

Reliability of Craniometric Traits in Reflecting Biological Affinities Among Populations

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Introduction

Craniofacial morphological traits are commonly used by physical anthropologists to assess the relationships among individuals, groups or populations, in order to reconstruct human population history. However, despite such an habitual use, some scholars have questioned the reliability of these features in reflecting phylogeny and population history, because of processes such as integration among traits, convergence and parallelism, that could lead to confounding results (Collard and Wood, 2000; Hlusko, 2004). According to other scholars, different cranial regions – and, consequently, different traits – are more or less susceptible to these processes, with some of them more correlated to true genetic relationships. Concerning human skull, for instance, both facial morphology and the shape of the neurocranial vault have been often linked to climatic adaptation and to dietary or masticatory practices (Roseman, 2004; Lieberman *et al.*, 2004). On the other hand, the shape of the basicranium has been proposed to be the most genetically determined and only minimally influenced

by environmental factors, thus preserving a clearer signal of phylogeny and population history (Harvati and Weaver, 2006). The present contribution intends to verify the following two hypotheses: 1) cranial morphology can be used as a reliable proxy to infer genetic relationships among the populations; and 2) some craniofacial morphological traits are more suitable than others in producing a better correlation between the resulting phenotypic affinities and the true genetic affinities among the populations.

Materials and Methods

We used 57 craniofacial measurements for 1515 male and 1233 female individuals in order to assess quantitatively the morphological relationships among the populations (data and definitions of craniometric variables from Howells, 1989). We assigned *a priori* the specimens to nine population groups according to their geographic provenance and ethnic affiliations (Tab.1). These nine groups were the same defined schematically by Cavalli-Sforza *et al.* (1994), because we based their genetic relationships on the *F_{ST}* genetic distance matrix reported by Cavalli-Sforza *et al.* (1994).

Group	Population samples from Howells' data	N	N males	N females
Sub-Saharan Africans	Teita, Dogon, Zulu, Bushman	410	195	215
European Caucasoids	Norsemen, Norwegians, Zalavars, Magyars, Austria Berg	330	173	157
Extra-European Caucasoids	Dynastic Egyptians, Iranians, Indians	124	67	57
Northeast Asians	Buryats, Koreans, Northern Japanese, Southern Japanese, Ainu	376	211	165
Arctic Northeast Asians	Greenland Inuit, Chukchis, Orochis, Yakuts	138	68	70
Amerindians	Arikara, Indian Knoll, Pecos Pueblo, Santa Cruz, Peruvians	351	190	161
Southeast Asians	Southern Chinese, Hainan, Atayal, Philippines, Taiwanese, Sumatrans, Nicobarese	228	162	66
Australians and Papuans	Lake Alexandrina tribes, Tasmanians, New Guinea Papuans	204	106	98
Pacific Islanders	Guam, Caroline, Gilbert, Marianas, Tolai, Fijians, New Caledonians, New Hebrides, Solomon Isl., Mokapu Hawaiians, Rapa Nui Islanders, Moriori, Maori, Marquesas, Society Isl., Tahitians, Tongans	587	343	244
Total		2748	1515	1233

Tab. 1. Composition of the 9 population groups with sample sizes (N) by sex.

In order to find possible relations between cranial morphology measures and genetic measures, that allow to display patterns of relationships among population, we compared the genetic distances with the craniofacial distances. The comparison between these two kinds of distances was done using the well-known correlation coefficient, r^p , and the rank (i.e., Spearman's) correlation coefficient, r^s . Correlation coefficient r^p was calculated after the morphological distances (that is, the percentages of errors of attributions) were transformed as *ln ratio*. This is a common transformation used in the logistic regression called *logit transformation* (Hosmer and Lemeshow, 2000, p. 6). In order to calculate the "morphological" (that is, the craniofacial) distance between any pair of populations, we considered suitable a discriminant analysis approach (Subhash, 1996).

In fact, it is intuitive that many errors of attribution (that is, to attribute to population B many crania coming from population A and vice versa) should indicate that the crania from the two compared populations are morphologically more similar each other. On the contrary, few errors of attribution should indicate that the crania from the two compared population are morphologically more different each other. Therefore, the "morphological" distance, expressed as a percentage of errors of attributions (misclassified cases), was calculated through a linear discriminant analysis on the logarithmic transformation of a selection of variables from the original database of 57 measurements. In fact, an expert (G.D.) selected a subset of twenty measurements on the basis of his experience in order to reduce the number of variables (Tab. 2).

Code	Description	Code	Description
BNL	Cranial base length	FMB	Bi-frontal breadth
BBH	Basio-bregmatic cranial height	NAS	Nasio-frontal subtense
ZYB	Bi-zygomatic breadth	EKB	Bi-orbital breadth
BPL	Face length	MLS	Malar subtense
NLB	Nasal breadth	SOS	Supraorbital projection
MAB	Maxillary breadth	GLS	Glabellar projection
MDB	Mastoid breadth	FRS	Frontal subtense
DKB	Bi-dakryal breadth	PAC	Parietal chord
WYNB	Minimum nasal bone breadth	PAS	Parietal subtense
ZMB	Zygomaxillary breadth	PAF	Parietal subtense fraction

Tab. 2. List of the twenty variables used in this study (for a complete description, see Howells, 1989).

Logarithmic transformation was used mainly for three reasons: 1. to reduce the asymmetry; 2. to linearize the variables; 3. to reduce the internal variability and to produce homoscedastic variables. From these three reasons, another biological reason rises: using the logarithmic transformation we can reduce the scale difference between male and female, underlining the true differences between the variables.

Results

Table 3 shows a visualization of the comparison between morphological distances and genetic distances. The same genetic distances were used for males and female; morphological distances, on the contrary, were calculated separately for males and females because of the obvious influence of sexual dimorphism on the expression of craniofacial morphology of the sexes.

Comparison	Genetic distance	Males morphol. distance	Females morphol. distance
Sub-Saharan Africans vs Pacific Islanders	2505.4	2.4	4.1
Sub-Saharan Africans vs Australians and Papuans	2472.0	5.0	3.8
Sub-Saharan Africans vs Amerindians	2261.4	0.3	1.6
Sub-Saharan Africans vs Southeast Asians	2206.3	5.3	9.6
Sub-Saharan Africans vs Arctic Northeast Asians	2008.5	1.1	1.1
Sub-Saharan Africans vs Northeast Asians	1979.1	3.4	5.5
Amerindians vs Pacific Islanders	1740.7	9.9	6.2
Sub-Saharan Africans vs European Caucasoids	1655.6	3.3	5.4
Amerindians vs Australians and Papuans	1457.9	2.0	1.2
Australians and Papuans vs European Caucasoids	1345.7	5.0	5.1
European Caucasoids vs Pacific Islanders	1344.7	10.5	9.2
Amerindians vs Southeast Asians	1341.7	8.8	6.6
Sub-Saharan Africans vs Extra-European Caucasoids	1340.0	3.1	5.9
Southeast Asians vs European Caucasoids	1240.4	13.1	10.8
Southeast Asians vs Australians and Papuans	1237.9	2.6	1.8
Arctic Northeast Asians vs Pacific Islanders	1181.2	3.6	5.7
Australians and Papuans vs Extra-European Caucasoids	1179.1	1.2	1.3
Arctic Northeast Asians vs Southeast Asians	1039.4	2.6	1.5
Amerindians vs European Caucasoids	1038.2	8.0	8.5
Arctic Northeast Asians vs Australians and Papuans	1012.5	0.6	0.0

Comparison	Genetic distance	Males morphol. distance	Females morphol. distance
Amerindians vs Extra-European Caucasoids	955.5	2.7	2.8
Extra-European Caucasoids vs Pacific Islanders	953.7	2.9	1.3
Southeast Asians vs Extra-European Caucasoids	939.6	7.9	6.5
Northeast Asians vs European Caucasoids	938.2	11.5	9.9
Australians and Papuans vs Pacific Islanders	808.7	12.3	11.4
Arctic Northeast Asians vs European Caucasoids	746.7	3.7	4.4
Amerindians vs Northeast Asians	746.5	8.2	12.9
Northeast Asians vs Australians and Papuans	734.4	4.1	4.2
Northeast Asians vs Pacific Islanders	723.8	13.9	14.9
Arctic Northeast Asians vs Extra-European Caucasoids	708.2	1.5	0.0
Northeast Asians vs Extra-European Caucasoids	640.4	1.4	4.1
Northeast Asians vs Southeast Asians	630.5	18.8	19.9
Amerindians vs Arctic Northeast Asians	577.4	2.3	2.6
Northeast Asians vs Arctic Northeast Asians	459.7	9.7	8.5
Southeast Asians vs Pacific Islanders	436.7	9.3	10.0
European Caucasoids vs Extra-European Caucasoids	154.7	11.3	10.7

Tab. 3. Results of the comparison between morphological distances and genetic distances. In order to facilitate the visualization, genetic distances are presented in decreasing order.

It can be observed for both sexes some relation between morphological distance (the percentages of errors of attribution) and genetic distance. For instance, the Sub-Saharan African population group presented many small values of percentage errors, in good accordance with their higher values of genetic distances from almost all the other comparative groups. The comparisons between much more genetically related population groups, on the contrary, produced several greater morphological distance values. This correspondence is not complete, since several morphological values did not agree to this rule, but a certain trend seems perceptible.

Concerning the results of correlation analysis, the higher correlation is obtained using the correlation coefficient r^p . The results suggest that a negative monotone association between genetic and morphological distances, both for male (-0.35) and for female (-0.31), exists.

Discussion

The results showed that some relation exists between craniometric distances and genetic distances when craniofacial metric data are logarithmically transformed. A possible explanation for this finding may be that logarithmic transformation reduces greatly scale differences among the variables, thus allowing also to the small-scale measurements to express their morphological – that is, biological - contribution. Another interesting finding was that such a correlation was observed when a subset of twenty measurements was selected out of the 57 original variables. This selection was made by a trained expert anthropologist who used his opinion about the most differentiating morphological features among the populations. We find, therefore, advisable in the field of physical anthropology research that one uses his own experience to choose properly the set of variables to employ, instead of gather together as many as variables is possible starting from the belief that “much is better”! It is also worth of note that our selected subset of variables do not include the most traditional and frequently used measurements, such as greatest length, breadth and height of the cranium, and that well 15 out of the 20 selected measurements are from the facial district, whose morphology is usually considered less genetically determined and consequently less informative concerning biological relationships. Finally, we are aware that our study is not conclusive, because of the presence of many comparisons that do not agree to the general trend. We think that morphological variation is produced under an enough complicate polygenic control, but that it is also subject to some non biological (that is, environmental and behavioural) factors. Therefore, we will intend to develop shortly some aspects related to such problems; for instance we will try to select new sets of measurements in order to obtain a better correlation, and to find more useful measurements in the comparison of local populations within the nine main groups analyzed here.

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