

## A Nonracial Craniofacial Perspective on Human Variation: A(ustralia) to Z(uni)

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**ABSTRACT** Dental and craniofacial measurements were collected for 57 samples from Asia, the Pacific, the aboriginal western hemisphere, and Europe. The craniofacial dimensions include many that are not obviously under the control of specific selective forces. Similar configurations for these in different samples should yield indications of recency of common ancestry according to the logic expressed by Darwin and evident in the relationships indicated by nuclear DNA comparisons. Dental dimensions, however, vary according to the length of time that different intensities in selective forces have been in operation. The craniofacial measurements were transformed into C scores and used to generate Euclidean distance dendrograms. When all the material was used to generate a single dendrogram, the European and Amerindian samples sorted into two regionally identifiable clusters, and the Asian and Pacific material sorted into the three clusters identified in separate previous studies: a Mainland Asian cluster, a Jomon-Pacific cluster and an Australo-Melanesian cluster. Since these clusters are based on variation in traits that are basically nonadaptive in nature, no hierarchical ranking is possible. The clusters simply reflect degree of relationship. This technique holds forth the promise of producing a nonracial assessment of the relationships of all the peoples of the world, past and present.

There is a spectrum of variation in what is confusingly labeled "anatomically modern" *Homo sapiens* that is rarely taken into account in appraisals of human evolution in general and individual fossil specimens in particular. In tooth size alone, the difference between the average condition in Australia and that in Europe (or China) would satisfy the criterion used to indicate specific difference (Gingerich, 1974, 1979, 1980; Gingerich and Schoeninger, 1979), yet there is obviously no reproductive barrier between Australians and anybody else in the world. All living human beings are demonstrably members of the same species even though there are average visible differences between the various geographically situated populations of the world. The spectrum of variation is there, however, and it should be possible to deal with it in such a fashion that we can determine how much of it is due to differences in the intensity of specific selective forces and how much of it is due to the length of time since the groups being compared

shared a common ancestor. There is almost certainly some ethnocentrism inherent in viewing the spectrum as running from Europe to Australia, but this quite literally does extend from one geographical extreme of the earth to the other, and, dentally at least, the Australian aborigines can legitimately stand for a morphological extreme in contemporary *H. sapiens* and Europeans come quite close to representing their antithesis (Brace, 1980; Brace et al., in press b).

The aboriginal inhabitants of Australia have been a continuing source of fascination for anthropologists and the general public alike ever since they were first encountered by itinerant Europeans almost 400 years ago. With the addition of an evolutionary perspective developed by Charles Darwin after his visit there a century and a half ago, that fascination invested them with more than just the status of benighted savagery that had previously prevailed. To be

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sure, much of that judgment continued unabated, but to it was added an implication of the "primitive" in an evolutionary sense. Whether overt or unspoken, there has been a general assumption that Australian Aborigines represent the survival of an earlier stage in human evolution. Whatever their age or sex, they have been repeatedly designated by the collective term "primitive man," a kind of Pleistocene vestige that has been regarded as a veritable living fossil.

This sort of appraisal has the same kind of typological essentialism to it that underlies the urge to identify cladistic status or "race" (Brace, 1988). But if cladistic assessment and racial designation are equally subjective enterprises, what can we do to make sense in our consideration of those aforementioned Australian Aborigines or any other human group during the course of an investigation of the spectrum of variation in *H. sapiens*?

There are in fact two general approaches that can be productive in very different ways to help us understand the nature and relationships of any given population. One such approach is to assess the adaptive state of separate traits one by one in the perspective of the intensity and temporal duration of the individual selective force that applies to each. The other is to assess the similarities to and differences from other populations, both near and far, by using traits and configurations that have little adaptive significance in and of themselves. No one study of limited scope can hope to do complete justice to both approaches. At best, one can aspire to provide an illustration of how and why each one can work. We attempt to do this in the sections that follow.

#### THEORETICAL BACKGROUND

##### *The demise of racial classification*

A generation and more ago, physical anthropology considered racial classification to be one of its principal tasks, and the preferred technique used in the pursuit of this goal was the comparative use of nonadaptive traits (Hooton, 1926, 1931). Subsequently the enthusiasm for the use of nonadaptive dimensions of morphology waned (Hooton, 1946), and, with the Fisherian insistence that selection was the sole mechanism controlling evolution, it became the accepted view that all aspects of morphology were controlled by selection and nothing could be regarded as non-adaptive (Dobzhansky,

1944; Lack, 1961; Gould and Lewontin, 1979). The rise of the synthetic theory of evolution redirected scholarly enthusiasm towards the study of characteristics with measurable adaptive value, and the maturation of the science of genetics focused attention on traits with simple and discoverable modes of inheritance, whatever their adaptive significance. Partially as a result of these developments, the relevance of skeletal studies in general came under an increasingly vocal attack (Boyd, 1950) that has continued up until the present (Renfrew, 1987). Initially, however, this simply served to shift the basis on which classification was established from the morphological phenotypic level to the serological genotypic level.

Classification involved the identification and naming of a presumably fixed number of "races," whose individual members each contained traits considered to be uniquely characteristic of the "race" in question. Still earlier, during the nineteenth century, there was a general consensus in physical anthropology that the various "races" had been fixed entities for an immeasurably long period of time, possibly reflecting original creations—separate and unequal (Brace, 1982). With the superficial addition of an evolutionary dimension to the expectations of physical anthropologists as the twentieth century proceeded, the idea grew that each "race" had a different evolutionary trajectory, and that each had evolved to a greater or lesser extent in comparison to each other (Coon, 1962). The assumption of differences in timing and degree of that evolution allowed the preservation of an assumed hierarchy no different in effect from the idea that differences in worth had existed *ad initio*, and it underlies the invidious comparisons that continue to be offered (Rushton, 1985, 1987, 1988).

Finally, the concept of race itself was shown to be devoid of biological justification (Livingstone, 1962; Brace, 1964a,b). Consequently the whole enterprise of racial classification, once at the core of professional physical anthropology, was deprived of its scientific credibility and basically ceased to exist. The social scientist, cognizant of the inequities and injustices perpetrated in the name of "race," could well cry "good riddance."

But human beings are not identical clones, and their differences have regional and temporal aspects to them that should certainly

be the legitimate concern for biological anthropologists. Some investigators have actually chosen to deal with one or another trait whose manifestation can be associated with differences in the intensity or duration of specific selective forces (Livingstone, 1958, in press; Brace, 1967, 1977, 1979, 1980; Brace et al., 1987, in press c). Others have concentrated on particular single gene phenomena and investigated the evidence for genetic drift and the founder effect in island populations or other remote genetic isolates (Glass et al., 1952; Friedlaender and Steinberg, 1970; Neel, 1970; Morton and Lalouel, 1973). Somewhat more ambitious attempts have been made to use multiple loci to assess within and between group similarities and differences of a more extensive regional nature (Smouse et al., 1982).

Until recently, however, the whole matter of population relationships that used to be subsumed under the rubric of "racial classification" has been left relatively untouched. Underlying this de facto abdication of concern is the sometimes privately expressed fear that any attempt to deal with this matter would simply allow observers to establish a hierarchical ranking of human groups with all of the invidious implications once associated with the racial classifications of the past. We propose to show, however, that the matter of relationships can be treated in perfectly objective fashion without the implications inherent in the terms "race," "type" or whatever, and in such a way that no group can be judged either more or less fit, "higher" or "lower," or better or worse than any other. In this endeavor, our efforts represent an extension of the pioneering work initiated at Mainz by Schwidetzky and those who have continued in that tradition (Schwidetzky and Rösing, 1984; Sokal and Yuyterschaut, 1987; Sokal et al., 1987, 1988; Harding and Sokal, 1988).

#### *Lessons from molecular biology*

The accumulating record of ongoing and successful research in molecular biology may have shown us a way out of the dilemma inherent in "classification." Certainly it is worth the effort to look at the matter and see if the underlying logic can be extended to deal with morphology as well as with molecules.

The study of mitochondrial DNA has produced promising and provocative results (Wallace et al., 1985; Cann et al., 1987;

Smouse and Li, 1987; Cann, 1988; Excoffier and Langaney, 1989), but there are some stochastic problems and other pitfalls that keep it from being our best general model (Weiss, 1987; Spuhler, 1988, 1989). The appraisal of nuclear DNA on the other hand, and despite some of its own attendant problems, can function as our basic example. Ideally this would be best approached by codon sequencing. In practice, however, this is a tedious and nearly interminable process. Doubts have also been expressed by some concerning the effectiveness of what has been demonstrated by crude "brute force" DNA-DNA comparisons because of some of the methodological problems involved (Marks, 1988; Marks et al., 1988). In addition, it was thought that the different adaptive significances of individual base pairs have not been taken into account, and further doubts were expressed because of the indeterminant nature of just what is being measured when a stated level of concordance is reached (McKenna, 1987). This has been anticipated by the molecular geneticists who note that perhaps 90% of the genome does not code for anything and hence is adaptively neutral, designated by the term "junk DNA" (Ohno, 1970; Nei, 1983, 1987). Given this, the differences observed should be mainly related to time elapsed since divergence (Sibley and Ahlquist, 1983, 1987a). In any case, the arguments over why it should or should not work have been effectively muted by the obvious fact that it does. Although arguments continue about various aspects of fine tuning, the overall pictures of phylogenetic relationship it has produced for birds, primates, and other living creatures (Sibley and Ahlquist, 1986, 1987a,b; O'Brien, 1987) have convinced many observers that DNA-DNA hybridization comparisons work. Furthermore, they work precisely because so much of the genome has no adaptive significance. The logic of why this should be so was articulated by Charles Darwin himself when he observed that "as a general rule, . . . the less any part of the organisation is concerned with special habits, the more important it becomes for classification" (Darwin, 1859: 414). And he continued with the converse, noting that "adaptive characters, although of the utmost importance to the welfare of the being, are almost valueless to the systematist" (1859:427).

By "classification" he did not mean any kind of ranking in the eyes of a putative "creator" or position in a hypothetical chain

of being. Rather he was simply referring to degree of relationship between one individual or group with another where that degree of relationship reflects evolutionary history—the time elapsed since descent from a common ancestor. Darwin, of course, was speaking of aspects of the phenotype, and, although it is now obvious that his logic also works at the genotypic level, it would be interesting to see if we could put it to the test at the phenotypic level at which he conceived of it in the first place.

#### *Nonadaptive features and population relationships*

There remains the problem of whether there is such a thing as a “non-adaptive trait” and, if indeed there is, how we could recognize any number or even one of such. We can argue that old-fashioned physical anthropology managed to discover them in almost ludicrous abundance. For example, one need only scan the papers and monographs of two or three generations ago to encounter countless enumerations of traits that have yet to be shown to have any vestige of adaptive significance. What possible difference in selective value might there be in having a cranial contour that is ovoid as opposed to pentagonal—or any other of the myriad of named shapes? Why on Earth would it be better to have high rounded orbits under some circumstances and low rectangular ones under others? And when one turns to the assessment of the “soft parts,” the same kinds of questions remain. What can we learn about human survival capabilities from an assessment of differences in lip seam development? And of what value were those extensive investigations of female breast form other than as measures of the ostensibly legitimized lechery of a previous generation of male investigators (Ploss, 1872; Ploss and Bartels, 1899; Ploss et al., 1938; Mercier, 1873; Stratz, 1898, 1901; Hoerschelmann, 1904; Lipiez, 1907; Witkowski, 1907; Bloch, 1909; Rothe, 1912; Hooton, 1918; Holl, 1920a,b; Martin, 1928a)? Those who insist that selection must be the main controlling factor, even if we cannot see how it works, have been compared by Gould and Lewontin to the figure of Dr. Pangloss in “Candide,” who maintained, despite the mounting record of personal disasters, that all was for the best in this the best of all

possible worlds (Gould and Lewontin, 1979). Both the “hyperselectionists” and the pious eighteenth-century objects of Voltaire’s satire represent the conviction that, although the workings of nature on the one hand and God on the other may be beyond the grasp of human reason, the nature of the world assumed by their various manifestations of a priori faith continues to be fully valid even if not discernible or testable (Brace et al., in press c).

#### *The construction of nonracial clusters*

Although this will continue to remain a controversial point, we suggest that there is a pragmatic approach that may well produce a de facto solution. With the demonstration by human geneticists that “. . . on a per character basis, anthropometric traits discriminate better than genetic traits” (Spielman and Smouse, 1976:328), and the pragmatic support of the theoreticians of numerical taxonomy (Sneath and Sokal, 1973), we have been encouraged to use morphometrics in an attempt to deal with human population relationships. Furthermore, referring back to the example of the DNA–DNA hybridizers, if we simply include a plethora of dimensions, we might be able to produce the same kind of “brute force” results. We have inadvertently done something very much like this, and we take this occasion to display the preliminary results. This was inadvertent because we actually had tried to use a set of measurements designed to discriminate between populations in features that presumably differed because of differences in selective force intensity (Brace et al., 1989, in press a). Although we did succeed in getting a picture of population relationships that served our purposes, we discovered that the picture became even sharper when we simply added more measurements without any regard for the possible adaptive significance of the underlying dimension. In fact, we have merely rediscovered what eighteenth century naturalists such as Buffon and Blumenbach had realized, namely, that the best results will follow from the use of the “greatest possible number of characters” (Mayr, 1965:73). In the same somewhat inadvertent vein, the satisfactory nature of our results demonstrates in empirical fashion the aptness of Sneath and Sokal’s observation that, although there may be redundancy in the use of correlated variables, it is more than “coun-

terbalanced" by the additional information obtained (Sneath and Sokal, 1973:106).

Actually, what DNA-DNA hybridization studies and our own morphometric efforts have produced are branching diagrams depicting phenetic relationships using large quantities of available but unweighted characters. To use Cain and Harrison's term, these are phenograms (Cain and Harrison, 1960:3; Mayr, 1965) in the classic sense of numerical taxonomy (Sokal and Sneath, 1963; Sokal, 1965; Sokal et al., 1965; Sneath and Sokal, 1973), or "numerical phenetics" as Mayr prefers (Mayr, 1965, 1982:222). Although there is a perception that this approach "has become a bit unfashionable lately," our efforts might just qualify as a representation of the "comeback" expected by the author of that comment (Dawkins, 1986:281).

One choleric critic has characterized the use of DNA-DNA hybridization to generate such diagrams for the purpose of indicating population relationships as "a dubious mixture of phenetic and cladistic methodology" (McKenna, 1987:57), but at least it avoids the manifest subjectivity of standard cladistic procedure (and see Schwartz, 1984, for a particularly risible example of the latter). In any case, we present a series of dendrograms for modern and recent prehistoric human groups that we suggest have several advantages. First, they agree well with linguistic, ethnographic, and historical accounts, and they can be checked against the available archaeological information. Second, this approach provides a means of dealing with human biological variation that can be used to group and compare human populations without the attendant danger of creating anything comparable to a racial typology with the possible attribution of relative worth that was inevitably associated with this activity in the past. In essence, it is a nonracial and noninvidious means of comparing the general biological similarities and differences of human populations. And, finally, it allows us to deal with both past and living populations, something that is beyond the reach of those who confine their analysis to the study of the genome itself.

#### DATA SELECTION AND TREATMENT *Craniofacial variables*

In the course of investigating the evidence for dental reduction in the recent human past, we had to deal with the question of

whether the reduction recorded in a given area actually took place *in situ* or whether it was the result of immigration and dilution or replacement by a population from some other area. Since we were attempting to test the continuity or lack of continuity between prehistoric and modern groups, we were restricted to the use of variables that could be assessed with equal ease on both. Of necessity, this meant that we had to seek our data on skeletal material. And, since our initial focus was on odontometrics, it was only logical that our test should focus on the use of the craniofacial material that provided us with our dental samples.

To avoid the possible taint of subjectivity associated with the assessment of character state or other kinds of nonquantitative analysis, we chose to restrict our efforts to the collection of craniofacial metric information. We started with a selection of the measurements used by Howells in his study "*Cranial Variation in Man*" (Howells, 1973) and added a few variables that we hoped would improve our ability to test similarities and differences. In successive years, we added further measurements, until we now have a full two dozen. The complete roster appears in Table 1.

Since we added items to our list after we had started, this means that the groups mea-

TABLE 1. *Craniofacial measurements used in this study*

1	Nasal height (Martin No. 55) <sup>1</sup>
2	Nasal bone height (Martin No. 56[2])
3	Piriform aperture height (Martin No. 55[1])
4	Nasion prosthion length (Martin No. 48)
5	Nasion basion (Martin No. 5)
6	Basion prosthion (Martin No. 40)
7	Superior nasal bone width (Martin No. 57[2])
8	Simotic width
9	Inferior nasal bone width (Martin No. 57[3])
10	Nasal breadth (Martin No. 54)
11	Simotic subtense <sup>2</sup>
12	Inferior simotic subtense
13	FOW subtense at nasion
14	MOW subtense at rhinion <sup>3</sup>
15	Bizygomatic breadth (Martin No. 54)
16	Glabella opisthocranium (Martin No. 1)
17	Maximum cranial breadth (Martin No. 8)
18	Basion bregma (Martin No. 17)
19	Basion rhinion
20	Width at 13 (fmo-fmt)
21	Width at 14
22	IOW subtense at nasion <sup>3</sup>
23	Width at 22 (fmo-fmo)
24	Minimum nasal tip elevation

<sup>1</sup>Martin numbers are from Martin (1928b).

<sup>2</sup>Howells (1973).

<sup>3</sup>Woo and Morant (1934).

sured at the beginning of our project were represented by fewer variables than the ones most recently studied. In some cases, it was possible to return to the collections and add the variables not measured on the first visit. It was in the course of this that we discovered the curious fact that our ability to cluster and distinguish was more dependent on the sheer quantity of variables used than it was on the care with which we selected them, a finding that provides empirical support for the intuitively based position taken by the promoters of numerical taxonomy (Sneath and Sokal, 1973). We also discovered that, beyond the first twenty or thirty individuals per group, our reliability in constructing our assessments was not changed even when we increased our numbers to one or two hundred cases for each of the variables.

*Data treatment: C score computation and use*

To start with, we collected data from a series of samples using the measurements listed in Table 1. In Table 2, we show the names of the groups we tested along with the number of individuals used in each and the locations of the collections in which they are stored.

We thought that comparisons of the kind we wished to make would be accomplished best by concentrating on relative proportion or "shape" alone and reducing the effect of sheer size on the results of our analysis. To accomplish this, we converted our data to C scores according to the procedure described by Howells (1986). This adjusts for size by comparing each measurement on an individual to the overall size of all measurements of

TABLE 2. Average and range of N and location of collections for the samples used in phenograms (footnotes give locations at which skeletal collections are housed)

Population	N		Population	N	
	Range	Average		Range	Average
Admiralty Islands <sup>1</sup>	2-3	3	Japan, Chiba <sup>2</sup>	73-80	79
Ainu <sup>2,3</sup>	78-114	85	Japan, Kofun <sup>16</sup>	9-25	19
Andaman Islands <sup>4</sup>	22-26	25	Japan, Tohoku <sup>17</sup>	83-109	102
Australia, North <sup>5</sup>	18-19	19	Japan, Tokyo <sup>3</sup>	116-119	119
Australia, South <sup>5</sup>	19-22	22	Japan, Kyushu <sup>16,18</sup>	29-32	31
Baining, New Britain <sup>1</sup>	8-13	12	Jōmon, Early/Middle <sup>2,19</sup>	5-19	14
Burma <sup>4</sup>	36-38	38	Jōmon, Late <sup>2,19</sup>	9-37	27
California, South <sup>6</sup>	27	27	Korea <sup>3</sup>	17	17
China, East Coast <sup>7</sup>	196-241	224	Maori <sup>1</sup>	27-41	39
China, Hong Kong <sup>8</sup>	47-52	50	Marquesas <sup>1,14</sup>	33-40	37
China, Neolithic <sup>9</sup>	21-33	27	Michigan Indians, North <sup>20</sup>	7-15	12
China, North <sup>3</sup>	41-44	42	Michigan Indians, South <sup>20</sup>	33-53	45
China, Sichuan <sup>10</sup>	83-92	89	New Caledonia <sup>12</sup>	20	20
China, Yunnan <sup>9</sup>	80-106	97	New Hebrides, Vanuata <sup>12</sup>	13-14	14
Dayak, Borneo <sup>3</sup>	10-13	13	New Ireland <sup>1</sup>	4-6	6
Denmark <sup>11</sup>	14-22	16	Northwest Coast <sup>6</sup>	48-50	50
Denmark, Neolithic <sup>11</sup>	26-32	30	Norway <sup>21</sup>	44-46	46
Easter Island <sup>1</sup>	15-17	16	Péru <sup>6</sup>	18	18
England <sup>4</sup>	33-42	41	Philippines, Visayas <sup>20</sup>	29-41	36
Fiji <sup>12</sup>	7-8	8	Plains Indians <sup>6</sup>	3	3
France <sup>12</sup>	38-40	40	Ponape <sup>3</sup>	5-9	8
France, Neolithic <sup>13</sup>	3-6	5	Ralum, New Britain <sup>1</sup>	62-71	70
Germany <sup>1</sup>	24-41	36	Samurai <sup>3</sup>	25-32	30
Guam <sup>14</sup>	55-79	69	Siberia <sup>1</sup>	5-7	7
Gulf of Papua, New Guinea <sup>4</sup>	14-15	15	Southwest Indians <sup>6</sup>	7	7
Hawaii <sup>14</sup>	76-91	87	Thailand <sup>22</sup>	72-87	82
Irian Jaya, W. New Guinea <sup>4</sup>	6	6	Trobriand Islands <sup>4</sup>	10-11	11
Italy <sup>15</sup>	42-50	46	Vietnam <sup>12</sup>	7-10	9
			Yayoi <sup>16</sup>	28-37	35

<sup>1</sup>American Museum of Natural History, New York.

<sup>2</sup>Sapporo Medical College.

<sup>3</sup>University Museum, University of Tokyo.

<sup>4</sup>Duckworth Laboratory, Cambridge University.

<sup>5</sup>Department of Anatomy, University of Edinburgh Medical School.

<sup>6</sup>Lowie Museum, University of California Berkeley.

<sup>7</sup>Institute of Anthropology, Fudan University, Shanghai.

<sup>8</sup>Prince Philip Dental Hospital, University of Hong Kong.

<sup>9</sup>IVPP, Beijing.

<sup>10</sup>Chengdu College of Traditional Chinese Medicine.

<sup>11</sup>Panum Institute, Copenhagen.

<sup>12</sup>Musée de l'Homme, Paris.

<sup>13</sup>Institut de Paléontologie Humaine, Paris.

<sup>14</sup>B.P. Bishop Museum, Honolulu.

<sup>15</sup>Peabody Museum, Harvard.

<sup>16</sup>Department of Anatomy, Kyushu University Medical School, Fukuoka.

<sup>17</sup>Department of Anatomy, Tohoku University Medical School, Sendai.

<sup>18</sup>Department of Anatomy, Nagasaki University Medical School.

<sup>19</sup>Laboratory of Physical Anthropology, Kyoto University.

<sup>20</sup>Museum of Anthropology, University of Michigan.

<sup>21</sup>Anatomical Institute, University of Oslo.

<sup>22</sup>Siriraj Hospital, Bangkok.

the cranium. C scores are similar to ratios in that they both are measures of relative size. The advantage of a C score over a simple ratio is that the C score reflects the relative size of a given feature in comparison to the average relative size of all the other traits used, whereas a ratio can reflect only relative size in comparison with a single referent. C scores are calculated as follows. First, individual unweighted measurements are converted into sex-specific standardized scores (Z scores), where each Z score represents the number of standard deviation units by which the value in question departs from the grand mean of that variable for all the samples used in a given analysis.

This can be represented as:

$$Z_{ij} = \frac{(X_{ij} - \bar{X}_i)}{\sigma_i}, \quad (1)$$

where  $i$  = number of the measurement (e.g., 1 . . . 24),  $j$  = number of the individual,  $X_{ij}$  = value of measurement "i" for individual "j,"  $\bar{X}_i$  = overall sex specific average value for measurement "i," and  $\sigma_i$  = overall sex specific standard deviation for measurement "i."

From Z scores, C scores are calculated as the difference between the Z score of a single measurement for a given individual and the mean Z score of that individual for all the measurements used in the analysis.

The mean Z score of an individual is calculated as follows:

$$\bar{Z}_j = \frac{\sum_{i=1}^N Z_{ij}}{N}, \quad (2)$$

where  $\bar{Z}_j$  = the average Z score for all the variables for individual "j" and  $N$  = the number of variables used (e.g., 24 if all are represented). Given this, the C score for variable  $i$  for individual  $j$  is:

$$C_{ij} = Z_{ij} - \bar{Z}_j. \quad (3)$$

As Howells described this procedure, it has the requirement that all variables be present on each of the specimens used. This frequently presents a problem in the analysis of prehistoric populations since the number of complete specimens is often small to nonexistent.

Others have occasionally used various multiple regression procedures for interpo-

lating missing variables, but we decided against this. In our analysis we use up to 24 measurements, but, instead of calculating an average Z score only for individuals with all 24 variables, we calculated average Z scores if 15 or more variables were present on any one individual. These average Z scores were then used to compute the C scores for each of the variables present in each individual as in equation 3. A mean C score was then calculated for each variable by sex and by population, and these sex-specific C scores were used to generate the male-female midsex mean C scores ( $\bar{C}_{ij}$ ) that we then used as the basis of our group-by-group comparisons.

More formally,

$$\bar{C}_{ij} = \frac{\sum_{j=1}^{n_{J_f}} C_{ijJ_f} + \sum_{j=1}^{n_{J_m}} C_{ijJ_m}}{2}, \quad (4)$$

where  $i$  = number of the measurement (e.g., 1 . . . 24),  $j$  = number of the individual,  $J$  = a population, e.g., Japan,  $J_f$  = females only from population  $J$ ,  $J_m$  = males only from population  $J$ , and, therefore,  $C_{ijJ}$  represents the C score for the  $i$ th measurement, for the  $j$ th individual among the females of the  $J$ th population.

Once we had generated a mean C score for each variable by population ( $\bar{C}_{ij}$ ), we analyzed the data using a cluster algorithm available in the Michigan Interactive Data Analysis System (Fox and Guire, 1976). This algorithm produces branching diagrams in which populations are arranged according to their Euclidean distance from one another. Groups are displayed as twigs on a tree where the distance between each branching point is roughly proportional to Euclidean distance (Sokal and Sneath, 1963; Sokal and Camin, 1965; Sokal, 1966; Sokal and Rohlf, 1969; Sneath and Sokal, 1973; Fox and Guire, 1976).

We did a series of trial runs to test whether our use of individuals with different numbers of variables present for the purpose of generating mean C scores had any effect on the nature of the clusters that were produced. In the case of the treatment of relatively large groups, i.e., those with  $N$ s of over 25 for each sex, the major clusters were exactly the same. In the cases with smaller  $N$ s, our procedure tended to produce more

satisfying results than was the case when only individuals with complete data were included. For example, it eliminated the curiosity of seeing an Amerindian group or two appear in the European or the Australo-Melanesian clusters. As will be seen in what follows, our results are sufficiently consistent for us to be confident in the validity of our procedure.

#### PRACTICAL APPLICATION *Japan*

Our first attempt to use this technique for a population analysis problem was focused on Japan. We used C scores as the input to generate a Euclidean distance dendrogram to see whether the modern Japanese clustered with their Jōmon predecessors or with other previous and modern Asian groups. First we restricted our attention to the data from the Japanese archipelago itself. Figure 1 shows that the modern Japanese fall into the same cluster as the Yayoi rice agriculturalists who entered Japan in 300 BC and also with the Kofun tomb builders, who were the immediate predecessors of the emergence of the Yamato State in the sixth century. The Jōmon, associated with the development of pottery in Japan more than 10,000 years ago, fall into the cluster with the modern Ainu. This confirms the conclusions previously reached by the appraisals of craniofacial form (Koganei, 1903, 1927; Brace and Nagai, 1982) and the nonmetric characteristics of the dentition (Turner, 1976, 1986).

The Jōmon-Ainu association of a putative group of Samurai, killed during the overthrow of the Kamakura Shogunate in 1333, is an interesting demonstration of how this analytical approach can cast light on partic-

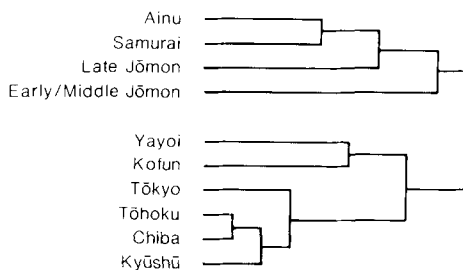


Fig. 1. Euclidean distance dendrogram comparing the prehistoric and modern populations of Japan. All dendrograms are based on C scores; see text for explanation.

ular aspects of population history and has been dealt with elsewhere in greater detail (Brace et al., 1989). It is a curious irony that the facial features associated with high social status in Japan and glorified in Japanese art evidently represent the genetic contribution that the despised Ainu have made to the traditional Samurai class.

Japan, however, for all its long and independent history, shares many cultural elements with the neighboring Asian mainland, and it has been a matter of long-term observation that the Japanese characteristically display facial features that ally them with their mainland Asian neighbors. At the same time, during work on the prehistoric Jōmon skeletal collections, we were struck by the similarities between the configuration of their features and those visible in some of the crania from Oceania. The obvious course of action was to test this by including Japanese, Oceanic, and mainland Asian crania in a single analysis. The results of this can be seen in Figure 2.

As can be seen, the Japanese along with the prehistoric Yayoi rice agriculturalists are included in the same cluster with the mainland Asian groups tested. The Mainland Asian cluster further is broadly separated into a northern and a southern component. The northern component includes the northern Chinese Neolithic, modern coastal Chinese, Koreans, and Japanese. The Ainu and the prehistoric Jōmon, however, fall into a cluster with Micronesians and Polynesians. This has been called the Jōmon-Pacific cluster (Brace et al., 1989, in press a, b).

#### *Oceania and Australia*

The process by which the settlement of Oceania was accomplished has been an active focus of interest by archaeologists and culture historians for some time (Green, 1973, 1986; Bellwood, 1975, 1979; Jennings, 1979), and some very contradictory models have been proposed. These range from the vision of a figurative Austronesian "fast train" from the Asian mainland, or the postulation of a Lapita "homeland" in the Bismarcks of northwestern Melanesia (Allen, 1984; Kirch et al., 1989), to the suggestion that Polynesians emerged by transformation out of eastern Melanesians somewhere in the neighborhood of New Caledonia (Terrell, 1986). This would appear to be an ideal situation in which to test the effectiveness of



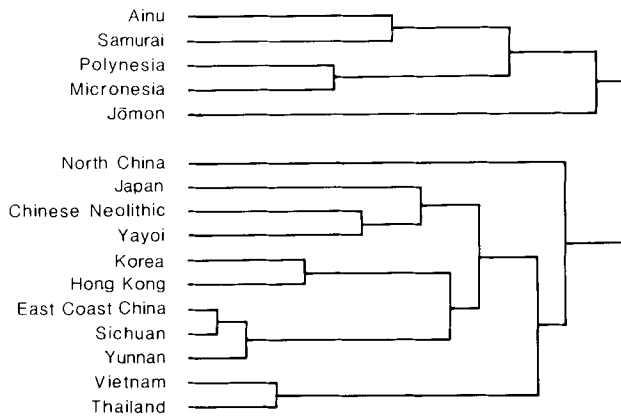


Fig. 2. Euclidean distance dendrogram comparing a series of populations from the Asian mainland, Japan, and the islands of Micronesia and Polynesia.

the approach we are advocating. We have presented a preliminary treatment of this matter elsewhere (Brace et al., in press a), but we have subsequently added some further populations to fill in areas previously unrepresented.

In dealing with this matter, we have had to organize things to consider the oft-reiterated observation that the Melanesian inhabitants of Oceania are closely related to Tasmanians, Australians, and the inhabitants of New Guinea (Sarasin, 1924; Wagner, 1937; Howells, 1973). Figure 3 shows what happens when we compare the various peoples of the Pacific with those who produced the Mainland Asian cluster. The Jōmon-Pacific cluster retains its identity, and all the groups found in Melanesia, New Guinea, and Australia form a separate coherent cluster, which we have termed the Australo-Melanesian cluster. It is a matter of added interest that the available specimens representing the Andaman Islands also fall into this cluster, although the tie is not close. Still, the Australo-Melanesian group with which they form their closest association is the westernmost for which we have data from the island of New Guinea itself. This, with other subjective hints previously noted, gives some support to the expectation that groups that would have been recognized as members of this cluster once may have been distributed west of New Guinea throughout what is now Indonesia.

With Easter Island, Hawaii, and the Maori of New Zealand in the far Pacific fitting comfortably in the same cluster with the

Ainu and the prehistoric Jōmon of Japan, there is virtually no likelihood that any members of what has been termed the Jōmon-Pacific cluster could have emerged by transformation from anything in either western or eastern Melanesia. And with the representatives of the latter from New Britain and New Ireland to New Caledonia and the New Hebrides solidly associated in the same cluster with both northern and southern Australian aborigines as well as groups from the Gulf of Papua in New Guinea, there is every reason to believe that the members of the Australo-Melanesian cluster have a common inheritance that goes well back into the Pleistocene. Archaeological evidence for human occupation of the Swan River region of southwestern Australia (Pearce and Barbetti, 1981) and the Huon Peninsula of northern New Guinea goes back more than 40,000 years (Groube et al., 1986) and is supported by prepottery sites of more or less comparable antiquity in the Bismarck Archipelago of western Melanesia.

Altogether, this sustains the suspicion previously offered, largely on the basis of tooth size alone, that an area extending from the Andaman Islands in the west through Borneo and the Philippines to the large islands of Melanesia and including New Guinea and Australia was populated by people of common ancestry and similar appearance during the latter part of the Pleistocene (Brace and Hinton, 1981). Figure 4 shows the putative extent of this related series of populations and suggests the routes by which their spread into the regions be-

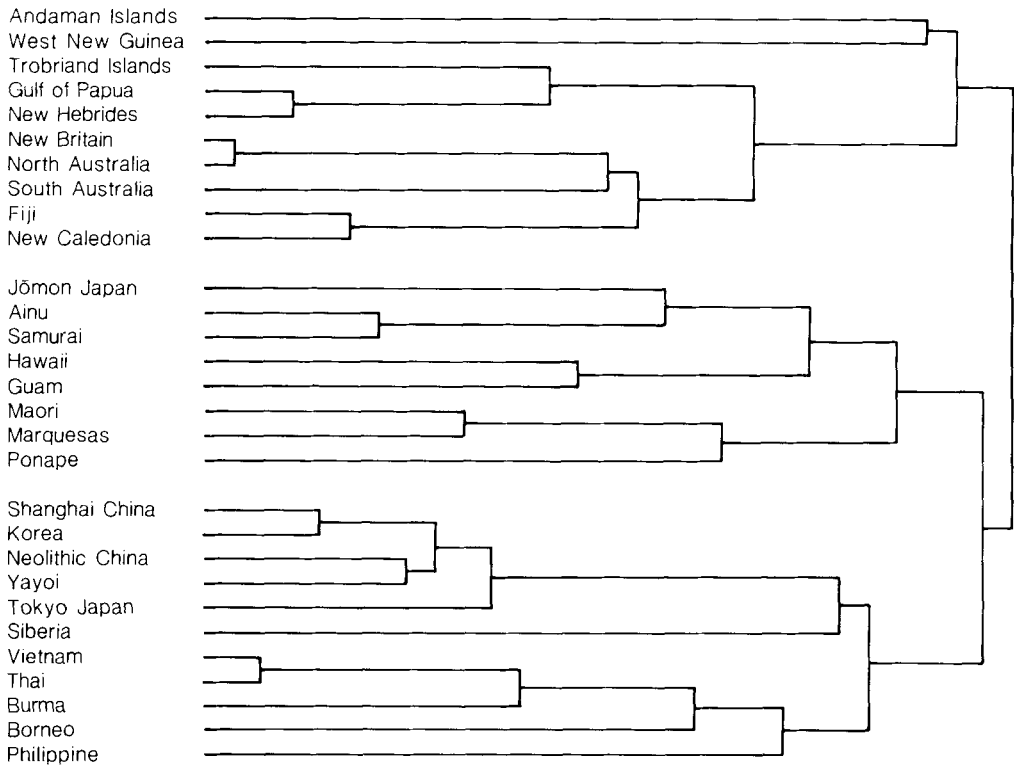


Fig. 3. Euclidean distance dendrogram comparing samples from the Asian Mainland, Micronesia, Polynesia, Melanesia, and Australia.

yond Wallace's line was presumably accomplished.

Then, to get a population of a very different appearance out into the small islands of the far Pacific between 4,000 and 2,000 years ago, some version of Bellwood's express train model has to be invoked. There have been archaeological attempts to identify a south-east Asian source (Solheim, 1964, 1972, 1976; Spoehr, 1973), and Turner has used data from dental morphology to suggest that what had been Sundaland at the time of lowered sea levels in the Late Pleistocene was the most likely area (Turner, 1986, 1987).

However, the oldest human skeletal material solidly aligned with the members of the Jōmon-Pacific cluster are the Early Jōmon specimens themselves from approximately 6,000 years ago in Japan. On purely archaeological evidence, the Jōmon goes back much farther than that (Ikawa-Smith, 1980; Pearson, 1986), and, if the 18,000-year-old Minatogawa skull from Okinawa can be used as

further evidence (Suzuki, 1981; Suzuki and Hanihara, 1982; Turner, 1983, 1989, in press), then there is at least a tentative reason to offer Japan and the Ryukyu Archipelago as the source from which subsequent expansion produced the distribution of the related peoples who form the Jōmon-Pacific cluster. This possibility is illustrated by the routes of movement depicted in Figure 5.

#### *Other parts of the world*

The success we have had using this cluster-producing method to suggest population relationships in Asia and the Pacific has led us to extend our efforts to include representatives from other major regions of the world. Figure 6 shows what happens when a series of European and Amerindian groups is added to what has already been examined. It is no surprise to discover that the two additional series make distinct, separate clusters. In the Amerindian cluster, one of the constituent groups, the Southwest, appears to be less closely related to the others and, in

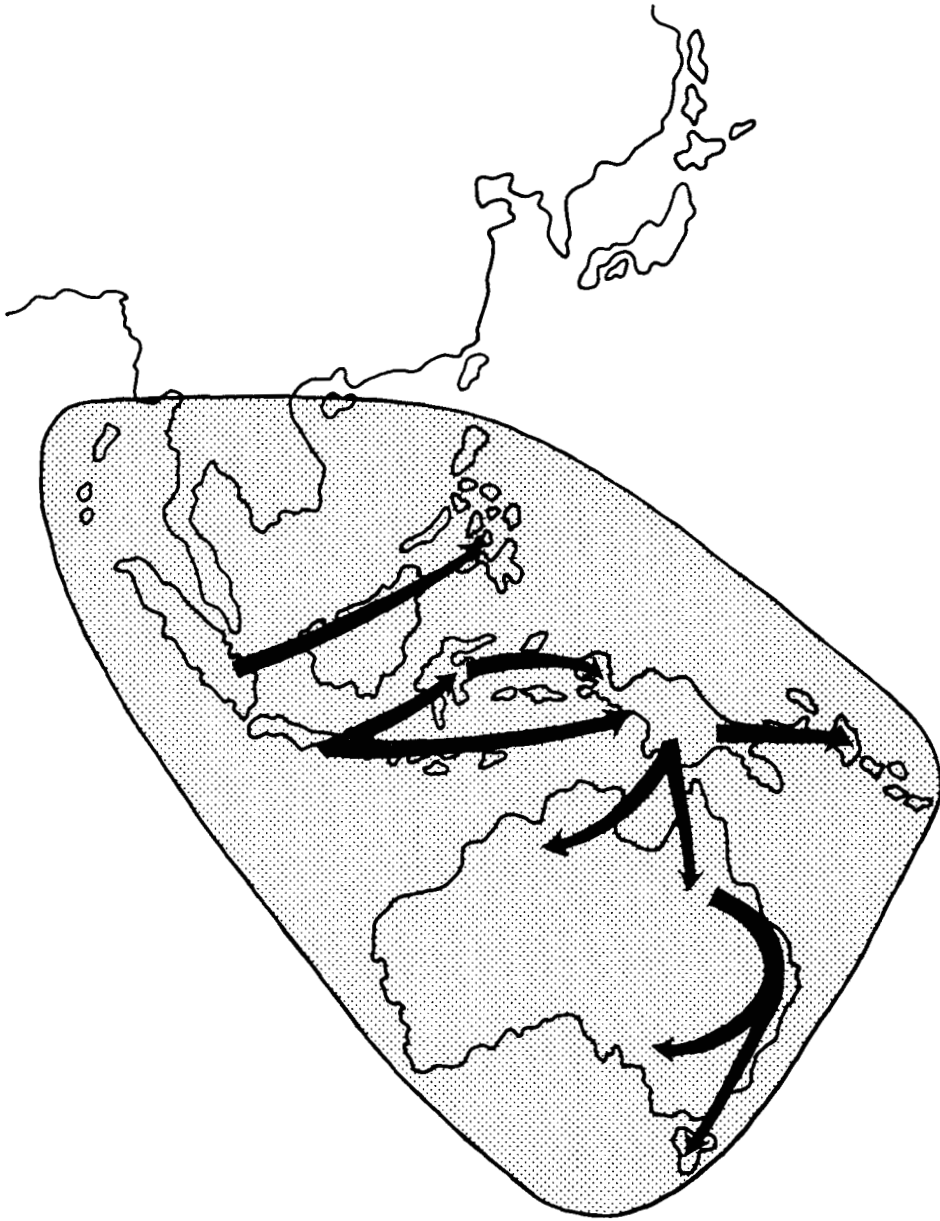


Fig. 4. The stippling represents the suggested area of occupation late in the Pleistocene of a large-toothed series of people of relatively similar appearance. The arrows show the presumed routes of initial Late Pleistocene movement into the Philippines and beyond Wallace's Line into the large islands of Melanesia and Australia. (Adapted from Brace and Hinton, 1981, with permission of the publisher.)

a sense, almost intermediate between the Amerindian cluster and the European cluster. As it happens, we were dubious about this even before we ran the cluster-

producing program, but we included it anyway since we had nothing else to represent that end of the Australia-to-Zuni spectrum. Our suspicions arose from the possibility

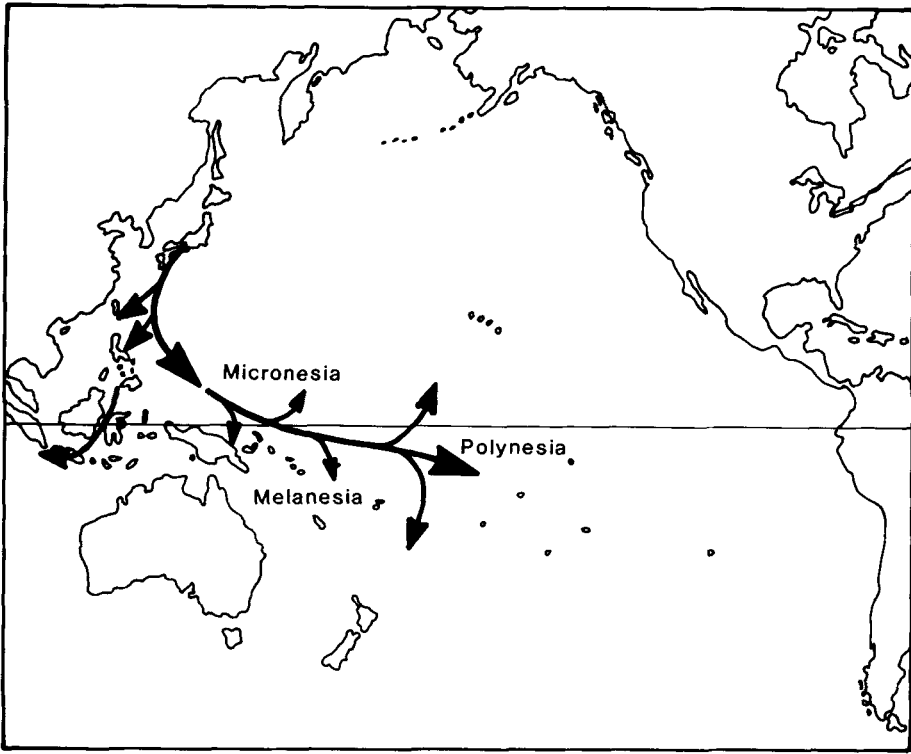


Fig. 5. The suggested route of spread of the Jōmon-Pacific movement from its hypothetical area of origin out into the small islands of the Pacific. (Adapted from Brace et al., 1989, with permission of the publisher.)

that the form of the skulls from the American Southwest had been altered by artificial deformation. A great deal of the available material was rejected out of hand because the deformation was obvious. Although we tried to select specimens that did not appear to have been deformed, nonetheless we still had the uneasy feeling that there were virtually no completely undeformed individuals. Obviously we need to add many more representatives of each region treated before we can be more than tentative about the nature and extent of each such grouping.

What does come as something of a surprise, however, is the relatively complete separation of the Amerindian cluster from the Mainland Asian and the Jōmon-Pacific clusters. Evidently the 12,000 or 13,000 year time span since the presumed initial movement into the New World (Irving, 1985; Fagan, 1987; Haynes, 1988) was sufficient for the production of the distinctions observed. The computer program that produces dendrograms from our C scores also

generates Mahalanobis  $D^2$  figures, which express a numerical form of the Euclidean distance between any given group and each of the others (Sokal, 1965). It is our hope that we may eventually be able to use such figures as measures of separation time when we have been able to collect enough information on lineage change through time and on reliably dated separations of known groups. At the moment, however, this is a long way from being achieved, which is why we have not included a table of the already-ponderous matrix of  $D^2$  figures.

#### TOOTH SIZE AS A MODEL FOR ADAPTIVE TRAIT CONSIDERATIONS

Because of the quantity of information available and the various other reasons mentioned in extensive previous discussions (Brace, 1967, 1978, 1979, 1980; Brace and Mahler, 1971; Brace and Hinton, 1981; Brace and Nagai, 1982; Brace et al., 1984, 1987; Brace and Vitzthum, 1984), we have concentrated our consideration of dimen-

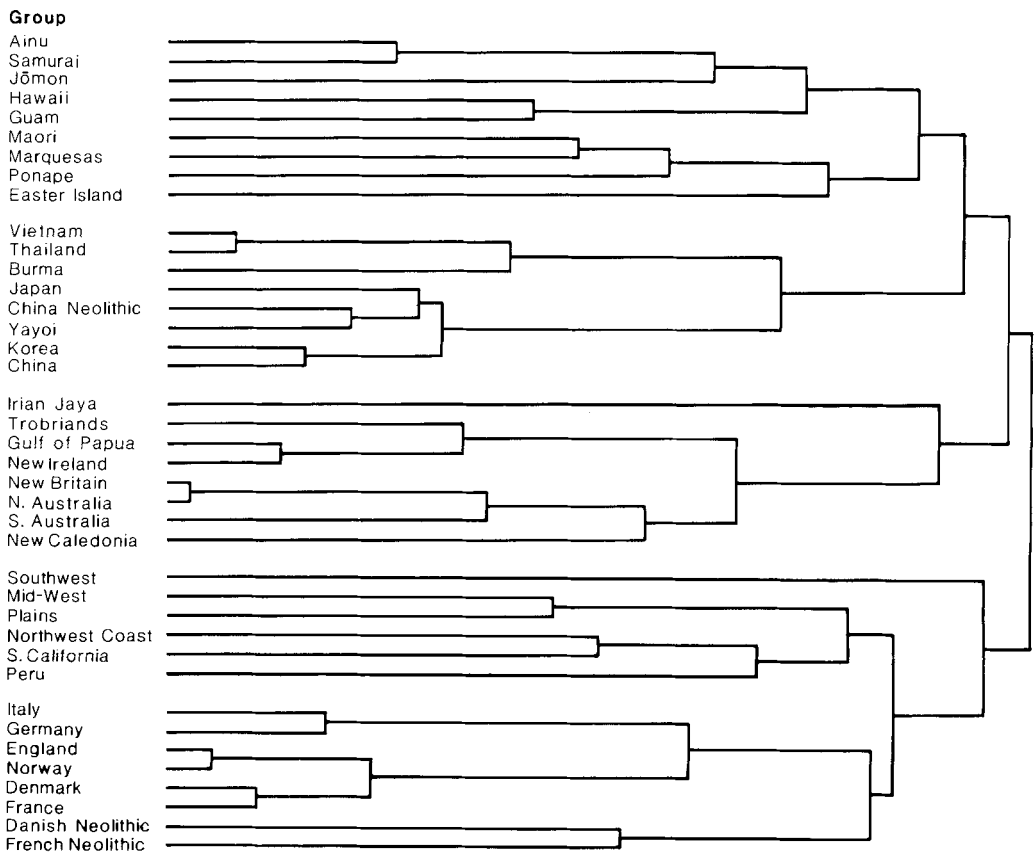


Fig. 6. Euclidean distance dendrogram showing the nature of the clusters when a series of representative Amerindian and European groups are added. The clusters shown in Figure 3 retain their identity, and Europe and the whole of the aboriginal western hemisphere appear as comparably identifiable clusters.

sions under obvious selective force control on the single trait of tooth size. We are aware, of course, that there are many parameters involved in tooth size, as can be seen when mesial-distal and buccal-lingual dimensions are treated separately or when anterior and postcanine or maxillary and mandibular teeth are compared (Brace et al., 1987). For purposes of simple demonstration, however, there is considerable heuristic value in treating tooth size as though it were a simple adaptive trait.

However, tooth size, like any other metric feature, shares a measure of common variance with body size as a whole. It would be desirable, then, to treat it in conjunction with some kind of body size index. Stature is notoriously poor as an indicator of body mass, and, furthermore, in many skeletal collections, there is no way to sort cranial

and postcranial remains by individual, if indeed the postcranium is represented at all.

On the other hand, the teeth on which our measurements have been made are usually still in or at least associated with the skulls of their original owners. Since cranial measurements can give us a fair approximation of brain size (Pearson, 1926), and since brain size is allometrically related to body size within a given species (Lande, 1979; Martin, 1983; Martin and Harvey, 1985; Riska and Atchley, 1985), we have used the cranial and dental dimensions of the collections studied to investigate the relations between tooth size and body size. Our measure of tooth size, TS, is the cumulative sum of the cross-sectional areas ( $MD \times BL$ ) of all the maxillary and mandibular tooth classes (Brace, 1980). To calculate brain size, we treated the height, width, and length measurements of

the brain case as though they were the major axes of an ellipsoid and used the standard formula to calculate its volume. Obviously we are aware that this will produce an overestimate of the actual size of the brain for several reasons (and note the attempt to correct for this made by Pearson in 1926), but it does give us a crude figure with which to work, and a case can be made that this will rise and fall in close approximation to the variation of true brain size itself.

Over a century ago, the English anatomist W.H. Flower used an even cruder index to determine whether the dentition in a given population was relatively large, medium, or small—"microdont, mesodont, and megadont" to use his terms (Flower, 1885). To do this, he measured the distance from the mesial surface of the maxillary first premolar to the distal surface of the third molar, a length that can be approximated by summing the mesial-distal dimensions of the five teeth involved. He then divided this figure by the nasion-basion length.

Flower's index, of course, is simply a proportion between two linear measures. Since our own appraisal of tooth size involves the calculation of areas and our approximation of brain size is a volumetric measure, we took the square root of the first and the cube root of the second in order to allow a direct comparison of Flower's index with our own. Despite the relatively crude approximations used by Flower, his measures show surprisingly high correlations with ours. For example, the correlation between our calculation of cranial volume and basion-nasion length is 0.813, and that between his length measure of the maxillary postcanine teeth and our cross-sectional area of the entire dentition is 0.926. Even though we believe that our own approach should yield a more reliable assessment, it is clear that Flower's index does indeed produce an easily calculated and very useful assessment of relative tooth size.

Figure 7 compares the assessment of a series of Asian and Oceanic populations by Flower's method and by our own, where the left-to-right position of the bars on the graph is determined by increasing magnitude of the TS/cranial volume index. As can be seen, the populations that are placed in the Jōmon-Pacific cluster in our previous craniofacial analysis fall largely at the microdont end of the spectrum, the Australo-Melanesians all prove to be megadont, and the Mainland Asians are in between, just as

Flower himself observed over 100 years ago when he treated groups from those areas (Flower, 1885).

When we break down our comparisons to single dimensions and plot tooth size and brain size separately on the same graph, as in Figure 8, it is obvious that they vary in quite unrelated fashion for the same set of populations plotted here in the same order as in Figure 7. The brain size-tooth size correlation across these groups in fact is negative, being  $-0.384$ . This provides a graphic demonstration of the point that tooth size and body size have become decoupled during the recent course of human evolution (Brace et al., 1987). A full treatment of the changes in human tooth size that have followed the alterations in the relevant selective forces is being presented elsewhere (Brace et al., in press c).

#### CONCLUSIONS

A full understanding of the course of evolution requires the study of both phylogenetic relationships and the dynamics by which individual traits change through time, Darwin realized this 130 years ago with a clarity that has been appreciated by too few. Now that we have the advantages of both data and techniques that were unavailable in the past and can put his suggestions to the test, his genius seems ever more impressive.

But the effort to apply these to deal with problems in human phylogeny and evolution has suffered from their association with the invidious enterprise of racial classification in the physical anthropology of yesteryear. This is clearly expressed by Colin Renfrew in his recent book "Archaeology and Language," in which he says, "craniometry, the study and measurement of human skulls, has in recent years enjoyed about as much prestige in scientific circles as phrenology" (Renfrew, 1987:4). He continues, "there are at present few conclusions that can be relied upon" (p. 5) and concludes, "it would in my view be wrong to place much weight upon conclusions drawn from physical anthropology until the methodology is better developed" (p. 93).

We would argue, however, that the problem is less with the methodology than with the vision, or, rather, the lack of vision, of its users. As we have been able to show above, the use of nonadaptive traits to survey some representative human populations has enabled us to produce an assessment of the strength of their genetic relationships one to

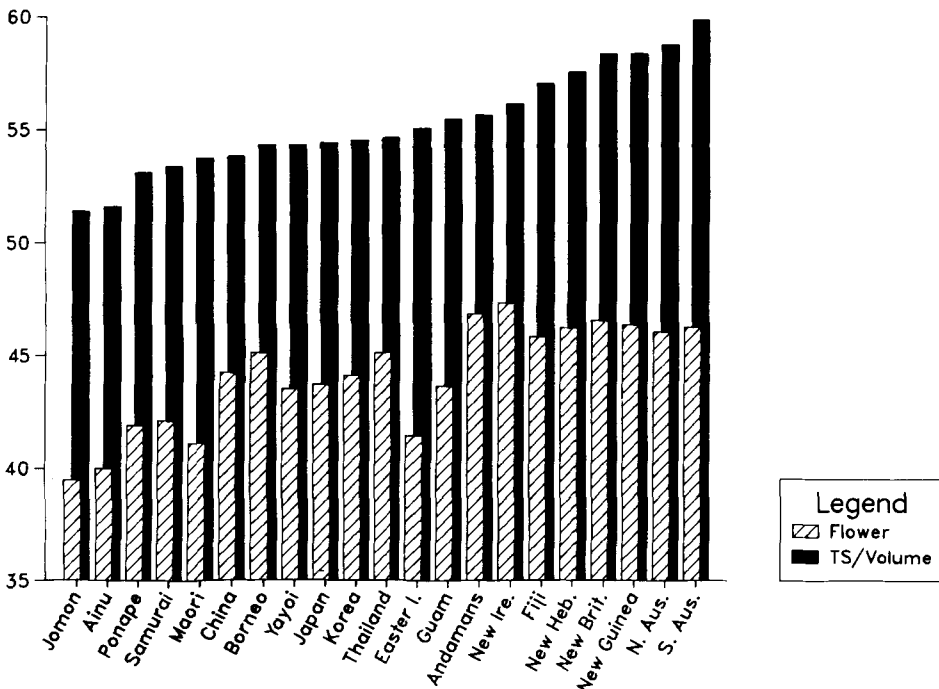


Fig. 7. The tooth size/cranial volume index for a series of Jōmon-Pacific, Mainland Asian, and Australo-Melanesian populations compared to Flower's index for the same groups. The increase in magnitude from left to right is keyed to the TS/BS index. Based on the data in Tables 3 and 4.

another. Then, when we turned to the treatment of a trait under the changing influence of selection for different known periods of time in different areas of the world, we have been able to make interpretive sense out of a specific instance of evolutionary change. It is our hope that other investigators will follow this lead, dealing with still further human populations and other traits in the manner that we recommend. By these means, a coherent picture of human populations relationships and trait modifications—in sum, human evolution—has a very real chance of emerging in the near future.

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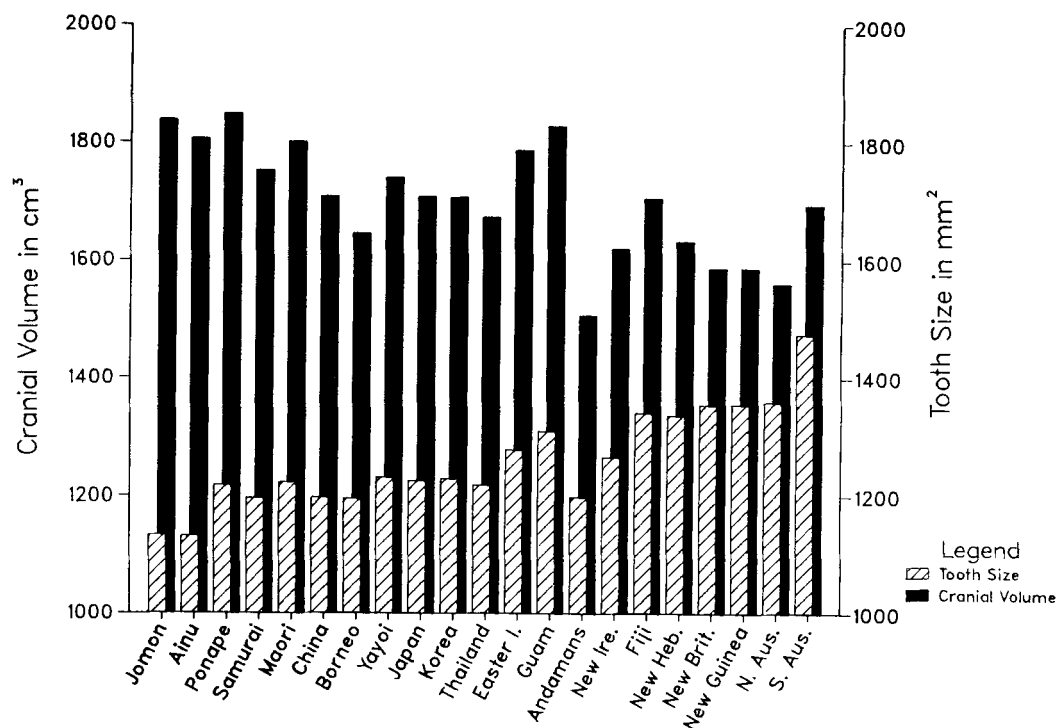


Fig. 8. Absolute tooth size and cranial volume figures for the same groups in the same order as that seen in Figure 7. Based on the data in Tables 3 and 4.

TABLE 3. Total tooth size (TS), cranial volume (CV), summed mesial-distal dimensions for maxillary P1-M3, nasion-basion figures, Flower's index, and the TS/CV index for a series of Asian and Pacific groups

Population	Basion-nasion	P1-M3 Length	Flower's index	Cranial volume	Tooth size	TS <sup>1/2</sup> /cranial volume <sup>1/3</sup>
Jōmon	102.90	40.60	39.5	1,838.1	1,134.3	27.5
Ainu	104.15	41.68	40.0	1,805.4	1,132.3	27.6
Maori	102.80	42.22	41.1	1,800.6	1,223.0	28.8
Easter Island	107.40	44.42	41.4	1,786.8	1,278.6	29.5
Ponape	103.00	43.13	41.9	1,848.2	1,218.1	28.4
Samurai	101.14	42.62	42.1	1,751.7	1,196.5	28.7
Yayoi	99.14	43.09	43.5	1,740.3	1,231.4	29.2
Guam	102.43	44.65	43.6	1,828.2	1,310.9	29.6
Japan	99.24	43.34	43.7	1,708.6	1,225.8	29.4
Korea	97.31	42.88	44.1	1,707.3	1,229.3	29.4
China	97.00	42.87	44.2	1,708.3	1,197.3	29.0
Thailand	95.81	43.22	45.1	1,673.7	1,218.3	29.4
Borneo	96.89	43.72	45.1	1,645.4	1,195.9	29.3
Fiji	99.52	45.57	45.8	1,706.1	1,341.9	30.6
N. Australia	99.13	45.64	46.0	1,560.8	1,359.7	31.8
S. Australia	100.98	46.67	46.2	1,694.2	1,474.8	32.2
New Hebrides	97.64	45.12	46.2	1,632.4	1,337.6	31.1
New Guinea	97.80	45.31	46.3	1,587.4	1,356.0	31.5
New Britain	98.39	45.77	46.5	1,587.3	1,355.2	31.5
Andamans	92.23	43.20	46.8	1,506.5	1,198.5	30.2
New Ireland	96.13	45.45	47.3	1,620.4	1,266.0	30.3

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TABLE 4. Average and range of *N* for the TS/Cranial Volume index

Population	Cranial volume <i>N</i>	TSN	
		Range	Average
Jōmon	23	17-73	49
Ainu	106	91-196	137
Ponape	7	8-15	11
"Samurai"	28	29-50	42
Maori	40	1-26	9
China	227	25-234	108
Borneo	13	3-11	6
Yayoi	36	25-64	48
Japan	331	153-305	264
Korea	17	13-44	22
Thailand	82	50-75	63
Easter Island	15	1-21	10
Guam	68	38-89	70
Andaman Islands	27	1-19	7
New Ireland	6	3-21	8
Fiji	7	2-5	3
New Hebrides	14	3-14	11
New Britain	71	13-67	42
New Guinea	15	2-11	6
N. Australia	18	143-150	149
S. Australia	21	164-338	209

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