

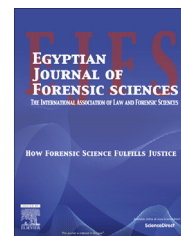
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# Digital dermatoglyphic variation and migratory pattern of ethnic Liberians

Godwin Mbaka<sup>a,\*</sup>, Adedayo Ejiwunmi<sup>b</sup>, Olusegun Alabi<sup>c</sup>, Timothy Olatayo<sup>d</sup>

<sup>a</sup> Department of Anatomy, Lagos State University College of Medicine, Ikeja, Lagos, Nigeria

<sup>b</sup> Department of Anatomy, College of Medicine of the University of Lagos, Idi-Araba, Lagos, Nigeria

<sup>c</sup> Department of Mathematical Sciences, Federal University of Technology, Akure, Ondo State, Nigeria

<sup>d</sup> Department of Mathematical Sciences, Olabisi Onabanjo University, Ago-Iwoye, Ogun State, Nigeria

Received 17 May 2016; revised 21 June 2016; accepted 21 June 2016

### KEYWORDS

Ridge-count;  
Dermatoglyphic variation;  
Ethnic Liberians

**Abstract** The magnitude of digital dermatoglyphic variation among ethnic Liberians was examined using a total of 427 people comprising 218 males and 209 females. The three major tribes of ethnic Liberians which comprised Kwa, Mande and Mel exhibited significant finger ridge-count asymmetry and diversity. Also using one way multivariate analysis of variance to access finger ridge-count asymmetry and diversity the finding was consistent with our univariate Fst analysis. The magnitude of inter-group differentiation as measured by Fst showed unbiased values for the four principal component scores ranging from 0.034 to 0.096 in males and 0.025 to 0.050 in females. The females showed lesser differentiation and this perhaps might be explained from the migratory pattern due to difference in marital mobility. The Fst value showed that the Mande population was the most heterogeneous while the Mel population was the most homogeneous. In keeping with the trend that asymmetry and diversity values tend to decrease from the northern to the southern hemisphere, the Mel population with greater ridge-count differentiation might have migrated from far north to their present location in southwestern Liberia. This is consistent with the map location of major ethnic tribes.

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### 1. Introduction

Archeologists and anthropologists have investigated the diversity of humans for many decades.<sup>1</sup> Dermatoglyphics, the study of the patterns of epidermal ridges has become one of the fore-

most indices in determining genetically related groups in multi-ethnic populations. It is also a valuable means of tracking the migratory pattern of these genetically related groups within a large demographic expression. Several studies have demonstrated variation in pattern among ethnic groups within a population.<sup>2,3</sup> Furthermore, large differences are said to exist between migratory populations and the original population within the same ethnic group.<sup>4</sup> This is largely because dermatoglyphic patterns genetically determined are heritable and is believed to follow a polygenic pattern of inheritance.<sup>5</sup>

\* Corresponding author.

E-mail address: [mbaakagm@yahoo.com](mailto:mbaakagm@yahoo.com) (G. Mbaka).

Peer review under responsibility of The International Association of Law and Forensic Sciences (IALFS).

<http://dx.doi.org/10.1016/j.ejfs.2016.06.005>

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Epidermal ridges laid down between tenth and eighteenth weeks of gestation remain unchanged except for increase in size.<sup>6-8</sup> However, it had been previously observed that in spite of the pivotal role of genes in determining dermatoglyphic expression, some aspects of dermatoglyphic variabilities are determined by such environmental factors as radiation drugs and hormones.<sup>9,7</sup> These have been observed to occur within the first trimester of pregnancy.<sup>10</sup>

Dermatoglyphics have been used extensively to study the origin and structure of human populations.<sup>11</sup> Its utilization has become increasingly common as the perception grows that they may offer new insights regarding ancient affinities among native population and variabilities in multi-ethnic society.<sup>12,13</sup> This assumption was strengthened by previous accounts that dermatoglyphics portrayed expected ethno-historical and geographical patterns convincingly.<sup>2,14-16</sup>

Although freed American slaves founded Liberia, this small West African country with a population of about 3.6 million<sup>17</sup> is made up of mostly indigenous Africans with slave descendants comprising only 5% of the population. Apart from the slave descendants, Liberia is made of 16 tribes, having 29 indigenous languages. This represents sub-strata of three major tribes namely Kwa, Mande and Mel. They are the three major ethno-linguistic groups. The ancestral origins of these tribes are rather vague. More so, the historical data about their settlement are lacking. This exercise therefore might prove a useful tool in investigating the ancient affinity/variability among the native population by means of univariate analysis of their dermatoglyphic finger patterns.

Using the Fst statistics formulated for quantitative traits, by Williams-Blangero,<sup>18</sup> the magnitude of inter-population variation among the major tribes<sup>19</sup> would be determined. Finally, the genetic drift within the micro-geographical arrangement would be equally assessed.

## 2. Materials and methods

This study was conducted among the Liberian refugees living in the Government established Camp in Oru, a town located in the Southwest Region of Nigeria. The database covered 13 tribes with the exclusion of slaves' descendants (American-Liberians). The exercise was conducted at designated centers within the camp. Subjects were made to dip the tip of their fingers (right and left) on a soaked stamp-pad. The digital patterns were obtained by assisted rolling of the inked digits on duplicating paper placed on a hard flat surface bearing the name, tribe and the sex of the subject. The sample distribution was uneven and unselected. A total of 427 people were examined comprising 218 males and 209 females. The exercise cut across all age group excluding those with obvious physical or genetic disabilities.

The finger pattern types were classified into four main categories- arches, ulnar loops, radial loops and whorls (double loops). The fingerprint classification is based on the recognition of the triradii.<sup>8</sup> According to Stevenson et al.,<sup>8</sup> this follows Galton's original classification that recognized three basic patterns of fingerprints; the whorl that has two triradii, the loop, one triradius and the arch with no triradius. A triradius is defined as the meeting place of three dermal lines that make angles of approximately 120° with one another.<sup>8</sup> Using the method of Jantz,<sup>19</sup> the variables analyzed are the sum-

maries of the ridge counts of the ulnar loop (UL), radial loop (RL) and the whorls. The total ridge count (TRC) consists of first choosing the larger of the radial or ulnar count of the whorls and then summing these with the ulnar or radial loop counts over all 10 digits. The absolute ridge count (ARC) is the sum of all ridge counts over all the 10 digits.

Variation among samples was tested using simple one-way ANOVA for different sexes. The original variables were also transformed to principal component scores extracted from the sample correlations, covariance matrix among Radial, Ulnar, TRC and ARC.

The magnitude of differentiation among populations was tested using the univariate Fst for quantitative variables presented by Relethford.<sup>20</sup>

$$F_{st} = \left[ \frac{\sum_{i=1}^g w_i c_{ii}}{2 + \sum_{i=1}^g w_i c_{ii}} \right]$$

where  $c_{ii} = (x_i - x)^2/g_w$  and  $w_i$  is relative population size weight,  $x_i$  is the mean for group  $i$ ,  $x$  is the grand mean and  $g_w$  the pooled within group additive genetic variance. If  $p_w$ , the pooled within group phenotypic variance is used in place of  $g_w$ , then one obtains a minimum Fst.<sup>20</sup>

Fst values were computed among all the samples. The ridge count differentiation of the population was obtained after merging into major ethnic groups.

The linearity of Fst for quantitative variables was tested with samples subjected to statistical analysis using chi-square to test the magnitude of variation.

## 3. Results

Table 1 shows the mean summary ridge counts and sample sizes, by sex, for each population. Table 2 gives the correlation matrix and within sample deviations for the four variables. All variables were strongly inter-correlated except ulnar and TRC count as well as radial and ulnar count which were weakly correlated in females. The lowest correlation was between radial and ulnar counts. TRC was the most highly correlated with radial counts because the higher count used in TRC was commonly a radial count. ARC, as the sum of all counts was highly correlated with radial, ulnar and TRC. Generally, the males exhibited higher standard deviation than females in all counts.

Table 3 shows F ratio, minimum Fst values and their standard errors for the four summary variables by sex. All three variables and four principal components exhibited significant ( $p < 0.05$ ) inter group variability for males, although male ulnar count was less significantly variable. But in females, all variables exhibited less significant inter group variation although female ulnar counts were highly significant ( $p < 0.05$ ). It was obvious that females were less differentiated than males particularly for radial, TRC and ARC counts except for ulnar counts.

The difference between males and females Fst values was significant for radial counts and close to significance for ulnar counts. In both sexes, the radial counts yielded the lowest Fst.

### 3.1. Chi-square analysis

The relationship between the subgroup tribes in both sexes were equally assessed using chi-square analysis. The formula:  $\chi^2 = \sum [(O - E)^2/E]$ . According to the hypothesis:

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