International Journal of Modern Anthropology
Int. J. Mod. Anthrop. (2011) **4** : 12 - 27
Available online at www.ata.org.tn ; doi: 10.4314/ijma.v1i4.1

Original Synthetic Report

Anthropological significance of dermatoglyphic trait variation: an intra-Tunisian population analysis.

Imene Namouchi

Imene Namouchi obtained her doctorate in Genetics from the Faculty of Sciences of Tunis. She's Department Director at ISAJC, University of Tunis. She has contributed to research in Human Genetics particularly on dermatoglyphics and on the socio-epidemiology of the autism.
E-mail: imen_namouchi@yahoo.fr

Laboratory of Human Genetics and Anthropology, Faculty of Pharmacy, University of Monastir, Tunisia
& ISAJC of Tunis, University of Tunis, Tunisia

Abstract – ***Background:*** The human dermatoglyphic traits present variations within and between populations and could be used for estimating the genetic distances between populations. ***Aim:*** This study aims to characterize the dermatoglyphic traits in the Tunisian population and to analyze eventual differences between men and women and between individuals according to their geographical distribution. ***Subjects and Methods:*** Several dermatoglyphic traits have been determined and analysed for 343 Tunisians belonging to six groups distributed on different Tunisian regions. For statistical analysis, the percent frequency, chi square test and t-test were used. The cluster analysis was applied on D^2 Mahalanobis distance matrix. ***Results:*** The chi-square test revealed high significant differences between the sexes for the frequencies of arches in the case of the fifth finger and for the frequencies of loops in the case of the fourth left finger and the first left finger. The difference of the distribution of whorl type between men and women was statistically significant for the fourth left finger. While no significant differences were found between sexes in finger ridge counts. ***Conclusion:*** The intra-Tunisian population analysis shows that Tunisians living in the North and the expanded East Centre of Tunisia are genetically very close, while Tunisians from the extreme East Center and the South of Tunisia are relatively less close to them. This conclusion agrees with that deduced from recent molecular marker analyses and shows that the multivariate analysis of a high number of quantitative digito-palmar dermatoglyphic traits represents a powerful and shrewd tool in intra-population analyses.

***Key words*:** Dermatoglyphics, Fingerprints, Tunisian population, Cluster analysis, Intra-population analysis

Introduction

Dermatoglyphics attracted a great number of scientists from all sections of biology, medicine and biological anthropology (Chen Yao-Fong et al., 2008) and links between dermatoglyphics and diseases or congenital abnormalities have also been explored (Tarca, 2001; Kumar et al., 2003; Miliĉić et al., 2003; Saha et al., 2003). In fact, dermatoglyphs are used as easily accessible tool to assess genetically determined diseases (Miliĉić et al., 2003; Temaj et al., 2009). Moreover, dermatoglyphics have been used extensively to characterize human populations and most studies have focused on dermatoglyphic variables within and between various populations across the world (Crawford and Duggirala, 1992; Demarchi et al., 1997; Reddy et al., 2001; Weisensee and Siváková, 2003; Arrieta, 2003) or between sexes (Esteban and Moral, 1993; Kusuma et al., 2002). In the latter and in more recent studies, the dermatoglyphic traits are used for estimating the genetic distances between populations (Temaj et al., 2009; Cheng et al., 2009).

Fingerprints or dermatoglyphs consist of patterns formed by parallel ridges on bare skin of fingertips. They are typical for higher primates, but occur sporadically in other mammals (Henneberg et al., 1997). The dermatoglyphic patterns of dermal ridges that constitute human fingerprint are formed during early intrauterine life, between the 7th and 21st week of gestation (Miliĉić et al., 2003) and are fully formed at about seven months of foetus development (Maltoni et al., 2003; Sharma et al., 2008). It has been reported that ridges are influenced by blood vessel-nerve pairs at the border between the dermis and epidermis during prenatal development (Kahn et al., 2008). Factors such as inadequate oxygen supply, unusual distribution of sweat glands and alterations of epithelial growths could influence ridge patterns (Schaumann and Alter, 1976).

The finger ridge configurations do not change throughout the life of individuals by environment or age factors except in events such as bruises and cuts of the fingertips (Henneberg et al., 1997). This property makes fingerprints a very attractive biometric identifier (Maltoni et al., 2003; Karmakar et al., 2009). Finger ridge counts and frequencies of all palm patterns follow the genetic modes of major genes. The distribution of interdigital patterns has been proven to follow a multi-allelic major gene mode of inheritance (Meenakshi et al., 2006; Bhasin, 2007; Cheng et al., 2009).

A similar mode of inheritance has also been observed for finger ridge counts in which significant genomic linkage has been found on chromosomes 5 and 1 (Medland et al., 2007). However, no Mendelian modes of inheritance have been discovered for most dermatoglyph characteristics in pedigree studies because of either low inheritance or a too large number of contributing genes (Sengupta and Karmakar, 2004).

In the present study, I investigate for the first time several dermatoglyphic traits in a representative sample of the Tunisian population in order to analyze eventual differences between men and women and between individuals according to their geographical distribution and to compare the obtained data with those found in other studied populations.

The current general Tunisian population is composed mainly by Berbers, natives of North Africa, mixed with some peoples from the different civilizations that have settled this region in historical times, particularly Arabs who, unlike the precedents, settled permanently in Tunisia following their substantial expansion in the 7^{th} century. Berbers and Arabs accepted mixed marriages until became a common unique population except for few Berber groups. These Berber groups are small, often not exceeding 4000 individuals. Although known as Berber communities, they only remember some words of their ancestral Berber language and are slightly mixed with others outside the group. The general Tunisian population was studied according to several genetic and molecular markers (eg. Chaabani and Cox, 1988; El Moncer et al., 2010).

Here I will confront the deduced conclusion with that emanating from the most important recent molecular study in order to estimate the anthropological significance of dermatoglyphic trait variation. In addition of this anthropological contribution present data will be used in future studies as control data for comparison with those obtained in sick Tunisians.

Subjects and Methods

The sample included 343 unrelated healthy Tunisians: 233 men and 110 women, of different ages (ranging from 18 to 58 years) and randomly-chosen. All individuals are divided according to their geographical membership in 6 groups.

As shown in Figure 1, the two groups 1 and 2 belonged to the North, area I (Group 1: Tunis district and Group 2: Bizerte – Jendouba – Béja – Nabeul), the two groups 3 and 4 represent the expanded Tunisian East Center, area II (Group 3: Zaghouan – Siliana – Kairouan – Sidi Bouzid and Group 4: Sousse – Monastir – Mahdia – Sfax), the two groups 5 and 6 represent the West Center and the South, area III (Group 5: Le Kef – Kasserine – Gafsa – Tozeur and Group 6: Kébili- Gabès – Medenine – Tataouine).

Figure 1. Location of the three areas obtained on the cluster tree:
Area I: GP1 and GP2; Area II: GP3 and GP4; Area III: GP5 and GP6.

Finger and palmar prints of both hands were collected and analyzed according to the Cummins and Midlo (1961). The number of ridges counted on each finger consisted of 10 variables of the finger ridge count FRC : finger ridge count right for each finger on the right hand (FRC R_1 – FRC R_5) and the finger ridge count left for each finger on the left hand (FRC L_1 – FRC L_5). The counting was carried according to Holt (1968) (Figure 2).

According to Holt (1968), the ridge count consists of the number of ridges which cut or touch a straight line running from the triradius to the core or center of the pattern. Between-sex comparisons were carried out by means of chi-square contingency analysis for qualitative variables and t-test was used to examine quantitative variables for sexual comparisons. Discriminant analysis was carried out with the six groups according to their geographical distribution and the cluster analysis was applied on D^2 Mahalanobis distance matrix.

Results

The different pattern types are broadly classified into three principal patterns namely whorls, loops and arches and their frequencies are given in Table 1. In both sexes, loops were the most predominant pattern type followed by whorls and arches. The percentage of arches varied from 1.5 % to 14.15 % for men and from 3.6 % to 20.45 % for women. The chi-square test revealed high significant differences between the sexes (χ^2 = 10.520; P = 0,001) for the frequencies of arches for the little left (the fifth) finger. The percentage of loops varied from 51.3 % to 79.8 % for men and from 49.05 % to 79.55 % for women. The chi-square test revealed significant differences between the sexes for the frequencies of loops for the fourth left finger (χ^2 = 3.908; P= 0.048) and for the first left finger (χ^2 = 4.395; P = 0.036).

The percentage of whorls varied from 17.2 % to 44.45 % for men and from 15.45 % to 45.9 % for women. The difference of the distribution of whorl type between the sexes was statistically significant (χ^2 = 4.221; P = 0.04) for the fourth left finger.

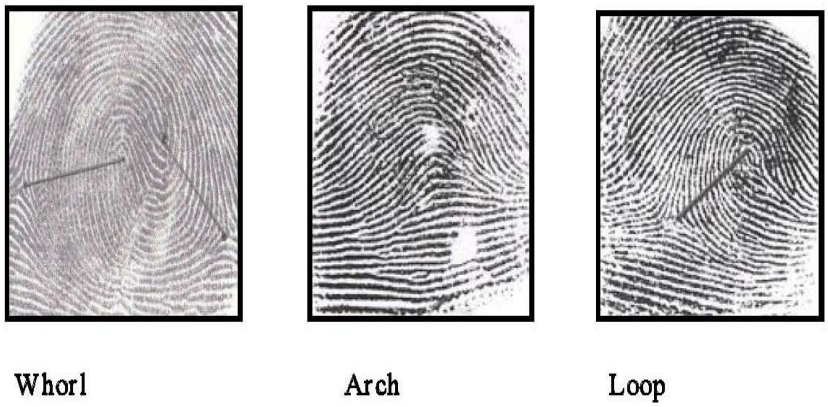

Figure 2: Main types of finger patterns.
The lines on the loop and whorl patterns connect the triradius and the core, these lines are used in counting ridges. In the case of whorls, the higher ridge count was taking.

Table 1. Frequency of digital pattern types.

	Men			Women		
Type of finger	Arch	Loop	Whorl	Arch	Loop	Whorl
R.thumb	4.3	47.2	48.5	3.6	53.6	42.7
L.thumb	5.2	56.7	38.2	6.4	44.5	49.1
Average	4.75	51.95	43.35	5.0	49.05	45.9
R. index	13.7	52.8	33.9	19.1	55.5	25.5
L. index	14.6	53.6	31.8	21.8	52.7	25.5
Average	14.15	53.2	32.85	20.45	54.1	25.5
R. middle	7.3	77.3	15.5	6.4	77.3	16.4
L. middle	13.7	67.4	189	11.8	70.0	18.2
Average	10.5	72.35	17.2	9.1	73.65	17.3
R. ring	4.3	49.4	46.4	3.6	58.2	38.2
L. ring	4.7	53.2	42.5	3.6	64.5	30.9
Average	4.5	51.3	44.45	3.6	61.35	34.55
R. little	1.7	78.1	20.2	1.8	83.6	14.5
L. little	1.3	81.5	17.2	8.2	75.5	16.4
Average	1.5	79.8	18.7	5.0	79.55	15.45

Results of descriptive statistics comparing quantitative digito-palmar dermatoglyphic traits for men and women are presented in Table 2. The highest number of ridges in both sexes is always on the first finger. The total finger ridge count in men on the left hand (TFRCL) is 69.897 (SD = 23.105) and is 71.931 (SD = 22.859) on the right hand. In women, this ridge count is 67.364 (SD = 25.717) on the left hand and is 68.436 (SD = 22.329) on the right hand. The results of the t-test have not shown significant differences between sexes in finger ridge counts.

Results of multivariate discriminant analysis of the six examined Tunisian groups for 15 quantitative digito-palmar dermatoglyhic traits revealed that out of five canonical discriminant functions, the first two ones explained 62.3 % of variance. Standardized canonical discriminant function coefficients are given in Table 3. Table 4 shows coordinates of group centroïds in discriminant space. The discriminant function 1 has the highest correlation with variable TFTC while the discriminant function 2 describes the variability of the TFRCR.

Table 2. Descriptive statistics for quantitative digito- palmar dermatoglyphic traits of men and women.

	Men		Women	
Variable	Mean	SD	Mean	SD
Right hand				
FRCR1	19.017	6.735	17.709	6.137
FRCR2	12.004	6.477	10.955	6.838
FRCR3	12.167	5.505	12.000	5.405
FRCR4	15.107	5.588	14.927	5.084
FRCR5	13.760	4.732	12.855	4.397
T FRCR	71.931	22.859	68.436	22.329
a-b RCR	38.790	5.905	38.473	5.604
Left hand				
FRCL 1	17.133	6.483	16.718	6.504
FRCL2	11.335	6.563	10.645	7.052
FRCL3	12.262	6.468	12.055	6.692
FRCL4	15.313	6.004	15.200	5.583
FRCL5	13.897	4.482	12.782	5.531
T FRCL	69.897	23.105	67.364	25.717
a-b RCL	40.356	19.362	39.509	4.964
TFRC	141.914	44.825	135.809	47.071

Table 3. Standardized canonical discriminant functions of original variables.

Variables	1	2	3	4	5
FRCLI	3.094	0.640	1.645	1.636	0.558
FRCLII	2.849	0.934	1.738	0.362	0.238
FRCLIII	2.815	-0.138	1.723	0.966	-0.112
FRCLIV	2.505	-0.368	1.523	1.475	0.060
FRCLV	1.935	0.690	1.784	0.810	-0.098
FRCRI	-0.124	-2.457	5.763	-2.083	1.797
FRCRII	0.090	-3.135	5.017	-1.842	1.834
FRCRIII	1.162	-1.720	4.524	-1.686	1.346
FRCRIV	0.652	-1.866	3.978	-2.589	2.211
FRCRV	0.633	-1.828	3.487	-1.011	1.370
TFRCL	-4.493	0.607	-5.253	-1.076	1.183
TFRCR	3.514	12.531	-15.922	8.993	-6.065
TFTC	-11.126	-5.644	-3.140	-4.516	-2.781
PRCL	-0.322	0.040	0.052	-0.084	-0.335
PRCR	-0.183	-0.062	-0.025	0.077	0.824

Abbreviations: FRCL : Finger ridge count left; FRCR : Finger ridge count right; TFRCL: Total of finger ridge count left; TFRCR : Total of finger ridge count right; TFRC : Total of finger ridge count of both hands; PRCL : Palmar ridge count left; PRCR : Palmar ridge count right.

Table 4. Canonical scores of group means

Group	1	2	3	4	5
1	0.220	-0.156	-0.215	0.034	-0.116
2	0.028	-0.190	0.227	0.178	0.069
3	-0.034	0.213	-0.189	0.051	0.254
4	0.167	0.377	0.145	-0.004	-0.137
5	-0.563	-0.038	-0.012	-0.090	-0.072
6	0.332	-0.175	0.149	-0.498	0.137

The squared quantitative dermatoglyphic distance D^2 values for the six groups are shown in Table 5. The cluster tree based on Mahalanobis distances is given in Figure 3. The shortest genetic distance at 0.25 is between people from North of Tunisia (GP1 and GP2), followed by that between people from expanded East Centre (GP3 and GP4). Thus people of these 4 groups (GP1, GP2, GP3 and GP4) belonged to North and the expanded East Centre of Tunisia is genetically very close. On the other hand GP5 and GP6 people from regions of the extreme West Centre and particularly from the South of Tunisia are separated from the precedents representing two other clusters with largest genetic distances.

Table 5. Per character D^2 values.

	1	2	3	4	5	6
1	0.000					
2	0.683	0.000				
3	0.676	0.742	0.000			
4	0.876	0.842	0.576	0.000		
5	1.523	1.095	0.904	1.394	0.000	
6	0.580	0.640	0.748	0.701	1.169	0.000

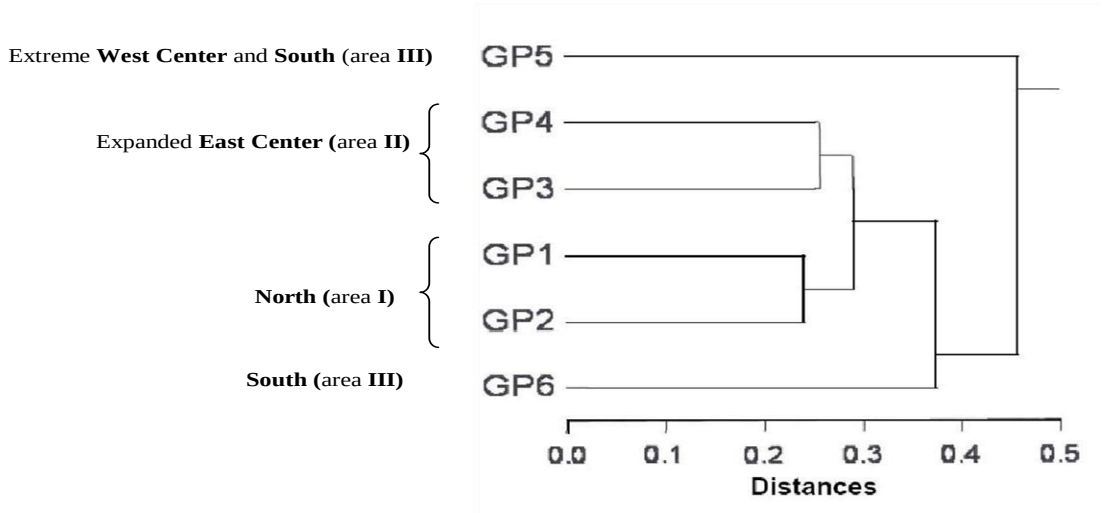

Figure 3. **Cluster tree based on Mahalanobis distances.**

Discussion

The present study provided the first data on the dermatoglyphic trait variation in the Tunisian population. The analysis of finger pattern type showed that in both sexes, loops were the most common pattern followed by whorls and arches and that differences between sexes are significant for the frequencies of arches for the fifth left finger and for the frequencies of loops for the fourth left finger. Similarly, finger patterns studied in the Berber population of the high Atlas (Marrakesh, Morocco) have shown a higher frequency of loops followed by whorls and arches in both sexes but this Moroccan Berber population is particularized by greater arch frequencies when compared to data describing the other North African populations (Algeria, Libya, Tunisia) (Sabir et al., 2005).

An eastern Andalusia population was described by more whorls and radial loops in males and by more arches and ulnar loops in females (Luna and Pons, 1987). The South African populations were well investigated with regard to digital patterns. In Zimbabwean subjects, ulnar loops were the most predominant pattern type in both sexes, followed by whorls in males and arches in females; however the sex differences between the digital pattern types were not statistically significant (Igbigbi and Msamati, 2002).

Similarly, a higher frequency of loops was also seen in both sexes among the Kenyans and Tanzanians. (Igbigbi and Msamati, 2005). However, in Malawians, arches were found to be the most predominant digital pattern in both sexes, followed by radial loops in men and whorls in women and it was demonstrated that the sex differences between these digital patterns were not statistically significant (Igbigbi and Msamati, 1999).

The reasons for sexual dimorphism observed in the dermatoglyphic patterns, can be supported by the fact that differences in heritability and developmental variation among sexes might account for these patterns (Meier, 1980). On the other hand, bimanual differences have been attributed to developmental instability, measured by fluctuating asymmetry of bilateral traits which in the particular case of dermatoglyphics, must result from environmental assaults during early embryonary (Cummins and Midlo, 1961).

Differences in total ridge count frequencies between different populations may be expected, since the frequencies of arches, loops and whorls vary between populations. In our present study, the TFRC has not shown significant sexual dimorphism. In both sexes, the highest number of ridges was always observed on the first finger. The total finger ridge count in men and women (TFRCL) was higher on the right hand than on the left one.

In the Murcia, a Spanish population, it was reported that the highest mean of ridge counts was shown by the thumb of each hand in males and females, as a result of both elevated frequency of whorls and pattern width while the lowest number of ridges corresponded to index finger in both right and left hands for males and females which can be explained by the high frequency of arches and radial loops in this finger as well as the small pattern width (Esteban and Moral, 1992).

Another study on sub-Saharan Africans has also shown that the values of TFRC found among the Zimbabweans were higher in men than in women (Igbigbi and Msamati, 2002). These results were also comparable to those obtained in the Zulus of South Africa (Grace and Ally, 1973). The Southern Nigerians have a significantly higher TFRC than those previously reported for the Zulu. In Malawian subjects, women had significantly higher TFRC than men (Igbigbi and Msamati, 1999). This conclusion is contrary to that reported in Kenyans and Tanzanians (Igbigbi and Msamati, 2005).

Hajn and Gasiorowski (1999) have shown in their study of the Czech and Polish populations, that men had higher TFRC than women. In agreement with these results, TFRC of the Araucanian Indians from Patagonia, showed sexual differences and were most important in men (Arquimbau et al., 1993). The mean total ridge count for the Chibcha-speaking Amerindian tribes, for males and females, and both hands was lower in these groups compared to other North, Central and South American Indians (Garruto et al., 1979; Segura-Wang and Barrantes, 2009).

The study of the quantitative dermatoglyphic traits in Albanian and Turkish populations living in the South-West Kosovo showed significant differences between the Albanian and the Turkish males for two fingers, and on palms for a-b RC, b-c RC and c-d RC on both hands and b-c RC on the left hand, and between females for six fingers and almost all palmar traits. The differences found between the two populations show that although Albanian and Turkish populations share the same territory, they have different origins and customs, and the marriages between these two communities are extremely rare (Temaj et al., 2009).

The intra-Tunisian population analysis was done applying a higher level of differentiation based on the multivariate discriminant analysis of the six examined Tunisian groups for 15 quantitative digito-palmar dermatoglyphic traits and was represented in a cluster tree based on Mahalanobis distances. This tree shows that Tunisians living in the North and the expanded East Centre of Tunisia are genetically very close, while Tunisians from the extreme East Center and the South of Tunisia are relatively less close to them.

This conclusion agrees with that deduced from molecular marker analyses and shows that the multivariate analysis of several quantitative digito-palmar dermatoglyphic traits represents a powerful and shrewd tool in intra-population genetic differentiation. In fact in a molecular recent study (El Moncer et al. 2010) a set of 16 Alu and 3 *Alu*/STR compound systems has been analysed in 268 autochthonous Tunisians from the north-centre and the south. The two sampled populations showed no significant differentiation from one another in any of the three *Alu*/STR systems while the analysis of the 16 Alu markers reveals a significant genetic differentiation between them. In addition *Alu*/STR system analyses explain the major causes of this slight genetic differentiation between North-Center and the South of Tunisia reflecting a mixed origin of Tunisian population: The presence of a sub-Saharan component revealed by three specific *Alu*/STR combinations is more noticeable in the north-centre sample than in that of the south. While analysis of two *Alu*/STR combinations, specific to North African ancestral populations, suggests that the ancient Berber component is relatively more substantial in the north and centre regions than in the south.

Acknowledgements

Our deep gratitude goes to Pr. Saida Ben Arab for her help and assistance during our collaboration. We would like to express our special thanks to Pr. Hassen Chaabani for his critics, corrections and suggestions and also for his encouragements. We are also extremely grateful to Pr. Esther Esteban Torne for her critics and suggestions. We thank all persons in charge in the "Police Technique et Scientifique de Tunis" for their help particularly Mr. Mohamed Mostapha.

References

Arquimbau R., Esteban E., Fananas L., 1993. Finger dermatoglyphics in Delta de l'Ebre: a Mediterranean population, Anthropol. Anz 51:267-274.

Arrieta I., 2003. Dermatoglyphic variation in Spanish Basque populations. Human Biology, 75: 265-91.

Bhasin M. K., 2007. Genetics of Castes and Tribes of India: Dermatoglyphics. Int. J. Hum. Genet., 7 2: 175-215.

Chaabani H. and Cox D. W., 1988. Genetic characterisation and origin of Tunisian Berbers. Hum. Hered. 38 : 308-316.

Chen Y.-F., Zhang H.G., Shen C.-Fu., LAI Chun-Hung., 2008. A dermatoglyphic study of the Amis aboriginal population of Taiwan. Sci. China Ser. C-Life Sci., 51 (1):80-85.

Cheng Xu, Hui Li, Sameer Gupta, Shangling Pan, Jingrong Hou, Li Jin. 2OO9. Dermatoglyphic changes during the population admixture between Kam and Han Chinese. HOMO—Journal of Comparative Human Biology 60 (2009) 143–157.

Crawford M.H., Duggirala A.R., 1992. Digital dermatoglyphic patterns of Eskimo and Amerindian populations: relationships between geographic, dermatoglyphic, genetic and linguistic distances. Human Biology, 64: 683-704.

Cummins, H. & C. Midlo. 1961. Fingerprints, Palms and Soles. An Introduction to Dermatoglyphics. Dover Publications, New York, USA.

Demarchi D.A., Giordano A.R., Marcellino A.J., 1997. Dermatoglyphics in Araucanian Indians from Patagonia and multivariate comparisons with other Argentinian aboriginal populations. Human Biology, 69: 227-39.

Esteban E., Moral P., 1992. Quantitative finger dermatoglyphics in the Mediterranean region of Murcia, Spain. International Journal of Anthropology, 7(2); 17-25.

Esteban E., Moral P., 1993. Finger dermatoglyphics in a Mediterranean population (Murcia, Spain); pattern types and pattern intensity index. Anthropologischer Anzeiger, 51:159-167.

El Moncer W., Esteban E., Bahri R., Gayà-Vidal M., Carreras-Torres R., Athanasiadis G. , Moral P., Chaabani H., 2010. Mixed origin of the current Tunisian population from the analysis of Alu and Alu/STR compound systems. Journal of Human Genetics, 55: 827–833.

Garruto R., Plato C., Hoff C., Newman M., Gajdusek D., Baker P., 1979. Characterization and distribution of dermatoglyphic features in Eskimo and North, Central and South American Indian populations. Birth Defects-Orig. 15: 277-334.

Grace H.J., Ally F.E., 1973. Dermatoglyphics of the South African Negro. Human Heredity, 23: 53-58.

Hajn V., Gasiorowski A., 1999. Quantitative values on fingers and palms in Czech and Polish populations. Biologica, 37: 107- 115.

Henneberg M.J., Lambert K.M., Leigh C.M., 1997. Fingerprint homoplasy: Koalas and humans. Natural Science.

Holt S.B., 1968. The genetics of dermal ridges. Thomas, Spingfield, Illinois, 195 p.

Igbigbi P.S., Msamati B.C., 1999. Palmar and digital dermatoglyphic patterns in Malawian subjects. East Afr. Med. J., 76: 668-671.

Igbigbi P.S., Msamati B.C., 2002. Palmar and digital dermatoglyphics of indigenous black Zimbabweans. Med. Sci. Monit., 8:757-761.

Igbigbi P. S., Msamati B.C., 2005. Palmar and digital dermatoglphic traits of Kenyan and Tanzanian subjects. W.A.J.M., 24 (1): 26 – 30.

Karmakar B., Malkin I., Kobyliansky E., 2009. Genetic Determinants of 22 Quantitative Dermatoglyphic Traits in the Chuvashian Population of Russia: Complex Segregation Analysis. The Open Anthropology Journal, 2, 64-73.

Kumar A., Manou S. J., 2003. Palmar dermatoglyphics as diagnostic tool: Mayer-rokintansky-Kuster- hauser syndrome. Indian J. Dermatol. Venereol. Leprol., 69: 95-96.

Kahn H.S., Graff M., Stein A.D., Zybert P.A., Mckeague I.W. and Lumey L.H., 2008. A Fingerprinr Characteristic Associated with the early prenatal environment. American Journal of Human Biology, 20: 59- 65

Kusuma Y.S., Babu B.V., Naidu J.M., 2002. Finger ridge count correlations among four tribes of Andhra Pradesh, India. Collegium Antropologicum , 26:319-323.

Luna F., Pons J., 1987. The dermatoglyphics of the eastern Andalusia. International Journal of Anthropology, 2 (2): 183- 190.

Maltoni D., Maio D., Jain A.K., Prabhakar S., 2003. Handbook of Fingerprint Recognition. Springer Verlag. New York.

Medland, S.E., Loesch, D.Z., Mdzewski, B., Zhu, G., Montgomery, G.W., Martin, N.G., 2007. Linkage analysis of a model quantitative trait in humans: finger ridge count shows significant multivariate linkage to 5q14.1. PLoS Genet. 3, 1736–1744.

Meenakshi S., Balasubramanyam V. and Rajangam S., 2006. Dermatoglyphics in amenorrhea- qualitative analysis. The Journal of Obstetrics and Gynecology of India, 56 (3): 250-254.

Meier, R. 1980. Anthropological dermatoglyphics: a review.Yearbook Phys. Anthropol. 23: 147-178.

Miliĉić J., Petković Z. B., Božikov J., 2003. Dermatoglyphs of Digito-Palmar Complex in Autistic Disorder: Family Analysis. Croatian Medical Journal, 44: 469-476.

Reddy B.M., Pfeffer A., Crawford M.H., Langstieh B.T., 2001. Population substructure and patterns of quantitative variation among the Gollas of Southern Andhra Pradesh, India. Human Biology, 2:291-306.

Sabir B., Cherkaoui M., Baali A., Lemaire O., Dugoujon J.M., Boetsch G., 2005.Characterisation of the digital dermatoglyphic in a berber population of the high Atlas (Marrakesh, Morocco). International Journal of Anthropology, 20 (3-4): 277- 289.

Saha S., Loesch D., Chant D. et al., 2003. Directional and fluctuating asymmetry in finger and a-b ridge counts in psychosis: a case-control study. BMC Psychiatry, 3.

Schaumann B., Alter M., 1976. Dermatoglyphics in medical disorders. Springer-Verlag. New York, 258 p.

Segura-Wang M., Barrantes R. 2009. Dermatoglyphic traits of six Chibcha-speaking Amerindians of Costa Rica, and an assessment of the genetic affinities among populations**.** Int. J. Trop. Biol. 57 (1): 357-369.

Sengupta M., Karmakar B., 2004. Mode of inheritance of finger dermatoglyphic traits among Vaidyas of West Bengal, India. Annals of Human Biology, 31:526-540.

Sharma P. R., Gautam A. K., Tiwari P. K., 2008. Dermatoglyphic variations in five ethno-geographical cohorts of Indian populations: A Pilot study. The Internet Journal of Biological Anthropology, 2 (1).

Tarca A., 2001. Contribution à l'étude de la pathologie des dermatoglyphes. Antropo, 1:51-60.

Temaj G., Milicic J., Skaric Jurié T., Behluli I., Smolej Narancic N., Hadziselimovic R., Nefic H., 2009. Comparative Analysis of Dermatoglyphic Traits in Albanian and Turkish Population Living in Kosovo. Coll. Antropol., 33 (4): 1001–1005.

Weisensee K. E., Siváková D., 2003. A comparison of Slovakian Haban Populations using Finger Ridge Count data. Stud. Tribes Tribals, 1:73-76.