0	2.4	2.4	7.1	7.1	0	3.9
Tented arch	0.8	1.6	0.8	0	0	0.8	7.1	7.1	3.1	3.1
Radial loop	3.1	3.1	1.6	3.9	7.1	5.5	3.9	1.6	3.9	9.4
Ulnar loop	33.1	35.4	63.0	42.5	64.6	34.6	25.2	52.8	33.9	61.4
Plain whorl	37.0	30.7	20.5	35.4	8.7	17.3	37.8	18.1	28.3	6.3
Double loop whorl	21.3	7.1	1.6	3.9	0	38.6	7.1	5.5	4.7	0.8
Central pocket whorl	0	15	2.4	11.0	17.3	0.8	8.7	7.9	22.0	15.0
Lateral pocket whorl	0	0	3.1	3.1	0	0	3.1	0	3.1	0
Accidental whorl	0	0	0	0	0	0	0	0	0.8	0

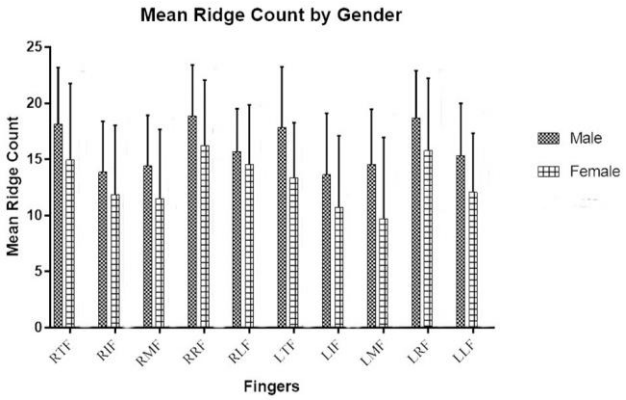

Fig. 2: Comparison of mean ridge count between males and females in the pooled population. The ridge count is consistently greater in males than females on all ten fingers; RTF: Left Thumb Finger, RMF: Left Middle Finger, RIF: Left Index Finger, RRF: Left Ring Finger, RLF: Left Little Finger, LTF: Left Thumb Finger, LMF: Left Middle Finger, LIF: Left Index Finger, LRF: Left Ring Finger, LLF: Left Little Finger.

The Igbo sub-population had on average a greater mean TRFC and average finger ridge count (AFRC) compared to the other groups (Table 4). On each of the ten fingers, the Igbos had ridge counts greater than the Yorubas and it is only on the left ring finger (RRF) that the Ibibio had count greater than the Igbo. These count differences on the significant at $p<0.05$. The ridge counts on all fingers were significantly correlated with each other. These correlations were all positive. The strongest correlations were between LIF and RIF (0.813) followed by LRF and RRF (0.781) while the least correlation was between LRF and RTF (0.336) (Table 5).

RTF: Left Thumb Finger, RMF: Left Middle Finger, RIF: Left Index Finger, RRF: Left Ring Finger, RLF: Left Little Finger, LTF: Left Thumb Finger, LMF: Left Middle Finger, LIF: Left Index Finger, LRF: Left Ring Finger, LLF: Left Little Finger, TTRC: Total Left Ridge Count, TLRC: Total Left Ridge Count, TFRC: Total Finger Ridge Count, AFRC: Average Finger Ridge Count

A total of 127 feet were examined and categorized into slanting (FTSL), horizontal (FTHL), roof (FTRF), hook (FTHK) and staircase (FTSC) foot types. No FTSC was observed, so this was not included in further analysis. Slanting foot type (FTSL) dominated the foot types with a joint prevalence of 38.6% while FTHL was 22.0% and FTHK 8% (Table 6, Table 7). The difference in percentage occurrence among the sexes was not statistically significant ($p>0.05$). Results further showed that the Ibibio population had a majority FTRF type (72.7%), the remaining were slanting type. No roof or hook foot type was observed in that population (Fig. 3).

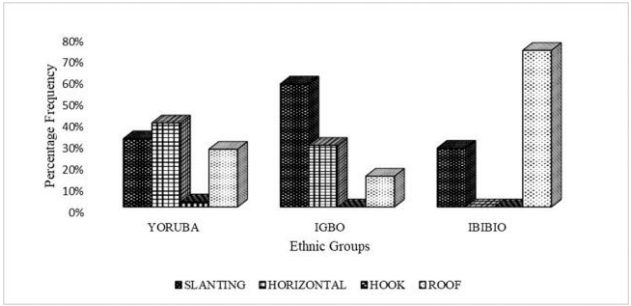

Fig. 3: Frequency of the observed foot types in each of the three populations.

Table 4: Descriptive statistics of ridge counts in each of the ten fingers for all studied populations

FINGERS	Population	N	Mean	Std. Deviation	Std. Error	F	Sig.
Right Thumb	Yoruba	41	16.20	6.321	0.987	0.677	0.510
	Igbo	42	17.64	5.127	0.791		
	Ibibio	44	16.45	6.645	1.002		
	Total	127	16.76	6.059	0.538		
Right Index	Yoruba	41	12.80	5.596	0.874	1.630	0.200
	Igbo	42	14.14	5.340	0.824		
	Ibibio	44	12.09	5.075	0.765		
	Total	127	13.00	5.362	0.476		
Right Middle	Yoruba	41	12.56	5.065	0.791	1.756	0.177
	Igbo	42	14.43	6.057	0.935		
	Ibibio	44	12.45	5.165	0.779		
	Total	127	13.14	5.478	0.486		
Right Ring	Yoruba	41	16.85	3.864	0.603	0.973	0.381
	Igbo	42	17.79	5.854	0.903		
	Ibibio	44	18.45	5.873	0.885		
	Total	127	17.72	5.300	0.470		
Right Little	Yoruba	41	13.39	3.707	0.579	7.454	0.001
	Igbo	42	15.07	5.602	0.864		
	Ibibio	44	17.00	3.313	0.499		
	Total	127	15.20	4.530	0.402		
Total Right Ridge Count	Yoruba	41	71.80	19.832	3.097	1.185	0.309
	Igbo	42	79.07	24.908	3.843		
	Ibibio	44	76.45	20.224	3.049		
	Total	127	75.82	21.800	1.934		
Left Thumb	Yoruba	41	15.27	4.995	0.780	1.086	0.341
	Igbo	42	16.93	6.114	0.943		
	Ibibio	44	15.45	5.777	0.871		
	Total	127	15.88	5.659	0.502		
Left Index	Yoruba	41	12.41	5.366	0.838	0.992	0.374
	Igbo	42	13.29	6.631	1.023		
	Ibibio	44	11.45	6.013	0.907		
	Total	127	12.37	6.030	0.535		
Left Middle	Yoruba	41	12.78	5.807	0.907	1.380	0.255
	Igbo	42	13.43	7.123	1.099		
	Ibibio	44	11.18	6.395	0.964		
	Total	127	12.44	6.488	0.576		
Left Ring	Yoruba	41	17.22	4.788	0.748	0.089	0.915
	Igbo	42	17.71	4.950	0.764		
	Ibibio	44	17.36	6.545	0.987		
	Total	127	17.43	5.469	0.485		
Left Little	Yoruba	41	13.59	4.219	0.659	0.755	0.472
	Igbo	42	14.71	5.969	0.921		
	Ibibio	44	13.45	5.200	0.784		
	Total	127	13.91	5.176	0.459		
Total Left Ridge Count	Yoruba	41	71.27	20.130	3.144	0.955	0.388
	Igbo	42	76.07	27.560	4.253		
	Ibibio	44	68.91	24.866	3.749		
	Total	127	72.04	24.410	2.166		
Total Finger Ridge Count	Yoruba	41	143.07	38.831	6.064	0.889	0.414
	Igbo	42	155.14	50.883	7.851		
	Ibibio	44	145.36	41.359	6.235		
	Total	127	147.86	43.957	3.901		
Absolute Finger Ridge Count	Yoruba	41	173.20	64.849	10.128	4.324	0.015
	Igbo	42	223.71	99.777	15.396		
	Ibibio	44	194.27	66.668	10.051		
	Total	127	197.20	80.723	7.163		

+N: Count, F: variation between sample means / variation within the samples, Sig: P-value.

Table 5: Pearson Correlation table for counts on the ten fingers

	RTF	RIF	RMF	RRF	RLF	LTF	LIF	LMF	LRF	LLF	TRRC	TLRC	TFRC	AFRC
RTF	1.000													
RIF	0.508**	1.000												
RMF	0.565**	0.708**	1.000											
RRF	0.397**	0.493**	0.573**	1.000										
RLF	0.575**	0.539**	0.607**	0.649**	1.000									
LTF	0.582**	0.468**	0.479**	0.561**	0.591**	1.000								
LIF	0.628**	0.813**	0.684**	0.578**	0.502**	0.540**	1.000							
LMF	0.552**	0.630**	0.756**	0.536**	0.561**	0.533**	0.705**	1.000						
LRF	0.336**	0.465**	0.529**	0.781**	0.599**	0.553**	0.661**	0.667**	1.000					
LLF	0.409**	0.452**	0.505**	0.601**	0.688**	0.605**	0.549**	0.567**	0.703**	1.000				
TRRC	0.772**	0.838**	0.883**	0.745**	0.811**	0.658**	0.774**	0.752**	0.650**	0.639**	1.000			
TLRC	0.614**	0.667**	0.724**	0.732**	0.703**	0.775**	0.845**	0.853**	0.858**	0.810**	0.844**	1.000		
TFRC	0.719**	0.781**	0.834**	0.769**	0.786**	0.749**	0.844**	0.837**	0.789**	0.758**	0.957**	0.963**	1.000	
AFRC	0.631**	0.682**	0.762**	0.736**	0.738**	0.695**	0.766**	0.791**	0.746**	0.711**	0.871**	0.898**	0.921**	1.000

** Correlation is significant at the 0.01 level (2-tailed).

Table 6: Percentage of foot type by gender

GENDER		Foot Type				Total
		Slanting	Horizontal	Hook	Roof	
Male	Count	23	18	0	31	72
	% within gender	31.9	25.0	0.0	43.1	100.0
Female	Count	26	10	1	18	55
	% within gender	47.3	18.2	1.8	32.7	100.0
Total	Count	49	28	1	49	127
	% within gender	38.6	22.0	0.8	38.6	100.0
Pearson Chi-Square			4.727			
Asymptotic Sign. (2-sided)			0.193			

Table 7: Percentage of foot type by population

Frequency foot type by tribe							
			FOOT TYPE				Total
			Slanting	Horizontal	Hook	Roof	
TRIBE	Yoruba	Count	13	16	1	11	41
		% within tribe	31.7	39.0	2.4	26.8	100.0
	Igbo	Count	24	12	0	6	42
		% within tribe	57.1	28.6	0.0	14.3	100.0
	Ibibio	Count	12	0	0	32	44
		% within tribe	27.3	0.0	0.0	72.7	100.0
	Total	Count	49	28	1	49	127
		% within tribe	38.6	22.0	0.8	38.6	100.0
F			12.842				
Sig.			0.000				

Table 8: Pearson Correlation table of fingerprint pattern against foot types.

		FTRF	FTSL	FTHL	FTHK
Left Thumb Arch	RTA	-0.12	0.16	-0.05	-0.02
Left Thumb Whorl	RTW	0.15	-0.08	-0.05	-0.11
Left Thumb Ulnar Loop	RTU	-0.14	0.06	0.07	0.13
Left Thumb Radial Loop	RTR	0.13	-0.14	0.01	-0.02
Left Index Arch	RIA	-0.24**	0.33**	-0.1	-0.03
Left Index Whorl	RIW	0.20*	-0.22*	0.05	-0.09
Left Index Ulnar Loop	RIU	-0.08	0.09	-0.04	0.12
Left Index Radial Loop	RIR	0.04	-0.14	0.12	-0.02
Left Middle Arch	RMA	-0.23**	0.31**	-0.08	-0.03
Left Middle Whorl	RMW	0.05	-0.20*	0.18*	-0.05
Left Middle Ulnar Loop	RMU	0.07	0.04	-0.14	0.07
Left Middle Radial Loop	RMR	0.03	-0.1	0.09	-0.01
Left Ring Arch	RRA	NA	NA	NA	NA
Left Ring Whorl	RRW	0.15	-0.14	-0.04	0.08
Left Ring Ulnar Loop	RRU	-0.09	0.07	0.04	-0.08
Left Ring Radial Loop	RRR	-0.16	0.17	-0.01	-0.02
Left Little Arch	RLA	-0.12	0.20*	-0.08	-0.01
Left Little Whorl	RLW	0.23**	-0.1	-0.14	-0.05
Left Little Ulnar Loop	RLU	-0.09	0.01	0.08	0.07
Left Little Radial Loop	RLR	-0.16	0.03	0.15	-0.02
Left Thumb Arch	LTA	-0.14	0.13	0.01	-0.02
Left Thumb Whorl	LTW	0.24**	-0.12	-0.11	-0.1
Left Thumb Ulnar Loop	LTU	-0.20*	0.03	0.17	0.12
Left Thumb Radial Loop	LTR	0.02	0.09	-0.13	-0.02
Left Index Arch	LIA	-0.24**	0.39**	-0.17	-0.04
Left Index Whorl	LIW	0.08	-0.14	0.05	0.08
Left Index Ulnar Loop	LIU	0.06	-0.12	0.09	-0.05
Left Index Radial Loop	LIR	0.09	-0.08	-0.01	-0.02
Left Middle Arch	LMA	-0.28**	0.28**	0	-0.04
Left Middle Whorl	LMW	0.02	-0.08	0.05	0.13
Left Middle Ulnar Loop	LMU	0.13	-0.09	-0.03	-0.09
Left Ring Radial Loop	LMR	0.16	-0.1	-0.07	-0.01
Left Ring Arch	LRA	-0.14	0.23*	-0.1	-0.02
Left Ring Whorl	LRW	0.07	-0.03	-0.06	0.07
Left Ring Ulnar Loop	LRU	0.01	-0.12	0.14	-0.06
Left Ring Radial Loop	LRR	-0.08	0.17	-0.11	-0.02
Left Little Arch	LLA	-0.16	0.29**	-0.15	-0.02
Left Little Whorl	LLW	0.20*	-0.19*	-0.01	-0.05
Left Little Ulna Loop	LLU	0	-0.07	0.07	0.07
Left Little Radial Loop	LLR	-0.15	0.13	0.02	-0.03

When the foot types and fingerprint patterns were correlated to determine if an association exists between the two variables, a Pearson correlation test showed that some significant associations existed between some foot types and some fingerprint patterns. There were 20 of such significant correlations involving mostly the roof and slanting foot types with whorl and arches mostly on the index, middle and little finger. All the correlations were weak, the highest being 0.39 between LIA and FTSL (Table 8).

A linkage analysis of all the markers showed that the general population had four linkage groups (LG) designated LG1-LG4 (Fig. 4). LG2-LG4 contained two markers each with the bulk of the markers clustering on one large linkage group (LGI). The LG1 covered a distance of 323.9 cM. Particular patterns on the same finger in different hands were observed to mostly be closely linked on the map: RTW and LTW, LIW and RIW, RLW and LLW, and so on. Whorls on eight (8) of the ten (10) fingers (except whorls on the ring fingers) were located in tandem on the large linkage group. The RRW and LRW are linked on one of the smaller groups while the other two smaller linkage groups have the ring ulnar patterns (RRU and LRU) on one and the little ulnar patterns (RLU and LLU) on the other respectively. The radial loop patterns also link up around the same position, though they are punctuated by arch patterns on the left and right middle fingers, and right index and thumb fingers. Though all the foot types were on the same linkage group, the FTHL was closest to the whorls and lay between RMW and RLR, while the FTHK was between LTA and RMR (arch and radial loops). The FTHL was on the extreme of the map after LTU and RTU (closer to the ulnar loops) (Fig. 4).

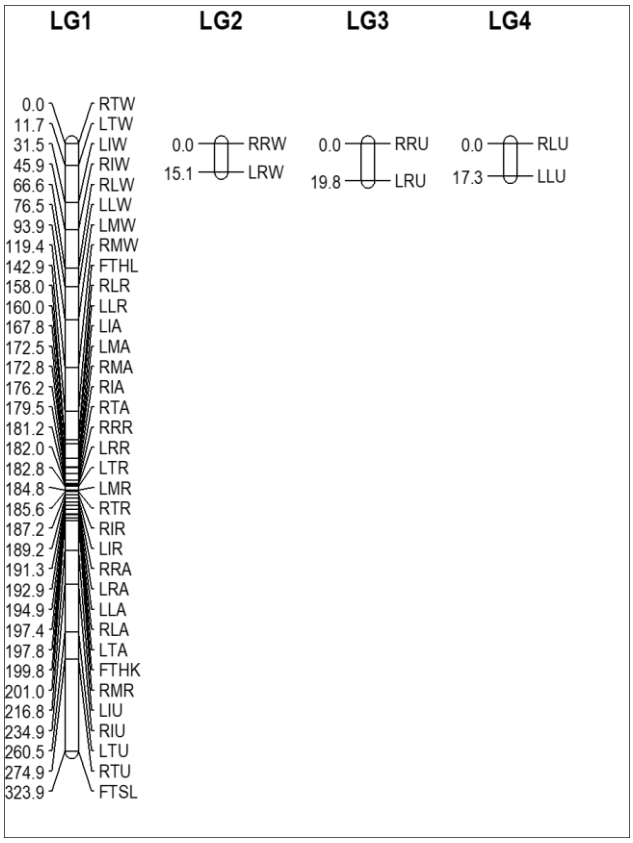

Fig. 4: Linkage maps of the 44 traits in the pooled population: traits clustered into four linkage groups.

When these linkages were resolved by each population, the radial loop markers, and arches maintained their relative clustering position on the largest linkage

group (LG1) in all three populations, similar to the position observed in the pooled population. The whorl markers, while still linked together was more likely to form a separate linkage group as was seen in LG2 I and LG4 in Yoruba, LG2 and LG3 in Igbo and LG 3 in Ibibio. The ulnar loop pattern is distributed into different linkage groups in all populations, with the ulnar loops on the thumbs and the little finger the most likely to be on separate linkage groups (Fig. 5a, 5b, 5c).

A segregation pattern analysis for the markers indicated that the RTW, RRW, RRU, LIW, RIW and LMU all segregated in a 1:1 pattern (Table 9). RMW, LIU, LMW, LTW, RLW, LLW and FTHL all segregated in a 1:3 pattern. RIW and LMU consistently segregated in a 1:1 pattern even when examined in a population-by-population basis. LIU also consistently segregated in a 1:3 pattern in the divided and pooled populations. RRU segregated 1:1 in the Ibibio, Igbo and pooled populations and 3:1 in the Yoruba population. RTW segregated 1:1 in the Ibibio, Yoruba and pooled populations and 3:1 in the Igbo and Ibibio populations where it presented two segregation patterns. When observed only in the ethnic subpopulations, 10 of the markers presented two segregation patterns which disappears when the pooled population is analyzed. When a dendrogram is constructed for the three populations based on the observed markers, the Igbos and Yoruba recently diverged from each other compared with the Ibibio (Fig. 6).

DISCUSSION

This study presented the types and frequency of fingerprints and foot patterns in three Nigerian populations, including Yoruba, Igbo and Ibibio. The study identified the distribution, association and segregation patterns of the two traits between and among the sampled ethnic populations. It was necessary to examine the percentage occurrence of the different fingerprint patterns and foot types in this study to establish that the sample was robust and representative enough of each group for use in genetic linkage investigation and segregation analysis. The frequencies observed in this study agree largely with what has been previously observed for Nigeria in general and particularly for some of these populations. Similar percentages have been observed for the Yoruba (Adetona and Lawal, 2024; Igbigbi et al., 1994; Jantz and Brehme 1978) and the Igbos (Igbigbi et al., 1994). The Ibibio share the same geography and language group as the Annang, so it is not surprising that the observed fingerprint pattern in our study is in agreement with what has been reported for the Annang (Ekanem et al., 2009).

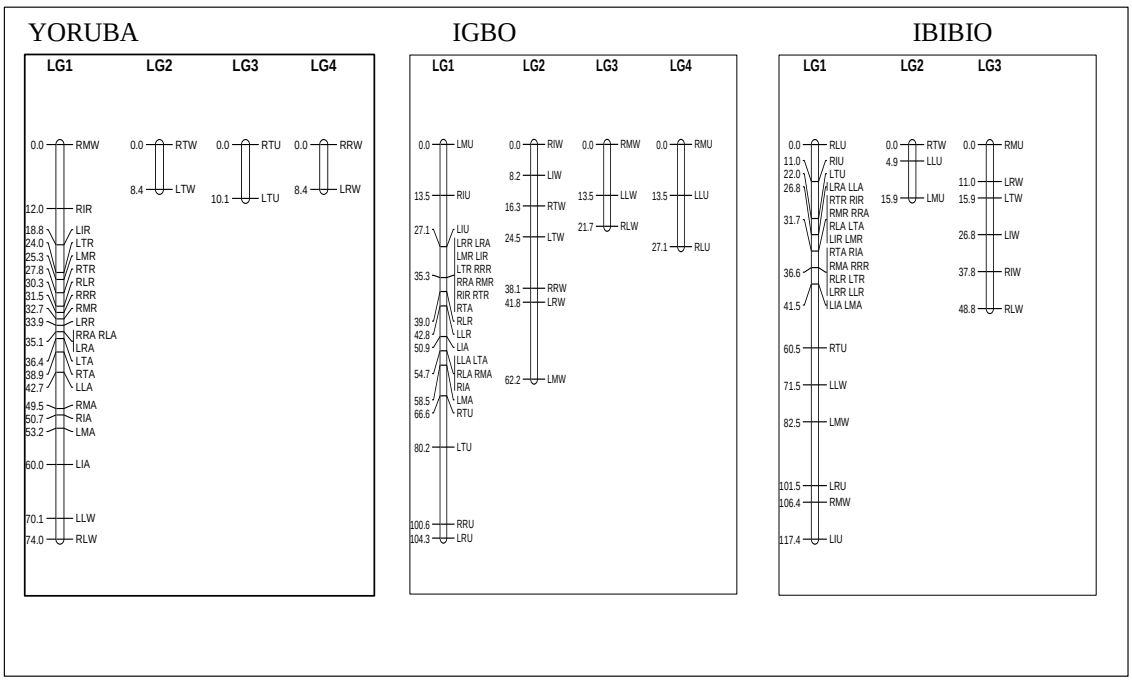

Fig. 5 a, b, c: Linkage maps of the 44 traits in the each of the three populations respectively.

Table 9: Segregation pattern of the different traits in the studied populations

Population/Pattern	1:1	1:3	3:1
Pooled	RTW, RRW, RIW, RRU, LIW, LMU	RMW, RLW, LTW, LIU, LMW, LLW, FTHL	
Ibibio	RTW[a], RIW, RIU[b], RRW, RRU[d], RLW[e] LTU, LIW LMU, LRW[f], LRU, LLU	RTU, RIU[b], RMW, RMU[c], RRU[d], RLW[e], LIA, LIU, LMA, LMW, LLW, FTSL	RTW[a], RMU[c], RLU, LRW[f], FTRF,
Igbo	RIW, RIU[g], RMW[h], RMU, RRW[i], RRU[j], RLU, LTW, LTU[k], LMW, LMU, LLU, FTSL,	RIU[g], RTU, RMW[h], RRU[j], RLW, LTU[k], LIA, LIW, LIU, LMA, LRU, LLW, LLR, FTRF, FTHL	RTW, RRW[i], LRW,
Yoruba	RTW, RTU, RIW, RIU, RMW, LTU, LMU, LRW, LRU, FTHL	LIA, LIW, LIU, LIR, LMW, FTRF, FTSL	RMU, RRW, RRU, RLW, RLU, LTW, LLU,
Traits with subscript demonstrated more than one mode of segregation with different values	a, b, c, d, e, f: χ^2 = 3.27; p=0.07 g, h, i, j, k: χ^2 = 3.43; p=0.06	b, d, e: χ^2 = 3.03; p=0.08 k: χ^2 = 2.57; p=0.11	j, h, j, a, c, f: χ^2 =3.03; p=0.08 i: χ^2 = 2.57; p=0.11

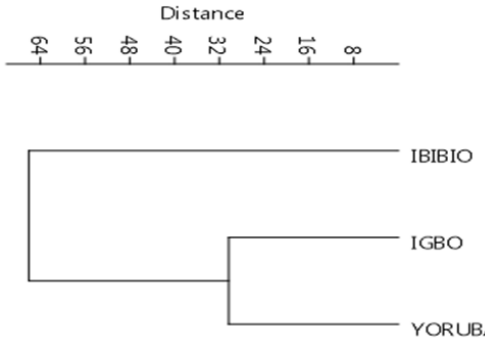

Fig. 6: Dendrogram showing relationship of the three populations based on the foot types.

Furthermore, the percentage occurrence of each of the fingerprint patterns agrees with earlier findings by other researchers. For instance, the prevalence of ulnar loop pattern on the little finger is consistent with several other populations. Abue et al. (2013) reported a higher percentage of ulnar loop pattern (58.93%) in their study of an undefined population in Lagos, southwestern Nigeria, while other studies on the Ijaw, and Okrika and Ikwerre ethnic groups both from the south-south Nigeria also recorded high prevalence of ulnar loop pattern among the subjects according to Otobo and Tarimobo-Otobo (2016) and Osunwoke et al. (2008), respectively. Also, our findings largely agree with other investigations that have been reported among the Indians (Kapoor and Badiye 2015), Philippines (Gutierez et al., 2012), and the Spanish (Martín et al., 1996). In contrast, Cho (1998) reported more whorl dermatoglyphic patterns among the New Zealand Samoans with percentages ranging from 55.6 in males to 65.6 in females. Singh and Garg (2004) studied finger dermatoglyphics among the Rajputs of Himachal Pradesh, India and found out that the whorl pattern is the most frequent in both male and female subjects of the population. It is believed that dermatoglyphic traits are inherited within populations with slow changes. These changes are distinct enough for individualization and genetic differentiation, a phenomenon that has been attributed to admixture (Cheng et al., 2009; Meier 1975). It is also widely accepted that interactions between genes and the environment, as well as gene flow and genetic drift, may influence fingerprint patterns of populations (Arrieta et al., 2003; Arrieta et al., 1987; Meier 1975).

The fingerprint ridge count showed that the fourth (ring) finger of both hands usually has the highest count, as has been observed by Jantz and Brehme (1978). This trend in the ridge count for this finger might not be unconnected with the fact that this finger has the lowest percentage of arch patterns compared to the first three fingers which possess even a greater surface area than it (Sharma et al., 2022). The Left counts on all fingers were significantly correlated with each other. These positive correlations indicated that the same gene or group of genes may be responsible for the counts observed on all the fingers. This study further demonstrated that the strongest correlations were between the same fingers on both hands as seen between LIF and RIF (r = 0.813), LRF and RRF (r = 0.781), and LMF and RMF (r = 0.756) indicating that they are possibly influenced by the same or linked genes. Total ridge count on all ten fingers, and multivariate ridge count on the ring, index, and middle have been previously linked to regions on chromosome 1 (1q42.2) and chromosome 5 (5q14.1) respectively (Medland et al., 2007).

The association between each pattern per finger combination was examined with a linkage analysis of all the traits. Evidence of shared inheritance and transmission pattern was observed. This is evident in that the same pattern on the same fingers on different hands frequently clustered to the same linkage groups. This strong correlation of pattern types on contralateral digits is obviously genetic and was also observed in some other study (Ho et al., 2016; Li et al., 2022). The majority of the traits were mapped to a large linkage group which included the foot types, indicating that the same or closely linked genes may be responsible for differentiation of the hands and digits. In fact, Li et al (2022) using genome wide association studies and segmenting the patterns into whorls and non-whorls found 43 markers across multiple ethnicities which were mapped to 18 loci involved in embryonic limb development. Possible epigenetic involvement on whorls development through the genes *ADAMTS9-AS2* on chromosome region 3p14.1, *OLA1*, and an intergenic region on chromosome 12 near *TBX3* and *MEDI13L* has also been suggested by Ho et al. (2016) and Walsh et al. (2016). In this study whorls on eight (8) of the ten (10) fingers (except whorls on the ring fingers) were located in tandem on the large linkage group, but were also the most likely to break into smaller groups or combine with other markers when specific populations were examined. This further indicates that there may be several genes or gene groups on different chromosomes involved in whorl development and inheritance. The whorls segregated in a 1:1, 1:3 and 3:1 pattern further confirming the involvement of several linkage groups or genes.

The radial loop pattern was the most stable of all the patterns, maintaining relatively the same position on the linkage groups in more than one population. The difference in the linkage and segregation pattern of the radial loop and ulnar loop respectively may indicate that these traits are not determined by the same gene or variant, and may need to always be treated as different when studying their inheritance. The ulnar loop markers were consistently found in two or more linkage groups. Whorls and ulnar loops appeared to be the most dominant patterns with different analyses in this study including a segregation pattern analysis. Other patterns had consistent segregation patterns in the pooled population but presented two segregation patterns which possibly indicates some level of penetrance or pleiotropy for these traits (Adekoya et al., 2020; Li et al., 2022).

The foot types were linked with the fingerprint patterns in such a way that the FTHL was closest to the whorls and lay between RMW and RLR, the FTHK linked tightly with the arch and radial loop, and the FTSL more closely linked to the ulnar loops. These linkages indicate associated genetic relationship between lower leg phenotypes and fingerprint patterns (Li et al., 2022). Foot pattern inheritance was previously shown to be semi-dominant (Adekoya et al., 2020), but this study reveals a

segregation pattern of 1:3 for the FTHL, 1:1 and 1:3 for the FTSL pattern. The distribution of these foot types, as with fingerprint patterns differ in different populations (Adekoya et al., 2020; Paul et al., 2023).

The human dermatoglyphic and foot pattern and traits presents/possesses variations within and between populations which can be used to estimate genetic distances between populations (Crawford and Duggirala, 1992; Arrieta et al., 2003; Namouchi, 2011; Cheng et al., 2009).

The dendrogram constructed based on these markers divided the populations into two genetic groups with one group comprising only the Ibibio and the other, the Yoruba and the Igbo. The variation when used to estimate genetic relationships among the three ethnic groups involved in the study successfully revealed previously established population relationships using other marker types and linguistics (Eberhard et al., 2024; Akpan et al., 2024). Similar performance of dermatoglyphics patterns was observed when used to estimate the population distances within the Brahmin caste of India (Kamali et al., 1991; Karmakar et al., 2002). This showed that the evaluated traits can infer interpopulation relationships and help to understand population structures as was previously documented by different authors (Gualdi-Russo et al., 1994; Segura-Wang and Barrantes 2009).

Conclusion

This study highlighted dermatoglyphic and foot types variations in three Nigerian ethnic groups. Dermatoglyphic patterns on the ten fingers, as well as foot characteristics, were observed among the male and female individuals of ethnic studied ethnicities. The ulnar loop pattern constituted the majority of fingerprint patterns observed in the combined population. Slanting and roof foot types are the most prevalent foot types in the sampled populations with further analysis showing divergence between the Yoruba and the Igbo populations. The print patterns segregated into expected 1:1 and 1:3 ratios. The study provides an insight into the genetics of fingerprint patterns and foot types in these ethnic groups, a precursor to understanding the forensics and genetic structure of the Nigerian populations based on the traits evaluated.

Authors' Contribution

UUA, ODA, and KOA conceived and designed the experiment. UUA, JHO, OAA, and OAB performed the study. UUA and STF conducted the fingerprint and footprint analyses. HBA, KOA and BO supervised and coordinated the experiments. ODA performed statistical analyses of experimental data. UUA, JHO and STF prepared the draft of the manuscript. All authors critically revised the manuscript and approved the final version.

Availability of Data and Material

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing Interests

The authors declare that they have no competing interests.

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