

## HUMAN CRANIOFACIAL FORM AND THE EVIDENCE FOR THE PEOPLING OF THE PACIFIC

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### INTRODUCTION

Up through the Middle Pleistocene, human beings, like most other placental mammals, did not inhabit any of the areas of the Pacific east of Wallace's Line. Humans at the grade level of *Homo erectus* did occupy the Asian mainland starting before the Middle Pleistocene, and their presence has been demonstrated in China and Java which latter, during the recurrent periods of lowered sea level, was intermittently a continuous part of the mainland itself. At one time it had been thought that the distribution of Lower Paleolithic artifacts from Java throughout Southeast Asia and up into northern China provided a more accurate picture of the extent of human occupation. Serious questions concerning the dating of some of that material have been raised (Hutterer 1985; Bartstra and Basoeki 1989), although recent archaeological evidence from Thailand would appear to confirm a hominid presence before the beginning of the Middle Pleistocene (Pope *et al.* 1986).

Then sometime after the beginning of the Late Pleistocene, humans began to move across those water gaps that had previously prevented the eastward extension of most placental land mammals. By the time that the inhabitants of western Europe could be characterized as Late Neanderthals, there were human inhabitants in New Guinea, the larger islands of the Bismarck Archipelago, and Australia (Pearce and Barbetti 1981; Groube *et al.* 1986). Since the evidence is principally archaeological, it does not allow us to say anything directly about the appearance of the people themselves. However, the earliest scraps of human material from Niah Cave in Sarawak (Kennedy 1979) and Tabon Cave in Palawan (Macintosh 1978) to Keilor near Melbourne (Weidenreich 1945) and the Cossack dune site in Western Australia (Freedman and Lofgren 1979) lead us to expect that the makers of the artifacts looked like robust versions of recent Australian aborigines. One could even posit that the first human occupants of what has been termed "Near Oceania" (Pawley and Green 1973:4) east of Wallace's line were essentially Southeast Asian "Neanderthals", where that term is taken to mean humans with fully

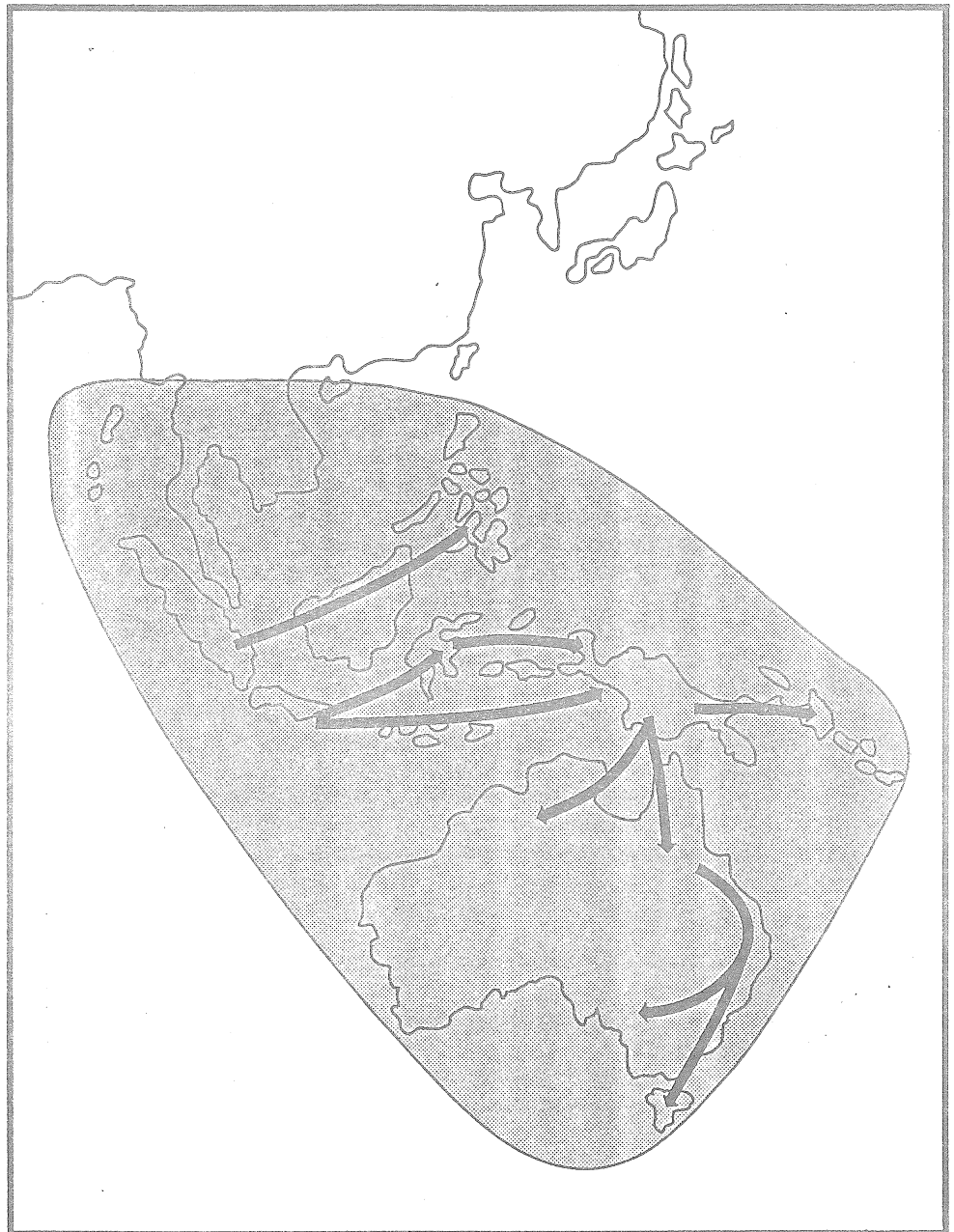
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Indo-Pacific Prehistory Assn. Bulletin 11, 1991:247-269 (P. Bellwood ed., *Indo-Pacific Prehistory 1990*, Vol 2)

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**FIGURE 1: THE PROBABLE EXTENT OF THE DESCENDANTS OF THE SOUTHEAST ASIAN PALEOLITHIC POPULATIONS AT THE END OF THE PLEISTOCENE**  
The arrows suggest the directions of movement by which their spread was accomplished starting 50,000 years ago (from Brace and Hunt 1990:351).

modern brain size but where Middle Pleistocene levels of tooth size and postcranial robustness and musculature were retained (Brace 1988:118) - in essence, "archaic" *Homo sapiens*.

A sequence of development from full scale *Homo erectus* represented by the Trinil finds, beginning with Dubois' original "Pithecanthropine" discovery a century ago, up through the late Middle Pleistocene Solo specimens and via the Wajak skulls in Java has long been regarded as a plausible background for the emergence of the Australian Aboriginal configuration in the Late Pleistocene (Weidenreich 1945, 1951; Brace and Hinton 1981; Kramer 1989). The arrows in Figure 1 show the hypothetical routes by which those Southeast Asian "Neanderthals" moved into Near Oceania, and the stippled portion shows the extent of the area occupied by their descendants at the end of the Pleistocene (Brace and Hunt 1990:351).

The spread of human groups into "Remote" Oceania (Pawley and Green 1973:1, 4) did not begin until well after the Pleistocene had ended at approximately 10,000 BC. The question that concerns us here, however, is whether the people who accomplished that post-Pleistocene spread into the smaller islands of Oceania were derived from the same people who had moved across Wallace's Line earlier in the Late Pleistocene, or whether they moved out directly from the coast of mainland Southeast Asia (Bellwood 1986, 1988), or from some other source such as the Japan-Ryukyu archipelago (Brace and Nagai 1982; Brace and Hunt 1990; Brace *et al.* 1990).

#### MATERIALS AND METHODS: THEORY AND APPLICATION

The populations we have sampled are listed in Table 1 and the variables we used in order to compare them are presented in Table 2. A more extended description of the latter can be found elsewhere (Brace and Hunt 1990). In previous analyses we had found that, when craniofacial measurements are employed to compare the living and prehistoric peoples of Asia and Oceania, these form three separate and relatively unrelated clusters (Brace *et al.* 1989; Brace and Hunt 1990; Brace *et al.* 1990). Somewhat by trial and error we found that we needed at least five or six related groups before a cluster would remain stable. In similar fashion, we also found that it was easier to demonstrate the relationships of populations to these clusters by using large numbers of measurements on only fifteen or twenty individuals of each sex rather than by using fewer variables and increasing the numbers of individuals to fifty or one hundred or more (Brace and Hunt 1990). Our original expectation was that, by using judiciously selected and, we hoped, diagnostic measurements, we could handle large numbers of individuals and populations to greatest effect. Instead, we discovered that Howells' more laborious approach yielded better results in actual practice (Howells 1973a, 1989).

This somewhat belated discovery was made when we remeasured a few groups used in earlier studies in the hopes of refining our test battery so that we could use a minimum number of key dimensions to produce the maximum degree of regional differentiation. Instead, what we found was that the most important thing was the quantity and not the nature of the traits used. This put us in the awkward position of having to go back and

Group	N's in Dendrogram		N range for mean Z-score	
	Female N	Male N	Female N	Male N
Africa	57	59	58-59	59
Ainu	23	33	28-50	41-65
Amerind	83	100	85-102	115-134
Andaman Islands	10	10	12-14	10-13
Asia Mainland N	260	525	309-379	595-694
Asia Mainland S	52	81	55-58	85-93
Athabaskan	23	19	23	19
Australia N	6	12	6	12
Australia S	9	10	10-12	10-11
Borneo, Dayak	4	6	4-5	6-8
China Neolithic	8	14	9-51	19-90
Eskimo	71	83	71-73	83-85
Europe	113	206	126-143	224-264
Fiji	3	4	3	4
India	45	68	45	68
Jōmon	4	2	9-27	4-27
Micronesia	28	32	37-51	50-71
Mongol	21	29	21-23	29-30
New Britain	30	37	32-35	39-49
New Caledonia	10	10	10	10
New Ireland	2	2	2	2-4
Philippines	19	26	20-27	31-39
Philippine Negrito	8	15	8	15-16
Polynesia	70	61	83-99	70-90
Purari Delta	6	8	6	8-9
Tasmania	4	5	4	5
Thai Neolithic	2	3	4-15	5-18
Trobriand Islands	1	9	1-2	9
Vanuatu	6	7	6-7	7
Yayoi	9	12	10-27	19-52

TABLE 1: SAMPLES AND NUMBERS USED IN THIS STUDY

remeasure as many groups as we could. Even so, our test battery of two dozen variables has to be regarded as no more than the bare minimum necessary to accomplish our objectives and, as will be seen, some of our tests had to be made with somewhat less than our full battery.

For those workers who are either just beginning in the field or who are interested in making an independent test of our findings, we recommend using fifty or more variables as Howells does in his most recent exemplary work (Howells 1989). The logic is essentially the same as that used in DNA sequence comparisons and is based on the fact that, like much of DNA, there is no specific adaptive value to most of the craniofacial variables that can be measured (Brace and Hunt 1990). There is, of course, the difficulty of finding

more than a handful of individuals in a given sample with a full complement of fifty or sixty dimensions. Where prehistoric material is concerned, it is often a problem to find even one such individual. The use of regression techniques to interpolate missing variables, of course, artificially inflates common variance and reduces the validity of any subsequent treatment. Pragmatically then, we use the largest number of variables possible for the samples available.

Variable Number	Measurement Name
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 Opisthocranion (Martin No. 1)
17.	Maximum Cranial Breadth (Martin No. 8)
18.	Basion Bregma (Martin No. 17)
19.	Basion Rhinion
20.	Width at 13 (fmt-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>4</sup>

<sup>1</sup>Martin numbers are from Martin 1928

<sup>2</sup>Howells 1973-a

<sup>3</sup>Woo and Morant 1934

<sup>4</sup>Brace and Hunt 1990

TABLE 2: CRANIOFACIAL MEASUREMENTS USED IN THIS STUDY

The question of whether a given dimension is adaptive or not and how one can determine this is dealt with at greater length elsewhere (Brace and Hunt 1990; Brace *et al.* in press a; Brace and Tracer ms.; Brace, in preparation). In brief, adaptive features such as skin pigmentation, nasal elongation or adaptive anemias are not confined to geographically, genetically, culturally and linguistically circumscribed populations. Nor are they generally found as part of a configuration of co-occurring features. Instead, their

distributions and frequencies coincide with the distribution and intensity of the controlling selective forces operating on the requisite genetic material that inevitably flows across the boundaries of adjacent populations. In most instances, the selective forces to which adaptive traits respond are distributed in unrelated fashion and are not themselves limited by human population boundaries. Consequently, adaptive traits occur as clines that are largely independent of each other.

Where traits occur in identifiable configurations associated with circumscribed geographical areas and where such configurations are clearly different from the ones found elsewhere at the same latitude, or where the same configuration occurs at very different latitudes, then one has reason to suspect that the configuration in question is determined more by the accident of sharing available genes between adjacent groups than it is to the action of any significant amount of natural selection. Individual aspects of a configuration may very well be under selective force control, but there is real reason to question whether a regionally identifiable configuration as a whole ever has any adaptive significance (Brace and Tracer ms.). The picture of population clusters from given areas that emerges from morphometric analysis then is a picture of relatedness in which there can be no associated implication of adaptive differences. No given regional cluster is more adapted or less adapted - better or worse - than any other such regional cluster. Since the clusters demonstrated are based solely on shared genetic material of trivial adaptive significance, there can be no invidious or hierarchical implications. The number and nature of the clusters will depend on the number of actually related populations utilized. The result is a non-racial picture of human population relationships and distinctions that can be expanded to global extent or refined and focused in regional and sub-regional fashion depending on the interests of the investigator (Brace and Hunt 1990; Brace in preparation).

In our own case, the analysis we produce using between eighteen and two dozen variables must be regarded as a useful but somewhat crude first step. The clusters we have produced are reliable and real enough, but subsequent more detailed studies should be able to refine the relationships of their individual components to a much greater extent. In addition to populations of Oceania and Asia, we acquired data on samples from all of the other major geographic provinces of the world. With all of this as a background, then, we should be in a position to tell whether or not the separate manifestations we see in Oceania and adjacent areas are comparable to variants on a local theme or whether they can be considered the equivalent of major geographic distinctions. Ultimately, this should bring us closer to being able to assess just how long it must have taken for such differences to have arisen.

After we had collected the raw data, we converted the measurements into sex-specific Z-scores. These were then used to generate sex-specific mean C-scores. The methods and procedures have been described in detail in previous presentations (Howells 1986, 1989; Brace *et al.* 1989; Brace and Hunt 1990:346-347; Brace *et al.* 1990; Brace and Tracer ms.). From these we calculated mid-sex mean C-scores which were used as input for a Euclidean Distance cluster program (Fox and Guire 1976). The cluster pattern shown in

Figure 2 summarizes the results when representatives of all the major geographical areas of the world are analyzed in this fashion. Each named branch can be separated into a series of constituent populations, but these generally tie in with each other rather than with populations from other named branches (Li *et al.* 1991; Brace and Tracer ms.). The most parsimonious representation of the living peoples of the world then is seen in the eight regional clusters shown in Figure 2.

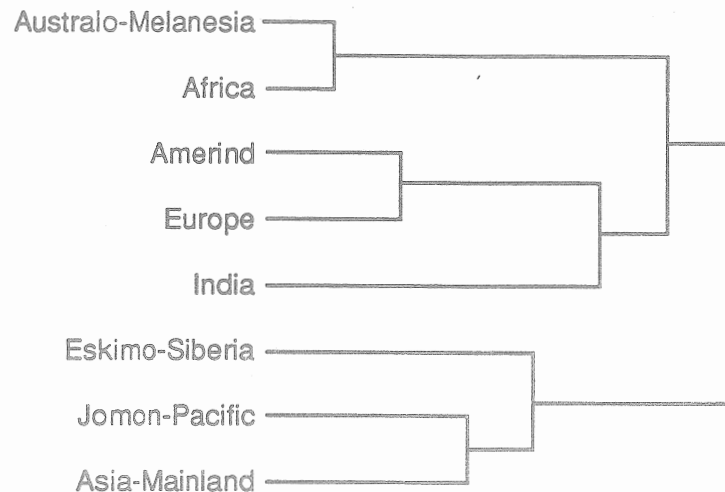


FIGURE 2: A EUCLIDEAN DISTANCE DENDROGRAM SHOWING THE SIMILARITIES AND DIFFERENCES OF THE EIGHT NAMED MAJOR GEOGRAPHIC CLUSTERS OF MODERN *HOMO SAPIENS*.

C-scores for measurements on 24 craniofacial variables from samples of each of the main regions were used as input for the generation of the clusters.

The proximity of the European and Amerind branches as well as the African and Australo-Melanesian ones is due to the large number of nasal measurements in our battery, and is more a reflection of the long term similarities in the kinds of environmental stress in the backgrounds of the groups compared rather than any measure of actual relationships (Brace *et al.* in press a). It was our assessment of the contribution of individual measurements to the construction of this dendrogram that led us to the belated realization that relationships are best delineated by traits that have the least adaptive significance - just as Darwin advised us in the first place (Darwin 1859:427).

When nasal prominence is treated using the outer edges of the orbits as a point of reference - Woo and Morant's measure of "facial flatness" (1934) - and the dendrogram is generated using indices instead of raw measurements, then the Amerind-European tie disappears. This manipulation, however, made no changes in the relative placement of all but two of the populations that were the focus of the current study, so they were not used in the initial comparisons presented here in Figure 3.

In addition, when we turned our attention more specifically to the human groups in and around the Pacific Basin, we found that neither African nor European groups, individually or collectively, add anything to our ability to deal with the placement of particular groups farther east. Consequently, we have not used them in the treatment that follows. Figure 3 displays a Euclidean Distance picture of the morphological proximity and distance between twenty-seven groups from localities in and around the Pacific Basin and including South Asia. The India branch includes six groups ranging from Calcutta to Sri Lanka. These consistently tie with each other before the cluster as a whole ties to the rest of the world (Brace and Tracer ms.). We include the India branch here, however, because of the role it plays in defining the Andaman Island sample.

Leaving aside the India and Andaman twigs for a moment, the three major clusters displayed in Figure 3 are the same as those previously discovered in works specifically focused on Micronesia (Brace *et al.* 1990), Japan (Brace *et al.* 1989), China (Li *et al.* 1991) and the circum-Pacific margin (Brace *et al.* in press a). In previous analyses, we have called these (1) the Mainland Asian cluster, (2) the Jomon-Pacific cluster, and (3) the Australo-Melanesian cluster. Each of these deserves a brief consideration.

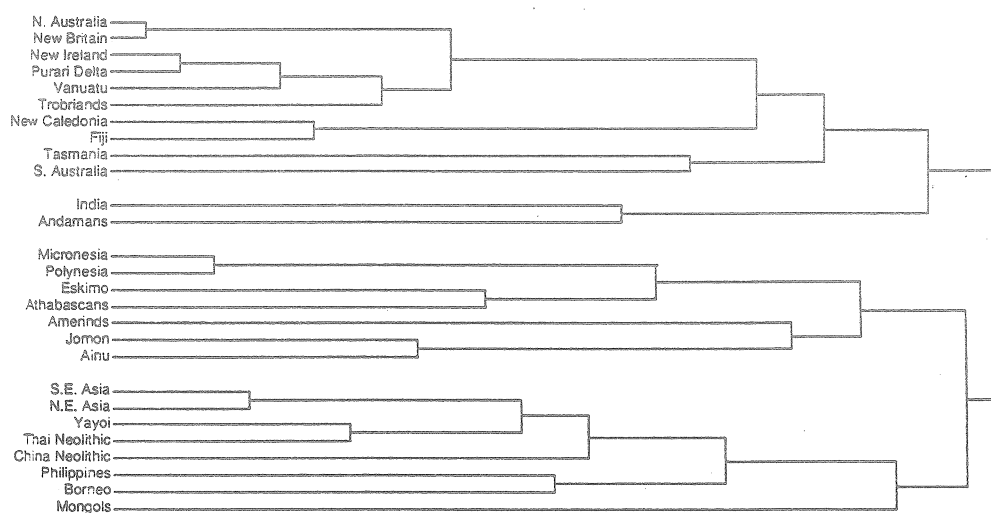


FIGURE 3: EUCLIDEAN DISTANCE DENDROGRAM SHOWING THE THREE MAIN CLUSTERS OF THE PACIFIC BASIN AND SOUTH ASIA AND THEIR CONSTITUENT COMPONENTS.

South Asia and the Andaman Islands form a separate cluster, and Amerinds, Eskimos and Athabascans are not divided into their constituents, falling instead into the Jomon-Pacific Cluster.



### The Mainland Asian Cluster

The members of this cluster that are not physically located on the Asian Mainland itself are the Japanese and Yayoi groups, and the Philippine, Borneo and Sumatra samples from Island Southeast Asia. The Yayoi are the rice agriculturalists who moved from Korea to southwestern Japan in the third century BC. Not only were they obviously from the Asian Mainland in the first place, but their morphological characteristics clearly ally them with the northern branch of the Mainland Asian cluster members - most specifically with the Chinese Neolithic and the modern coastal Chinese and Koreans.

The Island Southeast Asia samples fall into the southern branch of the Mainland Asia cluster when all the constituents of that cluster are run as separate twigs (Li *et al.* 1991), and they clearly represent the results of the southward movement of human populations made possible by the Neolithic subsistence techniques that spread via the Philippines on the one hand and Peninsular Southeast Asia on the other.

As for the modern Japanese themselves, there is little average difference between the various samples found throughout the archipelago. The samples we measured in Tohoku (the northeast), Tokyo (the center) and Kyushu (the southwest) all form a tight cluster when treated separately (Brace *et al.* 1989). For the purposes of the present demonstration we have lumped them all together as a single group. Although there are several hypotheses concerning the origin of the modern Japanese and what relationship, if any, they have to the pre-agricultural inhabitants of the islands, our own data ally them firmly with the peoples of the Asian mainland and only remotely with the prehistoric Jomon. As we have noted in detail elsewhere (Brace *et al.* 1989), this leads us to prefer the hypothesis that regards the Japanese as the direct and largely unmodified descendants of the Yayoi invaders of more than two thousand years ago. Not only do they exhibit morphological characteristics that ally them comfortably with the Mainland Asian cluster, but our data can be most easily accounted for by suggesting that the Japanese actually had their origins on the Asian mainland before the end of the Pleistocene.

As has already been mentioned, our data also show that, while the Mainland Asian cluster has an overall coherence, it is divided into northern and Southeast Asian components (Brace *et al.* 1989, 1990; Li *et al.* 1991). The southern component includes Vietnam, Thailand and Burma (Myanmar). The northern component here includes Hong Kong and western (Yunnan, Sichuan), eastern (Shanghai), and northern (Henan, Hebei) Chinese, Koreans and Japanese. The Neolithic of both China and Southeast Asia plus groups from Borneo and the Philippines tie with the Mainland Asian cluster at another remove, and the Mongols tie in as a remote last step. Since the Mongols are the most peripheral of the Mainland Asian groups, using them to typify the cluster as a whole as "Mongoloids" is misleading at best (Li *et al.* 1991). In addition, such usage tends to perpetuate the typological essentialism of the "racial anthropology" of yesteryear with all of its associated invidious baggage. The employment of geographic terms that can be expanded or contracted as needed can avoid many of these problems.

### The Jomon-Pacific Cluster

The bulk of the samples in this cluster comes from modern Polynesian and Micronesian groups, but it also includes the Jomon of Japan who date back to a time long before there were any people at all in Micronesia or Polynesia. Elsewhere we have noted that all of the various Jomon groups cluster together, whether from Hokkaido, Honshu or Kyushu and Early, Middle or Late Jomon (Brace *et al.* 1989). There are reductions in tooth size and general skeletal robustness that can be seen through time in the Jomon series, but the pattern of their morphological characteristics retains its identity. For purposes of the present analysis, then, we have lumped them together to form a single sample. Their modern descendants in Japan are clearly the Ainu of Hokkaido, but it is interesting to note that the people who lost their lives as a result of the destruction of the Kamakura Shogunate in AD 1333 also fit within this cluster. The identification of a major Ainu element in the Samurai class in Japan has been the focus of a separate treatment (Brace *et al.* 1989). Likewise the suggestion that the Jomon inhabitants of the Japan-Ryukyu archipelago were the most likely ancestors of the modern Micronesians and Polynesians has also been developed at greater length in a previous work (Brace *et al.* 1990).

As can be seen in Figure 3, when the Amerind and Eskimo-Siberian branches of Figure 2 are left as single entities to be compared with the partially separated representatives of the Jomon-Pacific, the Mainland Asian and the Australo-Melanesian clusters, they get forced into joining one of them - the Jomon-Pacific cluster as it happens. If we were to represent them by their many constituent samples, they become separated once again. As Figure 3 shows, however, when we represent them as single twigs they both become allied with the members of the Jomon-Pacific cluster - the Amerinds with its Polynesian and Micronesian constituents and the Eskimo-Siberians plus Athabascans with the Jomon and Ainu constituents. Parenthetically, the arrangement shown in Figure 3 lends some independent credence to Greenberg's suggestion concerning the ancient differences between the Amerind, Athabaskan and Eskimo linguistic families (Greenberg 1987a, 1987b).

Since the Jomon sample includes specimens that date from 7000 years ago this represents the oldest constituent of this cluster, which is why the term Jomon-Pacific was used in the first place. The Amerind tie provides equally convincing if less direct evidence for the considerable antiquity of the configuration under consideration. The samples used to produce the Amerind branch range from the coast of California, the Great Plains, the American Midwest, the mid-Atlantic coast, the Valley of Mexico, Peru and Tierra del Fuego, and they are all presumed to have descended from the first people to have crossed the Bering Strait in the Late Pleistocene 12,000 years ago or perhaps earlier (Brace *et al.* in press a). In any case, they provide support for the idea that identifiable aspects of what can be seen in the features of the Jomon, the surviving Ainu of Japan and in Remote Oceania are part of a coherent configuration that dates back more than 10,000 years.

It is not surprising that the Amerinds, Eskimos, and Remote Oceania eventually tie with the Mainland Asian cluster before any of the other major clusters of the world, and it is not surprising that the Amerind and Eskimo-Siberian groups show closer affinities with

the earliest known Holocene samples from the northeast edge of the Old World - namely the Jomon of Japan. What is somewhat surprising, perhaps, is that the Remote Oceanic groups also tie with the Jomon of Japan before they link up with the Mainland Asian cluster. This raises the possibility that serious consideration should be given to seeking the origins of the people of Remote Oceania in the Japan-Ryukyu archipelago rather than on the mainland of South China or Southeast Asia-Borneo. The general lack of the full amount of skin pigmentation associated with long-term residence in the tropics suggests descent from a population that had more than 50,000 years of association with a temperate latitude. The relative reduction in tooth size also suggests an origin in the northern part of the Old World since it was the particular food-preparation practices associated with survival in the north during the last glaciation that initiated the whole process of dental reduction (Brace, Smith and Hunt 1991).

Finally, the recent demonstration that the Ainu language has a substantial number of Austronesian cognates and that there may well have been an Austronesian substratum to Japanese (Murayama 1989) also suggests a more northerly presence and possible origin for that language family than has traditionally been recognized. Ainu, in fact, has been called a "very Old AN-language .... older than the AN-substratum of Japanese" (Murayama personal communication 1989). For all of these reasons, prehistoric Japan merits serious consideration as a possible source for both the biological and linguistic ancestors of the modern inhabitants of Remote Oceania.

#### The Australo-Melanesian Cluster

There is nothing new to the observation that, morphologically, the inhabitants of Melanesia, New Guinea and Australia have something in common. Their appearance as members of a single cluster *vis-à-vis* the other two major clusters in Figure 2 then is comfortably in line with the impressions of previous scholars (Sarasin 1924:224; Wagner 1937:144; Howells 1973b:48, 172; Allbrook 1976:216; Brace and Hinton 1981; Brace and Hunt 1990).

The terminal Pleistocene Kow Swamp skeletal material and the earlier Cossack dune site and Willandra Lakes specimens (Thorne and Wilson 1977; Freedman and Lofgren 1979; Thorne 1984; Habgood 1985) show that those traits we tend to think of as "Australoid" already existed in Australia well back into the Late Pleistocene. In addition, the appraisal of prehistoric skeletal material at Wajak in Java (Dubois 1890, 1922; Weidenreich 1945), Gua Kepah on the west coast of the Malay Peninsula (Huxley 1863; Mijsberg 1938) and at Niah Cave in Sarawak (Brothwell 1960) has given support to the idea that people who displayed the morphological characteristics now common in Melanesia, New Guinea and Australia once inhabited the Malay Peninsula and the adjacent islands of Borneo and Java at the very least.

Such a view is given further superficial reinforcement by the observation of attributes of the hair and skin of remnant hunters in the Philippines, the Malay Peninsula and the Andaman Islands (Pickering 1851; Haddon 1912; Wollaston 1912). With the large islands of the Bismarck Archipelago, New Guinea and Australia occupied by at least 40,000 years

ago (Pearce and Barbetti 1981; Groube *et al.* 1986), it is not at all unreasonable to suggest that the ancestors of the modern members of the Australo-Melanesian cluster occupied an area similar to the extent of the stippling shown in Figure 1. The arrows show the putative routes of expansion into territory that had been unoccupied prior to about 50,000 years ago.

Today, however, much of peninsular Southeast Asia, Indonesia and Borneo has little if any trace of surviving members of the Australo-Melanesian cluster. Instead, the predominant population belongs to the southern branch of the Mainland Asian cluster who presumably moved south after the development of agriculture and displaced and/or absorbed the hunter-gatherer (foraging) peoples who had lived there since the Pleistocene. In some instances, such as the Philippines and the Malay Peninsula, the foragers continued to exist as recognizable entities interspersed with the more recently arrived cultivators. The various interactions between these disparate groups has led to the somewhat complicated cultural mosaic now visible in Southeast Asia and the Philippines (Hutterer 1976).

#### Negritos

While many early observers were intrigued by the various possible implications of a presumably widespread pygmy "race" (Pickering 1851:175; T.H. Hurdey 1963:178, 1870:404-405; Radcliffe-Brown 1922:6), others have suggested that, in Oceania and possibly elsewhere, they were merely short-statured versions of their non-pygmyoid neighbors (Simmons 1973:23, 1976, 319; Howells 1977:180; Omoto 1984:146, 1985:128). We have attempted to apply our methods to the material available in order to test the various possibilities.

While we could not get measurements for the Semang of the Malay Peninsula, we were able to make them on usable samples of Philippine "negritos" and Andaman Islanders. When we ran these two Southeast Asian groups against samples of the eight major geographic clusters, the Philippine negritos tied in with the Mainland Asian cluster and most closely with the other Philippine samples in the southern component. This last point conforms to the conclusions reached by Omoto on the basis of his analysis of serological gene frequencies (Omoto 1984, 1985).

In a previous analysis (Brace and Hunt 1990), we were able to demonstrate that the Andaman Islanders tie in with the Australo-Melanesian cluster as a last step before that group as a whole joins in with the rest of the world. That, however, was before we had any usable samples from the Indian subcontinent - South Asia. After we were able to add a series of South Asian representatives, the Andaman Islanders tied in with them as a last step before the link connecting them collectively with the rest of the world. In Figure 3, that link ties South Asia with the Australo-Melanesian cluster, but, when representatives of all of the world are included, South Asia ties with Europe and the connection with Australo-Melanesia and the Andamans is completely removed. Evidently that last tie in Figure 3 is just something that the computer does because the Euclidean Distance

algorithm forces it to do so. A tie at that level, then, is mainly statistical artifact with no real anthropological implications.

Elsewhere (Li *et al.* 1991; Brace and Tracer *ms.*), the effort to deal with aspects of the proportions between craniofacial variables was successful in highlighting population distinctions that were not so clear when the C-scores were based on raw measurements. When nine of our variables were transformed into proportions of each other, we were able to eliminate the Amerind-European linkage evident in Figure 2. Just to see what would happen, we tried that approach in our comparison of the Andaman and Philippine negrito samples with the other major blocks represented. Specifically, we used transformations involving variables 6, 13, 16, 17, 18, 19, 21, 22 and 23. Six new variables were created by these transformations: 6/19, 13/21, 16/17, 16/18, 17/18, and 22/23. The nine untransformed variables were then eliminated from the battery to avoid redundancy. This left us with a total set of 21 variables.

When the transformed variables were rendered as C-scores and entered into the Euclidean Distance program, the Andaman and Philippine negritos display a closer tie with each other than with anyone else, followed by a joint tie with the Australo-Melanesian cluster. South Asia links with this grouping at a further step unless Europe is included in the analysis at which point those two tie loosely together and only link to the rest of the world at the last possible step. When the analysis is performed this way, the tie between the Andamans and South Asia almost completely disappears. If we leave Europe out of the picture as in Figure 4, the tie between the Andaman and Philippine negritos and the Australo-Melanesian cluster is clearly demonstrated. The later linkage with South Asia is remote enough so that it is little more than statistical artifact.

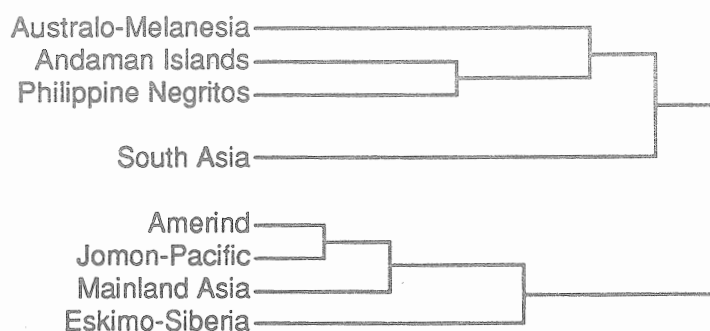


FIGURE 4: EUCLIDEAN DISTANCE DENDROGRAM CONSTRUCTED WITH THE USE OF TRANSFORMED VARIABLES

The original point in making the transformations was to highlight some of the nasofacial proportions that differentiate Europeans and Amerindians, but they also produced another result that was of particular importance in the comparison of our South Asian and Near Oceania populations. This was the elimination of sheer size as an important consideration. The transformations render all of the major cranial dimensions

as proportions rather than as raw measurements. This eliminates gross bulk which is normally such an important element in the multivariate assessment of group relationships, and, when size alone is discounted, the strength of the relationship between the Andaman and the South Asian groups shown in Figure 3 is greatly reduced. As it happens, much of our South Asian sample is made up of people who are at the bottom end of the spectrum of sheer human bulk, and at least some of the affinity between them and the Andaman sample shown in Figure 3 is contributed by the common manifestation of very small size. All of this lends a measure of credence to the old general anthropological expectation that the dark-skinned and curly-haired aborigines from the Andamans east through Peninsular and Island Southeast Asia to the "Negrito Islands" (T.H. Huxley 1870:404) of Melanesia represent something in the way of variations on a common theme.

Although it has been our experience that the Euclidean Distance program is quite successful at demonstrating major genetic relationships, we are aware that it is not quite so effective in handling instances of intermediate status. The algorithm demands that a case be put in one cluster or another. A true intermediate, then, may be placed in one particular cluster as opposed to another based only on the tiniest difference in percentage of common variance. In order to produce a less "either-or" assessment of the groups in question, we employed a discriminant function procedure that generates probability figures stating the likelihood that a given sample can be excluded from membership in the others with which it is compared. This procedure also has its limitations, and these are discussed in detail elsewhere (Brace and Tracer ms.). Briefly, it is quite effective in showing who is different from whom, but it is less successful in demonstrating necessary similarities.

Table 3 shows the significance levels of the distinction between the Philippine negritos and the Andaman Islanders from each other and from the eight major geographic clusters when the comparisons are made using both transformed and untransformed variables. It is vanishingly unlikely that either configuration could occur in an Eskimo-Siberian sample, and it is not much more likely that either could be found in Europe. The one cluster from which the Philippine negritos are least likely to be excluded is the Mainland Asian cluster ( $P=.772$ ). The Andaman Islanders, for their part, are unlikely to be distinguished from South Asians ( $P=.333$ ). When transformed variables are used, the Andaman Islanders are about equidistant between South Asians and Philippine negritos, although they are even less likely to be distinguished from the negritos ( $P=.329$ ) than from South Asians ( $P=.239$ ). When we compared the Andaman Islanders to the roster of possibilities shown in Table 3 but without including a specific comparison with the Philippine negritos, they fell almost equally between South Asians ( $P=.284$ ) and Australo-Melanesians ( $P=.246$ ).

It should be remembered that these  $P$  values do not indicate the likelihood of inclusion. The algorithm simply indicates the probability of exclusion when the groups against which comparisons are being made are considered to constitute the total universe of possibilities. Even though we included representatives of all the major populations of the world in running our tests, there is no necessity *a priori* that the samples being

compared must be encompassed by some or indeed any of them. Still, it is interesting to note that the Andaman Islanders are least likely to be excluded from either Philippine negritos or South Asians. Given their geographic placement about half way in between those two clusters, such a finding is not surprising.

Group Name	P Value for Exclusion			
	Philippine Negrito		Andaman Islands	
	Raw	Trans	Raw	Trans
Australo-Melanesia	.032	.035	.141	.077
Amerind	.052	.043	.151	.115
South Asia	.008	.004	.333	.239
Eskimo-Siberia	.001	.001	.001	.001
Europe	.001	.001	.018	.015
Jōmon-Pacific	.062	.093	.062	.092
Africa	.009	.012	.073	.037
Mainland Asia	.772	.739	.052	.093
Andaman	.063	.072	—	—
Negrito	—	—	.169	.329

TABLE 3: PROBABILITY LEVELS GENERATED BY DISCRIMINANT FUNCTION THAT THE PHILIPPINE NEGRITOS AND ANDAMAN ISLANDERS CAN BE DISTINGUISHED FROM THE GROUPS NAMED IN COLUMN ONE

The initial assessment of the Philippine negritos based on untransformed variables, however, was something of a surprise even though it is so clearly in agreement with Omoto's most recent genetic analysis (Omoto 1985). Negrito skin color and hair form suggest residence in the tropics for a far longer period of time than the post-Pleistocene span during which members of the Mainland Asian cluster have extended their range southward and eastward. That time span was not enough to produce such phenotypic responses in the tropics of the New World, and one has to suspect, therefore, that the Philippine negritos have a tropical ancestry that goes back many thousands of years before the entry of members of the Mainland Asian cluster into the tropics. This is what leads to the expectation that those negritos should show some kinship with the obvious descendants of the Pleistocene inhabitants of Near Oceania, namely the modern Australo-Melanesians.

When that expectation is fulfilled as it is in the results of the analysis based on transformed variables shown in Figure 4, the question then arises: why did Omoto's genetic analysis present such a different picture? The only thing we can suggest is that at

least some of the red cell enzymes, proteins and antigens that he tested are under strong selective force pressures. HB beta, for example, is famous for its variants related to the distribution and intensity of particular kinds of malaria (Livingstone 1989), and malaria is known to be a major health problem in the southwest Pacific (Black 1956). Simply because of the nature of the traits chosen for analysis, Omoto may have unwittingly produced a picture that emphasized the effects of selection rather than one of similarities due solely to kinship. Actually, when Omoto compared the Philippine negritos to a wider spectrum of human populations throughout the world in an earlier run, his results (1981: Figure 1) look remarkably like our Figure 4. Depending on the frame of reference used, the conclusions reached by Omoto and ourselves may not be that far apart.

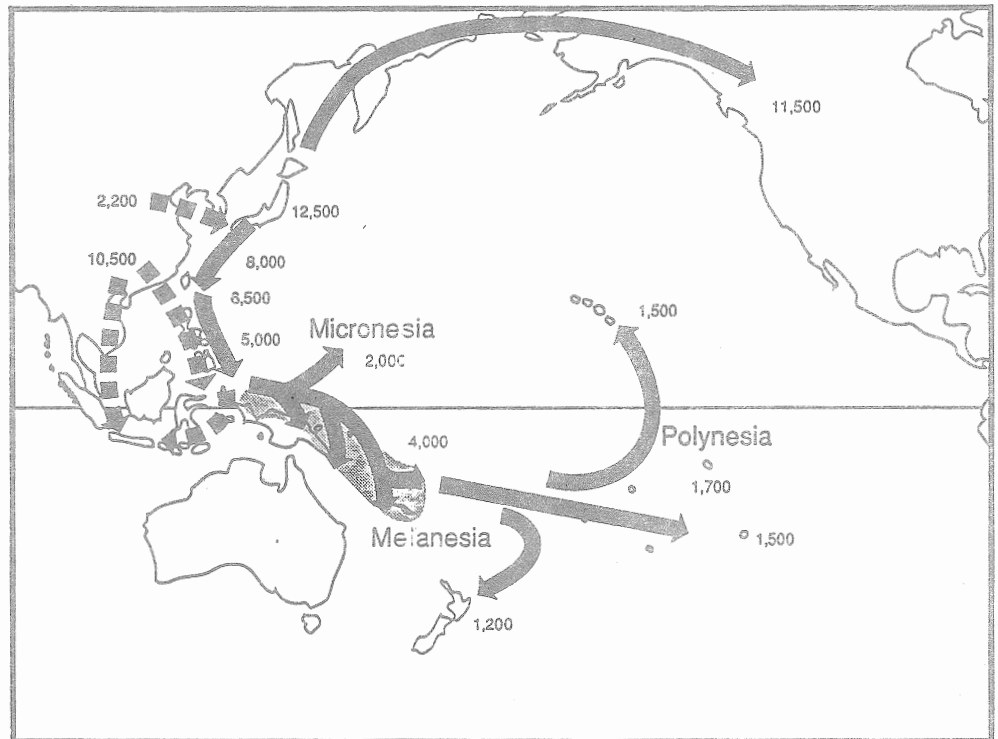
#### CONCLUSIONS

Contrary to the expectations of many (e.g. Turner 1987, 1990; Kirch and Green 1987), we can find no basis for deriving the inhabitants of the small islands in the Remote Pacific from Southeast Asia. The modern peoples of Southeast Asia tie in with the Mainland Asian cluster which is identifiable at least as far back as the Chinese Neolithic as much as 10,000 years ago (Meacham 1977; Li *et al.* 1991). The people of Island Southeast Asia - the Philippines, Borneo and Indonesia - clearly stem from the southern component of this Mainland Asian cluster, but just as clearly none of these provide credible models for the immediate ancestors of the peoples of Remote Oceania. In Japan, the Early Jomon - contemporaries of the Chinese Neolithic - already displayed the same constellation of features now demonstrable throughout Micronesia and Polynesia.

For these reasons also, we cannot see any basis for the attempt to derive the inhabitants of Remote Oceania by transformation out of anything now visible in the Bismarcks or in eastern Melanesia as is essayed by Terrell and others (Terrell and Fagan 1975; Houghton 1980; Allen 1984; Terrell 1986). In this regard, we agree with the conclusions recently expressed by Howells (1989:83) and Pietruszewsky (1990:88). Further, our data compel us to suggest that it was the Jomon people themselves who are the most likely ancestors for the more recent Micronesians and Polynesians. The geographic locus from which those expansions took place, then, would be the archipelago which includes Japan and the Ryukyus. This suggestion is illustrated by the solid arrows displayed in Figure 5. Obviously, this is more in line with the "fast train" model of Bellwood (1975, 1979; Spriggs 1989), although the immediate starting point for this particular movement cannot yet be shown to have been on the Asian mainland.

It is just possible that the techniques for successful exploitation of marine resources that sustained a substantial coastal population in Jomon Japan were the key to the successful occupation of the previously underutilized shores and islands of Oceania. This is supported by the similarity between early Hawaiian and Marquesan fish hooks and those of the Late Jomon in Japan (Reinman 1967:187). Fish hooks are present in the





**FIGURE 5: TERMINAL AND POST-PLEISTOCENE MOVEMENTS INTO AND AROUND THE PACIFIC BASIN.**

The solid arrows show the direction of movement of members of the Jomon-Pacific Cluster and their Amerind Relatives from the terminal Pleistocene northeast represented by earliest Jomon Japan at 12,500 BP (Ikawa-Smith 1982:27), moving northeast then south into the sub-Beringian western hemisphere at least by 11,500 BP (Haynes 1982:383), south to Okinawa by 8000 BP (Pearson 1977:1240), Taiwan by 6500 (Meacham 1988:97), the Philippines by 5000 (Bellwood 1985:107 ff., eastern Melanesia by 4000 (Shutler and Shutler 1975:66), the Marquesas by 1700 (Davidson 1981:22), Hawaii and Easter Island by 1500 (Tuggle 1979:189; Pawley and Green 1973:22) and New Zealand by 1200 BP (Davidson 1981:6). The broken arrows show the direction of movement by members of the Mainland Asian Cluster from the Neolithic of South China at 10,500 BP (Meacham 1977:423) and by the Yayoi into Japan by 2200 BP (Akazawa 1982:163).

Jomon as early as 9,500 BP at "one of the oldest sites where the use of marine resources is well documented" (Ikawa-Smith 1986:209) and indicate the development of the latter as a major subsistence strategy long before the people who later came to inhabit Remote Oceania had begun their move out into the Pacific.

At the moment, the puzzle is why the Filipinos show biological affinities with the Mainland Asia cluster but speak Austronesian languages. Obviously their ancestors had to have moved out from the Mainland either from South China or further down in Southeast Asia as we show in the broken arrows in Figure 5. The South China-Southeast Asian Neolithic provides a reasonable impetus for the forces generating such a movement. It is possible that the circumstances under which they adopted Austronesian from the Jomon-derived people who came in contact with them were similar to the circumstances that led to the spread of Austronesian in Melanesia.

The encounter with previously established Australo- Melanesian groups along the north shore of New Guinea and in the islands of Melanesia would have led to just the kind of biological and cultural mixing previously posited (Brace and Hinton 1981). A diagrammatic depiction of the path of movement of the incoming Jomon-Pacific people and the suggested area of intermixture is shown by the shading associated with the relevant solid arrow in Figure 5.

At the moment, we can see no other way to account for the fact that the Marquesans, the Hawaiians, the Easter Islanders and the Maori of New Zealand all cluster with the Ainu of Hokkaido, and, together, the aggregate clusters with Jomon skeletal material in Japan going back more than six or seven thousand years. With the Jomon cultural tradition in Japan going back another four or five thousand years in unbroken sequence (Ikawa-Smith 1986), there appears to be a compelling reason to take seriously the possibility that Jomon Japan was the source from which the Micronesians and the Polynesians were ultimately derived. Certainly, given the continuity of craniofacial configuration in each of the three main clusters for which we have evidence, the idea that either the southern branch of the Mainland Asian cluster or a Melanesian representative of the Australo-Melanesian cluster independently transformed itself into something that now falls into the same cluster as the Ainu and the earlier Jomon would have to be regarded as historically unlikely and biologically impossible.

#### ACKNOWLEDGMENTS

The research on which the results reported here were based was supported in part by the Horace H. Rackham School of Graduate Studies at the University of Michigan in 1983; The University of Michigan Museum of Anthropology Field Research Fund in 1984, 1985, 1986, 1988 and 1990; The Committee on Scholarly Communication with the People's Republic of China in 1985; by The LSB Leakey Foundation in 1986; by Diana Blaban Holt in 1987; the National Science Foundation, BNS-9616298, in 1987 and 1988; and by the generosity of the late E.B. Hoagland and the late G.W. and H.L. Brace. Essential assistance has also been provided by C.L. Brace V., M.L. Brace and R.C. Brace of Ann Arbor, Michigan; by G. Brace of Nanterre, France; J.K. Deetz, Berkeley, California; T.S.

Ellzey, Naperville, Illinois; B.R. Finney and W.G. Solheim II, Honolulu, Hawaii; M.A. Gordon and Chacma Inc., New York; M. and M. Harwit, Washington DC; F. Ikawa-Smith, Montreal, Canada; S. Murayama Tokyo, Japan; M. Nishimura, Ann Arbor, Michigan; and by P.D. Raspe, Cambridge, England. Access to the collections utilized has been previously acknowledged (Brace *et al.* 1989; Brace and Hunt 1990; Brace *et al.* 1990, in press a; Brace, Smith and Hunt 1991; Li *et al.* 1991). Finally, if it had not been for the pressure exerted by M.L. Brace, no invitation to participate in this conference would have been offered and this presentation never would have been prepared.

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