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Inheritance of Dermatoglyphic Asymmetry and Diversity Traits in Twins Based on Factor: Variance Decomposition Analysis

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A B S T R A C T

Dermatoglyphic asymmetry and diversity traits from a large number of twins (MZ and DZ) were analyzed based on principal factors to evaluate genetic effects and common familial environmental influences on twin data by the use of maximum likelihood-based Variance decomposition analysis. Sample consists of monozygotic (MZ) twins of two sexes (102 male pairs and 138 female pairs) and 120 pairs of dizygotic (DZ) female twins. All asymmetry (DA and FA) and diversity of dermatoglyphic traits were clearly separated into factors. These are perfectly corroborated with the earlier studies[1–3] in different ethnic populations, which indicate a common biological validity perhaps exists of the underlying component structures of dermatoglyphic characters. Our heritability result in twins clearly showed that DA_F2 is inherited mostly in dominant type (28.0%) and FA_F1 is additive (60.7%), but no significant difference in sexes was observed for these factors. Inheritance is also very prominent in diversity Factor 1, which is exactly corroborated with our previous findings[4]. The present results are similar with the earlier results of finger ridge count diversity in twin data[5], which suggested that finger ridge count diversity is under genetic control.

Key words: *dermatoglyphic asymmetry and diversity, variance decomposition analysis, twins*

Introduction

Bilateral asymmetry (difference of size and/or shape between supposedly identical right- and left-sided structures) of dermatoglyphic traits is the most interesting aspect in recent times. Since asymmetry is thought to have resulted from inability to buffer against adverse environmental noise[6], it is a good indicative of overall developmental homeostasis[7]. Thus very important in case of dermatoglyphic traits because dermatoglyphic features are formed before the 19th week of gestation[8,9] and thereafter are not amenable to change due to age and / or environmental factors. Therefore, increased dermatoglyphic asymmetry can be related to a nonspecific distortion at an early stage of embryonic development. There are some studies have observed higher asymmetry for finger ridge count[10–13]; as well as palmar a-b ridge counts[13–17]. Most of the above studies considered only one type of asymmetry, i.e., fluctuating asymmetry (FA), which is directionally random deviation (irrespective of sign) from perfect bilateral symmetry. While other type of asymmetry i.e., directional asymmetry (DA), which has a consistent bias within a species towards systematically greater development on one side (considered sign), has been neglected[18,19]. Thus, due to inadequate information in the literature, it becomes difficult to develop any satisfactory conclusion in this field.

There is another interesting type of dermatoglyphic variable – »intra-individual diversity« (Div) introduced by Holt[20] as a measure of digital differences evaluated by finding the sum of squares of deviations of the ten separate digital ridge-counts from their mean ($S / \sqrt{10}$). The importance of this trait was emphasized by Micle and Kobyliansky[1,2] who studied on a set of 66 dermatoglyphic variables and defined as diversity quantifies ridge differences between non-homologous fingers. Some studies demonstrated that diversity display ethnic variation ba-

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sed on a comparative study between groups of European and African ancestry[21] and suggested that inter-population comparison not only reveals ethnic differences of diversity, but also shows geographical variation among populations from Europe, the Middle East, and Africa, and also emphasized its suitability to use for comparative studies in dermatoglyphics. In a series of studies[22,23] investigated the finger ridge count diversity in males and females across the world and concluded that the structure of finger ridge count diversity on separate fingers differs in the population groups, and the left hand is more homogeneous than the right hand. However, genetic study on this variable is hardly available[24], although, there is evidence that diversity of ridge counts from finger to finger is under genetic control was suggested by Holt[20]. Holt[5] strongly recommended the indices of diversity traits especially- Div 9 (or, $S/\sqrt{10}$) and Div 11 (or, Shannon index- taking into account the frequency of each of the four basic finger pattern types on ten fingers) for genetic analysis. Therefore, a thorough understanding of the mode of inheritance of dermatoglyphic diversity traits is essential.

It is well known that twin data have played a central role to sort out genetic from environmental variation[25–30]. Twin studies have shown that increased dermatoglyphic asymmetry corresponds to a higher inter pair variability in a number of behavioral tests as well as to a greater test-retest instability[31,6]. Schizophrenia among DZ twins resulted in a greater inter pair variability for FA of dermatoglyphic traits when compared to unaffected pairs of twins[14], while the degree of asymmetry was related to clinical severity of disease[15]. Relatively few studies have attempted towards the extent and relative contributions of genetic and environmental effects on twin pedigrees[32–39]. However, very rare approach have attempted through genetic model fitting statistical procedures[30,40–42] to get proper results.

Further, we know that familial studies now have established hereditary factors are very important in the phenotypic expression of dermatoglyphic traits[40–47,18,4,24]. In this context also well known that the composite score of dermatoglyphic traits may be a more adequate measure of developmental homeostasis than any single trait[47–52]. This measure can be obtained from factor scores by principal component analysis, which is based on correlations among a number of indices. From this standpoint, to get a clear picture of this phenomenon, a comparative examination of biological validity of the underlying component structure of dermatoglyphic character is appropriate by principal component analysis[4,52,47,53].

Thus, the main goal of the present article is to evaluate the mode of inheritance, which represents the causal factors presumed to be operating on dermatoglyphic asymmetry and diversity traits based on principal component structure in a large number of twin data. The maximum likelihood ratio test was used to evaluate both the significance of putative genetic effects and common familial environmental influences on twin data.

Materials and Methods

Samples and traits

Dermatoglyphic prints were collected from twins-monozygotic (MZ) twins of two sexes (102 male pairs and 138 female pairs) and 120 pairs of dizygotic (DZ) female twins. The data were provided by the Anuchin Anthropological Museum, Moscow State University, Russia. Dermatoglyphic prints were analyzed and obtained following ink method described by Cummins and Midlo[54]. In the present report 16 asymmetry traits were used namely 8 directional asymmetry (DA) and 8 fluctuating asymmetry (FA). Total 11 diversity traits of finger and palmar dermatoglyphics (Appendix 1) were analyzed. The high genetic diversity of the people living in Moscow may also be responsible for high heritability estimates. Therefore, a genetically mixed population such as Moscow is expected to produce high heritability estimates and thus the present study on twins is important. The dermatoglyphic variables are presented in Appendix 1 and the formulae for calculating various indices are in Appendix 2.

Statistical Analyses

Z-transformation: For each value of dermatoglyphic traits was converted to normalize the data. The formula is: $Z = (Xi - \overline{X}) / SD$, where Xi, $\overline{X}$, and SD are the individual's measurements, average and standard deviation for the trait respectively. The transformed score has a mean of zero and a standard deviation of one. All further calculations are based on these transformed Z-scores.

Principal component analysis (PCA): PCA were performed using STATISTICA version 6 software (Stat Soft 2001). To avoid the problem of multiple comparisons, redundancy of information, and repetition of measurement error, we performed principal component analysis (PCA) using the original traits (FA, DA and Div) regardless of the sex and age of the individual to capture as much common variation as possible. The eigenvalue >1 criterion was used to extract factors for FA, DA and Div trait groups (Varimax rotation).

Genetic analyses: Variance decomposition analysis was performed to distinguish between different independent components that form the variation of the trait, including additive and dominant genetic effects and common family environment components. The analysis was performed on the traits, which were standardized before analysis. The MAN program[55] finds the best-fitting and most parsimonious model of the trait variability and produces maximum likelihood estimates of genetic, common family environment and individual residual environment components with corresponding standard errors. To find the best fitting and most parsimonious model, the likelihood ratio test has been used: $\chi^2 = -2(\log LH_G - \log LH_R)$, where G and R, are the general and restricted models respectively. The data were processed at the Tel Aviv University, Israel.

Results

Principal component analysis (PCA)

A clear separation of DA traits into 3 factors is easily interpretable in Table 1, which jointly accounted for more than 56% of the total variation. Factor 1 alone accounted for about 23% of the total variation, whereas factor 2 and 3 explain approximately 16% each. Similarly (Table 1) described the FA traits into 2 factors, which jointly accounted for more than 43% of the total variation. Factor 1 accounted for about 29% of the total variation, whereas factor 2 explains approximately 13%.

Table 2 described the Div traits into 2 factors, which jointly accounted for more than 88% of the total variation. Factor 1 accounted for about 76.11% of the total variation, whereas factor 2 explains approximately 11.94%, respectively. No significant differences were observed for these factors

Variance decomposition analysis

The parameter estimates are shown for general and most parsimonious models (Table 3), the lasts are given with asymptotic standard errors for DA_F2 and FA_F1. Only DA_F2 and FA_F1 had significant genetic variance components and therefore, variance decomposition analysis have done on these two factors. DA_F2 is inherited mostly in dominant type (28.0%) and FA_F1 is additive (60.7%). No significant difference in sexes was observed for these factors.

TABLE 1
ROTATED FACTOR LOADINGS OF DA AND FA TRAITS IN TWINS

Factors	Factor 1	Factor 2	Factor 3
Traits			
DA 2	0.71	–	–
DA 3	–	0.40	–0.53
DA 4	0.60	0.61	0.42
DA 10	–	–	0.79
DA 11	–	0.77	–
DA 12	0.41	–	0.43
DA 13	0.80	–	–
DA 14	0.34	0.44	–
V. P	1.81	1.40	1.27
C. V	22.66	40.13	55.95
Traits			
FA 2	0.33	–	
FA 3	–	0.59	
FA 4	0.81	–	
FA 10	0.54	–	
FA 11	0.53	–0.41	
FA 12	0.67	–	
FA 13	0.71	–	
FA 14	0.28	0.69	
V. P	2.36	1.08	
C. V	29.46	43.02	

Loading values below 0.25 are omitted. The V.P. is the variance explained by each factor. C.V is the cumulative proportion of the explained variance.

TABLE 2
UNROTATED FACTOR LOADINGS OF DIVERSITY TRAITS IN TWINS

Traits	Factor 1	Factor 2
Div 1	0.85	0.49
Div 2	0.87	–0.46
Div 3	0.94	–
Div 4	0.86	0.45
Div 5	0.87	–0.45
Div 6	0.98	–
Div 7	0.87	0.47
Div 8	0.89	–0.45
Div 9	0.99	–
Div 10	0.97	–
Div 11	0.31	–
V.P	8.37	1.31
C.V	76.11	88.05

Loading values below 0.25 are omitted. The V.P. is the variance explained by each factor. C.V is the cumulative proportion of the explained variance.

The parameter estimates are shown for general and most parsimonious models of Diversity traits in Table 4, the lasts are given with asymptotic standard errors. Among diversity factors only Factor 1 had significant proportion of genetic variance (62.2%). No significant sex differences were observed in both factors.

Discussion

Unfortunately, the existing information regarding mode of inheritance by the genetic model-fitting test especially on asymmetry and diversity traits are very limited and thus we are unable to provide an accurate explanation compared with such studies in other populations.

Factor analysis

Asymmetry: The application of factor analysis is not new in the study of dermatoglyphic asymmetry and diversity in different populations[1-3,52,24,53]. In the present study, the DA and FA of dermatoglyphic traits were clearly separated and these results are perfectly corroborated with earlier studies[1-3,52,24,53]. This similarity between general dermatoglyphic traits and their bilateral asymmetry is compatible with the suggestion of Jantz[56] that the genetic mechanisms responsible for dermatoglyphic traits may also mediate their bilateral asymmetry. Our results are also consistent with Martin et al.[57] suggested that there exits a genetic component in asym-

TABLE 3
VARIANCE DECOMPOSITION ANALYSIS OF DA AND FA TRAITS ONLY ON INHERITED FACTORS

Trait	Parameter	Model	
		General	Most Parsimonious
DA_F2	μ_m	–0.035	[0]
	μ_f	0.012	[0]
	σ_{AD}^2	0.000	[0]
	σ_{DO}^2	0.272	0.273 ± 0.081 (28.0% ± 8.3%)
	σ_{SB}^2	0.000	[0]
	σ_{RS}^2	0.702	0.702 ± 0.079 (72.0% ± 8.1%)
	LH	–704.30	–704.39
	χ^2 (p)	0.19 (0.98)	
FA_F1	μ_m	–0.092	[0]
	μ_f	–0.018	[0]
	σ_{AD}^2	0.533	0.574 ± 0.070 (60.7% ± 7.4%)
	σ_{DO}^2	0.039	[0]
	σ_{SB}^2	0.000	[0]
	σ_{RS}^2	0.370	0.371 ± 0.039 (39.3% ± 4.1%)
	LH	–662.69	–663.14
	χ^2 (p)	0.90 (034)	

μ_m, μ_f – mean values for male and female; σ_{AD}^2 – additive genetic variance; σ_{DO}^2 – dominant genetic variance; σ_{SB}^2 – sibling variance; σ_{RS}^2 – residual variance; [0] – Parameter was constrained to zero; ! – Parameter was constrained to be equal to upper one; in parentheses () percent of the total variance is given. For MP model parameters are given with standard errors.

TABLE 4
VARIANCE DECOMPOSITION ANALYSIS OF DIVERSITY TRAITS ON UNROTATED FACTORS

Trait	Parameter	Model	
		General	Most Parsimonious
Factor 1	μ_m	0.014	[0]
	μ_f	0.003	[0]
	σ_{AD}^2	0.620	0.620 ± 0.064; (62.2% ± 6.5%)
	σ_{SB}^2	0	[0]
	σ_{RS}^2	0.377	0.377 ± 0.034 (37.8% ± 3.4%)
	LH	–866.00	–866.01
	χ^2 (p)	0.02 (1)	
Factor 2	μ_m	0.069	[0]
	μ_f	–0.032	[0]
	σ_{AD}^2	0.061	[0]
	σ_{SB}^2	0	[0]
	σ_{RS}^2	0.932	0.994 ± 0.054
	LH	–922.23	–923.34
	χ^2 (p)	2.21 (0.14)	

μ_m, μ_f – mean values for male and female; σ_{AD}^2 – additive genetic variance; σ_{SB}^2 – sibling variance; σ_{RS}^2 – residual variance; [0] – parameter was constrained to zero; ! – parameter was constrained to be equal to upper one; in parentheses () percent of the total variance is given. For MP model parameters are given with standard errors.

metry variation between hands but environmental factors are more important.

Diversity: In the present study, we performed principal component analysis on the studied diversity traits. All diversity traits were clearly separated into two factors, which are perfectly corroborated with the earlier studies[1–3] in different ethnic populations, which indicate a common biological validity perhaps exists of the underlying component structures of dermatoglyphic characters.

Variance decomposition analysis

Asymmetry: The present findings clearly showed that DA_F2 is inherited mostly in dominant type (28.0%) and FA_F1 is additive (60.7%), but no significant difference in sexes was observed for these factors. We cannot compare our present results due to relatively a few studies have addressed the extent and relative contributions of genetic and environmental effects on the co-variation of twin pedigrees through genetic model fitting statistical procedures[40–44]. However, we can explain with the help of previous common studies. Our present investigation suggests that the relationship between MZ and DZ twins is due to common genes that affect dermatoglyphic traits. Comparison of our heritability results in twins may be similar conclusion with earlier studies[29,58,50,,26,59,60,61,40-42] that phenotypic expression of dermatoglyphic features appears to be controlled by distinct genetic entities in different digital regions and also in spite of the genetic component intrauterine environmental factors could influence to a great extent to be the differentiation of the dermatoglyphic pattern sizes. The present findings are also consistent with the assumption of earlier studies: The proportion of genetic variation is greater in digital patterns than interdigital areas, and environmental variation was found to be local which frequently involve in reciprocal interaction between twin pairs[28]; Lin et al.[62] concluded that finger ridge counts between MZ and DZ twins are genetically related to each other in different degrees, respectively.

Diversity: Inheritance is very prominent in Diversity (factor 1), which are exactly corroborated with our previous findings[4]. The present results are similar with the earlier results[5] of finger ridge count diversity on twin data. Holt[5] suggested that finger ridge count diversity is under genetic control.

Conclusion

The relationship between MZ and DZ twins is due to common genes that affect dermatoglyphic asymmetry

and diversity traits (factors) suggests is under genetic control of which DA is inherited mostly in dominant type and FA is additive.

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NASLJEĐIVANJE DERMATOGLIFSKE ASIMETRIJE I RAZLIKOVNE OSOBINE U BLIZANACA TEMELJENE NA FAKTORSKOJ ANALIZI DEKOMPOZICIJE VARIJANCE

SAŽETAK

Dermatoglifska asimetrija te razlikovne osobine velikog broja blizanaca (MZ i DZ) analizirani su temeljem glavnih faktora za evaluaciju genetskih učinaka i uobičajenih obiteljskih i okolišnih utjecaja na podatke o blizancima rabeći analizu dekompozicije varijance. Uzorak se sastoji od monozigotnih (MZ) blicanaca obaju spolova (102 muška i 138 ženska para) te 120 parova dizigotnih (DZ) ženskih blizianaca. Sve asimetrije (DA i FA) i različitost dermatoglifskih osobina jasno su odljeljeni na faktore. Oni su u skladu sa prethodnim istraživanjima[1–3] na različitim etničkim populacijama, a koja pokazuju kako postoji zajednička biološka vrijednost u pozadini komponentnih struktura dermatoglifskih karakteristika. Naši rezultati jasno su pokazali kako se DA_F2 nasljeđuje uglavnom kao dominantni tip (28,0%), dok je FA_F1 aditivan (60,7%), ali nikakva značajna razlika među spolovima nije primjećena za te faktore. Nasljeđivanje je

također bilo vrlo prominentno kod Fakktora 1, što izravno potvrđuje naše prethodne rezultate[1]. Ovi rezultati slični su prijašnjim rezultatima o broju grebena na prstima kod blizanaca[5], što upućuje na to kako je raznolikost broja grebena na prstima pod kontrolom gena.

APPENDIX 1
LIST OF THE DERMATOGLYPHIC TRAITS

22 quantitative traits
- Finger RC, I r
- Finger RC, II r
- Finger RC, III r
- Finger RC, IV r
- Finger RC, V r
- Finger RC, I l
- Finger RC, II l
- Finger RC, III l
- Finger RC, IV 1
- Finger RC, V 1
- Total Finger RC (TFRC)
- Absolute Finger RC (AFRC)
- PII, lh
- PII, rh
- PII, both h
- a-b RC, rh
- a-b RC, lh
- A-line exit, l
- A-line exit, r
- D-line exit, l
- D-line exit, r
- MLI

42 traits (diversity and asymmetry):

11 Diversity traits (Div)
- Div I = max – min fRC (lh)
- Div II = max – min fRC (rh)
- Div III = max – min fRC (both h)
- Div IV = S^2 for lh, (or S^2L)
- Div V = S^2 for rh, (or S^2R)
- Div VI = S2 (both h)
- Div VII = IIDL (for lh)
- Div VIII = IIDR (for rh)
- Div IX = S, (both h)
- Div X = S, (both h)
- Div XI = Shannon's index

15 Directional Asymmetry (DA) traits
- DA I = Div II – Div I
- DA II = PII, rh – lh
- DA III = a-b RC, r – l
- DA IV = hRC, rh – lh
- DA V = S^2, rh – lh
- DA VI = Div VIII – Div VII
- DA VII = atd angle, r – l
- DA VIII = a-b dist., r – l
- DA IX = ridge breadth, r – l
- DA X = fRC, Vr – Vl
- DA XI = fRC, IVr – IVl
- DA XII = fRC, IIIr – IIIl
- DA XIII = fRC, IIr – IIl
- DA XIV = fRC, Ir – Il
- DA XV = MLI, rh – lh

16 Fluctuating Asymmetry (FA) traits
- FA I = [Div I – Div II]
- FA II = PII, [rh – lh]
- FA III = a-b, RC, [rh – lh]
- FA IV = hRC, [rh – lhv
- FA V = [Div V – Div IV]
- FA VI = [Div VIII – Div VII]
- FA VII = atd angle, [r – l]
- FA VIII = a-b dist, [r – l]
- FA IX = ridge breadth [r – l]
- FA X = fRC, [Vr – Vl]
- FA XI = fRC, [IVr – IVl]
- FA XII = fRC, [IIIr – IIIl]
- FA XIII = fRC, [IIr – IIl]
- FA XIV = fRC, [Ir – Il]
- FA XV = MLI, [rh – lh]
- FA XVI = A1, asymmetry index

22 quantitative traits and 11 indices of diversity traits were excluded in the present study.

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; DA I to DA XV – indices of directional asymmetry; FA I to FA XVI – indices of fluctuating asymmetry.

APPENDIX 2
FORMULAE FOR SOME INDICES OF DERMATOGLYPHIC DIVERSITY AND ASYMMETRY

The directional asymmetry (DA) was computed by the following equation: $DA_{ij} = X_{iR} - X_{iL}$.

The fluctuating asymmetry (FA) was computed by using the absolute differences between the bilateral measurements. The distributions of the non-absolute differences for each individual were corrected (Livshits et al., 1988) to avoid additional influences (scaling effects) such as size of the trait or directional asymmetry, yielding the following equation for computing FA:

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

Where, x_i = 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, $S^2 = \sum_{i=1}^{10} q_i^2 - Q^2 / 10$; 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, $S\sqrt{5} = \sqrt{\sum_{i=1}^{5} (q_i^2 - Q^2 / 5) / 5}$;

In these formulae, qi is the ridge count for the ith 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 ith pairs of homologous right and left fingers.

Div XI. 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 ith finger of the right and left hand.