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Inheritance of Quantitative Dermatoglyphic Traits with Asymmetry and Diversity in Muzeina Bedouin Tribe: A Small Isolated and Consanguineous Population from South Sinai

Bibha Karmakar[1], Ida Malkin[2] and Eugene Kobyliansky[2]

[1] Indian Statistical Institute, Biological Anthropology Unit, Kolkata, India
[2] Tel Aviv University, Sackler Faculty of Medicine, Department of Anatomy and Anthropology, Human Population Biology Unit, Tel Aviv, Israel

ABSTRACT

The genetic factors contribute significantly to the determination of dermatoglyphic traits is well established. However, the controversies in views and findings of this issue are still inconclusive. The present study is an attempt to evaluate the inheritance of quantitative dermatoglyphic traits with asymmetry (DA and FA) and diversity (Div) through sibling correlations. Data include 218 individuals from (88 families) in a small isolate, the nomadic tribe Muzeina with a high degree of consanguinity (0.09) from South Sinai. Statistical analyses include sibling correlations, cross-correlations and genetic correlation (GC) – a ratio of sibling cross-correlation between traits divided on square root of the both traits sibling correlation product. The familial correlation coefficients for quantitative dermatoglyphic traits are perhaps expected lower in such a small isolated and consanguineous population than our previous studied in Indian populations and Chuvashian populations from Russia. These results indicate a simpler genetic basis due to high degree (0.09 inbreeding coefficient) of consanguinity in Muzeina Bedouin tribe. There is no evidence of major gene involvement, although a little genetic effect obtained from familial correlations on asymmetry (DA and FA) and diversity (Div) traits through sibling correlations. The significant interaction between sexes was found, which contradicts with the other populations perhaps due to high level of consanguinity. Lower correlation coefficients than in other non-consanguineous populations for quantitative dermatoglyphic traits indicate a simpler genetic basis due to high degree of inbreeding coefficient (0.09) in Muzeina. Dermatoglyphic asymmetry and diversity traits may be due to environmental factors rather than dominance in Bedouins, although a little genetic effect was found suggests a measure of developmental instability in human (FA).

Key words: *familial correlations, dermatoglyphics, Bedouins, South Sinai*

Introduction

Heritability of dermatoglyphic characters has a long history[1] that controlled by genetic factors and generally explained as a complex nature[2–4]. However, most of the conclusions of its genetic nature from various studies are contradictory[5–15].

In general, the relative contribution of genetic and environmental factors to phenotypic variation of dermatoglyphics differ from population to population[2,7,16–23]. In view of ethnic diversity, dermatoglyphics among the Bedouin tribe was selected because, studies are hardly available in Bedouins. Thus it would be interesting to determine whether any similarity exists with the present Bedouin population and the results of our previous studies on Indian and Chuvashian populations from Russia on different sets of dermatoglyphic traits (quantitative, asymmetry and diversity).

It was found since long back that the application of proper statistical techniques, the genetics of quantitative aspect of dermatoglyphics could be better demonstrated than the qualitative traits[7,24–29]. Therefore, to study 22 quantitative dermatoglyphic traits is quite appropriate.

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In the last few years, dermatoglyphic asymmetry and diversity have greatly broadened its scope and deserves a special attention for several reasons[30–50]. However, the actual utility of asymmetry is also limited because of inadequate knowledge of its genetic nature and thus, a through understanding of dermatoglyphic asymmetry is essential. The human body exhibits a variety of bilateral asymmetries (differences in the size and /or shape of supposedly identical right- and left-sided structures). Some of these asymmetries are inborn but others are acquired. According to the literature, there are mainly two types of asymmetry, namely (1) fluctuating asymmetry (FA), which is a random deviation, i.e., irrespective of sign, from perfect bilateral symmetry[40] and (2) directional asymmetry (DA), which reflects a consistent bias of a character toward systematically greater development on one side, i.e., considering sign[51].

The »intra-individual diversity«(Div) traits, introduced by Holt[7] 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/ v10). The importance of this trait was emphasized by several authors[31–33,36,35,52].

TABLE 1
DESCRIPTIVE STATISTICS AND SIBLING CORRELATION FOR DIV TRAITS

Traits	Sample	Descriptive statistics			Sex Difference p value	Sibling pairs		
		N	$\overline{X}$	SD		N	r	p value
Div_1	All	127	10.740	5.104	0.00066	90	0.049	0.65768
	Male	96	11.479	5.270				
	Female	31	8.452	3.785				
Div_2	All	133	10.805	4.954	0.00023	101	–0.030	0.77093
	Male	99	11.636	4.970				
	Female	34	8.382	4.083				
Div_3	All	105	12.943	5.127	0.00007	65	0.109	0.39009
	Male	80	13.838	5.247				
	Female	25	10.080	3.475				
Div_4	All	127	89.584	79.491	0.00114	90	0.068	0.54011
	Male	96	100.225	83.320				
	Female	31	56.632	55.414				
Div_5	All	133	89.504	75.001	0.00057	101	0.016	0.92583
	Male	99	100.537	78.057				
	Female	34	57.376	54.572				
Div_6	All	105	180.802	138.606	0.00150	65	0.119	0.35228
	Male	80	200.516	143.920				
	Female	25	117.716	98.127				
Div_7	All	127	3.847	1.772	0.00123	90	0.076	0.49198
	Male	96	4.103	1.801				
	Female	31	3.056	1.435				
Div_8	All	133	3.871	1.715	0.00056	101	–0.012	0.89678
	Male	99	4.142	1.726				
	Female	34	3.079	1.433				
Div_9	All	105	3.965	1.545	0.00146	65	0.071	0.59069
	Male	80	4.198	1.570				
	Female	25	3.218	1.214				
Div_10	All	105	15.752	7.108	0.00147	65	0.040	0.75610
	Male	80	16.880	7.064				
	Female	25	12.144	6.072				
Div_11	All	164	0.613	0.268	0.81917	143	0.156	0.06585
	Male	122	0.610	0.268				
	Female	42	0.621	0.269				

TABLE 2
DESCRIPTIVE STATISTICS AND SIBLING CORRELATION OF DA TRAITS

Traits	Sample	Descriptive statistics			Sex Difference p value	Sibling pairs		
		N	$\bar{X}$	SD		N	r	p value
DA_1	All	105	1.484	45.159	0.79447	65	–0.174	0.17090
	Male	80	2.162	44.346				
	Female	25	–0.686	48.554				
DA_2	All	149	0.739	18.991	0.37773	119	0.005	0.84056
	Male	110	1.509	19.616				
	Female	39	–1.432	17.158				
DA_3	All	217	–3.985	12.934	0.21793	201	0.121	0.08970
	Male	171	–3.407	12.779				
	Female	46	–6.133	13.416				
DA_4	All	105	–1.916	10.858	0.29705	65	0.041	0.75335
	Male	80	–2.429	11.610				
	Female	25	–0.274	7.971				
DA_5	All	105	1.567	79.744	0.78254	65	–0.132	0.30588
	Male	80	0.272	77.430				
	Female	25	5.714	88.306				
DA_6	All	105	–3.058	10.793	0.55416	65	0.015	0.89282
	Male	80	–2.610	9.156				
	Female	25	–4.495	15.035				
DA_7	All	215	–2.159	15.013	0.34063	201	0.071	0.32668
	Male	168	–1.610	14.636				
	Female	47	–4.124	16.302				
DA_8	All	217	–2.156	10.323	0.22250	201	0.093	0.19097
	Male	171	–1.698	10.189				
	Female	46	–3.858	10.748				
DA_9	All	217	1.735	8.930	0.74079	201	0.090	0.20521
	Male	171	1.624	8.753				
	Female	46	2.145	9.649				
DA_10	All	144	–5.028	31.078	0.60210	108	–0.036	0.72160
	Male	110	–5.778	31.223				
	Female	34	–2.599	30.941				
DA_11	All	145	–5.610	41.066	0.23597	113	0.087	0.36869
	Male	109	–7.875	41.557				
	Female	36	1.248	39.309				
DA_12	All	154	–2.485	44.582	0.66122	124	0.094	0.31196
	Male	115	–3.312	46.839				
	Female	39	–0.047	37.585				
DA_13	All	140	–3.269	62.058	0.89798	118	0.036	0.70721
	Male	102	–3.658	64.259				
	Female	38	–2.224	56.525				
DA_14	All	153	2.281	21.022	0.44742	124	–0.041	0.66761
	Male	114	1.584	21.871				
	Female	39	4.320	18.427				
DA_15	All	176	8.819	20.503	0.01198	133	0.058	0.52017
	Male	141	10.868	19.687				
	Female	35	0.563	21.914				

TABLE 3
DESCRIPTIVE STATISTICS AND SIBLING CORRELATION OF FA TRAITS

Traits	Sample	Descriptive statistics			Sex Difference p value	Sibling pairs		
		N	$\overline{X}$	SD		N	r	p value
FA_1	All	104	35.695	28.392	0.44978	65	0.039	0.76505
	Male	80	34.500	28.080				
	Female	24	39.676	29.669				
FA_2	All	148	14.002	12.604	0.62313	118	–0.067	0.48187
	Male	110	14.278	13.151				
	Female	38	13.205	10.988				
FA_3	All	213	9.995	8.223	0.75867	197	0.145	0.04459
	Male	171	10.094	7.787				
	Female	42	9.590	9.902				
FA_4	All	104	7.887	7.499	0.33829	65	–0.072	0.58297
	Male	80	8.193	8.079				
	Female	24	6.864	5.121				
FA_5	All	104	64.759	47.663	0.24208	65	0.047	0.72141
	Male	80	61.716	47.323				
	Female	24	74.902	48.395				
FA_6	All	104	6.707	8.617	0.18605	65	0.122	0.34336
	Male	80	5.907	7.153				
	Female	24	9.371	12.129				
FA_7	All	211	10.340	11.511	0.50121	197	0.202	0.00686
	Male	168	10.041	11.082				
	Female	43	11.508	13.133				
FA_8	All	61	8.131	7.076	0.36380	59	0.156	0.24643
	Male	44	8.566	7.699				
	Female	17	7.005	5.155				
FA_9	All	213	7.062	5.619	0.67465	197	0.011	0.91631
	Male	171	6.971	5.367				
	Female	42	7.432	6.604				
FA_10	All	142	18.868	23.580	0.94691	106	–0.043	0.67412
	Male	110	18.942	23.295				
	Female	32	18.613	24.916				
FA_11	All	144	22.406	33.874	0.67910	112	0.154	0.10751
	Male	109	23.074	33.898				
	Female	35	20.325	34.207				
FA_12	All	153	27.636	34.559	0.65333	123	0.142	0.12151
	Male	115	28.269	36.591				
	Female	38	25.720	27.856				
FA_13	All	138	35.676	48.272	0.23710	116	–0.083	0.38164
	Male	102	38.551	48.375				
	Female	36	27.529	47.702				
FA_14	All	151	15.458	14.025	0.29333	123	0.131	0.15665
	Male	114	16.061	14.765				
	Female	37	13.601	11.426				
FA_15	All	173	14.877	12.768	0.96598	130	–0.020	0.98080
	Male	141	14.855	12.491				
	Female	32	14.971	14.139				
FA_16	All	105	7.311	3.177	0.19622	65	0.058	0.65865
	Male	80	7.530	3.204				
	Female	25	6.611	3.045				

Holt[7] stated that diversity of ridge counts from finger to finger is under genetic control and thus study of dermatoglyphic diversity is essential.

In this article we therefore, evaluate the mode of inheritance, which represents the causal factors presumed to be operating on dermatoglyphic traits with asymmetry and diversity in South Sinai Bedouins.

Materials and Methods

Sample and traits

The Muzeina tribe inhabited for centuries in the Sinai desert, which especially occupied by the Bedouins and they originated mainly from Saudi Arabian Peninsula[53]. Muzeina tribe is characterized by strong biological isola-

TABLE 4
DESCRIPTIVE STATISTICS AND SIBLING CORRELATION OF FINGER RIDGE COUNTS

Traits	Sample	Descriptive statistics			Sex Difference p value	Sibling pairs		
		N	$\bar{X}$	SD		N	r	p value
FRC_1R	All	159	20.74	5.01	0.093	141	0.183	0.03301
	Male	117	21.11	5.19				
	Female	42	19.71	4.36				
FRC_2R	All	156	12.88	6.09	0.093	134	0.178	0.04240
	Male	115	12.43	6.26				
	Female	41	14.17	5.44				
FRC_3R	All	161	14.16	5.37	0.176	137	0.289	0.00096
	Male	120	13.83	5.40				
	Female	41	15.12	5.24				
FRC_4R	All	149	15.61	5.41	0.662	121	0.296	0.00100
	Male	112	15.51	5.64				
	Female	37	15.92	4.69				
FRC_5R	All	152	14.16	4.52	0.381	123	0.342	0.00084
	Male	114	13.98	4.57				
	Female	38	14.71	4.38				
FRC_1L	All	158	20.35	5.19	0.025	126	0.245	0.00772
	Male	119	20.82	5.40				
	Female	39	18.92	4.23				
FRC_2L	All	146	12.89	6.29	0.219	123	0.302	0.00097
	Male	107	12.52	6.45				
	Female	39	13.90	5.76				
FRC_3L	All	156	14.72	5.88	0.139	129	0.355	0.00079
	Male	116	14.31	5.86				
	Female	40	15.90	5.83				
FRC_4L	All	155	16.34	5.88	0.543	129	0.234	0.00881
	Male	115	16.50	6.06				
	Female	40	15.88	5.36				
FRC_5L	All	155	15.03	5.20	0.881	126	0.240	0.00844
	Male	118	15.06	5.32				
	Female	37	14.92	4.88				
TRC	All	164	148.29	44.32	0.823	143	0.251	0.00447
	Male	122	147.87	45.98				
	Female	42	149.52	39.61				
ARC	All	164	205.62	83.16	0.622	143	0.261	0.00294
	Male	122	203.85	85.94				
	Female	42	210.76	75.27				

TABLE 5
DESCRIPTIVE STATISTICS AND SIBLING CORRELATION FOR FINGERPRINT COUNTS AND OTHER TRAITS

Traits	Sample	Descriptive statistics			Sex Difference p value	Sibling pairs		
		N	$\bar{X}$	SD		N	r	p value
PII_L	All	155	7.27	1.70	0.020	125	0.260	0.00563
	Male	116	7.09	1.71				
	Female	39	7.79	1.58				
PII_R	All	157	7.31	1.60	0.176	135	0.372	0.00073
	Male	115	7.22	1.68				
	Female	42	7.57	1.35				
PII_B	All	149	14.65	3.07	0.041	119	0.370	0.00078
	Male	110	14.37	3.19				
	Female	39	15.44	2.60				
AB_RC_R	All	219	39.81	6.43	0.641	203	0.227	0.00159
	Male	173	39.90	6.68				
	Female	46	39.46	5.47				
AB_RC_L	All	218	41.27	6.19	0.345	204	0.215	0.00383
	Male	171	41.08	6.40				
	Female	47	41.96	5.38				
LINEAL	All	195	4.07	0.84	0.040	160	0.151	0.05991
	Male	156	4.01	0.86				
	Female	39	4.28	0.69				
LINEAR	All	195	4.03	0.90	0.437	163	0.007	0.87483
	Male	156	4.01	0.91				
	Female	39	4.13	0.86				
LINEDL	All	212	4.03	1.56	0.619	196	0.139	0.05241
	Male	167	4.00	1.56				
	Female	45	4.13	1.60				
LINEDR	All	216	4.72	1.43	0.633	198	0.118	0.09846
	Male	171	4.74	1.41				
	Female	45	4.62	1.53				
MLI	All	176	8.45	1.76	0.813	133	0.163	0.06323
	Male	141	8.44	1.77				
	Female	35	8.51	1.73				
Arch	All	149	0.15	0.44	0.36473	119	0.188267	0.04267
	Male	110	0.16	0.48				
	Female	39	0.10	0.31				
Whorl	All	149	4.80	2.90	0.04448	119	0.367683	0.00079
	Male	110	4.54	2.99				
	Female	39	5.54	2.52				
Lu	All	149	4.72	2.60	0.03272	119	0.403503	0.000708
	Male	110	4.97	2.68				
	Female	39	4.03	2.23				
Lr	All	149	0.33	0.70	0.96820	119	0.044177	0.648221
	Male	110	0.33	0.64				
	Female	39	0.33	0.87				

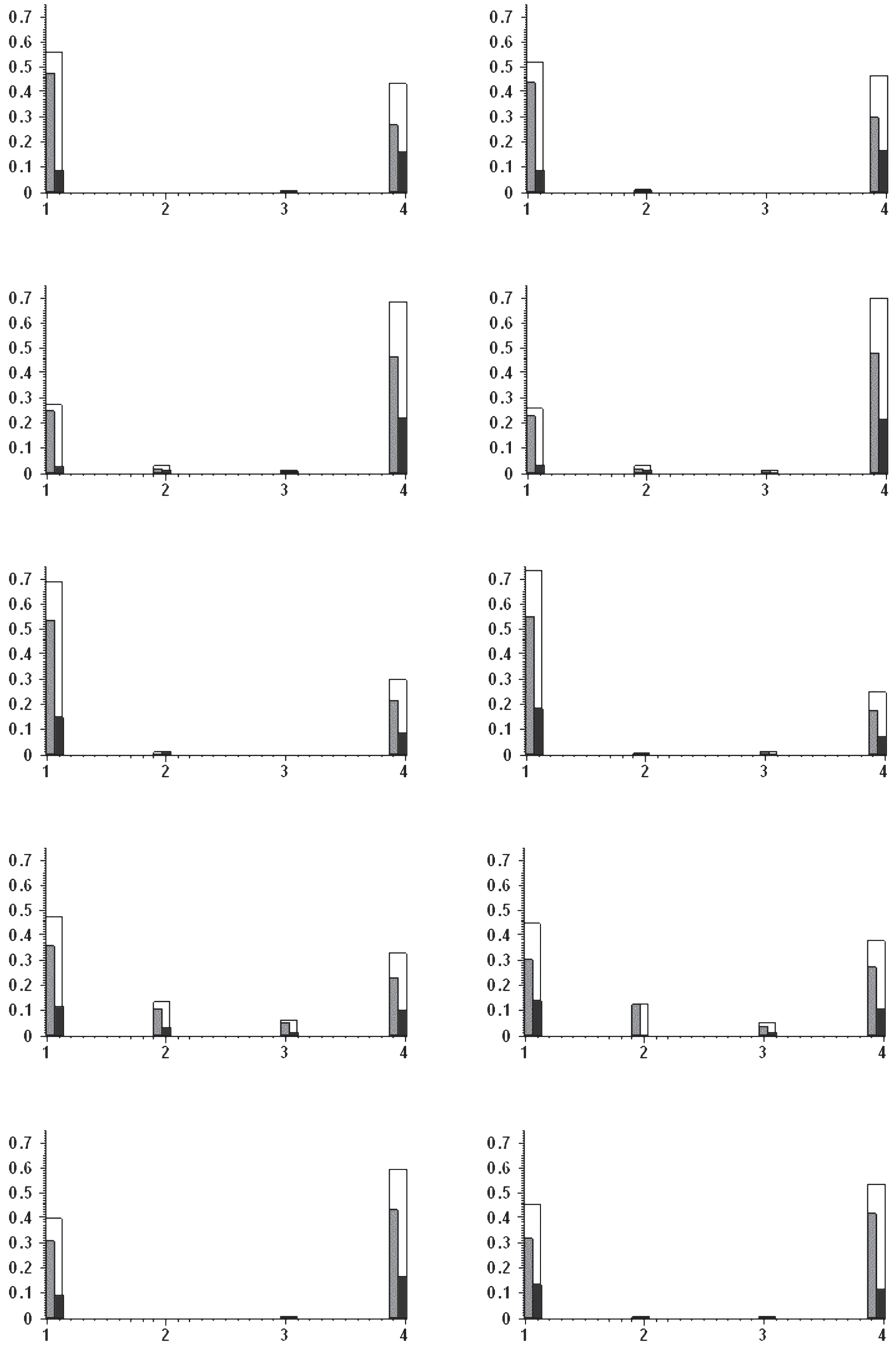

Fig. 1. Frequencies of different finger prints for each of 10 fingers. Left side – from f19 (upper) to f24, right side – from f25 (upper) to f29 (lu=1, lr=2, a=3, w=4. Light gray – male, dark gray – female, white – all).

tion, rarely intermix and show preference for first-cousin marriages. The frequency of such marriages is 15% and the inbreeding coefficient is 0.09. Dermatoglyphic traits were measured in offspring of 88 nuclear pedigrees having 199 sibling pairs. 22 generally used quantitative traits (12 finger and 10 palms); total 29 asymmetry traits (14 DA and 15 FA); and 11 diversity traits (Div) were considered in the present study. We analyzed frequencies of four types of finger patterns namely- Loop Ulnar (Lu), Loop Radial (Lr), Arch (A) and Whorl (W); and count of each type on 10 fingers was analyzed as four additional quantitative traits. The dermatoglyphic variables are presented in Appendix 1 and the formulae for calculating various indices are set out in Appendix 2.

Statistical analyses

The dermatoglyphic traits should not have significant environment variance component because of their nature. We have only one type of relatives (siblings) and therefore, we cannot distinguish between additive and dominant genetic variance components. So we tested sibling correlation of each trait as a measure of their inheritance. If for a pair of traits their sibling correlations are significant, then the significant cross-correlation between traits pair in siblings estimates the presence of shared genes taking part in formation of both traits. As a measure of genetic correlation (GC) we used a ratio of sibling cross-correlation between traits divided on square root of the both traits sibling correlation product. The data were processed at the Tel Aviv University computer center, Israel using the computer programs described by Nie et al.[54].

Results

Table 1 presents results of descriptive statistics for eleven intra-individual diversity (Div) traits. Sex difference in this trait have somewhat higher mean values in males than in females and almost all the differences (except Div_11) are statistically significant. While sibling correlations are non-significant ($p > 0.05$) for all eleven Div traits. Table 2 shows, out of fifteen indices of directional asymmetry (DA), neither sex difference, nor were significant sibling correlations found. Only DA_15 has marginally significant sex difference (0.012). Table 3 shows the results of sixteen fluctuating asymmetry (FA) indices. Sex differences are also having greater in females for some indices than males, as well as also larger in females than in males for some indices. However, analogously no sex differences were found for 16 FA traits. Only FA_3 and FA_7 traits were found significant (0.044 and 0.007) sibling correlations. Sibling cross-correlation of these traits was significant ($p=0.014$, GC=1). Table 4 presents pronounced inheritance of finger ridge count (FRC) for each digit, sibling correlation varies from 0.183 to 0.355 and almost all p-values are less than 0.01. Table 5 shows the results of four additional quantitative traits including counts of finger pattern types on 10 fingers. PII is a complex trait representing the sum of triradii located on the finger tips and sex differences are significant only for left hand (PII-L). High correlation coefficients in sibling vary from 0.260 to 0.372 respectively. Palmar a–b ridge count also significantly correlated, the values of coefficients are 0.227 and 0.215, while sex differences are non- significant. Correlations are low and non- significant sex differences for mainline terminations (MLD, MLA) and mainline index (MLI). The number of W has significant positive sibling cross-correlation with TRC ($p=0.008$), ARC ($p=0.001$), PII_L($p=0.001$), PII_R ($p=0.001$) and PII_B ($p=0.001$).

Table 6 presents significance of sibling cross- correlation between traits having significant inheritance. TFRC and AFRC show significant cross- correlation with almost all traits except a–b _R and a–b_L. There is signifi-

TABLE 6

GENETIC CORRELATION (GC) OF TRAITS HAVING SIGNIFICANT SIBLING CORRELATION (UPPER RIGHT CORNER) AND P–VALUE OF SIBLING CROSS–CORRELATION

	FRC_1R	FRC_2R	FRC_3R	FRC_4R	FRC_5R	FRC_1L	FRC_2L	FRC_3L	FRC_4L	FRC_5L	TRC	ARC	PII_L	PII_R	PII_B	AB_RC_R	AB_RC_L
FRC_1R		1.000	0.930	0.954	0.721	1.000	0.838	1.000	0.696	0.632	0.909	0.802	0.352	0.499	0.491	0.010	0.519
FRC_2R	0.031		0.898	0.939	0.877	0.998	0.934	0.850	0.782	0.776	1.000	0.969	0.757	0.801	0.827	0.121	0.636
FRC_3R	0.012	0.019		1.000	0.825	0.630	0.875	1.000	0.962	0.684	0.972	0.935	0.441	0.618	0.524	0.105	0.696
FRC_4R	0.012	0.016	0.001		0.860	0.646	0.840	0.928	1.000	0.835	0.900	0.765	0.322	0.486	0.461	0.017	0.559
FRC_5R	0.042	0.015	0.005	0.004		0.694	1.000	0.941	0.794	1.000	0.993	0.916	0.400	0.645	0.566	–0.143	0.288
FRC_1L	0.014	0.018	0.057	0.055	0.027		0.642	0.592	0.455	0.503	0.683	0.650	0.372	0.496	0.472	0.170	0.599
FRC_2L	0.025	0.015	0.005	0.007	0.001	0.017		0.825	0.677	0.989	1.000	0.994	0.648	0.794	0.747	–0.133	0.435
FRC_3L	0.003	0.015	0.001	0.001	0.001	0.016	0.004		0.882	0.654	0.982	0.944	0.472	0.644	0.580	0.109	0.707
FRC_4L	0.097	0.072	0.006	0.004	0.012	0.139	0.045	0.006		0.558	0.795	0.754	0.376	0.604	0.547	0.238	0.696
FRC_5L	0.135	0.072	0.042	0.014	0.001	0.095	0.005	0.034	0.145		0.777	0.757	0.570	0.657	0.665	–0.184	0.082
TRC	0.021	0.011	0.003	0.007	0.001	0.016	0.001	0.001	0.026	0.030		0.960	0.661	0.761	0.759	–0.114	0.473
ARC	0.041	0.015	0.004	0.016	0.003	0.019	0.002	0.001	0.033	0.032	0.005		0.845	0.911	0.914	–0.140	0.491
PII_L	0.385	0.068	0.174	0.337	0.190	0.198	0.045	0.110	0.311	0.115	0.052	0.011		0.982	0.984	–0.377	0.070
PII_R	0.134	0.018	0.019	0.074	0.010	0.039	0.004	0.008	0.043	0.028	0.008	0.001	0.001		1.000	–0.048	0.384
PII_B	0.154	0.017	0.054	0.097	0.029	0.054	0.008	0.019	0.077	0.031	0.009	0.001	0.001	0.001		–0.168	0.257
AB_RC_R	0.821	0.769	0.746	0.842	0.647	0.563	0.694	0.714	0.514	0.616	0.740	0.680	0.273	0.935	0.573		0.855
AB_RC_L	0.199	0.128	0.033	0.091	0.354	0.040	0.184	0.016	0.056	0.978	0.171	0.149	0.958	0.182	0.386	0.009	

cant cross- correlation between last two traits. The numbers of fingerprint are not included in Table 6. Because of very low frequency of Lr and A, numbers of W and Lu are negative linearly dependent.

Figure 1 presents frequencies of different finger prints for each finger. Frequency patterns are similar for corresponding fingers of left and hands. Nevertheless fingerprints do not always coincide for corresponding fingers. Proportion of coinciding patterns for corresponding finger pairs is as follows: F19–F25 0.80, F20–F26 0.81, F21–F27 0.73, F22–F28 0.56 and F23–F29 0.78. So it can be seen, that F22–F28 pair have most frequencies of A and Lr and lowest frequency of fingerprints coincidence. The number of left-right finger pairs having the same fingerprint varies from 1 to 5. The distribution of this value in the sample is shown on Figure 2

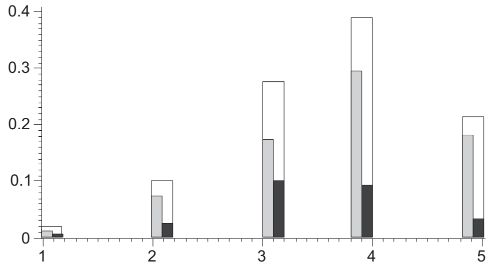

Fig. 2. Distribution of finger counts having the same fingerprint on the corresponding fingers pf left and right hand (light gray –male, dark gray –female, white- all).

Discussion

Sex differences are evident significant in the indices of intra-individual diversity (Div) among Bedouins, but display different levels when compared with other populations, perhaps due to high level of consanguinity. The strength of correlation of both DA and FA is much lower than theoretical value, indicating that along with the little genetic component, the environmental (intrauterine) factors are mainly considerable (Table1–3). Finger ridge counts: The present results (Table 4) of sibling correlation vary from 0.183 to 0.355 in finger ridge count (TFRC). High heritability ranges of correlations 0.5 to 1.0 in sib pairs for (TFRC) obtained by Holt[7] among twins; the theoretically expected values when the environmental influences are negligible. However, lower values were found by earlier studies[9,27,55–59]. Similarly, lower correlation values were found based on Factors[44,60,61]. Falconer[62] suggested that the correlations between genetically related individuals are significantly different. The observed differences emphasize the importance of sample structure in appreciation of the correlation values. For example, Holt[7] pointed out that to some degree of heterogeneity in her sample, which may have increased the values of the resulting correlation coefficients. Further, it is known fact that environmental differences or a strong genetic heterogeneity in a sample may inflate the correlation coefficients, whereas homogeneous populations present lower values of these correlation coefficients. Our results appear similar with these above observations. The low values of correlation coefficients may be a reflection of the strong consanguinity and the low variability of the TFRC indicate the characteristic features of the studied population. Our results also suggest clearly that a possible genetic basis for the ridge count of each finger or of groups of fingers. Pattern intensity index (PII): The present results (Table 5) of sex differences in PII are in complete agreement with earlier studies of different populations[45,46,63–66]. Significant correlation for PII indicated that the dominant nature of PII, which means controlled by genes, support our earlier study[44]. a–b ridge count: The results of palmar a–b ridge count (Table 5**)** reveal extreme homogeneity for sex differences and are similar to earlier studies in various populations[23,45,46,65,67–71]. However, significant sibling correlations (but low values) indicate its genetic nature and are similar with earlier studies[72]. It may be due to the isolated and inbred nature of our sample. Main lines (MLA, MLD) and main line index (MLI): All the results (Table 5) are homogeneous between sexes and sibling correlations are also non-significant. These results are very similar with earlier studies[47–49,72]. Cross- correlation between traits in siblings: Significant cross- correlations (Table 6) are almost with all traits except a–b ridge count indicating significant inheritance and are similar with earlier results[72]. The correlation coefficients for diverse dermatoglyphic traits are perhaps expected in such a small isolated and consanguineous population. In general, we found lower correlation coefficients than in other non-consanguineous populations.

Conclusion

The familial correlation coefficients of quantitative dermatoglyphic traits are perhaps expected lower in such a small isolated and consanguineous population than our previous studied in Indian populations and Chuvashian populations from Russia. These results indicate a simpler genetic basis due to high degree (0.09 inbreeding coefficient) of consanguinity in Muzeina Bedouin tribe. Sex differences are evident significant in the indices of intra-individual diversity (Div) among Bedouins, but display different levels when compared with other populations, perhaps due to high level of consanguinity. The strength of correlation of both DA and FA is much lower than theoretical value, indicating that along with the little genetic component, the environmental (intrauterine) factors are mainly considerable.

REFERENCES

1. GALTON F, Finger Prints. (Macmillan and Co., London, 1892). — 2. CUMMINS H, MIDLO C, Finger prints, palms and soles. (Dover Publ. New York, 1961). — 3. ROBERTS DF, Dermatoglyphics and human genetics. In: Dermatoglyphics – Fifty years later. (WERTELECKI W, PLATO CC. (editors). New York: Alan R Liss; p 529–538, 1979). — 4. MEIER RJ, Year Book of Physical Anthropology, 23 (1980) 147. — 5. KNUSSMANN R, Humangenetik, 8 (1967) 221. — 6. KNUSSMANN R, Humangenetik, 8 (1969) 208. — 7. HOLT SB, The genetics of dermal ridges. (CC. Thomas, Springfield (III), 1968). — 8. PENROSE LS, Ann Hum Genet, 33 (1969) 15. — 9. LOESCH D, Ann Hum Genet, 34 (1971) 27. — 10. SPENCER MA, ELSTON KK, NAMBOODIRI KK, POLLITZER WS, Hum Hered, 23 (1973) 414. — 11. WENINGER M, HOUSER AG, SCHEIBER V, Human Biology, 18 (1976) 713. — 12. JANTZ RL, OWSLEY DW, Ann Hum Biol, 4 (1977) 357. — 13. MATHEW S, MOHANOHAN HSR, Ann Hum Biol, 8 (1981) 567. — 14. CHAKRABORTY R, MATHEW S, SATYANARAYANA M, MAJUMDER PP, CHAKRABORTY R, MATHEW S, SATYANARAYANA M, MAJUMDAR PP, Am J Anthrop, 58 (1982) 431. — 15. MARTIN NG, EAVES LJ, LOESCH DZ, Ann Hum Biol, 9 (1982) 539. — 16. KOBYLIANSKY E, MICLE S, Intern J Anthropol, 1(1986) 49. — 17. KOBYLIANSKY E, LIVSHITS G, Am J Phys Anthrop, 70 (1986) 251. — 18. ARRIETA MI, IBRARRONDO MA, LOSTAO CM, Am J Phys Anthrop, 73 (1987) 89. — 19. KARMAKAR B, MALHOTRA KC, NARAIN P, Anthropologie, 27 (1989) 13. — 20. KOBYLIANSKY E, Hum Ecol, 9 (1990) 37. — 21. CRAWFORD MH, DUGGIRALA R, Hum Biol, 64 (1992) 683. — 22. JANTZ RL, ERIKSSON AW, BREHME H, Hum Biol, 65 (1993) 711. — 23. DEMARCHI DA, GIORDANO AR, MARCELLINO A, Hum. Biol, 69 (1997) 227. — 24. BONNEVIE K, J Genet, 15 (1924) 1. — 25. NEWMAN HH, Am J Phys Anthrop, 14 (1930) 331. — 26. GEIPEL G, Ibid, 39 (1941) 414. — 27. MATSUDA F, Jap J Hum Genet, 17 (1973) 293. — 28. SINGH S, Evidence of dominance in the finger ridge counts using multivariate analysis. In: Dermatoglyphics – Fifty years latter. WERTELECKI WW, PLATO CC. Birth defects: Orig. Art. Ser. 15 (1979) 529. — 29. DITTMAR M, Anthropol Biologica, 2 (1994) 39. — 30. HOLT SB, Ann Hum Genet, 24 (1960) 253. — 31. JANTZ RL, Am J Phys Anthrop, 4 (1975) 215. — 32. LEGUEBE A, VRYDAGH S, Coll Anthrop, 3 (1979) 225. — 33. LEGUEBE A, VRYDAGH S, Ann Hum Biol, 8 (1981) 519. — 34. JANTZ RL, WEBB RS, Am J Phys Anthrop, 57 (1982) 253. — 35. DITTMAR M, Am J Phys Anthropol, 105 (1998) 377. — 36. MICLE S, KOBYLIANSKY E, Hum Biol, 58 (19864) 85. — 37. MICLE S, KOBYLIANSKY E, Homo, 42 (1991) 21. — 38. KAREV GB, Anthrop Anz, 46 (1988) 245. — 39. KAREV GB, Am J Hum Biol, 2 (1990) 63. — 40. ARRIETA MI, CRIADO B, MARTINEZ B, LOBATO MN, GIL A, LOSTAO CM, Ann Hum Biol, 20 (1993) 557. — 41. ARRIETA MI, MARTINEZ B, NUNEZ M, GIL A, CRIADO B, TELEZ M, LOSTAO CM, Hum Biol, 67 (1995) 121. — 42. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Coll Antropol, 25 (2001) 167. — 43. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Homo, 53 (2003) 263. — 44. KARMAKAR B, MALKIN I, KOBYLIANSKY E, Anthrop Anz, 63 (2005) 365. — 45. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Homo, 59 (2008a) 317. — 46. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Coll Antropol, 32 (2008b) 467. — 47. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Int J Anthropol, 24 (2009a) 163. — 48. KARMAKAR B, MALKIN I, KOBYLIANSKY E, Anthrop Anz, 67 (2009b) 253. — 49. KARMAKAR B, KOBYLIANSKY E, Coll Antropol, 33 (2009c) 1007. — 50. SENGUPTA M, KARMAKAR B, Hum Biol, 78 (2006) 199. — 51. PALMER AR, STROBECK C, Ann Rev Ecol Syst, 17 (1986) 391. — 52. JANTZ RL, Hum Biol, 46 (1974) 663. — 53. KOBYLIANSKY E, HERSHKOVITZ I, Biology of Desert Populations – South Sinai Bedouins: Growth and Development of Children in Human Isolates. (Etudes et Rech. Archeologiques de l'Universite de Liege, Belgium, pp. 283, 1997). — 54. NIE NH, HULL CH, JENKINS JG, STEINBRENNER K, BENT DH, Statistical packages for the social sciences. (2nd Ed. McGraw-Hill, New York, 1975) — 55. PARSONS PA, Acta Genet (Basel), 14 (1964) 201. — 56. MI MP, RASHAD MN, Genetic parameters of dermal patterns and ridge counts. Hum Hered 25 (1975) 249. — 57. MATHEW S, Genetics of dermal ridges. (PhD.Thesis, Andhra University, India. 1980). — 58. DEVI S, Mode of inheritance of finger and palmar dermatoglyphic patterns in an endogamous population of Orissa. (Ph.D. Thesis, Utkal University, India, 2000). — 59. SENGUPTA M, KARMAKAR B, Ann Hum Biol, 31 (2004) 526. — 60. CHOPRA VP, Homo, 30 (1979)1. — 61. DAS CHAUDHURI AB, CHOPRA VP, J Ind Anthrop Soci, 18 (1983) 147. — 62. FALCONER DS, Introduction to quantitative genetics. (Edinburgh, Oliver & Boyd Co. 1981). — 63. IGBIGBI PS, MSAMATI BC, East Afr Med J, 76 (1999) 668. — 64. IGBIGBI PS, MSAMATI BC, Med Sci Monit, 8 (2002) 757. — 65. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Sexual dimorphism: 22 dermatoglyphic traits in five endogamous populations of West Bengal, India. In: Papers on Anthropology. Tartu University, Estonia, Vol XI, pp 93- 112, 2002a). — 66. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Anthrop Anz, 60 (2002b) 273. — 67. REDDY BM, MALHOTRA. KC, Homo, 36 (1985) 11. — 68. REDDY BM, MALHOTRA KC, Int J Anthropol, 2 (1987) 141. — 69. ARRIETA M.I, MARTINEZ B, SIMSON A, SALAZAR L, CRIADO B, LOSTAO CM, Anthrop Anz, 48 (1990) 65. — 70. GOMEZ. P, MARTIN J, Coll Antropol, 16 (1992) 395. — 71. KARMAKAR B, YAKOVENKO K, KOBYLIANSKY E, Am J Hum Biol, 18 (2006) 377. — 72. KOBYLIANSKY E, MICLE S, NEFESH R, HERSKOVITZ I, ARENSBURG B, Anthrop Anz 42 (1984) 291.

B. Karmakar

Indian Statistical Institute, Biological Anthropology Unit, 203 B.T.Road, Kolkata 700 108, India
e-mail: bibha@isical.ac.in

NASLJEĐIVANJE KVANTITATIVNIH DERMATOGLIFSKIH KARAKTERISTIKA S ASIMETRIJOM I RAZNOVRNOŠĆU KOD PLEMENA MUZEINA BEDOUIN: MALA IZOLIRANA POPULACIJA U KONSANGVINITETU IZ JUŽNOG SINAJA

SAŽETAK

Genetski čimbenici koji značajno doprinose determiniranju karakteristike dermatoglifa dobro su uspostavljeni. No, kontroverze kod pristupa u problematici su i dalje nejasne. Ova studija predstavlja pokušaj pri evaluaciji nasljednih i kvantitativnih dermatoglifskih karakteristika sa asimetrijom (DA i FA) i raznovrsnosti (Div) kroz srodne povezanosti. Obuhvaćeno je 218 pojedinca iz 88 obitelji unutar malog izolata, nomadskog plemena Muzeina sa visokim postotkom konsangviniteta (0.09) iz južnoj Sinaja. Statističke analize uključuju srodnu povezanost, unakrsnu korelaciju i genetsku korelaciju (GC) – omjer srodne unakrsne korelacije između karakteristika podijeljenih na kvadratnom korijenu od produkta srodne korelacije obje karakteristike. Koeficijenti familijarne korelacije za kvantitativne dermatoglifske karakteristike kod takvih malih izoliranih populacija uz prisutnost konsangviniteta su očekivani u nižoj vrijednosti nego kod naše prethodne studije kod populacije Indije i Chuvashian populacije iz Rusije. Ovi rezultati pokazuju jednostavniju genetsku osnovu zbog visokog stupnja (koeficijent srođivanja 0.09) konsangviniteta kod plemena Muzeina Bedouin. Nema dokaza o većoj umiješanosti gena, iako je mali genetski učinak uočen kod familijarne korelacije kod asimetričnih (DA i FA) i raznovrsnih (Div) karakteristika kroz srodne korelacije. Uočena je značajna interakcija između spolova, što je u suprotnosti sa drugih populacija, vjerojatno zbog visoke razine konsangviniteta. Korelacijski koeficijenti niži od onih u ne-konsangvinitetnim populacijama za kvantitativne dermatoglifske krakteristike upućuju na jednostavniju genetsku osnovu zbog visokog stupnja koeficijenta srođivanja u Muzeini. Dermatoglifska asimetrija i raznolikost obilježja se mogu vjerojatnije pojaviti zbog okolišnih čimbenika, nego radi dominantnosti kod Bedouina, iako pronađeni mali genetski učinak sugerira mjeru razvojne nestabilnosti kod čovjeka (FA).

APPENDIX 1

LIST OF UTILIZED DERMATOGLYPHIC TRAITS

11 Diversity traits (Div)	15 Directional Asymmetry (DA) traits	16 Fluctuating Asymmetry (FA) traits
Div_1= max – min FRC (lh)	DA_1= Div 2 – Div 1	FA_1= Div I – Div 2
Div_2= max – min FRC (rh)	DA_2= PII, rh – lh	FA_2= PII, rh – lh
Div_3= max – min FRC (r+l)	DA_3 = a–b RC, r – l	FA_3= a–b, RC, rh – lh
Div_4= S^2 l	DA_4= RC, rh – lh	FA_4 FRC, rh – lh
Div_5= S^2 r	DA_5= S^2, rh – lh	FA_5= Div 5 – Div 4
Div_6= S2 (r+l)	DA_6= Div 8-Div 7	FA_6= Div 8 – Div 7
Div_7= Sl	DA_7= atd angle, r – l	FA_7= atd angle, r – l
Div_8= Sr	DA_8= a–b dist. r-l	FA_8 = a–b dist. r-l
Div_9= Sv10, (r+l)	DA_9= ridge breadth, r-l	FA_9= ridge breadth, r-l
Div_10= S(r+l)	DA_10 = FRC, 5r – 5l	FA_10= FRC, 5r – 5l
Div_11= Shannon's index	DA_11= FRC, 4r – 4l	FA_11= FRC, 4r – 4l
	DA_12= FRC, 3r – 3l	FA_12= FRC, 3r – 3l
	DA_13= FRC, 2r – 2l	FA_13= FRC, 2r – 2l
	DA_14= FRC, 1r – 1l	FA_14= FRC, 1r – 1l
	DA_15= MLI, rh – lh	FA_15= MLI, rh – lh
		FA_16 = AI, asymmetry 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; 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 (FLAs) was computed by using the absolute differences between the bilateral measurements. The distribution of the non-absolute differences for each individual were corrected (Livshits et al., 1988) to avoid additional influences (scaling effects) like size of the trait or directional asymmetry, 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, 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, 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.

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 i^{th} finger of the right and left hand.