VII. INBREEDING LEVEL AND MORPHOLOGICAL DIFFERENCES BETWEEN AND WITHIN SOUTH SINAI BEDOUIN TRIBES

In the last part of this chapter we shall attempt to ascertain whether the distribution of the morphometric traits in the tribes and sub-tribes of Bedouins in South Sinai deviate from the norms observed in large populations with random matings. If, indeed, deviation should be observed, we could attribute a not inconsiderable portion of the observed genetic variability to inbreeding (albeit selection and genetic drift could also come into play).

Theoretical Background

In previous chapters we have discussed the possible drop in heterozygosity in the Bedouin tribes, and the possible influences of inbreeding (mainly first-cousin marriages) on the phenotype of the group. We now consider the link between inbreeding and morphometric traits in the Bedouin. Crow and Kimura (1970, p.83) in their discussion of inbreeding noted possible changes in the mean and variance of a trait (e.g. stature, weight, etc.) within populations with different levels of inbreeding under various models of dominance and epistasis

The concept that inbreeding leads to an increase in the proportion of homozygotes in the population, was developed via the inbreeding coefficient by Wright (1921). Wright was thus the first to offer a tool for estimating the extent of inbreeding in a population. This tool has been refined and adapted for various population conditions, both by Wright himself and by some of his associates (e.g. Kimura, 1955; Crow and Kimura, 1970; etc.). Crow and Kimura (1970) showed that the frequency of heterozygotes in the population drops at the rate of 1/2Ne (N= the effective population size) per generation (independetly of the number of alleles involved).

Let us here attempt to translate theory into practical terms. In an panmictic population the distribution of the genotypes for a given trait will appear approximately as follows: at the center of the distribution curve and around it there will be a concentration of individuals heterozygous for a particular trait, while the homozygotes will appear at the margins.

The Statistical Processing

Our age-tribal samples of Bedouin boys were small, primarily due to the small size of the total South Sinai Bedouin population. Hence we were forced to "increase" the samples by converting measures into standard scores for each age-tribal group separately, and by combining standard scores of all children of a particular tribe, regardless of age group. Taking these new distributions, we performed the necessary statistical manipulations, that is, the measures of skewness and kurtosis ("peakedness") for evaluating the new distributions and their deviations from the norm.

The computation of these two statistical measures (kurtosis and skewness) was done according to SPSS, Condescriptive Statistics (Novusis, 1990).

In a distribution which has a totally symmetric bell-shaped curve, skewness and kurtosis measures acquire the value of zero. It may be recalled that when the scores tend to trail off to the right, or positive end of the scale, it is considered positively skewed; conversely, when scores tend to trail off to the left, the negative end of the scale, it is negatively skewed. If the kurtosis value is positive, the distribution is more peaked (narrow and high, designated as leptokurtic), whereas a negative value implies a flattened curve (platykurtic).

In view of the small size of the samples on which our computations were based, we necessarily relied mainly on calculations specific for small samples (Johnson, 1949; D'Agostino and Pearson, 1973; Dunaveskeya et al., 1973) to determine the deviations from normal distribution as expressed in the measures of skewness and kurtosis.

Distribution of quantitative traits in the various tribes of South Sinai

The measures of skewness and kurtosis for the distributions of each of the studied morphometric traits among boys in four tribes are given in Table 84. As noted in the table, the several Bedouin tribes manifest only a few (2-3) traits that appear statistically significant, with no special tendency towards skewness or kurtosis.

On the basis of these results, we conclude that most of the physical traits in all of the Bedouin groups display a close approximation to a normal distribution, i.e. follow a fairly symmetrical bell-shaped curve. The few traits deviating from the normal curve may be products of genetic processes acting within small isolated groups, or indeed the result of inadequate sampling.

Although not statistically significant, it seems noteworthy that of the 41 traits considered, the distribution of 38 showed negative kurtosis in the Gebeliya tribe, 22 such in the Muzeina tribe, all 39 in the Hamada-Aleigat group, and 32 in the "other" or remaining tribes. There is indeed a tendency in large panmictic populations for some of the morphometric trait distributions to present negative kurtosis (Wolanski and Takai, 1976), but not at the rates and frequencies observed in the Bedouin tribes of South Sinai. As noted in Table 84, a negative skewness occurred less frequently than a positive skewness. Skewness and kurtosis differed both in regard to traits, and frequency of each among the tribes. For example, in the Gebeliya tribe the trait "Hand length" had a high negative kurtosis and a positive skewness tending towards zero, whereas in the Muzeina tribe this trait manifested positive kurtosis and a positive skewness (Table 84).

TABLE 84 Kurtosis (K) and skewness (S) for some metric trait distributions in different Bedouin groups.

TRIBES								
	Gebeliya (N=66)		Muzeina (N=253)		Hamada&Aleigat (N=64)		Others (N=134)	
Variable	K	S	K	S	K	S	K	S
Stature	-0.238	0.359	-0.336	0.187	-0.319	0.200	-0.249	0.059
Iliospinal height	-0.385	-0.019	-0.180	0.080	-0.612	0.349	-0.111	-0.037
Tibial height	-0.280	-0.132	-0.353	0.219	-0.832	0.346	-0.136	-0.005
Acromial height	-0.310	0.236	0.632*	0.419*	-0.439	0.274	-0.380	-0.037
Sitting height (1)	-0.109	0.493	-0.081	0.171	-0.679	0.219	-0.643	0.187
Foot breadth	-0.623	0.359	-0.338	0.110	-0.734	-0.291	-0.367	0.051
Foot length	-0.891	0.016	-0.234	-0.078	-0.320	-0.216	-0.541	0.071
Head length	-0.906	-0.236	0.095	-0.291	-0.396	0.070	-0.404	0.142
Head breadth	-0.699	-0.575	-0.512	0.048	-0.772	0.213	-0.758	0.351
Bizygomatic breadth	-0.994	-0.224	-0.436	0.204	-0.670	0.252	-0.758	0.208
Bigonial breadth	-0.231	-0.655*	2.543*	1.077*	-0.426	-0.260	-0.283	-0.480*
Morphological facial ht.	-0.845	0.075	-0.395	-0.079	-0.535	0.140	-0.015	-0.220
Biacromial breadth	0.309	-0.756*	-0.108	-0.030	-0.293	-0.253	0.203	-0.320
Biiliac breadth	-0.761	0.004	-0.140	0.163	-0.975	0.130	0.237	0.598*
Chest circumference	-0.195	0.527	-0.68*	0.072	-0.780	0.058	0.012	0.349
Body weight	-0.535	0.541	-0.140	0.324	-0.926	0.268	-0.316	0.085
Hand strength (L)	-1.128*	-0.029	-0.470	0.167	-0.293	0.059	-0.449	-0.013
Hand strength (R)	-0.218	-0.141	0.130	0.093	-0.326	0.075	-0.190	-0.029
Total arm length	-0.527	0.195	0.337	0.387*	-0.471	0.326	-0.424	-0.024
Upper body segment	-0.068	-0.231	0.777*	-0.412*	-0.318	0.251	0.098	0.263
Upper leg length	-1.147*	0.098	0.419	0.192	-0.728	0.198	0.248	0.286
Upper arm length	-0.307	0.374	0.481	-0.092	-0.045	0.703*	-0.139	0.258
Lower arm length	-0.213	0.143	1.393*	-0.021	-0.314	-0.004	-0.060	-0.184
Hand length	-0.629	0.003	0.172	0.212	-0.404	0.167	0.257	0.094
Trunk length	-0.130	0.177	-0.077	-0.001	-0.156	0.096	-0.608	-0.055

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Table 84: cont.

Body weight/Stature^3	-0.627	0.173	0.025	0.298	-0.585	-0.111	-0.053	0.286
Body weight/ Stature^2	-0.756	0.103	0.176	0.312	-0.641	-0.021	-0.321	0.114
Total arm length/Stature	-0.821	-0.279	0.063	0.066	-0.373	0.046	-0.228	-0.122
Sitting ht.(1)/Stature	-0.647	0.366	1.689*	0.015	-0.723	-0.175	-0.053	0.008
Leg length/Stature	-0.652	0.260	-0.275	-0.014	-0.911	0.027	-0.382	-0.427
Foot br./Foot length	-0.672	0.291	-0.097	-0.141	-0.219	0.462	-0.225	0.067
Head br./Head length	-0.653	0.555	0.525	0.495*	-0.836	0.121	-0.531	0.226
Biacromial br./Stature	0.111	-0.604*	-0.457	0.079	-0.722	-0.429	-0.332	-0.107
Biiliac br./Stature	-0.903	-0.088	-0.512	0.040	-0.824	-0.253	-0.722	0.217
Chest circumf./ Stature	-0.687	-0.083	0.257	-0.252	-0.560	0.162	-0.644	0.100
Body weight/Stature	-0.739	0.453	-0.032	0.247	-0.867	0.187	-0.295	-0.019
Body surface area	-0.530	0.459	-0.337	0.261	-0.957	0.141	-0.424	0.069
Body surface area/ Body wt.	-0.922	-0.219	0.075	0.024	-0.360	-0.195	0.003	0.069
Kj	-0.538	0.541	-0.136	0.324	-0.934	0.294	-0.306	0.081

Note: Sitting height (1) differs from Sitting height (2) - see Tests and/or explanations chapter. Upper arm and subscapular skinfolds were excluded from the analysis because they have highly positive skewed distributions also in panmictic conditions.

* $p \leq 0.05$

Adult Bedouin during argometric test (standing R. Nefesh)

Distribution of quantitative traits in the Muzeina tribe and its sub-tribes

In the Muzeina sub-tribes (Table 85), the distribution measures of the traits differ from those in the tribe proper (see Table 84). For example, in the Shadadine, 13 traits show significant kurtosis. Significant skewness obtained for 9 distributions (eight positive and one negative), the same in which significant kurtosis was displayed with the exceptions of body weight and sitting height.

When we combine the four sub-tribes Shadadine, Dararme, Gawanme and Gsenat into a single group, and weight the sample size for each sub-tribe to compute a group result, we obtain results which are almost identical to those obtained for the entire tribe which included all six sub-tribes without weighting their relative size in the general tribal population.Only in one trait, namely, hand length, is significant skewness observed in the distributions for the four sub-tribes, which was not observed for the tribe as a whole (Table 85).

In sum, the data on skewness and kurtosis provide no strong evidence of inbreeding on the expression of the various morphometric traits in the tribes or the sub-tribes. Yet, despite the lack of statistical significance for skewness and kurtosis in most of the distributions, we cannot ignore the relatively high values of these measures. We believe that such high values for most of the traits studied, at least suggest a tendency for deviation from the "normal" distribution.

As is known, skewness and kurtosis are sensitive measures of `normality' of distribution, and in samples smaller than 100 even the slightest deviations from the norm drastically affect their values. Thus, for instance, narrow and tall curves which are based on small samples are liable to show negative skewness because at one tail of the curve there is a fortuitous high frequency of cases. The fact that we obtain negative skewness for such a curve, however, can be misleading, and may not reflect the `true' distribution of the trait.

We therefore decided to employ two additional measures as a check on our skewness and kurtosis results. First, we constructed for each trait separately the distribution of its frequencies according to the `Frequencies-SPSS' procedure (SPSS, 1975). Because we replaced the raw scores of the individuals with standard scores, the x-axis carries units of standard normal deviates (at intervals of 0.5 units, ranging from +5.0 to -5.0), while the y-axis presents the frequencies in percentages; and second, we constructed distributions of traits representing different components of explained variance selected by Principle Component Analysis, and determined their deviations from the normal distribution.

In addition to the statistical tests, a detailed examination of the actual distribution pattern of the various morphological traits within the South Sinai Bedouins was also carried out.

TABLE 85 Kurtosis (K) and skewness (S) for some metric trait distributions in different Muzeina sub-tribes.

SUB-TRIBES								
	Shadadine (N=22)		Dararme (N=27)		Gawanme (N=30)		Gsenat (N=79)	
Variable	K	S	K	S	K	S	K	S
Stature	3.642*	1.548*	-0.211	0.215	-0.441	0.706	-0.487	0.117
Iliospinal height	3.422*	1.706*	-0.844	-0.020	-0.154	0.266	-0.149	-0.001
Tibial height	3.785*	1.438*	-1.024	0.329	0.143	0.312	-0.538	-0.164
Acromial height	0.929	0.743	-0.256	0.207	-0.550	0.549	-0.041	0.105
Sitting height (1)	0.932	-0.093	0.300	0.710	-0.040	0.208	-0.167	-0.169
Foot breadth	-0.354	-0.285	-0.538	0.711	-0.642	0.233	-0.269	0.001
Foot length	-0.765	0.050	-1.101	0.184	0.074*	0.290	-0.247	-0.201
Head length	0.297	-0.262	-0.554	-0.025	-0.117	-0.397	0.778	-0.666*
Head breadth	-0.951	-0.147	-0.356	0.237	-0.591	0.006	-0.600	0.247
Bizygomatic breadth	-0.062	0.558	0.554	0.177	-0.359	-0.020	-0.738	0.023
Bigonial breadth	1.890*	0.943*	0.823	-0.917*	7.029*	2.073*	-0.753	0.098
Morphological facial ht.	0.072	-0.344	-0.508	0.011	-0.264	0.187	-0.651	-0.219
Biacromial breadth	0.051	-0.435	0.690	-0.771	-0.018	0.005	-0.406	-0.002
Biiliac breadth	-0.613	0.262	0.009	0.134	0.910	-0.043	-0.185	0.109
Chest circumference	-0.111	0.330	-0.317	-0.077	0.627	0.732	-0.865	0.029
Body weight	1.616*	0.493	1.234	0.416	0.586	0.773	-0.418	0.305
Hand strength (L)	0.743	0.781	-1.187	-0.041	0.447	-0.012	-0.526	-0.123
Hand strength (R)	-0.863	0.108	1.337*	-0.155	-0.101	0.038	0.034	0.263
Total arm length	4.608*	1.306*	-0.858	-0.070	0.483	0.572	0.275	0.298
Upper body segment	0.142	0.904	0.171	-0.740	-0.723	-0.109	0.846	-0.193
Upper leg length	2.649*	1.421*	-0.766	0.006	-0.652	-0.255	1.654*	0.471
Upper arm length	-1.130	0.107	-0.279	-0.612	1.016	-0.447	-0.211	0.106
Lower arm length	3.257*	1.391*	-0.763	-0.177	-0.297	0.213	0.650	0.246
Hand length	0.760	0.570	0.108	-0.201	0.366	0.847	-0.494	-0.046
Trunk length	-0.034	-0.599	-0.450	-0.327	0.672	0.628	-0.197	-0.123
Body weight/Stature^3	1.019	0.132	-0.079	0.231	-0.246	-0.105	0.384	0.359
Body weight/ Stature^2	0.282	0.337	0.432	0.627	0.133	0.225	0.461	0.203
Total arm length/Stature	-0.608	-0.414	0.475	0.371	-0.536	0.008	-0.402	0.427
Sitting ht.(1)/Stature	4.292*	-1.403*	-0.551	-0.632	2.872*	1.154*	1,355*	0.043
Leg length/Stature	-1.217	-0.302	0.799	0.664	0.426	-0.498	-0.638	0.009

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Table 85: Cont.

SUB-TRIBES								
	Shadadine (N=22)		Dararme (N=27)		Gawanme (N=30)		Gsenat (N=79)	
Foot br./Foot length	-0.148	0.210	-0.075	-0.139	-0.552	0.061	-0.104	-0.148
Head br./Head length	-0.304	0.876	-0.458	0.080	2.974*	1.134*	0.320	0.477
Biacromial br./Stature	-0.864	0.328	-0.401	-0.558	-0.770	0.132	-0.221	0.103
Biiliac br./Stature	0.385	-0.175	-0.023	0.702	-0.668	-0.176	-0.364	-0.104
Chest circumf./Stature	0.319	0.801	-0.078	-0.198	0.191	-0.090	0.439	1.029*
Body weight/Stature	0.745	0.298	1.155	0.500	0.501	0.600	-0.294	0.092
Body surface area	2.195*	-0.928	0.491	0.322	0.042	0.590	-0.595	0.257
Body surface area/Body wt	0.557	0.406	0.643	0.323	-0.325	-0.164	0.390	0.042
Kj	1.658*	0.507	1.241	0.422	0.588	0.774	-0.404	0.299

* significant $p \leq 0.05$

For notes, see Table 84

Distribution of traits representing different components of morphology, as detected through PCA. Muzeina tribe.

The distributions of 8 variables (converted to standard scores) representing, according to PCA, different aspects of child morphology correlated weakly with one another, as noted in Table 86. These variables are examined relative to theoretical normal distribution in Figures 31-38.

Prof. Ben-David (Kobyliansky) taking head circumference measure from an adult Bedouin.

TABLE 86: A correlation matrix between eight morphological traits in Muzeina boys, aged 5-13 years.

PC[1]	LV[2]	Trait	St	LAL	CC	HB	UBS	HL	HAL
I	.958	Stature (St)	-						
I	.618	Lower arm length (LAL)**	.523	-					
I,II	.576	chest circumference (CC)*	.554	.346	-				
IV	.746	Head breadth (HB)	.205	.085	.206	-			
X	.476	Upper body segment (UBS)**	.517	.204	.259	.047	-		
VIII	.854	Head length (HL)	.301	.219	.157	.026	.231	-	
V	.694	Hand length (HAL)	.337	.167	.164	-.073	.233	.167	-
I	.439	Morphological facial ht.	.392	.258	.237	.082	.298	.123	.131

[1]PC= Principal Component

[2]LV= Loading Value

* Statistically significant negative kurtosis

** Statistically significant positive kurtosis

FIGURE 31: Standard Score Distribution of Body Height in Muzeina Boys, Compared to Normal Theoretical Distribution.

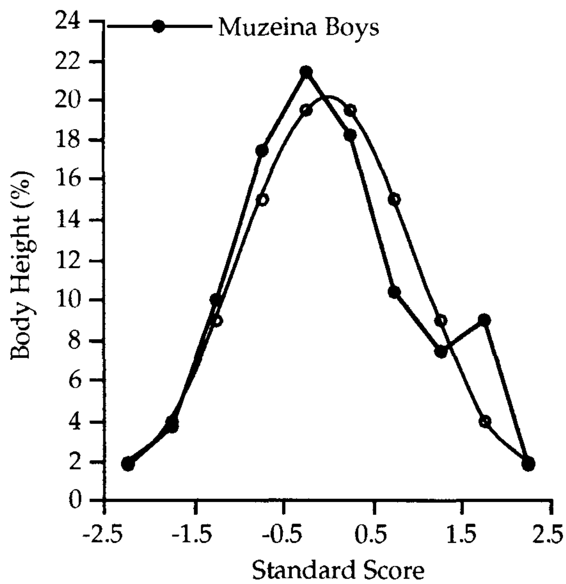


FIGURE 32: Standard Score distribution of Upper Body Length in Muzeina Boys, Compared to Normal Theoretical Distribution.

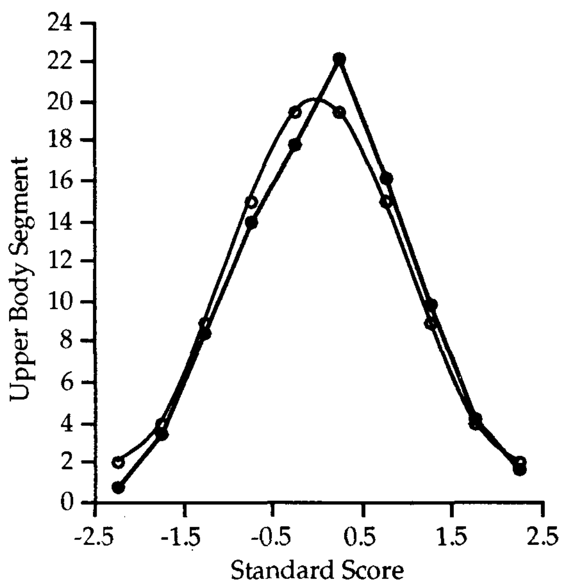


FIGURE 33:Standard Score Distribution of Facial Height in Muzeina Compared to Normal Theoretical Distribution.

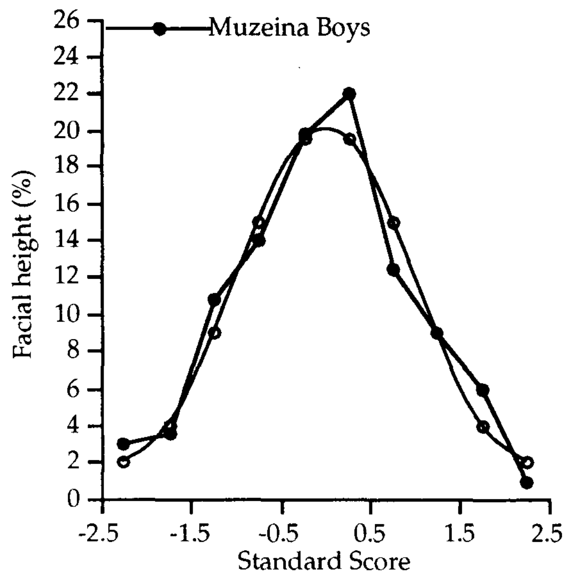


FIGURE 34: Standard Score Distribution of Head Length in Muzeina Boys Boys, Boys, Compared to Normal Theoretical Distribution.

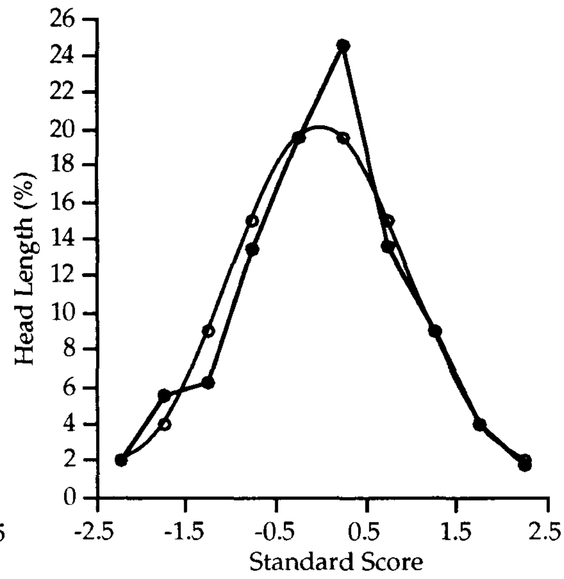


FIGURE 35:Standard Score Distribution of Hand Length in Muzeina Boys Compared to Normal Theoretical Distribution.

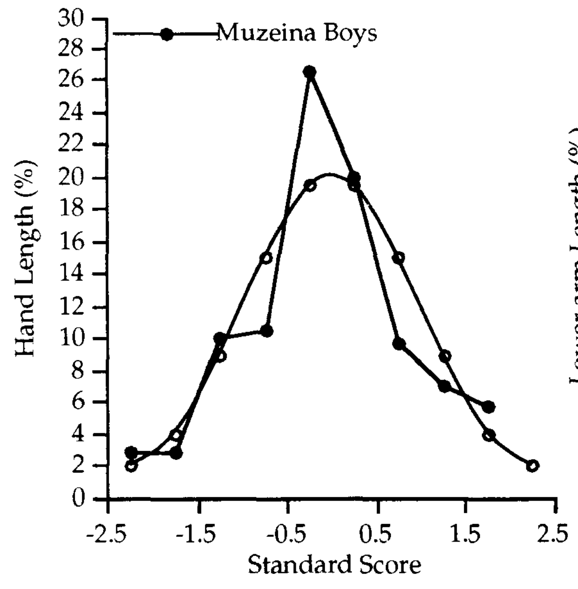


FIGURE 36: Standard Score Distribution of Lower Arm Length in Muzeina Boys, Compared to Normal Theoretical Distribution.

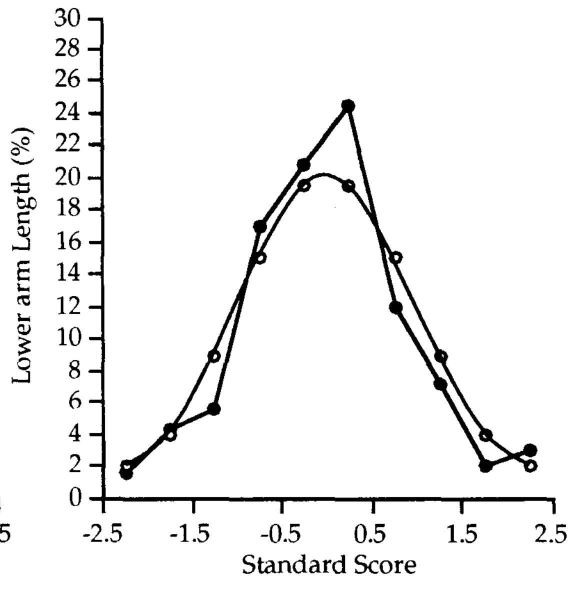


FIGURE 37: Standard Score Distribution of Chest Circumference in Muzeina Boys, Compared to Normal Theoretical Distribution,

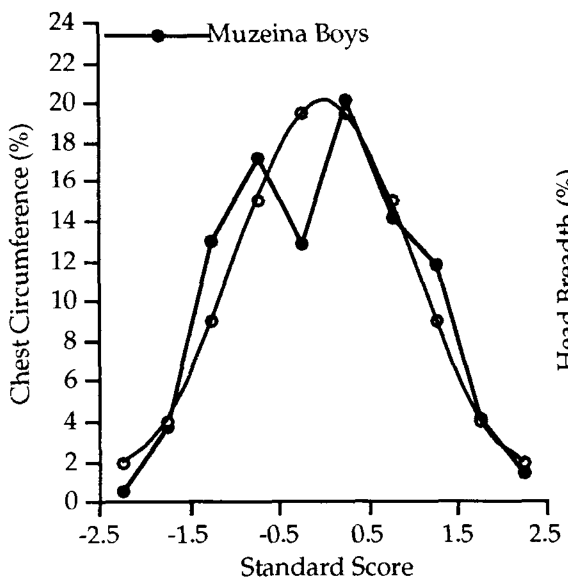
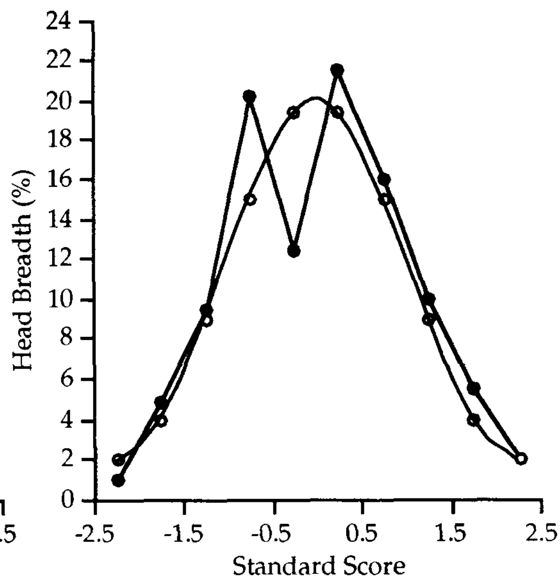


FIGURE 38: Standard Score Distribution of Head Breadth in Muzeina Boys, Compared to Normal Theoretical Distribution.



Three different types of distribution are recognized. First, more or less "bell-shaped" distribution curves are noted for stature, upper body segment length, and facial height (Figs. 31-33) second, there is a more narrow and peaked distribution for head length, hand length and lower arm length (Figs. 34-36); and third, one notes a bimodal distribution for chest circumference and head breadth (Figs. 37-38).

It would seem that two main forces may be acting on these traits, namely inbreeding and stabilizing selection. Inbreeding leads to a diminution in the number of heterozygotes and a reciprocal increase in the number of homozygotes.

On the further assumption of parallelism between the distributions of biochemical traits (whose gene frequencies are known) and that of quantitative traits (see Kobyliansky and Livshits, 1983), it becomes possible to use morphometric trait distributions to measure a decrease in heterozygosity of a population or group, provided that the observed phenomena are not the outcome of `disruptive selection' which there is no good reason to assume in the present instance. When a trait distributes normally, 50% of the cases will fall within the range of ±0.67 standard deviations from the mean, which we consider as indicative of heterozygosity in individuals. In a population in which effective inbreeding occurs, there will be a diminution in the proportion of cases falling into this range (±0.67 S.D. from the mean), a state which represents a decreased number of heterozygotes and a corresponding increase in homozygotic individuals.

This link between a drop in heterozygote frequency and inbreeding, expressed in terms of F, can thus be estimated from the following equation: $M_2 = M_1x(1\text{-}F)$, where M_1 is the theoretical percentage of heterozygotes in the normal distribution (panmictic condition) and M_2 the corresponding percentage in the new distribution (inbred condition). The difficulty, as already noted, is how to construct phenotypic units that can fit the various genotypes. On the assumption that the external expression of the trait is determined by a number of loci and that the non-additive component among these is low, we can then postulate the existence of a `super locus', that is, a single "imaginary" locus which is responsible for the phenotypic expression of the trait. Thus we could assume that the heterozygote cases indeed concentrate about the mean for the trait while the tails would contain the homozygote cases, as would be expected in a system of mono-loci. The diminution in the heterozygosity of such a `super locus' would be gradual, proceeding from the center to the tails.

We now return to the previously proposed computation system $M_2 = M_1x(1\text{-}F)$. If in a normal distribution of a trait 50% of the cases are at a distance of ±0.67 standard deviation from the mean, then in a population in which the inbreeding coefficient is F=0.09802 the 50 percent level will decrease to 45.1%, a drop of 4.9% in the number of heterozygous individuals for the given trait in the population. If we limit the range of heterozygosity in the distribution to only ±0.5 standard deviation from the mean, then for the Bedouin inbred population with F=0.09802 the expected number of heterozygous individuals will be about 34.5%. Now we may calculate the relative decrease in heterozygous individuals directly from the plotted metrical trait curves. In the two traits in which there is a bimodal distribution, the heterozygosity (within the range of ±0.5 S.D.) diminishes to 32.8% for chest circumference and 34.2% for head breadth. These observed values are very close to the expected 34.5% under an inbreeding pressure of F=0.09802.

The drop in the frequency of heterozygotes described above is understandable because of its linkage with inbreeding and explains the bimodal curves that were obtained for some of the traits.

We shall now attempt to ascertain the action of the second factor, stabilizing selection, on the shape of the curves observed. Stabilizing selection, or selection which acts against the tails and in favor of the middle of a distribution curve, is generally related to the increase in number of heterozygous cases. The effect of this mechanism is to reduce the variance in the population (Roughgarden, 1979, p.140). Evidence for stabilizing selection has been obtained in both human and animal studies. For example, it was found that among neonates with extreme values of weight and height, the mortality was higher than among neonates which were closer in these two respects to the population mean (Cavalli-Sforza and Bodmer, 1971; Ulizzi et al., 1981). The process whereby the individuals homozygous for morphologic traits are less resistant than the heterozygous individuals, coupled with the fact that heterozygous parents tend to be more fecund than homozygous parents (Goldstein and Kobyliansky, 1984; Kobyliansky and Livshits, 1983), lead to a constant increase in the number of individuals who are heterozygous for a given trait.

The influence of `stabilizing selection' (Se) on the frequency in the population of individuals heterozygous for a considered trait can be computed from the following equation: $Se = (M_{obs.} - M_{exp.})/M_{exp.}$, where $M_{exp.}$ = mean ±0.5 standard deviation. This equation indicates the relationship between the observed frequency of heterozygotes and that expected within the limits of a defined standard deviation. For example, in the trait of lower arm length, there is an increase of 19.1% in the frequency of the heterozygotes as derived from the following computation: Se =(45.6%-38.3%)/38.3% where 45.6% = the observed heterozygote frequency in the range of ± 0.5 S.D. from the mean of the lower arm length trait in the Muzeina tribe (Table 87), and 38.3% = the expected heterozygote frequency in the range of ±0.5 S.D. from the theoretical mean of the trait in a large population with random breeding.

TABLE 87 Changes in the frequency of "heterozygous"-modal individuals for some morphological traits, as affected by stabilizing selection and inbreeding.

Traits	Obs.-Exp./.Exp.
Stature	4.2
Lower arm length	19.1
Chest circumference	-14.4
Head breadth	-10.7
Upper body segment	9.4
Head length	15.1
Hand length	26.9
Morphological facial height	-4.7

Of the eight morphological traits examined (Figs. 31-38) six (stature, lower arm length, upper body segment, head length, hand length) show an increase in the frequency of heterozygotes, ranging from 4.2-26.9%, and three (chest circumference, head breadth, facial height) show a decrease (4.7-14.4%).

The question which naturally arises at this point is which of the traits are affected by selection and which by inbreeding? Or we could pose the further question that if each of the traits is affected by both these forces, which of the two ultimately determines the expression of the trait?

The answers to such and similar questions are not unequivocal. Insofar as we have selected traits which are not interdependent (see the correlation matrix, Table 86), let us also assume axiomatically that they are based on different genes (even though they are multifactorial). Inbreeding characterizes a given population. There is clear evidence of its existence in the Bedouin population (high F value) and, therefore, it comprises a factor in determining the expression of a trait, probably in a bimodal distribution. The evidence in the literature for the occurrence of selection against homozygous individuals is overwhelming, and consequently it also cannot be ignored. Hence, we conclude that in the Bedouin population, stabilizing selection `counteracts' the effects of inbreeding. It follows, therefore, that the true effect of stabilizing selection, as computed by percentage of individuals heterozygous for a particular trait, is actually higher but is somewhat offset by the influence of inbreeding.

Thus far we have assumed that the tribe (i.e., the Muzeina, Gebeliya and the like) is the biological unit in which the forces of selection and inbreeding act. This assumption is predicated primarily on the relatively high percentage of intermarriages among the sub-tribes (ca. 75%) and on the low rates of intermarriage between the tribes (3%). Yet, because female migration between sub-tribes is somewhat selective, and because the rate of first-cousin marriages is very high, it seems reasonable to assume that some of the morphological traits will distribute differently among the sub-tribes. To examine this assumption we chose eight morphometric traits which are poorly correlated (Table 86), in order to ensure independence of the variables. For four sub-tribes of the Muzeina for which the representative sample sizes were fairly adequate (Shadadine, Dararme, Gawanme and Gsenat), we computed the frequency distribution. Since all individual scores were standardized, all age groups for each sub-tribe could be combined. We postulated that if these four sub-tribes differ somewhat in their genetic composition, we should obtain as a result (at least for chest circumference and head breadth which are platykurtically distributed in the total Muzeina sample) a leptokurtic distribution for each trait in each sub-tribe. The genetic translation of this result would be a) a decrease in the percentage of heterozygous individuals compared to a panmictic "normal" population and a rise in the percentage of homozygous individuals; and b) distributions which are highly positively or negatively skewed. Whether a sub-tribe will manifest a positive or negative skewness for a specific metric trait is random. Genetically, this means that concentration of the homozygous individuals in each sub-tribe in one of the tails of the curve is random.

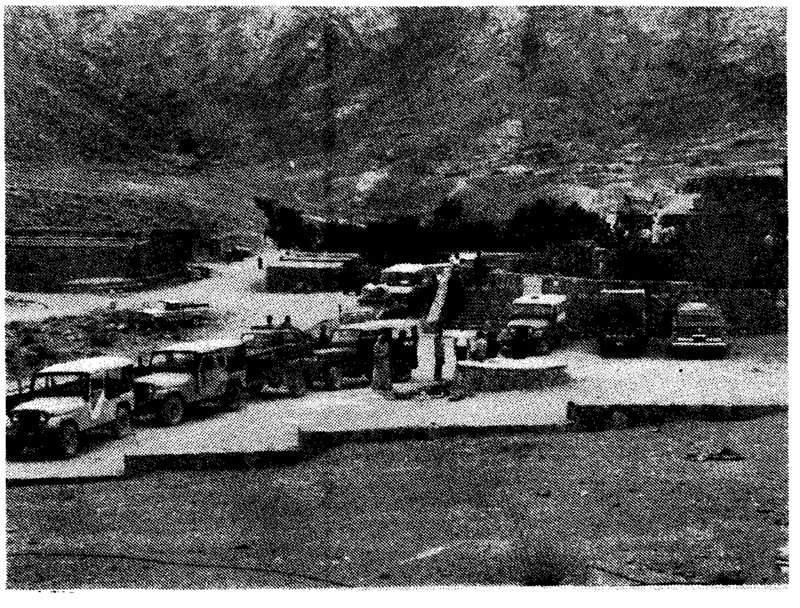
Our results show that, as expected, in two of the eight examined traits, namely, chest circumference and head breadth, there is a significant drop in most of the sub-tribes, in the percentage of individuals who are heterozygous for the trait. The mean frequency of "heterozygous" individuals for the trait of chest circumference is 32.8%, whereas the expected drop as a result of inbreeding (F=0.09802) is to 34.5% [from the computation of 38.3% X (1-F)]. Three sub-tribes show a clear decrease in the number of "heterozygous" individuals (Shadadine=33.4%; Gawanme=25.9%; and Gsenat=24.6%) and one shows an increase (Dararme=46.6%). Regarding the trait of head breadth, the observed mean of heterozygous individuals was 34.2%, also very close to the expected value. Among the sub-tribes, the frequency ranged from 31.0-36.7%. In all the remaining traits, there was no decline in heterozygotes; of the two traits which did show a decline in heterozygote frequency, only chest circumference displayed fortuitous intersubtribal fluctuations of "homozygous" individuals on both sides of the curve. For example, in the Shadadine most of the individuals "homozygous" for chest circumference (47.7%) concentrated at the left side of the curve and only 19.1% at the right side, while in the Dararme sub-tribe 36.7% of "homozygotes" concentrated on the right side of the curve (in contrast to the Shadadine) and only 16.7% on the left. However, for head breadth, the majority of "homozygous" individuals in all four sub-tribes concentrated on the left side of the curve. These results at first glance appear to be unlike the expected, i.e., random bunching of "homozygous" individuals on one side of the curve owing to randomness of the allele fixation, but since we are dealing with only four groups, the probability that most of the "homozygous" individuals will occur randomly on the same side of a curve for a particular trait in all four sub-tribes is fairly high. For the sake of completeness of the statistical analysis, we further tested whether the drop in number of heterozygotes expected as a result of inbreeding pressure, is also statistically significant for the two selected traits of chest circumference and head breadth.

We found that the kurtosis was indeed negative but its significance was only borderline. The various reasons that could account for the lack of significance of this parameter in most of the distributions have already been discussed.

We attempted another way of assessing the significance of the kurtosis values for chest circumference and head breadth. This time we used a test that takes into account only part of the overall distribution (±0.5 S.D. from the mean) and not all of it (as in the previously used test). Thus we hoped to reduce to a minimum the influence of extreme cases on the general nature of the distribution, for this is highly significant for such distributions as are based on small samples (Rokitzky, 1974). The underlying assumption of this test is that the difference between observed and expected frequencies will not be greater than the standard error of the observed values. Thus: S.E. of Obs. = $\pm\sqrt{p|n-p|}/n$ (Rokitzky, 1974, p.40), where n = the observed frequency and p = the expected frequency.

For chest circumference the data were: Exp. (P)=0.383x180=68.94, Obs. (N)=0.328x180=59.04, the Difference=9.9. According to the above formula, S.E. of Obs. (N) = 6.29, and because (Exp.-Obs)>S.E. of Obs. (9.90>6.29), the drop of kurtosis in the distribution of this trait is significant.

The same computation was made for head breadth, where the raw data were: Exp. (P)=0.383x187=71.62, Obs. (N)=0.342x187=63.95 and the Difference=7.67, resulting in S.E. (N)=6.48, and because 7.62>6.48 the drop in kurtosis for the distribution of this trait is also significant.



Leaving the Sinai