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Sexual Dimorphism in the Turkmenian Population in Two Types of Dermatoglyphic Traits: Discriminant Analysis

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ABSTRACT

The aim of this study is to compare the pattern of sex differences between two different sets of dermatoglyphic traits (22 quantitative and 42 indices of diversity and asymmetry). Finger and palmar prints of Turkmenian population (547 individuals) were used for Multivariate analyses includes Cluster, Discriminant and Mantel test of matrix correlations. All variables (two groups) scattered into a number of small clusters those are markedly similar between males and females. These results were confirmed by Discriminant analysis – the two groups of variables are almost similar, the percentages of correctly classified individuals are 64.14% (22 traits) and 65.45% (42 traits); and Mantel statistics – the Z values are within the level of non-significance, very good similarities in 22 (0.95) and good similarities in 42 (0.87) traits. Sex dimorphism is similar between two categories of dermatoglyphic variables may be used for sex – discrimination in different populations.

Key words: *sexual dimorphism, dermatoglyphic traits, discriminant analysis, Turkmenian population*

Introduction

Dermatoglyphic traits are genetically determined and conservative in their evolution is well known[1]. Our great advantage is that the dermal ridges are determined rather early in fetal life with no change thereafter, so that no allowances for changes with age are necessary. Therefore, dermatoglyphics are used in biological Anthropology to explore the affinities and biological relationships among human groups[2–6]. Assessment of these biological relationships on different sets of variables is mainly based on sex- relationship and bimanual (asymmetry) relationships[7–9]. Cummins and Midlo[1] in their classical work »Finger Prints, Palms and Soles«, summarized that sex differences are expressed with different intensity in diverse populations; and the level of bimanual asymmetry in both finger and palmar traits are higher in males than in females. The differences in the indices of pattern intensity and finger ridge counts usually have higher values in males[10–12]. Further, it is known that females may be more canalized in their growth and development than males[13–14] and thus they are less affected by environmental insults. The intrauterine environmental influences are more on the dermatoglyphic traits in males were postulated by several authors[15–17].

The possible effects of environmental stress on dermatoglyphic structure (early fetal life) may increase the level of asymmetry[18]. Mainly there are two categories of asymmetry – the directional (signed difference) and the fluctuating (random difference) asymmetry. These two categories differ in their biological significance; directional asymmetry (DAs) may be regarded as developmentally controlled, presumably having a genetic basis, whereas fluctuating asymmetry (FLAs) is considered as a result of developmental noise[18–23]. Therefore, research on the biological significance of two kinds of asymmetry in dermatoglyphic traits is surely needed among diverse populations.

Another important aspect – intra-individual diversity (Div) introduced by Holt[24,10] as a measure of digital differences evaluated by finding the sum of squares of deviations of the ten separate digital counts from their mean ($S/\sqrt{10}$). The importance of this trait was emphasized on

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a set of 66 dermatoglyphic variables by Micle and Kobyliansky[25]. Some studies demonstrated that diversity display ethnic variation based on a comparative study between groups of European and African ancestry[26]. Comparative studies in dermatoglyphics are not only reveals ethnic differences of diversity, but also shows geographical variation among populations from Europe, the Middle East, and Africa was suggested by Dittmar[27]. In a series of studies, Leguebe and Vrydagh[28,29] investigated the diversity of finger ridge counts in males and females across the world. They concluded that the structure of diversity of ridge counts on separate fingers differs in different population groups but there is similarity between males and females. However, these traits are generally been neglected in dermatoglyphic studies and thus important to include in dermatoglyphic research.

Although the above mentioned studies were useful and important in potential sex-differences but the results display differently in dermatoglyphic traits among various populations and thus controversial[4]. Therefore, studying sex-relationships among different sets of dermatoglyphic traits is very illuminating. Further, we have interesting results on the same issue in the Chuvashian[30–33] and in Indian populations[7,8,34,35] but studies in the Turkmenian populations are hardly available. The objective of this study is to compare the extent of sex-variation between two different sets of dermatoglyphic traits (22 commonly used traits and 42 diversity and asymmetry traits) through Multivariate analyses which includes-Cluster, Discriminant, and Mantel test of matrix correlation in the Turkmenian population.

Materials and Methods

Study population

The word Turkmen is thought to come from the Persian word »Tir« or in Turkic pronunciation »Tur« which means arrow and the word »Kamon« or the Turkic pronunciation »Keman« which means bow. The Turkmen are a Turkic people found primarily in the Central Asian states of Turkmenistan and Afganistan and in northeastern Iran (Figure 1).

They speak the Turkmen language which is classified as part of the Western Oghuz branch of Turkic languages family together with Turkish, Azerbajani, and Turkoman spoken in Iraq. Historically, all of the Western or Oghuz Turks have been called Turkmen, however today the terms are usually restricted to two Turkic groups: the Turkmen people of Turkmenistan and adjacent parts of central Asia, Iraq and Syria, which are similar but not identical ethnic groups. During the Ottoman period these nomads were known by the means of Turkmen which generally used to describe their way of life, rather than their ethnic origin.

The modern Turkmen people descend, at least in part from the Oghuz Turks of Transoxiana, the western portion of Turkestan, a region that largely corresponds to much of Central Asia as far east as Xinjiang. Oghuz

Fig. 1. Map showing geographic locations of studied samples.

tribes had moved westward from the Altay mountains in 7th century CE through the Siberian steppes and settled in this region, and also penetrated as far west as southern Russia and the Volga basin. These early Turkmens are believe to have mixed with native Iranian peoples and lived as pastoral nomads until the Russian conquest.

Genetic studies on Mitochondrial DNA (mtDNA) restriction polymorphism confirmed that Turkmen were characterized by strong presence of European Y and mtDNA lineages, similar to the European populations, but eastern Asian genetic component observed in Turkmen and Iranian populations with the frequencies of about 20%.

Turkmen is the name of the language of the titular nation of Turkmenistan; however, they also claim a good knowledge of Russian, a legacy of the Russian Empire and Soviet Union. Turkmenian ethnically belongs to the Fergana Middle Eastern Caucasoids whose language group is Altaic[36] and who live in the hot desert climate of Central Asia. The Turkmen were mainly a nomadic people for most of their history Turkmen lifestyle was heavily invested in horsemanship and as a prominent horse culture; Turkmen horse-breeding was an ages of old tradition.

The chosen rural population for this study is characterized by (i) demographically stable family structure; (ii) many Turkmen still live in extended families where various generations can be found under the same roof, same environmental conditions i.e. in an arid climatic zone especially in rural areas; (iii) most of the families have fairly similar biotic, economic, and professional conditions; (iv) they have not been exposed to the outside cultural influences, and thus the rate of inter-marriage with non-Turkmenians is extremely low. Turkmenian sample used in this study based on big populations and thus inbreeding values are close to zero. Turkmenian populations from the rural regions of 10 villages near Chardzevsk in Turkmenia were used for the present study. The sample consists of 745 individuals (309 males and 436 females) and was collected (1993) by a joint expedition of the Moscow State University Anthropological

Institute (Russia) and the Department of Anatomy and Anthropology, Tel Aviv University (Israel).

Dermatoglyphic print analysis

Dermatoglyphic prints of 547 individuals (293 males, 254 females) were collected according to the rolled print (inked) method of Cummins and Midlo[1]. The variables used in the present study were categorized into two main categories. The first category included the 22 usually studied quantitative traits (12 digital ridge counts, 2 palmar a-b ridge counts, 3 pattern intensity indices (PII), 4 palmar main line (A and D) endings, and – the main line index (MLI)). The second category included the 42 variables that represent the indices of diversity and asymmetry (11 intra-individual diversity indices, 15 directional asymmetry traits, and 16 indices of fluctuating asymmetry). Dermatoglyphic traits were evaluated for the most part by using the methods of Cummins and Midlo[1], Holt[10] and Penrose[37]. The indices of intra-individual diversity and asymmetry were calculated according to Jantz[26] and Kobyliansky et al.[38]. The dermatoglyphic variables are presented in Appendix 1 and the formulae for calculating various indices are presented in Appendix 2.

Statistical Analyses

Cluster analysis

The phenotypic correlations between dermatoglyphic variables were determined in males and females separately. The obtained matrices of correlations were used to calculate the Euclidean distances between each pair of traits. These results were constructed by the complete linkage method and grouped into dendrograms, following Hartigan[39].

Discriminant analysis

In the present study this analysis was used to compare the ability to sort individuals into male and female groups according to two categories of dermatoglyphic variables. The analysis was performed in two stages: (1) selecting independent variables on the basis of their discriminating power according to the Wilks step-wise method in which the variable minimizes the overall Wilks Lambda and maximizes the Mahalanobis distances; and (2) arranging a correct classification, based on a comparison between the sexes. The SPSS statistical software[40] was used for Discriminant analysis.

Mantel test

The Mantel test statistic, Z, is used to measure the degree of difference in the relationships between two matrices. It takes two symmetric similarity/dissimilarity matrices and plots one matrix against the other[41,42]. The quantity of Z is obtained from the procedure of the corresponding elements of the two half-matrices, which are multiplied and summed up. The test criterion is $Z=\Sigma$ Xij Yij, where Xij and Yij are the off-diagonal elements of matrix X and Y.

Significance tests were carried out by comparing the observed, Z value with its permutational distribution. This distribution was obtained by comparing one matrix, say X, with all the possible matrices, in which the order of the variables in the other matrix Y, has been permuted. If the two matrices show similar relationships, then Z should be the larger one. The MXCOM matrix comparison program was used for this analysis.

The data were processed at the Tel Aviv University Computer Center, Israel and at the Indian Statistical Institute, India.

Results

Cluster analysis

The cluster trees have been drawn based on the correlation matrices of 22 quantitative dermatoglyphic traits, and 42 dermatoglyphic traits of intra-individual diversity and asymmetry in males and females (Figure 1a, 1b and Figure 2a, 2b).

22 traits

The dendrograms, based on 22 quantitative dermatoglyphic traits in males and females, are presented in Figures 1a and 1b. Clearly, the cluster trees represent three main clusters for both sexes. Of the three, the first cluster is the broadest one and comprises variables of the ridge counts of individual fingers; total (TFRC) and abso-

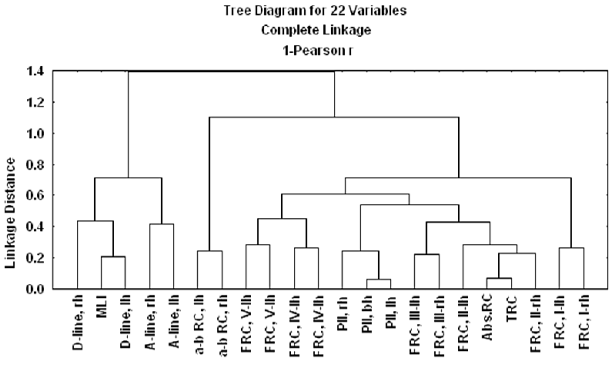

Fig. 1a. Turkmenia. Males (quantitative traits).

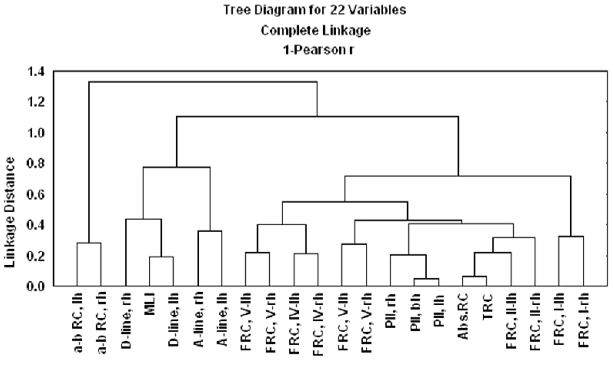

Fig. 1b. Turkmenia. Females (quantitative traits).

lute (AFRC) ridge counts and the pattern intensity index (PII). The PII counts are aggregated at the end of the first cluster in the area connecting the second cluster, and they appear in a separate component. The second cluster includes the palmar a-b ridge counts. The third cluster comprises the main line index (MLI) and its components. These results are very similar between males and females.

42 traits

The dendrograms based on 42 dermatoglyphic traits consist of intra-individual diversity as well as directional and fluctuating asymmetry; they are presented in figures 2a and 2b for males and females, respectively. The cluster trees can be classified into three main clusters. The first cluster comprises 11 intra-individual diversity indices of the finger ridge counts that they are joined by some other measures of FLAs indices. The second cluster is mainly aggregated by the indices of fluctuating asymmetry as well as directional asymmetry. The third cluster contains the variables of directional asymmetry and some indices of fluctuating asymmetry. All the variables form a number of small sub-clusters under the broad clusters and in general, these variables are scattered into a number of small clusters. The dendrograms between males and females are markedly similar; only a small number of rearrangements have occurred.

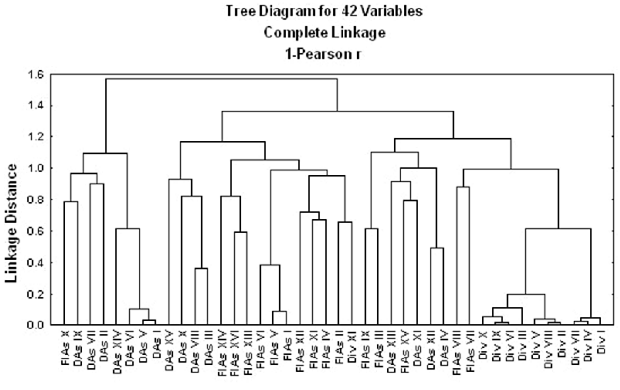

Fig.2.a. Turkmenia. Males (diversity & asymmetry)

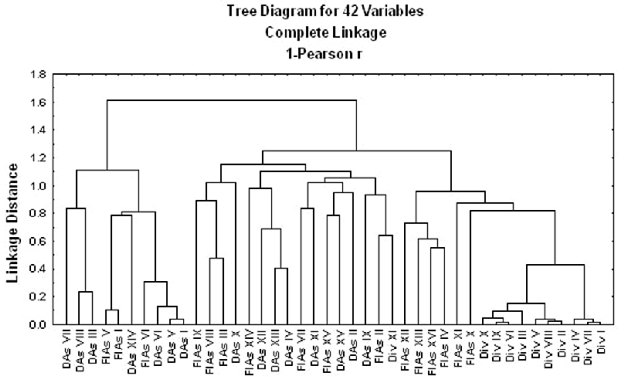

Fig.2.b. Turkmenia. Females (diversity & asymmetry)

Discriminant analysis

The variables manifesting a partial multivariate F-ratio, which were selected, are those that have values greater than 4 and are used in the discriminating procedure. In the first stage, those variables that are best able to discriminate between the two groups of dermatoglyphic variables are presented in Table 1. In the second stage, a sorting or a correct classification was made, whereby every individual was classified into a group as males and females based on the selected independent variables from the two groups of dermatoglyphic variables, which are presented in Table 2.

22 traits

Regarding the discriminating power of the 22 variables (Table 1), 5 variables were selected, namely, three ridge counts of individual fingers and two D and A line exits. The corresponding values of Wilks Lambda and Minimum D-Square values are almost similar. In this case, 64.14% of the individuals were correctly classified by sex (Table 2).

42 traits

Similarly for 42 traits, the selected number of variables by discriminating power is six (Table 1); these include one diversity and five FLAs and DAs. Similar results were also obtained from the Wilks Lambda and Minimum D-Square values. The percentage of correctly classified individuals by sex is 65.47% in this case.

TABLE 1
DISCRIMINANT ANALYSIS BETWEEN MALES AND FEMALES, THE SELECTED DISCRIMINANT TRAITS WITH F>4, AND THEIR WILKS LAMBDA AND MINIMUM D SQUARED VALUES

Variables	Wilks lambda	Minimum D squared
22 traits.		
Finger RC, I-lh	0.933	0.288
Finger RC, I-rh	0.924	0.333
Finger RC, III-lh	0.920	0.351
Finger RC, II-rh	0.908	0.406
PII rh	0.903	0.434
PII both h	0.890	0.498
Finger RC, IV-rh	0.884	0.531
Finger RC, V-lh	0.877	0.567
42 traits		
FlAs VI	0.966	0.140
FlAs XIII	0.943	0.243
DAs II	0.928	0.314
FlAs VII	0.911	0.395
FlAs X	0.894	0.475
FlAs IX	0.882	0.540
FlAs V	0.870	0.602

TABLE 2
RESULTS OF DISCRIMINANT ANALYSIS BETWEEN MALES AND FEMALES

22 traits		Predicted group	
Real group	No. of cases	Males	Females
Males	233	149 (63.9%)	84 (36.1%)
Females	309	119 (38.5%)	190 (61.5%)
Percent of correctly classified cases =62.55%			
42 traits		Predicted group	
Real group	No. of cases	Males	Females
Males	176	114 (64.8%)	62 (35.2%)
Females	210	68 (32.4%)	142 (67.6%)
Percent of correctly classified cases =66.32%			

Relationship between Cluster and Discriminant analysis

Regarding the discriminating power between the two groups, namely 22 and 42 variables (Tables 1 and 2) the results clearly show very marginal variations within the Turkmenian population. This result indicates that sex dimorphism is similar in two categories of variables and was confirmed by the next analysis using the Mantel test.

Mantel test of matrix correlations

With the aim of comparing these two categories of variables with respect to male vs. female, we performed the Mantel test of matrix correlations for significance tests within the Turkmenian population. The above Discriminant power of the two groups of variables, which proved to be almost similar between males and females, was confirmed by the similarity/correspondence test of the Mantel statistic, Z. The values of Z are within the level of non-significance, i.e., very good similarities in 22 (0.95) and good similarities in 42 (0.87) traits. The levels of similarity are: $0.9 \leq r$ (very good) and $0.8 < r \leq 0.9$ (good).

Discussion

Characteristics of the studied traits between sexes

It should be mentioned here that in our earlier papers in the Chuvashian population[30–33] we have studied sex comparisons – finger versus palmar dermatoglyphic traits with respect to qualitative, quantitative, diversity, and asymmetry traits. The palmar patterns exhibit more variation – significant sex differences compared with finger patterns – non-significant sex difference[30]. Indian populations (five) are revealed mostly uniform sex difference with respect to qualitative and quantitative finger ridge counts[8,34] but palmar traits display differently when compared with other human groups. However, we obtained in both sexes a common feature with factor 1- the digital pattern size factor (based on finger ridge counts) in the Chuvashian[32], Indian[7] and Turkmenian[43] populations and all the factors are similar in both sexes. This result fully corresponds to earlier studies- in Blacks and Whites populations[15], in German population[44], in Indian populations[45]. This similarity of results establishes its universality in human populations of diverse origin. Possible explanations[46] for the above findings of sex differences between finger and palmar traits are as follows: a) the differences are due to different durations of the growth period, relatively longer in palmar traits compared with finger traits during embryological development. b) The palmar dermatoglyphic pattern affinity corresponds better than fingers to the ethno historical background of the populations. c) The degree of universality of the principal factor (finger ridge counts) suggests that the variability of finger ridge counts is determined by the same genes that control the pattern types. With the above characteristics we may expect to obtain similar findings in Turkmenian population from the following analyses.

Cluster analysis

The similarity of the dermatoglyphic variables in males and females between the two groups is well reflected by the cluster analysis of the Turkmenian population (Figures 1a, 1b and 2a, 2b). Four main clusters were obtained from each of the two categories of variables that are exactly similar between the two sexes, although a number of rearrangements took place in the variables associated with these clusters. With the same objective and based on the same variables the dendrograms obtained by Micle and Kobyliansky[47] in Jewish populations, Karmakar et al.[35] in five Indian populations and in the Chuvashian populations[33]. Our present results are in agreement with these results and may suggest a common genetic background and the possible influence of environmental factors on the realization of sexual dimorphism.

Discriminant analysis

Our present results of Discriminant analysis by sex appears the percentages of correctly classified individuals are 64.14% (22 traits) and 65.45% (42 traits) which indicate lower percentage compared to the earlier study[25], 71.61% in the Israeli Jewish population. However, in this study a total of 66 dermatoglyphic variables including diversity and asymmetry were used. In a similar study on North African Jews, based on the same two categories of dermatoglyphic variables as were presented in our present study[48] correctly classified 60.06% and 69.16% of the individuals; in an Israeli population Micle and Kobyliansky[47] observed 69.6% and 68.8%; Karmakar et al.[35] with five different Indian populations, obtained 61.49% to 66.00% and 60.87% to 63.75%. These findings are similar to the present findings of Turkmenian population. The above results regarding the level of sexual dimorphism in different populations of differing geographic extraction suggest a common genetic background of the two categories of dermatoglyphic variables (22 quantitative traits and 42 indices of asymmetry and diversity), which provided similar possibilities of discrimination between sexes.

Conclusion

The obtained results of various statistical analyses based on the two different categories of dermatoglyphic traits, strongly suggest that the two different sets of dermatoglyphic variables may be used for sex- discrimination in different populations.

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SEKSUALNI DIMORFIZAM KOD DVA TIPA DERMATOGLIFSKIH NALAZA U TURKMENISTANSKOJ POPULACIJI: DISKRIMINANTNA ANALIZA

SAŽETAK

Cilj ove studije je usporediti spolne razlike između dva različita seta dermatoglifskih nalaza (22 kvantitativna i 42 pokazatelja raznolikosti i asimetrije). Otisci sa prstiju i dlanova turkmenistanske populacije (547 pojedinaca) su korišteni za multivarijatne analize, što je uključivalo klaster i diskriminantnu analizu te Mantel test matrice korelacije. Sve varijable (dvije skupine) koje su se raspršile u manje klastere nisu pokazivale veće razlike među spolovima. Ove rezultate je potvrdila i diskriminantna analiza – dvije skupine varijabli su gotovo jednake, sa postotkom točno klasificiranih pojedinaca 64,14% (za 22 značajke) i 65,45% (42 značajke); kao i Mantel statistika – Z vrijednosti su unatar granica i nisu statistički značajne, sličnosti su vrlo velike kod 22 (0,95), a velike kod 42 značajke (0,95). Seksualni dimorfizam je sličan kod obje kategorije dermatoglifskih varijabli i one se mogu koristiti pri razlikovanju spolova kod različitih populacija.

APPENDIX 1
LIST OF THE UTILIZED TRAITS AND INDICES

22 quantitative traits	15 Directional Asymmetry (DAs) traits
Finger RC, I r	DAs I = Div II – Div I
Finger RC, II r	DAs II = PII, rh – lh
Finger RC, III r	DAs III = a-b RC, r – l
Finger RC, IV r	DAs IV = hRC, rh – lh
Finger RC, V r	DAs V = S^2, rh – lh
Finger RC, I l	DAs VI = Div VIII – Div VII
Finger RC, II l	DAs VII = atd angle, r – l
Finger RC, III l	DAs VIII = a-b dist., r – l
Finger RC, IV 1	DAs IX = ridge breadth, r – l
Finger RC, V 1	DAs X = fRC, Vr – Vl
Total RC (TRC)	DAs XI = fRC, IVr – IVl
AbsRC	DAs XII = fRC, IIIr – IIIl
PII, lh	DAs XIII = fRC, IIr – IIl
PII, rh	DAs XIV = fRC, Ir – Il
PII, both h	DAs XV = MLI, rh – lh
a-b RC, rh	16 Fluctuating Asymmetry (FLAs) traits
a-b RC, lh	FlAs I = [Div I – Div II]
A-line exit, l	FlAs II = PII, [rh – lh]
A-line exit, r	FlAs III = a-b, RC, [rh – lh]
D-line exit, l	FlAs IV = hRC, [rh – lh]
D-line exit, r	FlAs V = [Div V – Div IV]
MLI	FlAs VI = [Div VIII – Div VII]
42 traits (diversity and asymmetry):	FlAs VII = atd angle, [r – l]
11 Diversity traits (Div)	FlAs VIII = a-b dist, [r – l]
Div I = max – min fRC (lh)	FlAs IX = ridge breadth [r-l
Div II = max – min fRC (rh)	FlAs X = fRC, [Vr – Vl]
Div III = max – min fRC (both h)	FlAs XI = fRC, [IVr – IVl]
Div IV = S^2 for lh, (or S^2L)	FlAs XII = fRC, [IIIr – IIIl]
Div V = S^2 for rh, (or S^2R)	FlAs XIII = fRC, [IIr – IIl]
Div VI = S2 (both h)	FlAs XIV = fRC, [Ir – Il]
Div VII = IIDL (for lh)	FlAs XV = MLI, [rh – lh]
Div VIII = IIDL (for lh)	FlAs XVI = A1, asymmetry index
Div VIII = IIDR (for rh)	
Div IX = S, $\sqrt{10}$ (both h)	
Div X = S, $\sqrt{5}$(both h)	
Div XI = Shannon's index	

Abbreviations: RC = ridge count; r = right; l = left; h = hand; PII – Pattern Intensity Index; MLI = main line index; Div I to Div XI = indices of intra-individual diversity of finger ridge counts; DAs I to DAs XV = indices of directional asymmetry; FlAs I to FlAs XVI = indices of fluctuating asymmetry

Appendix 2

Formulae for some indices of dermatoglyphic diversity and asymmetry

Computation of the directional asymmetry (DA) was effected by the following equation: $DAij = X_{iR} - X_{iL}$.

Computation of the fluctuating asymmetry (FA) was done by using the absolute differences between the bilateral measurements. In order to avoid additional influences (scaling effects) like size of the trait or directional asymmetry, the distribution of the non-absolute differences for each individual were corrected (Livshits et al., 1988) so as to yield the following equation for computing FA:

$$FA_{ij} = (X_{iR} - X_{iL}) - 1/n \sum_{i=1}^{n} (X_{iR} - X_{iL})$$

Where, xi = trait (x) of individual (i); R, L = right and left, n = size of the sample and FA_{ij} is the value of FA of trait (j) in the i^{th} individual.

Div I, Div II, Div III. Maximal minus minimal finger ridge counts in the five left (Div I), five right (Div II), or in the ten finger ridge counts (Div III). Div IV, Div V= $\sum_{i=1}^{5} q_i^2 - Q^2/5$, for the left (Div IV, S^2L), or right fingers (Div V, S^2R); Div VI, $S^2 = \sum_{i=1}^{10} q_i^2 - Q^2/1\,0$ Div VII, Div VIII $= \sqrt{\sum_{i=1}^{5} q_i^2 - Q^2/5}$, for the left (Div VII, IIDL), or right finger (Div VIII, IIDR); Div IX, $S\sqrt{10} = \sqrt{\sum_{i=1}^{10} (q_i^2 - Q^2/10)/10}$; Div X, $S\sqrt{5} = \sqrt{\sum_{i=1}^{5} (k_i^2 - Q^2/5)/5}$;

In these formulae, q_i is the ridge count for the i^{th} finger, Q is the sum of the five finger ridge counts of a hand (Div IV, V, VII, VIII) or of all the ten fingers (Div VI, IX, X), and k is the sum of ridge counts of the i^{th} pairs of homologous right and left fingers.

DivXI. Shannon's index, $D = -\sum_{i=1}^{4} P_i \log P_i$ where P_i is the frequency of each of the four basic finger pattern types on the ten fingers; Abs XVI, $AI = \sqrt{\sum_{i=1}^{5} (R_i - L_i)^2}$, where R_i and L_i are the ridge counts for the i^{th} finger of the right and left hand.