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BIOCHEMICAL HETEROZYGOSITY AND MORPHOLOGIC VARIATION IN A COLONY OF *PAPIO HAMADRYAS HAMADRYAS* BABOONS

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Abstract.—This analysis examines the association between genetic heterozygosity and individual morphologic variation in a captive population of *Papio hamadryas hamadryas* consisting of 403 juveniles and adults. The population structure of the colony was artificially generated and maintained and is thus rigorously defined. Subpopulations delimited by age, sex, and degree of inbreeding are also explored. Heterozygosity, as enumerated from six simple Mendelian biochemical loci, is compared with the residual morphologic variation of each individual for each of 20 quantitative traits. Use of a sequential Bonferroni technique nullifies all significant correlations. Principal-components analysis reduces the morphometrics to a single or few significant axes in each population. The first axis of the total population contains 86.07% of the variation in the sample and the absolute values of the factor scores exhibit a significant positive correlation with heterozygosity at $P < 0.05$. Correcting for age- and sex-related variation in the total population with a linear model subsequently demonstrates that no significant correlation between heterozygosity and morphologic variation exists. No significant relationship is found in the inbred animals or subpopulations when age and sex are controlled. Previous studies have indicated that individuals proximal to the population mean for a specific polygenic trait exhibit a higher biochemical heterozygosity than individuals distant from the mean. The results presented here, which are based on more loci than many studies and a well-defined population, do not support this relationship. Substructuring of a population by age and sex can lead to spurious correlations with univariate or multivariate techniques. Comprehensive indices of genetic variation and rigorous statistical techniques should be used in future analyses. Studies that fail to recognize these design elements should be interpreted with caution.

Key words.—Biochemical heterozygosity, morphologic variation, *Papio hamadryas hamadryas*, population genetics.

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Genetic heterozygosity at the loci encoding a polygenic, morphologic trait is purported to be inversely proportional to that trait's phenotypic variation (Falconer 1981). Lerner (1954) empirically demonstrated a negative relationship between the heterozygosity of individual organisms and their deviation from the group mean of morphological traits based on comparisons of morphologic variation between highly homozygous inbred strains and heterozygous cross progeny of various plants and animals. He ascribed this relationship to the improved fitness of a highly heterozygous organism as a product of developmental homeostasis. The generative mechanism of this phenomenon is deduced through the following argument. First, the effects of genes at the loci determining a polygenic trait are additive (Elston 1981). Second, genetic heterozygosity buffers the individual from impending ecological pressures by permitting more flexible adaptive responses than available to less heterozygous individuals (Mitton and Koehn 1985). Thus, heterozygous individuals are less likely to be eliminated by the forces of stabilizing selection and consequently, stabilizing selection acts differentially on a population, discriminately eliminating the more homozygous individuals. All things considered equal, the more heterozygous individuals within a population exhibit higher fitness values and eventually predominate. As a result, the morphologic measurements of the heterozygotes become representative of the population mean of any particular morphologic polygenic character. Furthermore, Kobyliansky and Livshits (1983) have suggested that inbreeding reinforces this process by supplementing the population of homozygotes acted upon by stabilizing selection.

The covariation between reduced phenotypic variation and heterozygosity has also been ex-

plained by theoretical models demonstrating that such a relationship is a simple consequence of the additivity of genic effects that control a quantitative trait (Chakraborty and Ryman 1983). Hence, no selective action is required. Chakraborty and Ryman (1983) also demonstrated that the theoretical relationship between morphologic variation and genomic heterozygosity is linear.

Additionally, it has been postulated that the genetic per locus heterozygosity of simple Mendelian loci, such as serum protein polymorphisms, provides a valid index of the amount of genetic variation of quantitative phenotypic traits (Hanford 1980; Kobyliansky and Livshits 1983; Livshits and Kobyliansky 1984a,b; Mitton 1978). Thus, the allelic variation of nonrandomly ascertained biochemical systems has been correlated with the variation observed in quantitative morphologic traits (Eanes 1978; Hanford 1980; Mitton 1978).

Numerous empirical studies of captive and natural populations of vertebrates and invertebrates have examined the relationship between morphologic variation and heterozygosity (reviewed in Mitton and Grant 1984; Zouros and Foltz 1987). Covariation has been detected at the interpopulation, interindividual, and intraindividual levels. Analyses of humans (Mueller 1984; Wolanski 1975, 1980; Livshits and Kobyliansky 1984a,b), butterflies (Eanes 1978), mollusks (Zouros et al. 1980; Kat 1982; Singh 1982), killifish (Mitton 1978), lizards (Soule 1979) and sparrows (Hanford 1980; Yezerinac et al. 1992) have suggested controversial and often antithetical results with no consistent pattern emerging.

Nonhuman primates are the closest living relatives of humans. This implies that their genome and morphologic features historically have been forged by similar forces and constraints. And although nonhuman primates manifest more genetic diversity than humans (Stringer and Andrews 1988), they exhibit similar sophisticated social and kin structures, complex mating schemes, developmental and generation times, and can be manipulated in captivity. This makes them attractive as a model to refine analytical and interpretive methods for human populations (Williams-Blangero 1991). Yet to date, no studies of nonhuman primates have directly examined the relationship between heterozygosity and morphometric variation.

This analysis tests the hypothesis that morphometric variation is higher in individuals exhibiting lower biochemical heterozygosity. Furthermore, this hypothesis is tested at an intrapopulational level that is comparing scores between individuals (Comuzzie and Crawford 1990; Schmitt et al. 1988; Yezerinac et al. 1992), versus the more conventional interpopulational perspective.

Materials and Methods

The serum samples and morphologic measurements were collected at the Institute of Experimental Pathology and Therapy of the United Soviet Socialist Republic Academy of Medical Sciences. The sample population used in this analysis consisted of 403 juvenile and adult baboons, *Papio hamadryas hamadryas,* of which 254 were female and 149 were male. The population structure of the baboon colonies had been artificially generated and maintained through seven generations. Recently imported animals and those with greater than 6.25% *Papio hamadryas anubis* ancestry were excluded to minimize the influence of hybridization. Prior to sexual maturity, males were transferred to male-only pens and retained until mated with a known group of females. This enabled the ascertainment of accurate pedigree data and thus the calculation of reliable inbreeding coefficients.

Of the markers examined, data were available only on the six systems that exhibited polymorphisms. These loci included *adenosine deaminase* (*ADA*), *6-phospho-gluconate dehydrogenase* (*6PGD*), glycine-rich *beta glifoprotein* or *factor B* (*BF*), *phosphoglucomutase 1* (*PGM1*), *phosphoglucomutase 2* (*PGM2*), and *transferrin* (*TF*). The premise that these loci are selectively neutral is supported by previous work in humans (Chakraborty 1984). Additionally, each of these loci is located on different chromosomes and thus not linked.

Twenty morphologic measurements were used in this examination. These included thigh length, leg length, upper arm length, forearm length, biiliocristal diameter, bitrochanteric diameter, transverse chest diameter, chest depth, biacromial diameter, head length, head breadth, chest circumference, upper arm circumference, calf circumference, biocular breadth, bizygomatic breadth, bigonial breadth, upper face height, trunk length, and crown-rump length. All measurements were reported in millimeters (O'Rourke 1980). Although no heritability estimates are available for these traits in *Papio hamadryas hamadryas,* it is reasonable to assume substantial

heritability based on studies of these characters in humans (Devor et al. 1986).

Individual heterozygosity (htz_i) was estimated by the enumeration of all heterozygous loci per individual (x) divided by the total number of available loci (n) [$htz_i = x/n$]. The degree of inbreeding was estimated from the inbreeding coefficient (F) of Wright (1922) (O'Rourke 1980; Crawford and O'Rourke 1978; Crawford et al. 1984) and was computed according to the method of Kudo (1962).

Descriptive statistics of each morphologic trait were calculated for the total population and for subsets of males and females. In addition, subpopulations partitioned into juveniles (age <60 mo), adults (age ≥60 mo), and inbred individuals were examined. Estimates of individual morphologic variation were computed by subtracting the mean value of a trait (x') from the individual's measured value of that trait (x), [$d = |x - x'|$]. The absolute value of this quantity is a measure of individual dispersion around a population mean of that trait. Product-moment correlations were calculated between d and heterozygosity.

Optimally, each morphologic trait would be fit to models of sex-specific growth to control for age and sex-related variation. Unfortunately, no such models of baboon growth exist using samples of sufficient size and composition to construct reliable growth charts (Mahaney pers. comm. 1993). Using our cross-sectional data, we regressed the morphometric characters on a natural logarithmic transformation of age. Compared with a linear regression, this substantially reduced the amount of residual variation of each trait, enhancing the power to detect a relationship with heterozygosity. The absolute values of the residuals were subsequently correlated to individual heterozygosity scores.

Examining a multitude of correlations ascertained from morphologic traits that covary undermines the assumption of performing independent tests. Therefore, we generated two synthetic measurements that retained the majority of information contained in each data matrix. First, a principal-components analysis was performed incorporating the original values of the 20 morphologic variables, and the principal-component scores of the first axis were retained. As we were most interested in the measurement of dispersion around an axis in either direction, the principal-component scores were subsequently converted to their absolute values. Second, a "composite morphologic score," calculated by dividing the sum of the absolute deviates of each individual's morphologic variables by the number of measurements, was calculated. These measurements were correlated with individual heterozygosity scores using parametric (product moment coefficient) and nonparametric (Kendall's τ and Spearman's ρ) correlation.

The experimentwise error rate was maintained near $P < 0.05$ by using a sequential Bonferroni technique (Rice 1989). The P values of each table were ranked from smallest (P_i) to largest (P_k) and beginning with the smallest P value compared sequentially to the inequality $P_i \leq \alpha/(1 + k - i)$, where i is the rank position of the P value. Neglecting to use a protected α while making multiple comparisons inflates the experimentwise error rate, increasing the probability of making a type I error.

The significance of the underlying structure of the morphologic variation within the total baboon population was explored with a MANOVA. Treatment groups were delimited by age and sex. All the morphometrics were included as independent variables.

A saturated linear regression, which tests all possible interactions, was performed to empirically control for age, sex, and an age-sex interaction. The dependent variable was the principal-component scores on the first axis of the principal-component analysis. The absolute values of the residuals of this analysis were subsequently tested for significant association with the individual heterozygosity scores.

To improve control of variation caused by age and sex, the saturated linear regression was repeated after replacing the independent variable age with ln(age), and the absolute value of the residuals was tested for covariation with the factor scores. This was performed for the total population as well as independently for each subpopulation.

Results

Biochemical heterozygosity demonstrates no significant correlation with age ($r = -0.037$, $P > 0.46$) or sex ($r = -0.037$, $P > 0.46$) in the total population. If Bonferroni's protected α is initially ignored, the dispersions around 10 morphologic measurements in the total population exhibit significant correlation with heterozygosity (table 1). Male and female subpopulations exhibit two and five significant correlations, respectively (table 1). No correlation between het-

TABLE 1. Correlations between individual mean heterozygosity and morphologic variation.

Morphologic measurement	Total ($N = 403$)	Males ($N = 149$)	Females ($N = 254$)
Thigh length	0.124*	0.200*	0.060
Leg length	0.111*	0.141	0.079
Upper arm length	0.112*	0.109	0.104
Forearm length	0.144*	0.158	0.129*
Biiliocristal diameter	0.138*	0.148	0.120
Bitrochanteric diameter	0.117*	0.084	0.145*
Transverse chest diameter	0.085	0.023	0.116
Chest depth	0.085	0.060	0.092
Biacromial diameter	0.128	0.123	0.149*
Head length	0.099*	0.070	0.103
Head breadth	0.003	−0.072	0.019
Chest circumference	0.078	0.034	0.094
Upper arm circumference	0.083	0.127	0.036
Calf circumference	0.110*	0.131	0.092
Biocular breadth	0.055	0.005	0.059
Bizygomatic breadth	0.082	0.064	0.110
Bigonial breadth	0.069	0.161*	0.001
Upper face height	0.104*	0.027	0.186*
Trunk length	0.135*	0.114	0.144*
Crown-rump length	0.087	0.106	0.065
Composite morphologic score	0.113*	0.107	0.115

* Indicates significant at $P < 0.05$ without sequential Bonferroni.

erozygosity and a specific measurement was consistently significant in all populations. No correlations are significant after applying the sequential Bonferroni technique. Correcting for ln(age) reduced the correlations even further, and no value is significant. The correlation of the composite morphologic scores with heterozygosity was significant in the total population ($P < 0.05$) but not in the male or female subpopulations (table 1).

Among the adults, no significant correlations were detected in the total male or female subpopulations with or without control of age-related variation (table 2). Additionally, the com-

TABLE 2. Correlations between individual mean heterozygosity and morphologic variation in adults.

Morphologic measurement	Total ($N = 195$)	Males ($N = 58$)	Females ($N = 137$)
Thigh length	0.003	0.043	−0.084
Leg length	0.019	0.102	0.048
Upper arm length	0.065	0.168	−0.006
Forearm length	0.057	0.070	0.074
Biiliocristal diameter	0.085	0.106	0.032
Bitrochanteric diameter	0.037	−0.032	0.021
Transverse chest diameter	0.049	−0.165	0.100
Chest depth	−0.005	0.151	0.010
Biacromial diameter	0.076	0.013	0.090
Head length	0.020	0.099	0.035
Head breadth	−0.015	0.038	−0.027
Chest circumference	0.015	−0.060	0.058
Upper arm circumference	0.096	0.151	−0.053
Calf circumference	0.002	0.055	−0.016
Biocular breadth	0.005	0.018	0.024
Bizygomatic breadth	0.018	0.011	0.097
Bigonial breadth	0.118	0.096	−0.052
Upper face height	0.012	−0.043	0.129
Trunk length	0.007	−0.006	−0.029
Crown rump length	0.022	0.129	−0.026
Composite morphologic score	0.044	0.046	0.019

* Indicates significant at $P < 0.05$ without sequential Bonferroni.

TABLE 3. Correlations between individual mean heterozygosity and morphologic variation in juveniles.

Morphologic measurement	Total ($N = 208$)	Males ($N = 91$)	Females ($N = 117$)
Thigh length	0.148*	0.287*	0.023
Leg length	0.063	0.210*	−0.062
Upper arm length	0.120	0.264*	0.033
Forearm length	0.138*	0.276*	0.026
Biiliocristal diameter	0.153*	0.297*	0.080
Bitrochanteric diameter	0.139*	0.289*	0.066
Transverse chest diameter	0.065	0.112	0.079
Chest depth	0.096	0.289*	−0.030
Biacromial diameter	0.168*	0.274*	0.067
Head length	0.061	0.215*	−0.018
Head breadth	0.059	0.143	−0.043
Chest circumference	0.122	0.234*	0.053
Upper arm circumference	0.061	0.113	0.012
Calf circumference	0.132	0.228*	0.001
Biocular breadth	0.033	0.106	−0.015
Bizygomatic breadth	0.121	0.257*	0.007
Bigonial breadth	0.023	0.117	−0.058
Upper face height	0.113	0.237*	0.023
Trunk length	0.119	0.264*	0.054
Crown rump length	0.176*	0.255	−0.040
Composite morphologic score	0.169*	0.269*	0.020

* Indicates significant at $P < 0.05$ without sequential Bonferroni.

posite morphologic scores were not correlated significantly with heterozygosity values in either the adult total or adult male and female subpopulations.

The total juvenile population exhibited six significant correlations with biochemical heterozygosity. The male subset displayed 14 significant positive correlations, but none were identified in the female juveniles (table 3). No significant correlations were observed in the juvenile total, male or female subpopulations when Bonferroni's protection was applied or when age-related variation was controlled. The composite morphologic score correlated significantly ($P < 0.05$) in the total and male juvenile subpopulations (table 3).

Contrary to the hypothesis of a negative correlation between heterozygosity and morphometric variation, the absolute values of the principal-component scores of the first axis of the total baboon population demonstrated a significant positive correlation with biochemical heterozygosity (table 4). This axis explained 86.07% of the variance contained in the morphometric dimensions. No significant correlation was identified between the principal-component scores of the first axis and heterozygosity in the male or female subpopulations (table 4).

The absolute values of the scores on the first axis of the adult total, male and female subpopulations did not significantly correlate with biochemical heterozygosity with and without control for age (table 5). The absolute scores on the first axis of the total juvenile and female juvenile subpopulation correlated significantly with estimated heterozygosity at $P < 0.002$ (table 6). The scores of the first axis of the male juveniles did not correlate significantly with heterozygosity. No significant correlations were found when the total juvenile, and each subpopulation were controlled for age.

The mean level of inbreeding in the subpopulation with inbreeding coefficients greater than zero is 0.026. Within this population, six individual morphologic traits exhibited a significant correlation with heterozygosity at $P < 0.05$ (table 7). These correlates were not significant after a Bonferroni correction. Nor was there significant correlation when age and sex were controlled (table 7). The correlation between heterozygosity values and the composite morphologic scores of animals in this subpopulation was not significant. In a principal-components analysis of the inbred population, the first axis explained 84.95% of the variance in the morphometric values. The absolute values of the principal component scores did not correlate significantly with individual heterozygosity scores with or without control for age and sex.

A MANOVA using the absolute values of the

TABLE 4. Principal-components analysis of morphologic measurements of total, male, and female populations.

Morphologic measurement	Loadings on principal axis one		
	Total	Male	Female
Thigh length	0.926	0.971	0.865
Leg length	0.903	0.921	0.877
Upper arm length	0.951	0.977	0.920
Forearm length	0.948	0.975	0.907
Biiliocristal diameter	0.918	0.961	0.901
Bitrochanteric diameter	0.973	0.986	0.951
Transverse chest diameter	0.922	0.962	0.886
Chest depth	0.962	0.986	0.934
Biacromial diameter	0.972	0.981	0.958
Head length	0.931	0.965	0.888
Head breadth	0.810	0.880	0.787
Chest circumference	0.927	0.916	0.951
Upper arm circumference	0.940	0.945	0.931
Calf circumference	0.917	0.894	0.954
Biocular breadth	0.866	0.939	0.746
Bizygomatic breadth	0.966	0.973	0.973
Bigonial breadth	0.885	0.949	0.795
Upper face height	0.953	0.953	0.956
Trunk length	0.958	0.981	0.953
Crown-rump length	0.912	0.990	0.817
Eigenvalue of first axis	17.21	18.27	16.19
Variation explained (%)	86.07	91.33	80.97
Correlation with heterozygosity	0.114*	0.100	0.123

* Indicates significant at $P < 0.05$.

TABLE 5. Principal-components analysis of morphologic measurements of adult baboons.

Morphologic measurement	Loadings on principal-axis one		
	Total	Males	Females
Thigh length	0.7946	0.7682	0.5194
Leg length	0.8246	0.5124	0.6305
Upper arm length	0.8433	0.7950	0.4275
Forearm length	0.8621	0.8068	0.5656
Biiliocristal diameter	0.6821	0.5506	0.6280
Bitrochanteric diameter	0.9370	0.6772	0.4209
Transverse chest diameter	0.7983	0.7450	0.5789
Chest depth	0.9070	0.8186	0.0146
Biacromial diameter	0.9183	0.6684	0.7939
Head length	0.8696	0.6979	0.7808
Head breadth	0.8358	0.3416	0.8886
Chest circumference	0.7459	0.3062	0.5358
Upper arm circumference	0.8433	0.5035	0.8200
Calf circumference	0.8583	0.5418	0.8102
Biocular breadth	0.7684	0.5654	0.4378
Bizygomatic breadth	0.9295	0.6213	0.7089
Bigonial breadth	0.8021	0.5977	0.8755
Upper face height	0.8583	0.4358	0.8233
Trunk length	0.8808	0.8834	0.8429
Crown-rump length	0.7571	0.8922	0.4182
Eigenvalue of first axis	14.05	8.67	10.67
Variation explained (%)	70.20	43.40	53.40
Correlation with heterozygosity	0.025	−0.025	0.069

* $P < 0.05$.

TABLE 6. Principal-components analysis of morphologic measurements of juvenile baboons.

Morphologic measurement	Loadings on principal-axis one		
	Total	Males	Females
Thigh length	0.9494	0.9649	0.9342
Leg length	0.8457	0.7946	0.8744
Upper arm length	0.9694	0.9730	0.9702
Forearm length	0.9734	0.9730	0.9742
Biiliocristal diameter	0.9016	0.9811	0.8544
Bitrochanteric diameter	0.9335	0.9811	0.9023
Transverse chest diameter	0.8298	0.8960	0.8065
Chest depth	0.9095	0.9649	0.8704
Biacromial diameter	0.9734	0.9811	0.9702
Head length	0.8617	0.9325	0.8304
Head breadth	0.5864	0.5351	0.6468
Chest circumference	0.9734	0.9811	0.9702
Upper arm circumference	0.8936	0.8960	0.8863
Calf circumference	0.7859	0.6324	0.9542
Biocular breadth	0.8058	0.7703	0.8304
Bizygomatic breadth	0.9654	0.9608	0.9742
Bigonial breadth	0.7899	0.8473	0.7825
Upper face height	0.9574	0.9649	0.9502
Trunk length	0.9574	0.9608	0.9582
Crown-rump length	0.8856	0.9811	0.8344
Eigenvalue of first axis	15.91	16.44	15.94
Variation explained (%)	79.60	82.20	79.70
Correlation with heterozygosity	0.233*	0.140	0.251*
Correlation with heterozygosity with age and sex correction	0.003	0.084	−0.068

* $P < 0.01$.

factor scores on the first principal-component axis of the total baboon population as the dependent variable demonstrated that the morphologic information of the data matrix was highly structured by age, sex, and age-sex interaction ($P < 0.001$). A saturated regression analysis was performed to control for differences caused by age, sex, and the age-sex interaction. The dependent variable was the principal-component scores on the first axis. The residuals were normally distributed and the absolute values of the residuals demonstrated no significant correlation with individual heterozygosity values ($r = 0.038$, $P > 0.49$). Repeating the saturated regression using the natural log transformation of age decreased considerably the amount of residual variation in the data matrix (30% versus 14%). The absolute values of the residuals still did not correlate significantly with heterozygosity scores ($r = 0.056$, $P > 0.26$).

DISCUSSION

This analysis tested the hypotheses that overall morphologic variation will be higher in individual nonhuman primates exhibiting lower bio-

TABLE 7. Correlations between individual mean heterozygosity and morphologic variation in inbred animals with (†) and without (‡) correction for age and sex-related variation.

Morphologic trait	$N = 118$†	$N = 118$‡
Thigh length	−0.161	−0.106
Leg length	−0.166	−0.142
Upper arm length	−0.208*	−0.062
Forearm length	−0.207*	−0.059
Biiliocristal diameter	−0.156	−0.143
Bitrochanteric diameter	−0.134	−0.086
Transverse chest diameter	−0.222*	−0.031
Chest depth	−0.123	−0.157
Biacromial diameter	−0.186*	−0.106
Head length	−0.135	−0.103
Head breadth	−0.027	−0.007
Chest circumference	−0.150	−0.107
Upper arm circumference	−0.120	−0.091
Calf circumference	−0.205*	−0.114
Biocular breadth	−0.212*	−0.235*
Bizygomatic breadth	−0.142	−0.097
Bigonial breadth	−0.140	−0.089
Upper face height	−0.157	−0.056
Trunk length	−0.154	−0.101
Crown-rump length	−0.156	−0.112

* Indicates significant at $P < 0.05$ without sequential Bonferroni.

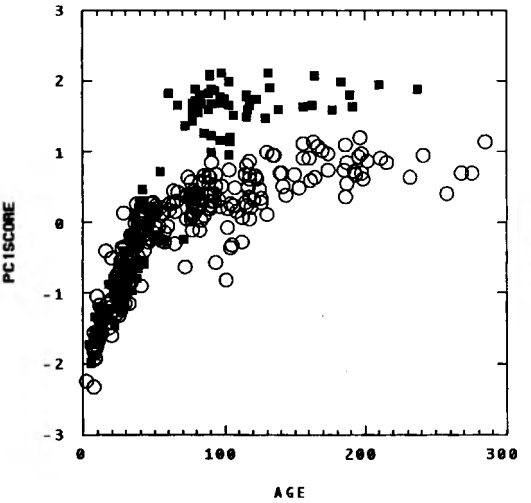

FIG. 1. Principal-component scores on the first axis of the total baboon population versus age in months for males (filled squares) and females (open circles).

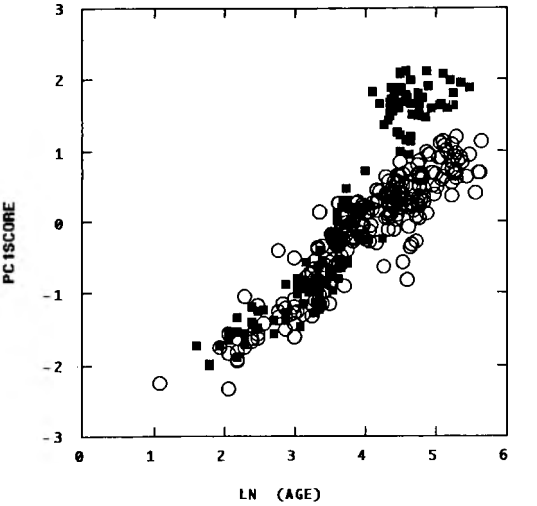

FIG. 2. Principal-component scores on the first axis of the total baboon population versus natural log age in months for males (filled squares) and females (open circles).

chemical variation. The hypothesis is not supported by this examination of a captive colony of *Papio hamadryas hamadryas*. This analysis has demonstrated no significant linear association between an individual baboon's biochemical heterozygosity and its morphologic variation in the total baboon population or any of the subpopulations. The first principal component of each analysis summarizes the great majority of the variation in the matrix of morphologic characteristics of the total baboon population and divided populations. The information contained in these scores probably represents a summary of variation in the size of individual animals. Thus, no significant linear association exists between the variation in size of an individual baboon and its biochemical heterozygosity. Indeed, most of the observed correlations were in the direction opposite that predicted by the hypothesis.

The relationship between morphologic variation and age for each sex is illustrated in figure 1. The difference in trends between males and females is obvious. Males and females demonstrate similar sizes until approximately sexual maturity and then begin to differentiate. Age-matched adult males are consistently larger than adult females. Unless these sources of structure are controlled in subsequent analyses of sexually dimorphic species such as *Papio,* spurious significant correlations between morphologic traits and heterozygosity values can be obtained. This may partially explain the disparate relationships between sexes obtained in the analysis by Comuzzie and Crawford (1990).

Using the inbreeding coefficients of each individual animal should have provided a more comprehensive index of genomic variability across many loci, exaggerating the relationship between heterozygosity and morphologic variation. Yet, this analysis finds no significant relationship between morphologic variation and heterozygosity in these inbred animals. This conclusion must be tempered by the lack of evidence for significant inbreeding depression on quantitative morphologic (O'Rourke 1980) and dental traits (Baume and Lapin 1983) in a population of baboons from this colony with a similar mean level of inbreeding, 0.10.

In a population that is mating randomly with respect to the loci investigated, the proportion of heterozygotes produced each generation remains the same. Selection against the more homozygous individuals in such a population suggests an age effect. That is, older individuals should also be more homozygous. Such a relationship was not observed in this analysis. This association would not be identified if, as Beardmore and Shami (1979) suggest, the less heterozygous individuals are eliminated prenatally. No evidence of such a phenomenon exists in this *Papio* colony.

The fundamental premise of the analyses in-

vestigating the relationship between genetic and morphologic variation is that the heterozygosity of various biochemical markers reflects the heterozygosity of the total genome or at least the heterozygosity of the loci that interact to produce the morphologic phenotype. Indeed, it has been suggested that allelic variation at as few as 12 such loci may correlate significantly with total genomic heterozygosity (Mitton and Pierce 1980). Previous analyses have even examined the association between heterozygosity at a single locus and individual morphologic variation (Mitton 1978; Yezerinac et al. 1992). On the contrary, other investigators have argued on the basis of analytical and simulation studies, that estimates of heterozygosity, extrapolated from a limited number of loci, much less a single locus, do not reflect the genetic heterozygosity of the individual (Chakraborty 1981, 1987). Estimation of genetic variability from six loci is a limitation of this analysis as well.

Furthermore, most analyses have estimated genetic variation by measuring allelic differences at loci encoding proteins that are amenable to simple collection and qualitative identification, for example, *6PGD*. Additional biochemical indices of genetic variation that are more labor intensive to measure, polymorphic loci with regulatory roles or more comprehensive indices of genomic variation using minisatellites, di- or trinucleotide repeats, have yet to be examined. Thus, extrapolations of total individual genetic heterozygosity from measured variation at nonrandom biochemical loci represent at most a biased sampling of genetic variation, much less an index of total genomic diversity. Indeed, evidence exists that the relationship between heterozygosity and morphological variation can fluctuate depending on the loci chosen for analysis (Comuzzie and Crawford 1990).

Moreover, estimates of genetic variation should be quantitated at neutral loci, yet many of the loci chosen for study (e.g., the ABO and MNs groups) have likely been influenced by selective forces. Last, the contention that biochemical variation correlates significantly with the loci responsible for morphologic ontogenesis has not been critically tested, mainly because definitive identification of the loci determining these polygenic traits is lacking.

Another premise is that the morphologic measurements examined represent a complete index of phenotypic variability. This allows the synthesis of a model known as the "modal phenotype" (Livshits and Kobyliansky 1984b). The "modal phenotype" represents the character measurements of the most "fit" individuals within a population. Subsequent to defining the most "fit" individuals within a population, the processes of stabilizing selection and developmental homeostasis become testable. The loadings of the first principal-component axes illustrate the high interdependence of these morphologic variables. Thus, the modal phenotype represents predominantly size, which is certainly not the only measure of fitness. Nor can any other single character state legitimately define a modal phenotype. In fact, support for the contention that any simple aggregation of morphologic measurements is a sufficient definition of fitness is lacking (Sober 1984). Moreover, Chakraborty (1987) has demonstrated that the practice of classifying individuals into different heterozygosity classes by phenotypes of a polygenic trait is quite error prone.

The delineation of the relationship between genetic heterozygosity and morphologic variation should be conducted with rigorous statistical techniques. For example, it is apparent that failure to use a protected α value while performing multiple tests inflates the experimentwise error rate (Rice 1989). Yet, this correction has commonly been neglected (Mitton 1978; Kobyliansky and Livshits 1983; Livshits and Kobyliansky 1984a,b; Yezerinac et al. 1992). The misinterpretations engendered by this approach have been documented elsewhere (Comuzzie and Crawford 1990; Rice 1989). As the understanding of the underlying genetic architecture of polygenic traits improves, more sophisticated methods such as the measured genotype approach (Boerwinkle et al. 1986) will be more useful if the pedigree structure of a population is known completely. Measured genotype models estimate directly the contribution of genetic variability at the locus physiologically responsible for a character to the variability of that trait.

Much of the inconsistency and contradiction evident in the literature stems from comparisons of relationships between different hierarchic levels of variation. For example, examining the relationship between genetic heterozygosity and morphologic variation at the level of the population may generate a different pattern than that apparent at the level of the individual (Soule 1979). Likewise, apparently homogeneous genetic populations at one level (e.g., protein polymorphisms) may demonstrate extensive variation at a different level (e.g., nucleotide sequence

variation). Furthermore, comparisons and criticisms are often drawn between analyses that have surveyed different loci and different morphologic measurements. The level at which the explanation of the relationships between morphologic variation and genetic variation is most valid is uncertain.

Phenotypic variation represents a complex interface between the genotype, the environment, and random events, and its expression is heavily restricted by phylogenetic, developmental, and physical constraints. Developmental homeostasis hypothesizes a relatively simple relationship between genomic variation and phenotypic expression. Heterozygotes are better buffered against environmental perturbations during development, leading to a phenotype that represents the optimal within a population of organisms. Yet, given the logical extreme that all phenotypic variation is dependent on selection, various selective forces would be operative during ontogenesis. These forces would be dynamic and thus fluctuating in intensity. The modal phenotype would also be shifting. This would engender a set of modal phenotypes that may exist only in a given ecological context. The existence of only a single modal phenotype would be dubious. A consequence of a strong shift in a selective force in a population with a single modal phenotype could be rapid population decline. If this is reasonable, one might expect that the search for a correlation between a mean phenotype and biochemical heterozygosity would be fruitless.

The relationship between morphologic variation and genetic variation as measured by biochemical polymorphisms has been examined on an individual and population level with negative results. Future investigations could be designed to address many of the critical shortcomings of all analyses to date, yet without a more sophisticated model of the genotype-phenotype relationship, their significance would be suspect.

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