

# The questionable contribution of the Neolithic and the Bronze Age to European craniofacial form

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Many human craniofacial dimensions are largely of neutral adaptive significance, and an analysis of their variation can serve as an indication of the extent to which any given population is genetically related to or differs from any other. When 24 craniofacial measurements of a series of human populations are used to generate neighbor-joining dendrograms, it is no surprise that all modern European groups, ranging all of the way from Scandinavia to eastern Europe and throughout the Mediterranean to the Middle East, show that they are closely related to each other. The surprise is that the Neolithic peoples of Europe and their Bronze Age successors are not closely related to the modern inhabitants, although the prehistoric/modern ties are somewhat more apparent in southern Europe. It is a further surprise that the Epipalaeolithic Natufian of Israel from whom the Neolithic realm was assumed to arise has a clear link to Sub-Saharan Africa. Basques and Canary Islanders are clearly associated with modern Europeans. When canonical variates are plotted, neither sample ties in with Cro-Magnon as was once suggested. The data treated here support the idea that the Neolithic moved out of the Near East into the circum-Mediterranean areas and Europe by a process of demic diffusion but that subsequently the *in situ* residents of those areas, derived from the Late Pleistocene inhabitants, absorbed both the agricultural life way and the people who had brought it.

craniometrics | Neolithic versus modern form | prehistoric versus modern European form | Basque and Canary Islands placement | Cro-Magnon reassessment

Among those who deal with the background of European history, there is a generally accepted view that the foraging way of life in the post-Pleistocene Mesolithic was succeeded by the Neolithic farming way of life. With the addition of metallurgy, the Neolithic morphed into the Bronze Age, which was succeeded by the Iron Age and the more recent European civilization (1–4). Further there is a general acceptance of the assumption that the farming way of life of the Neolithic arose in the Middle East  $\approx$ 11,000 years ago and spread to the western edge of Europe by about 6,500 years ago (5–10). Researchers have questioned whether that spread took place by cultural diffusion to *in situ* people (11) or whether it was a “wave of advance” or a matter of “demic diffusion,” the actual movement of groups of people (see refs. 1, 8, and 12–15). Some researchers have observed that, although the two possible modes of Neolithic spread need not be mutually exclusive (see refs. 9 and 12), principal components analysis of allele frequencies in living humans shows a southeast–northwest cline that favors the idea that the spread had been the result of actual demic movement rather than by diffusion of cultural elements to preexisting populations (see refs. 11–15).

Previous assessments of the Neolithic spread from the Middle East westward have been based on a consideration of tools and pottery on the one hand and genetically controlled aspects of living human populations on the other (14, 15). Here we offer an

assessment based on a comparison of a set of metric dimensions of both prehistoric and more recent human craniofacial morphology. Craniofacial analysis has been previously applied to this question, but the comparison to living populations was not done (16). It has already been shown that the quantitative treatment of craniofacial form produces a picture of the movement of human populations from Asia into the New World that is largely compatible with the picture produced by the molecular genetic comparison of nucleotide haplotypes (17, 18).

The underlying reason that such different approaches yield comparable results is that neither the nucleic acid components identified nor the particular craniofacial dimensions used have any obvious adaptive value. Both evidently behave in a manner compatible with what has been called the “neutral theory,” where the traits assessed are under genetic control and the differences between groups are principally the result of genetic drift (12–22). What they show, then, is the extent of genetically shared relationships between adjacent populations. Here we offer a comparable treatment of samples of recent and prehistoric human populations running from the Middle East to the western edge of the Eurasian continent, north to Crimea, east to Mongolia, and southward through Nubia and Somalia plus samples from North Africa and representatives of the Niger-Congo-speaking peoples of Sub-Saharan Africa (Table 1). Teeth and the tooth-bearing parts of facial skeletons of course do reflect differences in response to the forces of selection on different populations (23), but they were left out of our analysis.

## Neighbor-Joining Comparisons

A battery of 24 craniofacial measurements (Table 2) was used to compare the similarities and differences of living human populations and their prehistoric predecessors where possible throughout the area in question. The significance of the difference between any pair of the total sample can be assessed from Mahalanobis  $D^2$  figures (24), and a graphic depiction of the similarities and distinctions of the various groups tested can be seen from the dendrogram produced by using the  $D^2$  figures as input for the neighbor-joining procedure (Fig. 1) (25). To compute the Mahalanobis distances, we used a pooled within-group covariance matrix derived from all groups and weighted by sex and group sample size. The neighbor-joining method can be used for discrete differences, as is done with molecular data, or it can be used on continuous data, as we have done here (25). Assessments can also be made with canonical variate plots, which have the added advantage that single individuals can be placed in relation to the other samples used (Fig. 2) (29–32).

It is no surprise to discover that individual samples of recent humans tie more closely with other samples of extant people

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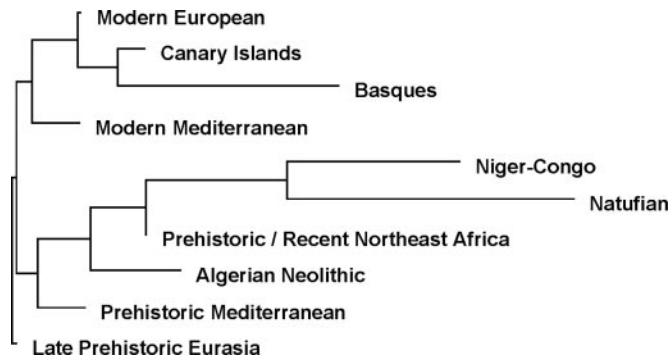


Fig. 3. Neighbor-joining dendrogram of combined adjacent groups from Fig. 1.

dendrogram relate to each other in exactly the same way as those in the 18-variable version shown in Fig. 3. The  $D^2$  figures that were used in the construction of Fig. 3 are printed in Table 3.

There are some generalizations that are apparent from the picture presented in both the greater individual numbers of twigs shown in Fig. 1 and the combined pattern shown in Fig. 3. When the maximum number of twigs is plotted, despite the very small numbers involved, the Late Pleistocene samples from Israel, Europe, and North Africa tend to link to each other before they tie to the modern representatives of each of the areas in question, as shown in Fig. 1. In that run, the Natufian of Israel ties to the French Mesolithic and then to the Afalou/Taforal sample from North Africa. These then link with the European Upper Palaeolithic sample and, somewhat surprisingly, with the Chandman (the Mongolian Bronze Age sample) and finally, at the next step, with the Danish Neolithic. One of the things that these geographically diverse groups clearly have in common is a degree of robustness that sets them apart from the recent inhabitants of the areas in which they are found.

Apart from the quantitative relationships shown in Figs. 1–4, most of the Neolithic samples in Europe share nonmetric features of the lateral edge of the orbit, the shape of the gonial angle of the mandible, and the configuration of menton that are present even when degrees of size and robustness vary between the regions represented. These nonmetric attributes all support the view that most of the Neolithic inhabitants of Europe tie more closely together with each other than with the living representatives of the areas in question. The principal exception to this generalization is one of the two small samples of the German Neolithic, the Mühlhausen sample, which ties closer metrically to the living inhabitants of the Middle East and North Africa. Metrically the other German Neolithic sample, Tauberbischofsheim, links with the living Central European samples. Nonmetrically, those two small German Neolithic samples also appear strikingly different from each other.

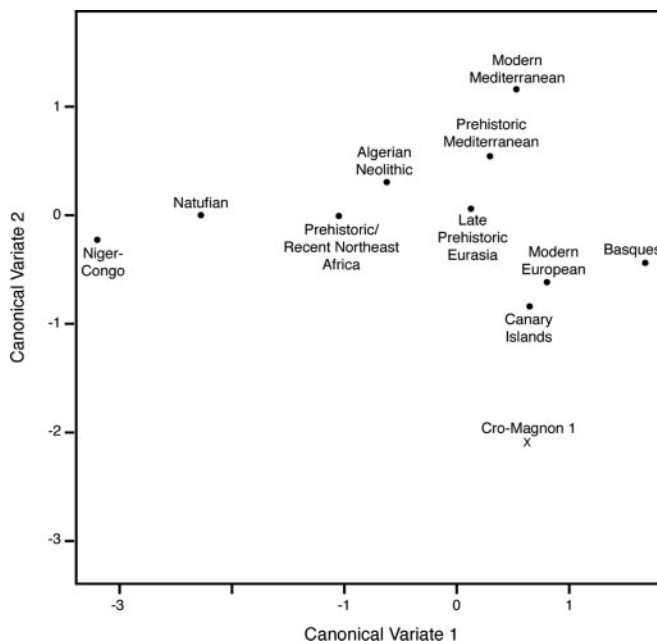


Fig. 4. Canonical variates 1 (58.1%) and 2 (16.2%) for the same groups represented in Fig. 3.

The Niger-Congo speakers (Congo, Dahomey, and Haya) cluster closely with each other and a bit less closely with the Nubian sample (both the recent and the Bronze Age Nubians) and more remotely with the Naqada Bronze Age sample of Egypt, the modern Somalis, and the Arabic-speaking Fellaheen (farmers) of Israel. When those samples are separated and run in a single analysis as in Fig. 1, there clearly is a tie between them that is diluted the farther one gets from Sub-Saharan Africa. The other obvious matter shown in Fig. 3 is the separate identity of the northern Europeans. This matter is treated in the next section.

**Basques, Berbers, and Canary Islanders**

When the number of variables is reduced from 24 to 18, the Basque sample can be compared with the others in the data set (Fig. 3). The Mahalanobis  $D^2$  figures for the samples used in Fig. 3 are shown in Table 3.

The Basque language is a linguistic isolate unrelated to any other language (37), and there is a long-held idea that the Basques may represent a modern survival of the Pleistocene human inhabitants of western Europe (38). Our measurements were made on the sample gathered from the French side of the French/Spanish frontier that runs through Basque country in southwestern France. These specimens were stored in the Broca

Table 3. Mahalanobis distance figures for the twigs in Fig. 3

|                              | 1     | 2     | 3     | 4     | 5     | 6     | 7     | 8     | 9     | 10 |
|------------------------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|----|
| 1. Modern Europe             | —     |       |       |       |       |       |       |       |       |    |
| 2. Modern Mediterranean      | 3.34  | —     |       |       |       |       |       |       |       |    |
| 3. Niger-Congo               | 16.42 | 16.26 | —     |       |       |       |       |       |       |    |
| 4. Late Prehistoric Eurasia  | 1.87  | 2.52  | 12.15 | —     |       |       |       |       |       |    |
| 5. Prehistoric Mediterranean | 4.19  | 3.90  | 15.60 | 2.65  | —     |       |       |       |       |    |
| 6. Prehist/Recent NE Africa  | 5.16  | 5.22  | 6.67  | 4.54  | 5.78  | —     |       |       |       |    |
| 7. Canary Islands            | 3.58  | 7.22  | 19.16 | 4.68  | 5.90  | 7.01  | —     |       |       |    |
| 8. Basques                   | 7.16  | 8.81  | 30.77 | 10.98 | 14.31 | 11.82 | 7.94  | —     |       |    |
| 9. Natufian                  | 21.00 | 19.93 | 14.66 | 14.00 | 16.59 | 15.31 | 20.62 | 33.97 | —     |    |
| 10. Algerian Neolithic       | 8.20  | 7.62  | 12.84 | 6.71  | 5.71  | 5.14  | 6.47  | 14.98 | 17.60 | —  |

**Table 4. Probabilities and squared Mahalanobis distances between Cro-Magnon 1 and reference samples**

|   | ModEur | ModMed | NigCon | LPEurasia | PrehMed | P/RNEAfr | CanIsl | Basq  | Natuf | AlgNe |
|---|--------|--------|--------|-----------|---------|----------|--------|-------|-------|-------|
| Cro-Magnon                              |        |        |        |           |         |          |        |       |       |       |
| Posterior probability                   | 0.49   | 0.01   | 0.00   | 0.39      | 0.03    | 0.01     | 0.07   | 0.01  | 0.00  | 0.00  |
| Typicality probability (F distribution) | 0.26   | 0.04   | 0.01   | 0.25      | 0.10    | 0.04     | 0.19   | 0.09  | 0.07  | 0.04  |
| Squared Mahalanobis distance            | 21.72  | 30.53  | 36.35  | 22.15     | 26.80   | 30.10    | 24.42  | 28.30 | 35.00 | 36.00 |

ModEur, Modern European; ModMed, Modern Mediterranean; NigCon, Niger-Congo; LPEurasia, Late Prehistoric Eurasia; PrehMed, Prehistoric Mediterranean; P/RNEAfr, Prehistoric Recent Northeast Africa; CanIsl, Canary Islands; Basq, Basques; Natuf, Natufian; AlgNe, Algerian Neolithic. The abbreviations used here are discussed in *Combining Samples*.

collection at the Musée de l'Homme in Paris. Paul Broca himself had promoted the view that the Basques represent the continuing existence of the kind of Upper Paleolithic population excavated at the Cro-Magnon rock shelter in the village of Les Eyzies in the Dordogne region of southwestern France in 1868 (38–41). Shortly thereafter the “old man” (“le vieillard”) found in that rock shelter was elevated to the status of typifying a whole “Cro-Magnon race” regarded as ancestral to not only the Basques but also the aboriginal inhabitants of the Canary Islands (38, 42–45).

When the Basques are run with the other samples used in Fig. 1, they link with Germany and more remotely with the Canary Islands. They are clearly European, although the length of their twig indicates that they have a distinction all their own. It is clear, however, that they do not represent a survival of the kind of craniofacial form indicated by Cro-Magnon any more than do the Canary Islanders, nor does either sample tie in with the Berbers of North Africa as has previously been claimed (38, 45–46). This is particularly well documented when the 18 variables are used to generate a plot of the first two canonical variates as shown in Fig. 4. In this figure, one can see a clear link between the Niger-Congo sample and the Natufians. The Prehistoric/Recent Northeast African sample also has a subsequent link to the Niger-Congo sample in Fig. 3. Yet the  $D^2$  values in Table 3 show that it is slightly closer to Late Prehistoric Eurasia than to the Algerian Neolithic, Modern Europe, and Modern Mediterranean and that it is farthest from the Niger-Congo, the Natufians, and the Basques. Although the Algerian Neolithic sample has an even more residual link to this cluster, the  $D^2$  figures in Table 3 show that it is almost as far from the Niger-Congo twig as from the Basques and Natufians. The generally high  $D^2$  values for the Natufian sample in Table 3 are almost certainly a reflection of the very small sample size.

To test the analysis shown in Fig. 3, Cro-Magnon (Fig. 4, ×) was removed from the European Upper Palaeolithic sample and run as a single individual. Interestingly enough, Cro-Magnon is not close to any more recent sample. Clearly, Cro-Magnon is not the same as the Basque or Canary Island samples. Fig. 4 plots the

first and second canonical variates against each other, but that conclusion is even more strongly supported when canonical variate 3 (not shown here) is plotted with variate 1. The probabilities of Cro-Magnon's ties to any of the groups in Figs. 3 and 4 are shown in Table 4. If this analysis shows nothing else, it demonstrates that the oft-repeated European feeling that the Cro-Magnons are “us” (47) is more a product of anthropological folklore than the result of the metric data available from the skeletal remains.

### Conclusions

The assessment of prehistoric and recent human craniofacial dimensions supports the picture documented by genetics that the extension of Neolithic agriculture from the Near East westward to Europe and across North Africa was accomplished by a process of demic diffusion (11–15). If the Late Pleistocene Natufian sample from Israel is the source from which that Neolithic spread was derived, then there was clearly a Sub-Saharan African element present of almost equal importance as the Late Prehistoric Eurasian element. At the same time, the failure of the Neolithic and Bronze Age samples in central and northern Europe to tie to the modern inhabitants supports the suggestion that, while a farming mode of subsistence was spread westward and also north to Crimea and east to Mongolia by actual movement of communities of farmers, the indigenous foragers in each of those areas ultimately absorbed both the agricultural subsistence strategy and also the people who had brought it. The interbreeding of the incoming Neolithic people with the *in situ* foragers diluted the Sub-Saharan traces that may have come with the Neolithic spread so that no discoverable element of that remained. This picture of a mixture between the incoming farmers and the *in situ* foragers had originally been supported by the archaeological record alone (6, 9, 33, 34, 48, 49), but this view is now reinforced by the analysis of the skeletal morphology of the people of those areas where prehistoric and recent remains can be metrically compared.

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