Patterns of Phenotypic Covariation and Correlation in Modern Humans as Viewed From Morphological Integration

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KEY WORDS craniometrics; covariance matrices; molecular distances; morphological distances

ABSTRACT Proportionality of phenotypic and genetic distance is of crucial importance to adequately focus on population history and structure, and it depends on the proportionality of genetic and phenotypic covariance. Constancy of phenotypic covariances is unlikely without constancy of genetic covariation if the latter is a substantial component of the former. If phenotypic patterns are found to be relatively stable, the most probable explanation is that genetic covariance matrices are also stable. Factors like morphological integration account for such stability. Morphological integration can be studied by analyzing the relationships among morphological traits. We present here a comparison of phenotypic correlation and covariance structure among worldwide human populations. Correlation and covariance matrices between 47 cranial traits were obtained for 28 populations, and compared with design matrices representing functional and developmental constraints. Among-population differences in patterns of correlation and covariation were tested for association with matrices of genetic distances (obtained after an examination of 10 *Alu*-insertions) and with Mahalanobis distances (computed after craniometrical traits). All matrix correlations were estimated by means of Mantel tests. Results indicate that correlation and covariance structure in our species is stable, and that among-group correlation/covariance similarity is not related to genetic or phenotypic distance. Conversely, genetic and morphological distance matrices were highly correlated. Correlation and covariation patterns were largely associated with functional and developmental factors, which probably account for the stability of covariance patterns. Am J Phys Anthropol 123:69–77, 2004.

Human phenotypic variation in general and craniometrics in particular are used to perform multivariate statistics focused on among-group or within-group variation. Patterns of association among traits (and the variation of those patterns among populations) are disregarded because of the properties of the most efficient distance indices (e.g., generalized Mahalanobis distance), which intrinsically account for relationships among traits and weight them in the final computation of the distance. However, among-trait relationships and associations can be explained after the concept of morphological integration (Chernoff and Magwene, 1999; Marroig and Cheverud, 2001; Olson and Miller, 1958; Waddington, 1957). Morphological integration can be defined, in a general sense, as the connections or relationships among morphological elements (Cheverud, 1996a). Usually, integration is studied through a statistical correlation of traits or growth, often combined with assessment of genetic correlation (Cheverud, 1995; Olson and Miller, 1958; Smith, 1996). Commonly, the main focus of morphological integration analyses is not the evolution of cranial morphology, but the potential evolution of the relationships between traits. This particular approach has important implications for morphological evolution, since the same selection pressures will lead to diverse coordinated morphological responses (Marroig and Cheverud, 2001).

Examining morphological integration in the skull is interesting because its development occurs in spatial and temporal continuity. Such systems are of importance because a wide variety of epigenetic mechanisms (both mechanical and molecular) require spatial and temporal proximity to function (Hall, 1987; Hanken and Thorogood, 1993; Smith, 1996). Cheverud (1996a) divided morphological integration in three classes: functional/developmental, genetic, and evolutionary integration. In the first case, morphological traits tend to be statistically associated when they share a specific function

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Received 8 October 2002; accepted 28 February 2003.

DOI 10.1002/ajpa.10302

and/or developmental origin. When genetic integration occurs, two characters tend to appear associated simply by pleiotropy or linkage disequilibrium. Finally, evolutionary integration acts by means of stabilizing the selection of traits involved in the same functional complex (Cheverud, 1996a; Marroig and Cheverud, 2001).

Morphological integration can be viewed as a factor stabilizing patterns of phenotypic correlation (C) and variance/covariance (V/CV). As stated elsewhere (Falconer, 1985; Page and Holmes, 1998; Williams-Blangero and Blangero, 1989), phenotypic variance is the sum of genetic and environmental components. Thus, if the phenotypic V/CV matrix is proportional to the genetic one, then the stability of such patterns must be considered of crucial importance to the study of human variation. In fact, constancy of phenotypic covariances is unlikely without constancy of genetic covariation (Lande, 1979; Marroig and Cheverud, 2001). Some models, as the mutation-stabilizing selection model of Lande (1979, 1980), predict the stability of the additive genetic variance/covariance patterns at equilibrium.

Proportionality of genetic and phenotypic V/CV matrices is also important, since several models applied to quantitative traits assume such proportionality (Konigsberg, 1990; Relethford and Blangero, 1990; Varela and Cocilovo, 2002; Williams-Blangero and Blangero, 1989). A theoretical Bayesian analysis after the original Boas anthropometric database performed by Konigsberg and Ousley (1995) strongly indicates that the additive genetic covariance is indeed proportional to the phenotypic one. Furthermore, empirical studies on different taxa of vertebrates (Cheverud, 1988; Roff, 1996), as well as a complete revision of New World monkey V/CV patterns (Marroig and Cheverud, 2001), demonstrated that phenotypic covariance structure is stable and that among-group covariance similarity is not related to the phylogenetic history of the group. Nevertheless, Ackermann (2002) observed that divergences in the pattern of facial variation among hominoids correspond to phylogenetic relationships among species. In her view, this fact suggests that the structure of V/CV may have diverged through time in the large-bodied hominoids (Ackermann, 2002). Thus, some contradiction about the phylogenetic signal of V/CV variation arose, and it probably depends largely on the taxonomic level observed. Both studies (Ackermann, 2002; Marroig and Cheverud, 2001) focused on covariation patterns at supraspecific levels. Besides the work by Konigsberg and Ousley (1995) on the proportionality of human genetic and phenotypic covariances, a global estimation of covariation structure and their among-population variability is lacking for modern humans.

Here we present a comparison of phenotypic (craniometric) C and V/CV structure among worldwide human populations. The objectives of the present work were 1) to explore if C and V/CV structure is affected by functional or developmental characteristics of the traits, 2) to estimate among-group fluctuations in covariation patterns, and 3) to test if C and V/CV structure adequately reflects the history and structure of human populations. In general terms, this work replicates that of Marroig and Cheverud (2001) and Ackerman (2002), but considering variation among modern humans.

TABLE 1. Cranial measurements considered in this study, and their developmental/functional categorization[1]

Code	Development	Function
GOL	Neural	Vault
NOL	Neural	Vault
BNL	Neural/facial	Base/nasal
BBH	Neural	Vault/base
XCB	Neural	Vault
XFB	Neural	Vault
ZYB	Facial	Zygo
AUB	Neural	Base
WCB	Neural	Vault
ASB	Neural	Base
BPL	Neural/facial	Base/oral
NPH	Facial	Nasal/oral
NLH	Facial	Nasal
JUB	Facial	Zygo/orbit
NLB	Facial	Nasal
MAB	Facial	Oral
MDH	Neural	Base
MDB	Neural	Base
OBH	Facial	Orbit
OBB	Facial	Orbit
DKB	Facial	Nasal
NDS	Facial	Nasal
WNB	Facial	Nasal
SIS	Facial	Nasal
ZMB	Facial	Zygo
SSS	Facial	Nasal
FMB	Facial	Orbit
NAS	Facial	Nasal
EKB	Facial	Orbit/nasal
DKS	Facial	Nasal
IML	Facial	Zygo
XML	Facial	Zygo
MLS	Facial	Zygo
WMH	Facial	Zygo
SOS	Neural	Vault
GLS	Neural	Vault
STB	Neural	Vault
FRC	Neural	Vault
FRS	Neural	Vault
FRF	Neural	Vault
PAC	Neural	Vault
PAS	Neural	Vault
PAF	Neural	Vault
OCC	Neural	Vault
OCS	Neural	Vault
OCF	Neural	Vault
FOL	Neural	Base

[1] Developmental and functional categories were taken from Marroig and Cheverud (2001). Measurements are listed according to original codes introduced by Howells (1973).

MATERIALS AND METHODS

Craniometric information was obtained from the Williams Howells dataset (Howells, 1973, 1989). Measurements are listed in Table 1. Radius and angles were not used, since their functional and developmental assignation is rather difficult (see below). In order to simplify reading, measurement codes as well as population names are those pro-

posed in the original publications (Howells, 1973, 1989). Data were available for 2,504 individuals divided into 28 worldwide populations (two additional populations, the South and North Maori, were removed from the original Williams Howells dataset because of their low sample sizes). The traits were corrected for sex-related size differences, using z-score standardization within each sex. This is a common method for removing sex-related size variation (Relethford, 1994; Williams-Blangero and Blangero, 1989). Two populations (Philippines and An-Yang) are only represented by males. Even when this bias may be of relevance at microregional levels, it is very likely that global among-population differences in V/CV will not be distorted by sexual dimorphism.

As a first step, pooled within-group craniometric C and V/CV matrices were computed for the total dataset and for each population. Secondly, we constructed design matrices simulating functional and developmental associations among traits, in order to compare them with the observed C and V/CV matrices by means of matrix permutation tests. Third, we focused on C and V/CV structure similarity among populations (or groups of populations) in order to find deviations from the average pattern. Finally, we selected specific populations from which genetic data were already published in the literature, to study the relationship of C and V/CV similarity patterns with classic phenotypic and genetic distances.

Morphological integration

In order to investigate whether function or development is related to the pattern of intertrait association, we carried out a series of matrix permutation tests comparing the *observed* pooled within-group C matrix against design matrices simulating functional and/or developmental relationships among pairwise characters. Hypothetical similarity between traits *expected* under a particular model (e.g., "correlation among traits is due to developmental factors") is used to construct a design matrix (Cheverud, 1995). The actual values assigned to the similarity in a design matrix are chosen arbitrarily by the investigator and depend on the model. Matrix permutation studies and construction of design matrices were well-described by Cheverud (1995), González-José et al. (2001), Livshits et al. (1991), and Sokal et al. (1992, 1997). An appropriate design matrix is critical to successful interpretation of an observed distance or similarity matrix (Sokal et al., 1997).

Design matrices were constructed considering two main factors (as well as their interaction) which could account for a correlation between traits: function and development.

Function. The evolution of different functional requirements leads to changes in craniofacial morphology and is the main factor responsible for the association among characters. In consequence, the similarity between pairs of traits involved in the same function will always be higher than between traits related to different functions. In this design, we assigned an arbitrary similarity value of 1 to traits sharing the same function, and a value of 0 to the opposite case.

Development. This tests the hypothesis that differences during the developmental onset of two traits make affinities closer among characters. Thus similarities are lower between traits (we separate them with a value of 0) which develop in the embryo at different moments. Conversely, comparisons between characters developing synchronically are assigned a similarity value of 1.

Function and development characteristics were assigned to each measurement, according to a simple scheme presented in Table 1 (expansion of all abbreviations used below). Both function and development were assigned following Marroig and Cheverud (2001). Since a single trait can operate in two different functional/developmental regions of the skull (e.g., NPH covers a direct distance from the oral functional region to the nasal one; BNL encompasses a dimension between landmarks that develops at different times: first the neurocranial part, and then the facial one), a value of 0.5 was arbitrarily assigned to cases in which at least one functional/developmental region is shared. In order to explore interactions between the functional and developmental components, we also considered a third design matrix obtained after multiplying the functional and developmental matrices.

Mantel tests (Mantel, 1967) were used to estimate the level of correlation between the observed and the design matrices. In addition, Smouse-Long-Sokal tests (Smouse et al., 1986) were used to yield partial matrix correlations. The Smouse-Long-Sokal method extends Mantel's statistic to three or more matrices, and tests whether an association between matrix A and B is significant when one or more matrices C, D, . . . are held constant. Mantel and Smouse-Long-Sokal tests were computed using the software NTSYSpc, version 2.10d (routine mxcomp). *P*-values reported here were obtained after 9,999 permutations (the observed correlation coefficient being tested became the 10,000th entry in the reference distribution of the Mantel test).

Population variability in C and V/CV matrices

C and V/CV matrices between 47 cranial traits were obtained separately for the 28 populations studied by Howells (1973, 1989). Because correlation and covariance matrices cannot be compared after the same statistical procedures, among-population comparisons were done separately for the C matrices and for the V/CV ones. To compare the similarity between patterns of correlation between populations i and j, a matrix of dimension 28 (number of populations) was constructed, whose elements are the Pearson product moment correlation (r_{ij}) between the within-group C matrix of populations i

TABLE 2. Alu-insertion frequencies for a subset of eight populations[1]

Alu-insertion	Norway (Norse)	Hungary (Zalavar)	Germany (Berg)	Africa (Zulu + Dogon + Teita)	Sau (Bushmen)	Amerindian (Peru)	Japanese (South Japan)	Chinese (Hainan)
APO	0.970	0.970	0.870	0.778	0.821	0.960	0.844	0.882
B65	0.619	0.450	0.350	0.558	0.654	0.290	0.412	0.471
Col3A1	0.022	0.120	0.030	0.229	0.167	0.000	0.156	0.029
HS2.43	0.053	0.000	0.070	0.004	0.000	0.000	0.000	0.000
HS4.14	0.672	0.570	0.820	0.501	0.393	0.740	0.824	0.969
HS4.32	0.586	0.670	0.550	0.354	0.321	0.270	0.438	0.438
HS4.65	0.000	0.030	0.020	0.104	0.115	0.020	0.056	0.219
HS4.75	1.000	0.990	0.970	0.789	0.607	0.980	1.000	1.000
PV92	0.254	0.120	0.100	0.320	0.300	0.700	0.857	0.853
TPA25	0.552	0.500	0.510	0.192	0.200	0.640	0.500	0.441

[1] In parentheses is William Howells sample, considered by us to be nearest skeletal sample to molecular one.

and j. Statistical significance was obtained using the Mantel permutation test, after 9,999 permutations.

V/CV matrices were tested for similarity with a modification of the random skewer method (Cheverud, 1996b; Manly, 1991; Pielou, 1984). This method is derived from the equation predicting multivariate response to selection (Lande, 1979). The first step consists of the computation of Δz, a vector of response to random selection:

$$\Delta z = W\beta$$

where W is an n × n phenotypic within-group V/CV matrix, and β represents an n × 1 random selection gradient vector measuring the selection acting on the traits (Ackermann, 2002). This vector is then applied to each of the V/CV matrices being compared, using the multivariate response to selection equation to obtain the expected evolutionary response vectors for comparisons. The random selection vector is known as the skewer, and it is generated from a uniform distribution of values between 0 and 1, standardized to a vector length of 1 (sum of squared elements = 1). Then, response vectors (rather than the matrix) corresponding to the two groups under comparison are tested for association by means of the average vector correlation between responses to 1,000 random selection vectors. This average vector correlation estimates the similarity among V/CV matrices. As with the correlation patterns, a 28-dimension matrix of covariance similarity is obtained after the average vector correlations. Vector correlations will be one when matrices are identical or proportional, and will decrease to zero when matrices lack a common structure (Marroig and Cheverud, 2001).

Genetic/morphological distances and patterns of similarity in C and V/CV matrices

We carried out among-groups comparisons between the similarity of their C and V/CV matrices, their morphological distance (generalized Mahalanobis distance), and their genetic distance (Nei distance computed considering a set of molecular traits). We constructed a reduced database, looking for coincidence between skeletal and molecular (*Alu*-insertions) information in roughly the same population. We chose *Alu* polymorphic insertions as DNA markers, because they are stable polymorphisms that are identical by descent, and the ancestral state of each *Alu* element is known, allowing the knowledge of the polarity of evolutionary change in population genetics analysis. The frequencies for the 10 *Alu* markers used in this work come from Romualdi et al. (2002) and Watkins et al. (2001).

Obviously, since molecular data are generally obtained from modern groups and skeletal measurements are collected from archaeological series, analysis was limited to groups that inhabited the same place but, necessarily, in different epochs. For example, the skeletal material from Zalavar was matched with the nearest population for which molecular data are available, i.e., modern Hungarians. The resulting reduced molecular-craniometric databases, as well as further population equivalences, are presented in Table 2. Nei's genetic distance for each pairwise comparison was obtained after the frequencies of the 10 *Alu*-insertions, and was presented in a genetic distance matrix used for the molecular analysis. Comparisons between 1) the correlation similarity matrix, 2) covariance similarity matrix, 3) Mahalanobis distance matrix, and 4) Nei distance matrix were performed after the Mantel test (9,999 permutations).

RESULTS

Morphological integration

Design matrices depicting functional and developmental relationships between pairs of traits were constructed, considering characteristics presented in Table 1. These matrices were tested for correlation against the pooled within-group C matrix for the whole dataset, and results are listed in Table 3. Results suggest that morphological integration is mainly determined by the effects of the functional and developmental characteristics of traits. Multiplication of both matrices also yielded significant correlation with C. Unfortunately, functional and developmental matrices are intercorrelated ($r_{\text{function vs. development}} = 0.573$; $P = 0.002$), and further improvement of functional and developmental traits' attributes is needed in order to separate their

TABLE 3. Mantel and Smouse-Long-Sokal tests results for comparisons between design matrices and pooled within-group correlation matrix[1]

Pooled within-group correlation matrix against	r	*P*
Developmental similarity	0.24	0.0001
Functional similarity	0.22	0.0001
Developmental/functional interaction	0.26	0.0001
Developmental similarity (function held constant)	0.15	0.0001
Functional similarity (development held constant)	0.10	0.0327

[1] Mantel correlation tests and their probability values were obtained after 9,999 permutations. See text for explanations.

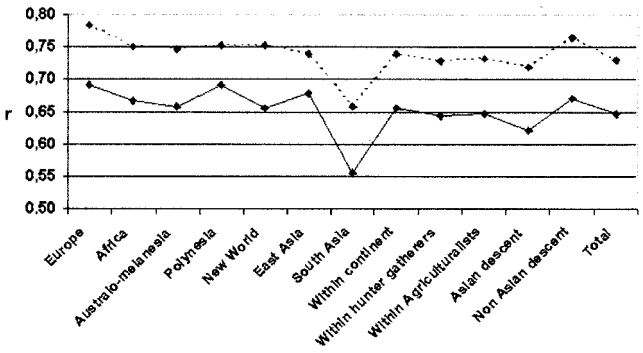

Fig. 1. Average similarity of comparisons of C and V/CV matrices among modern human populations. Average values are shown for all populations, and for several arrays of populations: within-continent average, hunter-gatherers, agriculturalist, Asian descent, and non-Asian descent. Here, Asian descent refers to a phylogenetic denomination involving all Asian and Amerindian groups. Dotted line, average similarity of V/CV matrices. Solid line, average similarity of C matrices.

relative effects. Mantel correlations of the pooled within-group C matrix with the functional design matrices and with the developmental matrices were also highly significant, but the r values were slightly lower. The Smouse-Long-Sokal test revealed that single effects of development (with function held constant) or function (with development held constant) are weaker than the summation of both effects, and this points to a coordinated functional/developmental constraint upon the trait's expression.

Population variability in C and V/CV matrices

Among-population comparisons between the C and V/CV matrices yielded very homogeneous figures, with high correlations between groups, and little variation in the magnitude of associations. All comparisons were significant at the 0.01 level. In the following, *matrix* correlation (or similarity) refers to the comparisons among population-specific trait C patterns, and *vector* correlation (or similarity) expresses the population-specific trait V/CV patterns. In general terms, results points to a high level and stability of similarity for all pairwise comparisons, with association between population-specific vector correlations being stronger than similarity between population-specific matrix correlations (average vector correlation = 0.73, SD = 0.0397; average matrix correlation = 0.64, SD = 0.0536). The highest value of vector similarity is found in the comparison Peru-Santa Cruz (r = 0.82), and the highest value of matrix correlation is found between Mokapu and Moriori (r = 0.77). Conversely, the lowest values were obtained between Andaman and Guam for the C similarity matrix (r = 0.49), and between Andaman and Phillipines (r = 0.61) for the V/CV similarity matrix. Several arrays of populations were tested for their average vector and matrix correlation structure, and the results are presented in Figure 1. Vector and matrix correlations tend to show the same pattern throughout the different arrays of samples, with European groups presenting the highest values of similarity, and South Asian groups presenting the lowest ones.

Clearly, results points to the existence of a common, stable pattern of correlation and covariance structure among modern human populations. Those results are coincident with the study by Marroig and Cheverud (2001) on neotropical primates, but do not agree with the results of Ackermann (2002) on Hominoidea groups.

Genetic/morphological distances and patterns of similarity in C and V/CV matrices

The next step in our study was to estimate the possible link between disruption of populations at the molecular and morphological levels, and differences in the population-specific C and V/CV similarity matrices, i.e., to determine if any two populations showing highly similar patterns of correlation and covariance structure are also strongly related in terms of molecular and morphological differences.

In Figure 2, we present the neighbor-joining trees obtained after Nei distances (derived from frequencies of *Alu*-insertions) and Mahalanobis generalized distances (expressing differences in craniometric measurements' centroids). Both molecular and craniometric data coincide in the existence of a European cluster and an Asiatic one, with the Amerindian and African branches in an intermediate position. A difference appears between the relative position of the Amerindian group and the remaining groups. In the molecular approach, the Amerindian sample rests near the Asiatic cluster, in opposition to the morphological data tree, where the Amerindian sample is near to a European group (Berg). Even when a certain lack of congruence is expected, since data were not collected strictly from the same population, the general topology of both trees is very similar. Because of the differences among the origins of samples in the molecular and morphological approaches, additional tests to evaluate the level of congruence between both types of data must be done. Hence we performed a series of matrix correlation tests. Additionally, the effects of C and CV similarity were estimated in this way. The aim of

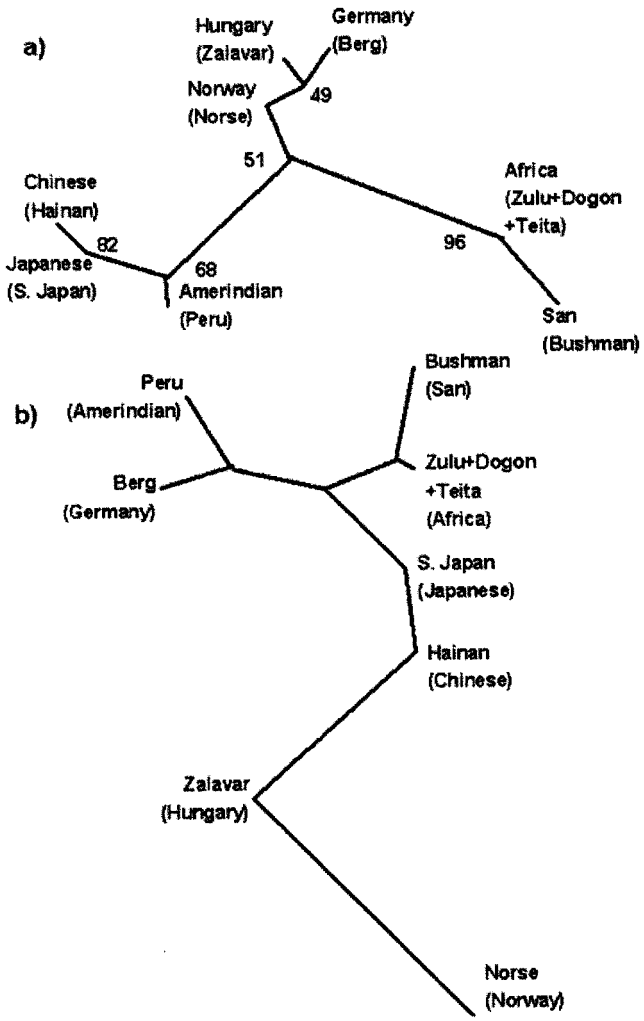

Fig. 2. Neighbor-joining trees obtained after (**a**) Nei distances (*Alu*-insertions) and (**b**) Mahalanobis distances (craniometrics). Analysis was performed upon eight populations listed in Table 2. Bootstrap values are shown in internodal edges for Nei distances (1,000 datasets were analyzed). All Mahalanobis distances were significant at $P < 0.001$.

this analysis was to compare the population patterning expressed by molecular and morphological attributes of the populations, and to evaluate the association between those patterns and the correlation and covariance spectrum of variation. Results of the Mantel test between 1) the C similarity matrix, 2) V/CV similarity matrix, 3) Nei distance matrix, and 4) Mahalanobis distance matrix are given in Table 4. If similarities between the population-specific patterns of intertrait correlation/covariance have any underlying phylogenetic meaning, then one must expect a negative, significantly correlation between the correlation and covariance similarity matrices and the molecular/morphological distance matrices. Note that under this hypothesis, a negative correlation is expected, because C and V/CV matrices express *similarity* among groups, while Nei and Mahalanobis matrices express *distance* among groups. However, matrix permutation tests coincide, to show that molecular (Nei) and morphological (Mahalanobis) distances were positively, highly significantly correlated ($r_{\text{Nei-Mahalanobis}} = 0.691$; $P = 0.005$). Additionally, neither correlation similarity nor covariance similarity correlated significantly with molecular or morphological distances. In the last row of the Table 4, we repeated the comparisons between morphological distances and C or V/CV similarity, but using data on the 28 populations. Results confirmed the seven-population tests, since Mahalanobis distances were not significantly correlated with the C or the V/CV similarity patterns.

DISCUSSION

Results on C and V/CV matrix similarity suggest that modern human populations share a very stable pattern of correlation and covariation, with strong association values between populations and a reduced spectrum of variability. In this sense, modern human populations behaved very similarly to other primate groups such as the platyrrhini (Marroig and Cheverud, 2001), but very differently from large-bodied Hominoidea (Ackermann, 2002). Even when levels of interpopulation variability are low, some differences among populations or groups of populations appeared, showing that South Asia is a macroregion of reduced similarity of intertrait C and V/CV. South Asian groups cover a surface more extended than for other populations (with the exception of Polynesia), and some of the groups are either highly admixed (Philippines) or highly isolated (Andaman). However, low values of C and V/CV similarity are produced mainly in comparisons involving the Anyang, in South China. High levels of heterogeneity at this level are probably due to errors in sampling or to an artificial grouping of individuals coming from different groups under a single denomination. Nevertheless, phylogenetically distanced groups showed similar patterns of C and V/CV, making admixing or artificial grouping a not very parsimonious way to explain low levels of similarity. Future research might be focused on those differences, in order to detect possible causes for disruption of the trait association pattern.

As already stated, a powerful hypothesis to explain the homogeneity of phenotypic correlation patterns and levels is that similarity in phenotypic correlations results from similarity in genetic correlation patterns. To explain both, important alterations of genetic patterns and the observed stability of phenotypic matrices require that genetic changes be coordinated with changes in the environmental matrices (Marroig and Cheverud, 2001). However, environmental variations must be viewed as a nondirectional factor, i.e., the magnitude and direction of their influence upon a single trait cannot be directly extrapolated to the entire, multivariate spectrum of among-group distances. This implies that patterns of craniometric variation can be considered selectively neutral on average (see Relethford, 2002). In this context, empirical studies seem

TABLE 4. Matrix correlation between Nei distances, Mahalanobis distances, correlation matrix similarity, and covariance matrix similarity among modern human populations[1]

	Correlation similarity	Covariance similarity	Morphological distance (D^2)
Nei distance (*Alu*-insertions)	−0.2035 ($p = 0.8038$)	−0.4737 ($p = 0.9825$)	0.6905 ($p = 0.0053$)
Mahalanobis distance (craniometrics)	−0.3051 ($p = 0.8297$)	−0.6764 ($p = 0.9963$)	
Mahalanobis distance (craniometrics)	0.0197 ($p = 0.5916$)	0.0676 ($p = 0.4284$)	

[1] Comparisons were made involving eight populations listed in Table 2, excepting for bottom row, where comparisons were computed based on 28 populations.

to demonstrate the lack of complementation between environmental and genetic or craniometric changes (Arnold and Phillips, 1999; Cheverud, 1996b; Rothhammer and Silva, 1990). But how are environmental and genetic variances coordinated in order to affect the phenotype? Morphological integration can be a clue to understanding such coordination. Integration is defined, in a general way, as the association of elements through a set of causal mechanisms so that the change in one element is reflected by change in another. Some of these mechanisms, particularly epigenetic mechanisms, would be reflected in a spatial or temporal association (Smith, 1996). Then, morphological integration is the final expression of the developmental/functional integration, which accounts for coordinated responses of genetic and phenotypic variation. In this sense, the pattern of developmental relationships among traits structures the pattern of correlations (Cheverud, 1988, 1996a; Marroig and Cheverud, 2001).

Our results seem to support this scheme in modern humans in two independent analyses: matrix permutation methods applied upon functional and developmental design matrices, and comparisons between patterns of correlation and covariance similarity, and genetic and morphological distances. In the first analysis, design matrix simulating functional and developmental characteristics of the traits is highly correlated with the pooled within-group correlation matrix, an expected result if morphological integration occurs.

Secondly, our results demonstrate that when human populations are tested for association between morphological, molecular, and C or V/CV similarity, morphological and molecular matrices tend to show similar patterns of population differentiation. Such patterns of among-population distances depicted by *Alu-insertions* and craniometrics follow the same trend shown in previous works after classical molecular markers (e.g., Cavalli-Sforza et al., 1994).

Comparisons of serological or molecular and morphological distance matrices can be traced back to the 1970s. In that decade, when there was a scarcity of statistical and laboratory techniques, several researchers pointed to high levels of taxonomic congruence between serological and craniometrical (or anthropometrical) differentiation (Pollitzer et al., 1970, 1977). In addition, linguistic craniometric distances seem to show stronger concordance with a hierarchy based on linguistic affinities (Ossenberg, 1977; Zegura, 1975).

As discussed elsewhere (González-José et al., 2002; Relethford, 1996; Relethford and Blangero, 1990; Templeton, 1999; Templeton et al., 1995), the topology of the molecular or morphological distance matrices is the final result of the history and structure of the populations. Thus, their meaning can only be ascertained as a complex interaction between bottlenecks, differential population effective sizes, gene flow, migration, isolation, selection, etc. Conversely, similarity in the C or V/CV structure was not associated with morphological or molecular distance matrices, indicating that the stability of those patterns is largely independent of the history and structure of the populations. Those results clearly refute the observations of Ackermann (2002) on large-bodied hominoids, whose differences in C and V/VC, rather than morphological distances, seem to be roughly congruent with phylogenetic (molecular) relationships among species. A possible explanation for those incongruent results rests on the fact that C and V/CV are probably highly constrained at the intraspecific value, while they play an important role in abrupt speciation events. (However, note that covariation patterns were highly constant at the supraspecific level in New World monkeys; see Marroig and Cheverud, 2001).

Even when morphology and molecular distance matrices reflected a similar pattern, this does not mean that selective forces play no role at all in the evolution of phenotypes, but argues for a double role of the stabilizing selection. Interaction between the phenotype and the external environment is denominated as external selection. Conversely, internal selection is modulated by the need of coadaptation of traits one to another rather than to an external environment, and is due to the interaction of the phenotype with other, internal characteristics of an organism (Cheverud, 1984, 1996a; Marroig and Cheverud, 2001). Both kinds of selection can be viewed as variants of stabilizing selection. Thus, potential adaptations must show some degree of developmental consistency to support selection by external environments (Lande, 1980). In other words, while phenotypic centroids have been evolving since the origin of modern humans and during the spread of populations throughout the whole world, the covariance structure remained relatively stable. The model of Lande (1979) could be the most parsimoni-

ous explanation to the ubiquity of the intertrait pattern of correlation and variance/covariance among human populations.

In concordance with previous research (Cheverud, 1988, 1996b; Konigsberg and Ousley, 1995; Marroig and Cheverud, 2001; Relethford, 2002; Roff, 1996), our results seem to show that phenotypic correlation is an adequate estimate of genetic correlation (Table 4, Fig. 2). Several mathematical models based on quantitative genetics were formally presented and implemented during the last decade. Those models require, as a fundamental assumption, the proportionality between genotypic and phenotypic covariance matrices. Thus, if this scheme is appropriate to describe the environmentally and genetically based phenotypic variation in modern humans, then the proportionality of genotypic and phenotypic matrices can be viewed as a more solid departure for models. Furthermore, models already used under this assumption can be handled and improved as a powerful tool to analyze genetic variability among human groups after skeletal remains.

CONCLUSIONS

Modern human populations show a common, stable pattern of intertrait correlation and covariance structure, probably as the effect of morphological integration. Integration at the functional and developmental level can be viewed as a potential factor to explain such morphological integration. Nevertheless, more factors should be explored in the future to elucidate possible selective forces directed to homogenize the intertrait pattern of correlation and covariance. Human populations are separated by a complex interaction between demographic structure and historical splits, and those separations are commonly represented by means of genetic matrices or dendrograms. Our results demonstrate that morphological differences are highly coincident with genetic ones. The data analyzed here clearly demonstrate that correlation and covariance patterns remain stable, even when populations are strongly distanced in their historical-structural aspects.

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