

Old World sources of the first New World human inhabitants: A comparative craniofacial view

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Human craniofacial data were used to assess the similarities and differences between recent and prehistoric Old World samples, and between these samples and a similar representation of samples from the New World. The data were analyzed by the neighbor-joining clustering procedure, assisted by bootstrapping and by canonical discriminant analysis score plots. The first entrants to the Western Hemisphere of maybe 15,000 years ago gave rise to the continuing native inhabitants south of the U.S.–Canadian border. These show no close association with any known mainland Asian population. Instead they show ties to the Ainu of Hokkaido and their Jomon predecessors in prehistoric Japan and to the Polynesians of remote Oceania. All of these also have ties to the Pleistocene and recent inhabitants of Europe and may represent an extension from a Late Pleistocene continuum of people across the northern fringe of the Old World. With roots in both the northwest and the northeast, these people can be described as Eurasian. The route of entry to the New World was at the northwestern edge. In contrast, the Inuit (Eskimo), the Aleut, and the Na-Dene speakers who had penetrated as far as the American Southwest within the last 1,000 years show more similarities to the mainland populations of East Asia. Although both the earlier and later arrivals in the New World show a mixture of traits characteristic of the northern edge of Old World occupation and the Chinese core of mainland Asia, the proportion of the latter is greater for the more recent entrants.

New World origins | craniometrics | prehistoric population relationships

The first Old World travelers to record their observations on the people they found living in the Western Hemisphere took it for granted that all humans ultimately descended from a single original pair as described in the Judaeo-Christian Bible. The exact location of that supposed initial Eden was not known, but it was generally assumed to have been somewhere in the Middle East of the Old World. Subsequently, thoughtful observers, such as Fray José de Acosta in the late sixteenth century and Thomas Jefferson in the eighteenth, realized that eastern Asia had to be considered the most probable immediate source when questions concerning the locus of New World human origins were raised (1). Some assumed that there was a link with wandering “Tartars” or the legendary “Ten Lost Tribes of Israel” (2), but, as faith waned in the Bible as a source of scientific information, the suggestion was proposed that human beings as well as the rest of animate nature were separately created in each of the geographic provinces of the world (3, 4). Charles Darwin then developed a non-Biblical explanation for the common origin for all living humans and made the case that the ultimate locus of human ancestry most probably was to be sought in Africa (5).

The fact that there is no skin color cline from the Arctic to the Equator in the native inhabitants of the New World indicates that occupation of the western hemisphere is of too shallow a time depth to have produced such an adaptive gradient. Skin

color, however, is so different from that found in sub-Saharan Africa that it clearly indicates long residence in the temperate rather than the tropical latitudes of the Old World. If the gradient in Australia is a product of some 60,000 years of occupation, then the picture north of the Equator had to have taken approximately three times as long *in situ* for selection to have produced the picture visible in the temperate zone (6). Genetic (7) and archaeological evidence (8) supports a northeast Asian source for the first human inhabitants of the Western Hemisphere. Some interpretations have suggested that the distribution of linguistically identifiable groups in the New World may have been the result of separate prehistoric population movements into the Western Hemisphere (9, 10).

From the sparse archaeological evidence and complementary molecular genetic data from living populations, an initial date of *ca.* 15,000 years can be postulated (11). Questions concerning the initial human settlement of the New World have involved such matters as the initial date of entry, route of access, whether there was a single or several dissimilar waves of people, and how these are genetically related both to living American Indian groups as well as to Asian and Pacific populations and possibly to other Old World peoples (12–14). Issues of geology, archaeology, and legal ownership are all involved (15–19).

Materials and Methods

Morphometric Comparisons. Recently these questions have been investigated by comparing patterns of the geographical distribution of human genetic and morphological features (20–26). Metric variables record inherited differences in cranial and facial form by documenting minor variations in the configuration of suture placement, length, and other details in the construction of the cranial vault and face. The various configurations of craniofacial form cluster regionally and are not distributed in clinal fashion related to the intensity of different selective force gradients. Furthermore, once established, configurations of facial form appear to remain relatively stable over considerable spans of time (27–29). Consequently, although details of facial form are distributed as regional groupings that may be viewed in the context of implied levels of biological relationship, these considerations must be made at a level well below that of the species. The human genotypic web is a subspecific, and therefore genetically open, system. None of the earlier human groups sampled in our data set, if they were all alive at the same time, would have been reproductively isolated in a fashion analogous to that of different species in a cladistic scheme. Because of this fact, the metrically indicated relationships depicted here, although of heu-

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Table 1. Craniofacial measures in the UMMA dataset (27)

Var. no.	Description
1	Nasal height
2	Nasal bone height
3	Piriform aperture height
4	Nasion prosthion length
5	Nasion basion
6	Basion prosthion
7	Superior nasal bone width
8	Simotic width
9	Inferior nasal bone width
10	Nasal breadth
11	Simotic subtense
12	Inferior simotic subtense
13	FOW (fronto-orbital width) subtense at nasion
14	MOW (mid-orbital width) subtense at rhinion
15	Bizygomatic breadth
16	Glabella opisthocranion
17	Maximum cranial breadth
18	Basion bregma
19	Basion rhinion
20	Width at 13 (fmt fmt)
21	Width at 14

ristic value in the examination of similarities and differences between groups of people across regions and through time, do not constitute a taxonomy in the strict sense of the term (30).

Here we integrate the results of the analysis of craniometric data showing the similarities and differences between prehistoric and recent samples representing the major regions of the Old World, the Pacific, and the New World. Our analysis is based on a set of 21 craniofacial measurements made of collections of human crania in the samples tested. These measurements are listed in Table 1. Preliminary studies (31–33) used C-scores and Euclidean distance clustering procedures to compare New World samples with a selected number of Old World groups. For the present analysis, we increased the number of Old World samples and added prehistoric material for comparison. The groups used, along with their sample sizes, are recorded in Table 2.

Table 2. Samples and *N*s used in the present analysis

Population	Female <i>N</i>	Male <i>N</i>	Total
Africa	52	54	106
Ainu	23	33	56
Athabaskan	27	21	166
Australia/Melanesia	74	92	166
China	139	166	305
Europe	152	190	342
Europe Upper Paleol	4	3	7
Inuit/Aleut	76	84	160
Jomon	6	3	9
Mongol	21	29	50
Mongolia Bronze	25	29	54
Neanderthal	2	2	4
Polynesia	75	64	139
Pueblo/Mexico/Peru	44	46	90
Somali/Nubia	15	38	53
South Asia	46	68	114
Southeast Asia	47	70	117
U.S.–Canada border	24	23	47
Upper Cave/Minato	0	3	3

After each bootstrap resampling of the original data (34–37), Mahalanobis distances were calculated for all pairs of the groups being compared. Then the neighbor-joining method of dendrogram building was used to display their similarities and differences (38). To quantify the relationships of the groups being compared, stepwise canonical discriminant function scores were calculated (39). To use data from the prehistoric samples where individuals with complete sets of measurements were hard to find, a multivariate procedure for imputing missing values was used (40).

Results

The resemblances and distinctions of samples representing the main geographic regions of the Old World are depicted in the neighbor-joining dendrogram displayed in Fig. 1. Also represented is the placement of the samples in relation to each other as determined by the first two discriminant functions. A composite of European Upper Paleolithic specimens from Czechoslovakia to France between 20 and 30 kya and a sampling of four European Neanderthals (from Gibraltar, France, and Italy) of ≈50 kya are also included.

Prehistoric and Recent Components of the Old World. The Neanderthal twig of the dendrogram (Fig. 1*A*) is separated from the others by a greater distance than that discernible between any other possible pair. On the other hand, no matter what samples are used, it always links to the European twig before any other. This link is confirmed by the plot based on the first two canonical discriminant function scores (Fig. 1*B*). Only when a third discriminant function (accounting for 9.6% of total variance) is used (or, alternatively, a third principal component) do Neanderthals separate noticeably from recent Europeans. The separation of the northeast Africans as well as the European and South Asian samples from sub-Saharan Africa is compatible with the picture of genetic attenuation when the core of the African continent is compared with its northeastern edge and to extra-African peoples (41). The tie between Africa and Australo-Melanesia also has parallels at the molecular genetic level, where an African degree of haplotype and microsatellite diversity has echoes in the southern part of South Asia and over into Melanesia and Australia (42–45). One explanation is that this haplotype dates back to the initial human spread from Africa across the tropics of the Old World. The morphological and genetic distinctions of populations at the northwestern and northeastern edges of the Old World would then be the result of the subsequent northward spread of peripheral extensions from the continuous tropical corpus of the Old World's main Paleolithic population concentration. Neither the genetic nor the morphological picture can give us any definitive estimate of the timing of that initial occupation of the tropics or the subsequent northward extensions.

The archaeological record, however, does provide some suggestions concerning population movements to the north. Such movements are crucial for establishing a temporal framework for the occupation of the northernmost edge of habitation in the Old World and for the extension of that occupation into the Western Hemisphere. The control of fire made occupation north of the tropics possible before the penultimate glaciation (46). At the western third of the temperate zone, a subsequent extension farther north was accompanied by the use of hafted projectile (Levallois) points—ultimately derived from the African Middle Stone Age with roots in the Acheulean more than 200,000 years ago (47). The subsequent distribution of the use of such tools eastward across the northern edge of human habitation to Mongolia and Siberia, but not to China and Japan or down toward Southeast Asia (8, 48), suggests an actual continuity between the makers, whether as the result of gene flow or an actual movement of people from the west.

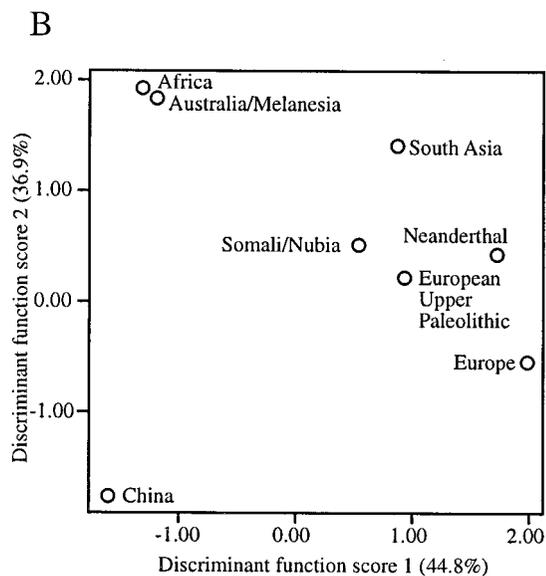
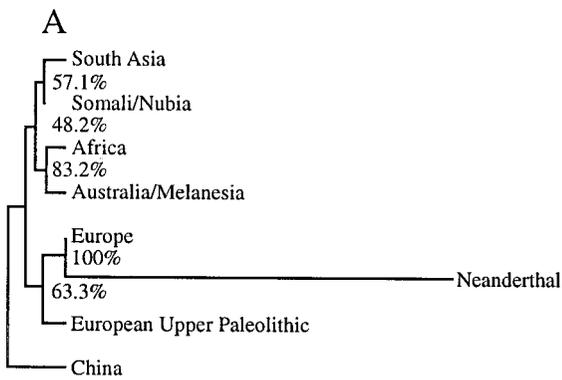


Fig. 1. A neighbor-joining dendrogram depicting the similarities and differences between major population groups in the Old World plus European Neanderthal and Upper Paleolithic samples (A). The sample sizes are shown in Table 2. The pattern was produced with the use of 1,000 bootstrap samples. The branch lengths of each line are based on Mahalanobis distances calculated from craniofacial metrics. The vertical distances between the lines are simply a matter of convenience and have no quantitative significance. The number at each juncture indicates the percentage of times per 1,000 runs that the tie in question occurred as indicated. However, the program does not calculate this number for the last node generated. The relative position of each sample is determined by the values of the first two canonical discriminant function scores (B) and is based on the Wilks' lambda statistic. The first discriminant function accounts for 45% of common variance, and the second accounts for 37%.

At that date—i.e., somewhat less than 200,000 years ago—it was Neanderthals who were making those tools at the western end of human occupation. If that picture of cultural continuity indicates an actual relationship, then it was Neanderthals who were also making those tools in Siberia, even though there is no unequivocal skeletal evidence to confirm their presence. The archaeological evidence shows that the Upper Paleolithic in Siberia arose by transformation from the preceding Mousterian *in situ* just under 40,000 years ago (49). Some have argued that the change in selective force pressure that accompanied the use of fire in processing food led to the reductions of tooth and jaw robustness that converted European Neanderthal into the early “modern” facial form at the northwest end of human habitation (50–51). In parallel fashion, the similar change in life ways shown

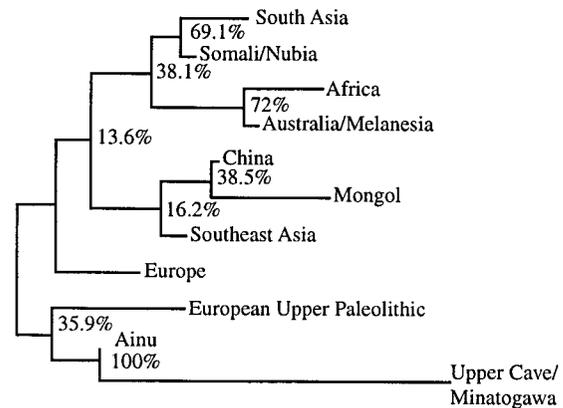


Fig. 2. A dendrogram showing the similarities and differences between the modern and European Upper Paleolithic groups compared in Fig. 1, to which are added a Late Pleistocene Asian (Upper Cave/Minatogawa) sample plus three more recent Asian samples. The neighbor-joining method was used on 1,000 bootstrap samplings to produce the pattern displayed. Only male specimens were used. The Neanderthal sample size was too small to include it in this analysis.

by the archaeological sequence at the northeast end of that continuum should have led to the transformation of a similar Neanderthal morphology into a related “modern” form for the same reasons.

Prehistoric and Recent Components of East Asia Compared with the Rest of the Old World. A brief test of such expectations is shown by the placement of the Late Pleistocene samples at both the western and the eastern ends of the Old World when they are compared with the regional representatives used in Fig. 1. To give a fuller representation of the living human form at the eastern edge of the Old World, Mongols from north central East Asia, Southeast Asians, and Ainus off the northeast edge of the continent were added to produce the pattern of resemblances and differences shown in Fig. 2. The Late Pleistocene sample from eastern Asia was made up of one individual from just under 30,000 years ago at the Upper Cave at Zhoukoudian just west of Beijing, China (27), and two individuals of just under 20,000 years ago at Minatogawa, Okinawa (52, 53). The sample is very small and consists of males only, so the groups used to construct Fig. 2 were restricted to males from each of the populations represented. The added Mongol and Southeast Asian samples cluster with the Chinese samples used in Fig. 1, but the East Asian Pleistocene and the Ainu samples cluster with the European Upper Paleolithic and latterly with modern Europe itself before showing any linkage with the rest of the world.

Comparison of Late Pleistocene and Recent Components of East Asia and the Northwestern Part of the Old World. Because the configurations represented in Africa, South Asia, and Australia/Melanesia are never linked with European, Asian, Oceanic, or New World samples, they were removed from the analyses when Oceanic and Western Hemisphere groups were being compared with the Old World. Fig. 3 shows the linkages and distinctions made when northern samples from Europe, Mongolia, China, and the Ainu of Japan are compared with Southeast Asia, Polynesia, and prehistoric groups in both Europe (Upper Paleolithic) and Japan (Jomon). The prehistoric Jomon and the Ainu of Japan are actually closer to the prehistoric and living European groups than to the core populations of continental Asia. The Polynesians of Oceania are close to being in between

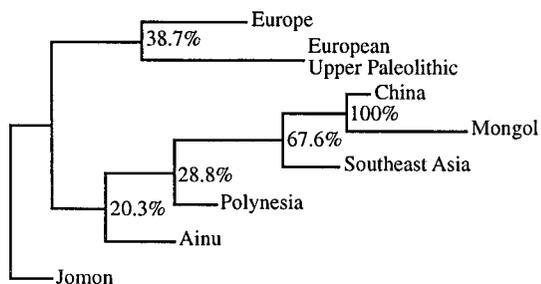


Fig. 3. A dendrogram of prehistoric and recent groups representing the northern edge of the Old World from Europe to Japan and ranging down to Southeast Asia and out into Oceania. The neighbor-joining method used 1,000 bootstrap samplings to produce the pattern displayed.

the European and Asian ends of the spectrum. Along with the Ainu and the Jomon, they could be described as Eurasian.

Comparison of Relevant Old World and New World Samples. When samples representing the original inhabitants of the Western Hemisphere plus a Mongolian Bronze Age sample are added to the roster used to construct Fig. 3, we get the picture displayed in Fig. 4. Sandwiched between Europe and the European Upper Paleolithic is the Bronze Age Mongolian sample and a group ranging along the U.S.–Canadian border from Montana/Alberta (Blackfoot) to northern Michigan (the Juntunen site) and Ontario (the Ossossone site). Next to link with this cluster is a group made up of samples ranging from the American Southwest down through Mexico and South America. Then Jomon, Ainu, and Polynesian samples are displayed as further steps away from that northern Old World/New World cluster, although they remain closer to it than to the mainland Asian cluster of China, Mongolia, and Southeast Asia. The final two groups in Fig. 4, Athabaskans from the Yukon drainage of Alaska and a combined Aleut–Inuit sample across the northern edge of the New World, tie more closely to the mainland Asian cluster than they do to any of the other samples tested.

Discussion

The fact that Late Pleistocene populations in northwest Europe and northeast Asia show morphological similarities suggests that there may have been actual genetic ties at one time. Those morphological similarities can still be shown between Europe and the descendants of the aboriginal population of the Japanese archipelago, i.e., the Ainu. This similarity provides some basis for the long-time claim that the Ainu represent an “Indo-European,” “Aryan,” or “Caucasoid” “type” or “race” (54, 55), however unfortunate those designations and their implications may be.

That there is no evidence that the Late Pleistocene occupants of the longer-inhabited western end of that human extent migrated eastward suggests that the genetic link may stem from a late Middle Pleistocene population spread across the northern edge of the Old World. Separate reductions of a common archaic level of robustness in the west and the east may account for the similarities in form of the living representatives at both ends of that range. When New World samples are added, those along the U.S.–Canadian border also tie in with that configuration, as does the Mongolian Bronze Age sample. An independent sign of that possible ancient continuity can be seen in the distribution of the X lineage of mitochondrial DNA that is present in low frequencies in Europe and across North America to the descendants of the pre-Columbian inhabitants of the Great Lakes area (56, 57). The distribution of Y chromosome haplotypes is also compatible (58).

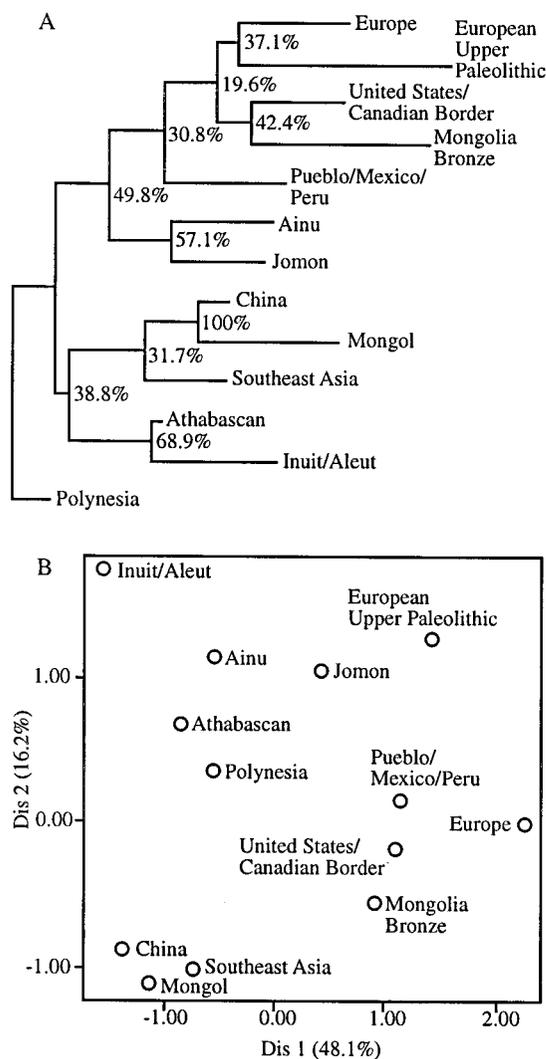


Fig. 4. A dendrogram based on the samples used to construct Fig. 3, plus a Bronze Age Mongolian group and four others from the Western Hemisphere. (A) The neighbor-joining method was used on 1,000 bootstrap samplings to generate the pattern displayed. (B) The relationships among the groups are also displayed by canonical discriminant function scores. The first discriminant function accounts for 48% of total variation, and the second accounts for 16%.

Fig. 4 supports the view that populations at the core of mainland East Asia (represented here by Mongolia, China, and Southeast Asia) only made partial contributions to the initial populating of the Western Hemisphere. It also suggests that the postagricultural expansion of that mainland East Asian population had an increasing impact on people at the northern and eastern edges of the continent as well as toward the south and out into the Pacific. The prehistoric Jomon of Japan, along with the living Ainu, still clearly resemble that northern stratum, although the latter are a bit closer to linking up with the mainland East Asian core. The same thing is true for the Polynesian samples, with the tie to the mainland Asian core being just slightly stronger than was true for the Ainu. The Inuits and the Na-Dene-speaking Athabaskans (the most recent groups to have left northeast Asia for the New World) show even more resemblance to the Chinese-related populations of mainland Asia.

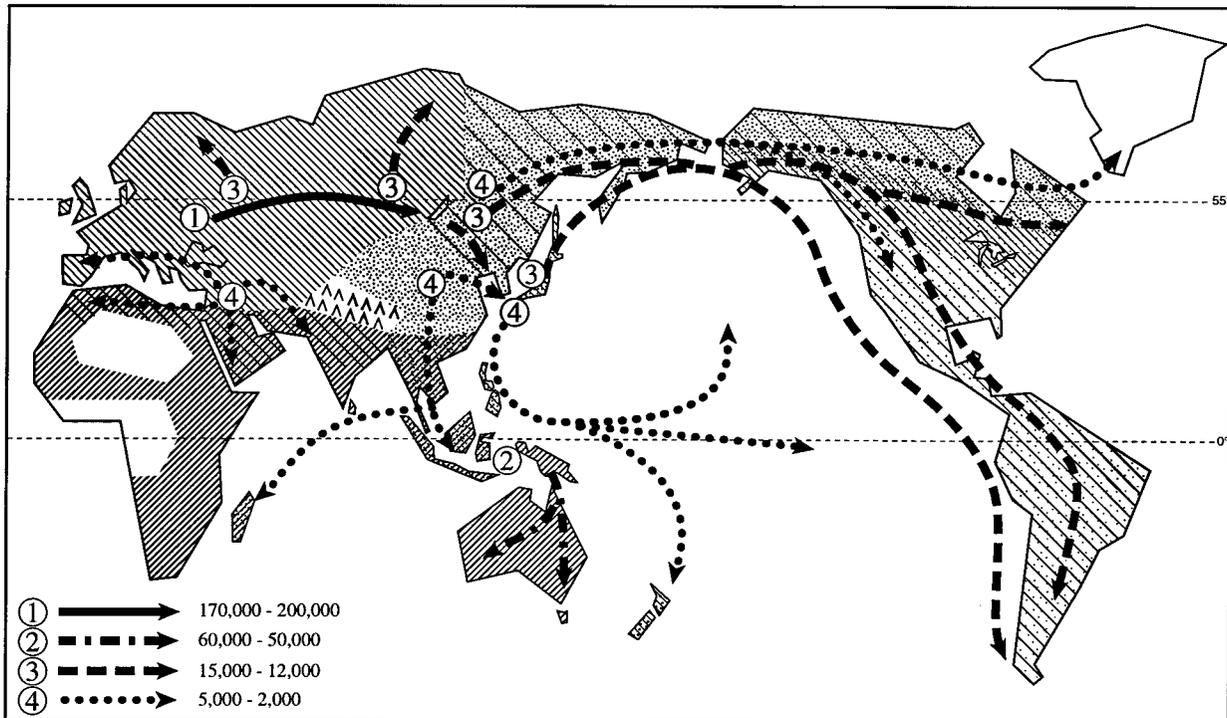


Fig. 5. The arrows indicate the spread of Levallois point makers eastward across the northern edge of the Old World between 200,000 and 170,000 years ago; the expansion from Southeast Asia to New Guinea and Australia 60,000 years ago; the spread to the northernmost portions of the Old World and the initial entry into the New World 15,000 years ago; and population movements at both the western and eastern edges of the Old World and into the New World after the development of agriculture after the end of the Pleistocene.

Conclusions

A combination of two different regional populations appears to have been involved in the initial human expansion into the Western Hemisphere. The regions in question were a mainland East Asian core located in China north of the Tropic of Capricorn and south of the Gobi Desert, and a northwestern component originally running from near Moscow to the Atlantic coast of Europe north of the Mediterranean Sea. The archaeological record indicates that both of these components had been separate in the Middle Pleistocene. The northwestern component expanded eastwards to exploit unoccupied terrain at the northern edge of Asia in the Middle Paleolithic *ca.* 200,000 years ago. The reduction in robustness that produced the “modern” form from an archaic version of *Homo sapiens* in the Late Pleistocene led to the emergence of people of similar appearance at the northwestern and northeastern edges of the Old World. Technological developments and climatic amelioration starting 17,000 years ago allowed the population segment across the northern edge of the inhabited Old World to extend north toward the previously uninhabited Arctic (8).

At the eastern end of this range, contact with the indigenous core population of mainland East Asia led to the incorporation of some of their genetic characteristics, making those who were first able to move across Beringia into the New World properly characterized as Eurasian. After the end of the Pleistocene, the development of agriculture led to a major expansion of the core population of mainland East Asia and its increasingly important contributions to the subsequent movements into the New World, Southeast Asia, and Oceania. A schematic representation of the placement of the original populations and their subsequent movements and combinations is depicted in Fig. 5.

The solid arrow labeled 1 represents the Middle Pleistocene movement across the northern edge of the Old World (49). The

arrow labeled 2 indicates the Late Pleistocene spread into Australia (59). Arrow 3 shows the terminal Pleistocene initial entrance into the New World (8, 11, 12), and the arrows labeled 4 show post-Pleistocene expansions made possible by the utilization of new food resources related in part to the development of agriculture (27). Arrows 1 and 2 represent single population expansions into unoccupied land. Arrow 3 represents movement into unoccupied land but by a population with both European and Asian roots. Arrow 4 represents a technology-based expansion of different populations into areas that, with the exception of Oceania, were already occupied. The consequence was a much greater rate of genetic exchange than had been true for any of the earlier movements.

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