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**Unanswered Questions and Misguided Answers:
An Overview of Current Problems with Late Pleistocene Contacts Between the
Old World and the New World, with the Sketch of an Alternative Paradigm**

How they got here is up in the air completely.
When they got here is up in the air completely.

Doug Owsley

Introduction

As reproduced in one of the latest issues of *Discover* (Wright, 1999: 63), the epigraphic lamentation of a National Museum of Natural History physical anthropologist was a direct response to the current crisis in the studies of the history of human presence in the Americas. The history of no other population has instigated such deep epistemological and social cleavages in the academia as the history of American Indians. Alternatively, since the discovery of the first Folsom points in 1926 and the first Clovis points six years thereafter, no significant advance in our understanding of the origins of Native Americans, the timing of their appearance in the New World, their early morphological characteristics or the size of the founding population has been accomplished. Whilst the academic fights are hot, the American prehistoric “questionnaire” remains blank.

Archaeologists are markedly divided into three groups: a conservative majority sticking to the 14,000-12,000-year-limit of human occupation of the Americas; a staunch minority voting for the dates up to 40,000 years; and a small group of romantic outliers that are ready to see human touch in geological facts dating back to 100,000-250,000 years (see overviews and discussions in Meltzer, 1995; Crawford, 1998: 16ff; Dillehay et al. 1992; Dillehay and Meltzer, 1991a).

Genetic laboratories make their own contribution to the reigning confusion. Some scholars (Wallace et al. 1985; Schurr et al. 1990; Torroni et al. 1992; also Novick et al. 1998) opine for a “severe bottleneck”, “dramatic founder effect” and multiple migrations into the New World, while the majority of others (Chakraborty and Weiss, 1991; Ward et al. 1991; Merriwether et al. 1995; Merriwether and Ferrell, 1996; Horai et al. 1993; Bailliet et al. 1994; Cann, 1994) demonstrate mutation drift equilibrium, lack of a populational bottleneck and a single migration. The existence of these equally influential but apparently mutually exclusive paradigms has led some researchers to doubt any possibility to resolve the contradiction by means of currently available genetic methods and on the materials of currently existing Amerindian populations (Bailliet et al. 1994: 32)¹.

¹ A similar skeptic note sounds in an earlier statement by Douglas Futuyama that “the genetic structure of North American Indian populations was altered forever when they were slaughtered and moved onto the reservations by whites” (Futuyama, 1986: 524).

Finally, the classification of American Indian languages remains a vexing puzzle after the vast majority of linguists (Campbell, 1997; Goddard, 1996; Heath, 1998: 143; also Morell, 1990) have dismissed the prodigious lumping effort of Joseph Greenberg (Greenberg, 1987). Chronologically Greenberg correlated his hypothesis with the Clovis bottomline of 11,500 BP and received support from some genetic and dental interpretations (Greenberg et al. 1986), while his opponents estimate the linguistic diversity between those American Indian languages that does not fall into the uncontroversial Na-Dene family as going back to 35,000-50,000 years (Nichols, 1990) and reject any correlations between genes and languages (Campbell, 1986). Alternatively the Greenbergians meet Nichols' historico-typological approach to linguistic diversity (Nichols, 1992) with equally harsh criticism (Ruhlen, 1994b).

Concerning the possibility of building a solid interdisciplinary fundament for the study of the origins of native Americans, Greenberg expressed himself pessimistically,

“Every time, it [mtDNA] seems to come to a different conclusion. I've just tended to set aside the mtDNA evidence. I'll wait until they get their act together” (quoted in Gibbons, 1996: 33).

For their own part, more and more geneticists seem to “get their act together” in rejecting Greenberg's three-wave hypothesis (Merriwether et al. 1995; Kolman et al. 1996; Forster et al. 1996; Karafet et al. 1997; Stone and Stoneking, 1998; Novick et al. 1998: 25).

The impasse that presently characterizes the prehistory of the Americas mirrors another controversial situation, namely the debate around the evolution of the human species. Two major theories here hold sway - the “Garden of Eden” or Out-of-Africa Model and the Multiregional Model.

“The debate has persisted and shows no sign of resolution despite the incorporation of new data and dates during the past decade” (Smith and Harrold, 1997: 113).

From the point of view of cranial and dental morphology, both sides seem to have successfully demonstrated to each other that neither Asian *Homo erectus*, European Neanderthals, nor African and Near Eastern “archaic” *Homo sapiens* bear any specific affinity to the moderns living in their respective regions (see, Howells, 1989: 83; Lahr, 1996a, with a refutation of multiregional associations and an excellent overview of the debate; also Lahr and Wright, 1996; Howells, 1996: XIII-XIV, with doubts concerning Lahr's African model; Corruccini, 1992, and Churchill et al. 1996, with particular anti-“Out-of-Africa” case studies; Scott and Turner II, 1997: 302, with a statement on modern African non-distinctiveness; Turner, 1992: 431, with a statement on the secondary evolutionary position of African dentition).

Genetic studies have so far failed to give sufficient support to either of the theories. The pioneering attempt of Cavalli-Sforza's team to read the global human history from DNA frequencies distributions (Cavalli-Sforza et. al. 1988; Cavalli-Sforza and Cavalli-Sforza, 1995) initially seemed to confirm the origins of modern humans from a single African population and the belief in the colonization of the Americas from Northeast Asia. Subsequently, however, it turned out that the microsatellite polymorphisms of the African populations used by Cavalli-Sforza as the chief indication of the greatest human antiquity in Africa is more likely to have been determined by other factors (greater population size and/or less severe bottleneck

than in other groups, accelerated mutation rates, selection etc.) (Aoki and Shida, 1993; Rogers and Jorde, 1995: 23-24; Harding et al. 1997: 772).

The situation appears even more convoluted since *no pre-sapiens* lineages have been detected in the modern human genetic pool (Manderscheid and Rogers, 1996: 2; Richards et al. 1996: 185). Some geneticists (Stoneking et al. 1992, with reference to Maddison et al's work) have argued that the chimpanzee control region is too distantly related to the human species to provide meaningful phylogenetic information. Moreover, despite their greater population size, modern humans are remarkably less diverse genetically than the great apes (Rogers and Jorde, 1995: 21).

In linguistics, the arguments in favor of a single proto-human language evolving in Africa around 50,000 years BP (Ruhlen, 1994a) confront with considerable criticism (Hock and Joseph, 1996: 484ff; Szulmajster-Celnikier, 1998) both on general methodological grounds and because the proponents of the "Proto-World" hypothesis have failed to demonstrate any specific relationship between the global cognates and living African languages as well as any specific importance of the typological features of the African languages for the evolution of non-African linguistic characteristics.

Frustrating as it may appear now, the overall picture contains multiple grains of a thorough consensus. Informed by the crossfire of the current debate, a future theory of human prehistory will necessarily assume the common origin of all living humans, will be sensitive to the specificities of regional evolution, will not be constrained by the imperative to derive human forms from apriori assumed non-human (not-fully-human) ancestors and will be increasingly more oriented on the integration of various branches of relevant knowledge into a functionally coherent interdisciplinary paradigm. The first step towards such a paradigm seems to be the emancipation of the Americas from the label of an "Asia-derived" cultural and genetic isolate and their inclusion in the orbit of potential homelands of modern humans. As Meltzer and Dillehay have rightly emphasized, instead of trying to prove or disprove early dates of human presence in the Americas,

"it is more profitable to discuss the ways in which we approach and attempt to resolve this problem" (Meltzer and Dillehay, 1991: 3).

The Return of the Americas

It is worth pointing out that the irrelevance of the Americas for the debate about the origins of humans and the location of their homeland was not established in the course of an intensive scientific scrutiny but rather retained as a cultural axiom from the pre-scientific period of Euro-American history. Pondering on the origins and destiny of the inhabitants of a newly discovered continent, Europeans have entertained two principal possibilities.

The chronologically earliest one was that American Indians represent the descendants of the Ten Lost Tribes of Israel, which fled Palestine as a result of the Babylonian invasion. Purported cultural similarities between Indians and ancient Jews were used as a chief historical argument. For instance, a XVII century explorer in North America, Father Lewis Hennepin, was quick to notice that both groups lived in tents, anointed themselves with oil, were "addicted to divination from dreams", bewailed the dead "with great lamentation", that women among the Jews and Indians mourned the dead a whole year by abstaining from dancing and feasting and wearing a hood and that the father or brother of the deceased took care of the widow (Hennepin, 1699. Vol. 1: 54).

A century later, after Captian Cook and Vitus Bering have independently discovered the narrow strait that separates Asia from North America, the myth of the shipwrecked Jews was replaced by the myth of Siberian hunters in search of wild game discovering a terrestrial passage to America. In 1797, a land commissioner, Gilbert Imlay (Imlay, 1969: 365-366), stated that, on the basis of “familiarity, or rather identity, of the persons and manners of the Americans and those of the Tartars of the north-eastern parts of Asia”, “the more reflecting part of mankind” was inclined to think that Indians peopled America from Northeast Asia. Imlay then continued with a statement that was destined to become the cornerstone of the anthropological and folk conceptions about Amerindian prehistory.

“We may now therefore conclude that no further inquiry will ever be made into the general origin of the American tribes”².

The latest summary of our multidisciplinary knowledge about the origins of Native Americans begins with a statement that clearly illustrates that no significant change or advancement has taken place here in the past 200 years.

“Since the initial European contact with the native peoples of the New World, a considerable body of scientific evidence has been compiled about the origins of those populations. *This evidence indicates extremely strong biological and cultural affinities between New World and Asian populations and leaves no doubt that the first migrants into the Americas were Asians, possibly from Siberia*” (Crawford, 1998: 3-4, italics added).

The world famous geneticist shares with his less savvy precursors the same trivial logical mistake: whatever biological or cultural similarities may exist between American Indians, on the one hand, and Siberians, Jews or whoever else, on the other, they do not automatically prove who derives from whom. *Similarities aside, not a single piece of causal evidence has ever been presented in favor of either the Ten Lost Tribes of Israel drama or the One/Two/ Three/Four Lost Tribes of Siberia action.* The scientific value of these ideas therefore is equal in the sense that they both are precious stones of collective imagination and myth-making and masterly parodies on scientific scrutiny³.

² Thomas Jefferson was among those few who, at the end of the XVIII century, was committed to a much more cautious view concerning the origin of Native Americans. As he wrote, “The question whether the Indians of America emigrated from another continent is still undecided” (Jefferson, 1905. Vol. 11: 79). He believed that the only means of determining the “filiation and descent” of Indians was by “knowledge and comparative view of their languages” (Jefferson, 1905. Vol. 11: 79, Vol. 9: 161, Vol. 6: 231). Having noticed the extreme diversity of North American Indian languages, Jefferson concluded that “a great number of those radical changes of language [that result not just in dialectal variation but in divergence in distinct languages – G. D.] having taken place among the red men of America proves them of greater antiquity than those of Asia” (Jefferson, 1905. Vol. 2: 141).

³ The essential equivalence of these two “theories” becomes even more remarkable in view of the latest discovery of X haplogroup in Native Americans that links them directly to Caucasoids (Brown et al. 1998). While this marker is not found in Asians or Africans, it is carried by several Caucasoid groups among whom are the Israeli Druze. Brown et al. hypothesize that X haplogroup was brought to America by a Caucasian population from the Near East. In the mid-XIX century, William Warren, a historian descended from an Englishman and an Ojibwa woman and having a native knowledge of the tribal lore, argued that the Sioux tribe - the Ojibwa’s traditional enemies - was a “portion of a tribe of the roving sons of Tartary, whom they

Symptomatically, American Indians themselves have persistently distrusted the European theories deriving them from Old World populations and throughout the contact history insisted on their origins in the Americas. Initially Indians rejected Hennepin's "Jewish hypothesis" (Hennepin, 1699: 51). Subsequently, when, in the winter of 1798-1799, a French explorer and future member of *La Société des Observateurs de L'Homme*, Constantin-François de Chasseboef, Count Volney, spread a world map in front of the Miami chief, Little Turtle, and explained to him the Bering Strait theory, he received a sensible retort:

"Pourquoi ces Tartares, qui nous ressemblent, ne seraient-ils pas venus d'Amerique? y a-t-il de preuves du contraire? ou bien pourquoi ne serions-nous pas nés chacun chez nous?" (Why those Tartars, who resemble us, could not come from America? Is there any evidence to the contrary? And also why could not we all have been born here?) (Volney, 1852: 712).

This Indian recalcitrance has survived until now as exemplified by the vociferous criticism of the Bering Strait theory recently exerted by the leading Native American scholar, Vine Deloria (Deloria, 1995). Indian political activists Russell Means and Ward Churchill (Means and Churchill, 1993) reviewed the current status of archaeological and genetic knowledge about the origins of Native Americans and concluded that "the footprints were going in the other direction", i.e. that people were moving from America into Asia and not vice versa. The same attitude is seen in the inclusion of the Bering Strait theory into a list of racial stereotypes that envelope Native Americans (Riding In, 1992; Echo-Hawk, 1994; Mihesuah, 1996: 46-47; Means and Churchill, 1993: 1; Vizenor and Lee, 1999: 128) and in the continuous reliance of Native Americans on tribal oral traditions portraying their autochthonous origins in the Western Hemisphere (Zimmerman, 1995; Bullchild, 1998; Means and Churchill, 1993: 3)⁴.

The gulf that separates academic (re)constructions of Native American prehistory, on the one hand, and ideas about time, authenticity and epistemological values coming from Native Americans themselves, on the other, constitutes one of the serious problems posed by processual archaeology (Layton, 1989; Anyon, 1991; Zimmerman, 1995; Ferguson, 1996; Watkins, 1998). Statements like the following

resemble in many essential respects", while the Algonquins formed a "portion of the ten lost tribes of Israel, whom they also resemble in many important particulars" (Warren, 1885: 61-62). These "particulars" included belief in dreams, the "veneration of the unseen God", the customs of fasting and sacrifice, "the never-failing separation of the female during the first period of menstruation", etc. (Warren, 1885: 65). His theory, Warren thought, would account for the great diversity of American Indian tongues. According to Brown et al., X haplogroup encompasses 25% of the Ojibwa, which is the highest percentage both in America and in the Old World. The Sioux, to be true, also contain this haplogroup but at lower frequencies of 15%. The coincidence nevertheless is striking: it can serve as a quirky advertisement both for Cavalli-Sforza's, Greenberg's, Ruhlen's and others' contention that genes and languages are connected and for William Durham's theory of gene-culture coevolution (Durham, 1991).

⁴ Native American rejection of the Bering Strait theory may take an utterly humorous turn. As barely literate Lakota holy man and Catholic catechist, Black Elk, said in 1944, "The Indian, if we came from Asia, we should have iron, because Christ was nailed on the cross with iron nails. I just cannot believe we came from Asia" (DeMallie, 1984, 318). Black Elk was wise enough to acknowledge that the Lakota did not know where people originally came from, and his willingness to question an idea that does not make sense because it is affirmed without sufficient evidence contrasts sharply with scientists' firm belief that they know how Indians arrived to America.

“Clearly, humans did not evolve in this hemisphere. Indians haven’t always been here, regardless of what their origin myths might say” (Clark, 1998: 24)

throw knowledge back into the times of arrogant Christian dogmatism.

At the beginning of the XX century, after the completion of the Jesup North Pacific Expedition work among the aborigines of Alaska, Northwest Coast and Northeast Asia, it was considered well-established that the physical and cultural similarities between the so-called Paleo-Siberian groups (Nivkhi, Yukagir, Chukchi, Itel'men and Koryak) and Native American populations from Alaska, Northwest Coast and British Columbia had to be interpreted as evidence for a reverse migration from America into Northeast Asia. Lev Sternberg (Sternberg, 1906), Waldemar Johelson (Johelson, 1905: 138-140) and later Alexander Chamberlain (Chamberlain, 1912a: 56-57) noted the morphological specificity of the Paleo-Siberian languages with respect to other Siberian dialects and argued for their classification as “Americanoid”. Franz Boas was the one who organized the multiple observations of the participants in the expedition into a general hypothesis.

“A consideration of the distribution, and the characteristics of languages and human types in America and Siberia, have led me formulate the theory that the so-called Palae-Asiatic tribes of Siberia must be considered as an offshoot of the American race, which may have migrated back to the Old World after the retreat of the Arctic glaciers” (Boas, 1910: 534; also Boas, 1905: 98-99).

This hypothesis soon acquired a wide currency as the following summaries of Chamberlain illustrate,

“Like the modern Asiatic Eskimos, they [the Paleo-Siberian groups – G. D.] represent a reflux from America to Asia and not *vice versa*. In brief, these peoples may be said to be “modified Americans” “ (Chamberlain, 1912a: 55-56, italics in original).

“The American Indians may thus be considered as an Asiatic people (sprung from the proto-Mongolian stock), considerably modified by their New World environment. By a refluent wave of migration they have “Americanized”, as it were, a large section of northeastern Asia” (Chamberlain, 1912b: 168).

Roland Dixon (Dixon, 1912: 59) arrived at the same conclusion by drawing comparisons between North American and Siberian mythologies:

“This Asiatic relationship must not, however, be regarded as furnishing evidence relating to the origin of the American Indian. It indicates a cultural relationship only, and far from pointing to an Asiatic source for the culture even, the bulk of the evidence would favor the theory that the similarity shown in the mythologies is the result of influences passing from America to Asia, and not in the reverse direction”.

The Jesupians have demonstrated sufficiently well that similarities between Northeast Asians and Native Americans can be interpreted in a reverse manner. However none of the turn of the century’s anthropologists questioned the initial premise that humans originated in the Old World and that the earliest populational movement across Bering Strait went from Siberia into the Americas.

To the best of my knowledge, nobody has ever made an effort to refute the “re-emigration” theory of the Jesupians, so one has to admit that it has simply fallen into

oblivion. Recently, however, this perspective has been revisited (Ousley, 1995) and gained support from mitochondrial genetic (Merriwether et al. 1995: 424; Hicks, 1995; Hicks, 1998), nuclear genetic (Karafet et al. 1997) and kinship studies (Dziebel, 1997b). Dixon's conclusion about American origins of Asiatic mythological motifs appears to be valid not only for Northeast Siberia but at least for a vast territory occupied by Finno-Ugrian and Altaic groups. Drawing on Terrence Turner's conception of diachronic structure of a myth (Turner, 1985), it proved to be possible (Dziebel, 1997a: Ch. 3) to derive major Old World creation and heroic motifs (Creation from an Egg, Earth-Diver and others) from a single prototype represented by the Bird-Nester motif. The latter is widely distributed in North and South America (Lévi-Strauss, 1964; Lévi-Strauss, 1971) and goes back to the earliest times of human presence on the American continent (Lévi-Strauss, 1971: 542-543). In the Old World, it is found in a fully "Americanoid" form only among the Kets in southwestern Siberia (Ivanov, 1982), whose linguistic relationship to Na-Dene has recently been demonstrated (Ruhlen, 1998), and in a slightly modified version among the Altai and the Tofalar in southern Siberia. Taking into account that myths might rather richly encode actual social relations in a group (Turner, 1985), their role as a source of information about deep human history should not be underestimated.

One more study is worth mentioning herein. Fifteen years ago, Jeffrey Goodman (Goodman, 1981) called attention to a group of skeletal finds in western North America dated 50,000-70,000 BP by amino acid racemization technique and argued that humans must have had originated in America and that Cro-Magnon man represents the early migrants into the Old World. This idea received sympathetic responses from some cultural anthropologists (Fogelson, 1987) and Native American activists (William Means, an Oglala coordinator of the International Indian Treaty Council, as quoted in Zimmerman, 1995: 28) but turned out to have been grounded in hopelessly wrong archaeological dates (Turner, 1982; Bada, 1985). Goodman himself was quick to mitigate his idea by allowing humans to appear in any part of the world as a result of a non-biological intervention into the lineage of *Homo erectus* (Goodman, 1983).

Despite individual errors of interpretation, the increasing number of scholars is willing to hypothesize the influence of the New World human evolution on the Old World human evolution. This approach has its own history and, in view of the current boom in the evolutionary approach to genetic, craniological, dental and other data, it is worthwhile exploring it here at a greater length.

Phenetic Evidence for Human Evolution

Craniology

With the revival of the interest in the evolutionary aspects of physical morphology some two decades ago, researchers have built up a consistent framework of relationships between modern human populations and recent human skeletal remains. The first generalizing study appeared in 1989 and was devoted to the worldwide examination of skull shapes (Howells, 1989). Howells arrived at several important, although unexpected conclusions:

"No support for lineages deriving separately from the stage of *Homo erectus*
 No support for a special eastern common ancestry for East Asiatics and Australians
 No support for a sub-Saharan first source for anatomical moderns, i.e., *Homo sapiens sapiens*" (Howells, 1989: 83).

Howells was positive about the lack of significant intraregional variation and evolutionary specificity among Africans (Howells, 1989: 71) and the morphological uniformity of living humans with respect to Neanderthals and “archaic” *sapiens* exemplified by the 80,000-100,000 year-old Border Cave skull (Howells, 1989: 65). He noted a boundary that sets apart Mongoloids, American Indians and Polynesians from Caucasoids and Africans (Howells, 1989: 77), high intraregional heterogeneity and specificity of American Indians (identified by some markers as joining Caucasoids (Howells, 1989: 79, 65)) and Polynesians (Howells, 1989: 83).

Marta Lahr characterized by Christy Turner (Turner, 1992: 431), as the “worker...who will do the best job of integrating the widest range of relevant information”, postulated a coherent functional complex constituted by the features of size, shape and robusticity of the cranium (Lahr, 1996a: 257-258). She formulated two conditions that have to be met in order to identify the ancestral human population: the ancestral population should be cranially undifferentiated with respect to living populations and it should include within its range of variation certain “archaic” features, like large dentitions, large size and cranial tori and ridges (Lahr, 1996a: 224).

The former condition is ambiguous since a skull “undifferentiated” with respect to living populations may belong a population *not genetically connected* to modern groups. Lahr’s formulation should be qualified to the effect that a prehistoric population genetically linked to living humans must be craniologically hyperdifferentiated, i.e. must display a higher degree of diversity with respect to modern populations, with recognizable morphological and metrical references to particular modern craniological types.

Then, if the condition of robusticity and large size is unquestionable, that of large dentition looks unconvincing. There are historically well attested cases of increasing tooth size as was observed in prehistoric Peruvian skeletal materials from 10,000 BP to 1,000 BP (Scott, 1979).

The general evolutionary tendency observed from the late Pleistocene onward is cranial gracialization systemically linked to size reduction and varying dimensional changes in different populations (Lahr, 1996a: 260). Cranio-dental dimensions, Lahr argued (Lahr, 1996a: 263), have a strong genetic basis and constitute therefore a valid source of information about human origin and dispersion. Gracialization is a process that affected most strongly Sub-Saharan African crania (Lahr, 1996a: 283) placing them therefore not at the source but at the end of the craniological scale of evolution. Howells (Howells, 1989: 13) noted that Khoisan skulls are very small, which also excludes them from evolutionary primary morphological types. To a lesser degree, gracialization affected Caucasoid crania (Lahr, 1989: 253, 263). Australian skulls demonstrate a remarkable case of local evolution favoring reduction in breadth and length but the maintenance of upper facial breadth and an increase in palatal breadth. They also seem to have retained to a large degree the features of robusticity (Lahr, 1996a: 257; Lahr and Wright, 1996: 157) and developed large dentition.

A paradoxical relation to modern human skull variation was observed among prehistoric Native Americans, although Lahr’s sample here was poor. Late Pleistocene and early Holocene skulls from Tepexpán (Mexico) and Lagoa Santa (Brazil) met important criteria for the ancestral human cranial morphology, namely large size and robusticity marked by the presence of tori and ridges at high frequencies. The retention of this archaic pattern among recent populations from around the world was recorded only in the Patagonians and Fueguians (Ona, Tehuelche and others) (Lahr, 1996a: 114, 142, 145-146, 222). The specificity of the last group is estimated as so

great as to make differences between other regional world populations “statistically insignificant” (Lahr, 1996a: 215-216). Alternatively the American specimens display close affinities with late Pleistocene/early Holocene skulls from Northern Africa and Palestine (Taforalt, Afalou, Natufian) (Lahr, 1996a: 208, 220, 232-237, with multivariate clustering figures) in terms of size and robusticity as well as with Australian skulls in terms of robusticity. Neves and Pucciarelli (Neves and Pucciarelli, 1989; Neves and Pucciarelli, 1991; Pucciarelli, 1998) have sufficiently demonstrated the startling relationship between South American and Australian (South Pacific) crania and less pronounced connection between the former and Asian samples especially in Paleo-Indian samples from both South and North America (also Lahr, 1989: 322; Steele and Powell, 1992).

The marked “archaic” (“pre-*sapiens*”) features (pronounced superorbital torus, marked postorbital constriction, sloping forehead, large browridges, etc.) and considerable morphological diversity (involving both dolichocranic and brachicranic extremities) of Native American crania were noted earlier by Givens (Givens, 1968) and several other scholars (see, Steele and Powell, 1992: 309). Davis et al. (1980) invoked these peculiarities to argue for a great antiquity of human presence in the Americas. Holocene non-Mongoloid (“German” or “Dutch”) skulls found near the Missouri River were discussed by Aleš Hrdlička and William Holmes (Holmes, 1912: 31). The latest contributions to the late Pleistocene skeletal record of North America, including Spirit Cave and Kennewick men as well as the widely publicized Umatilla Reservation findings, display a lack of typical Mongoloid features and affinities with dolichocranic Caucasoids and/or South East Asians (Hall, 1997b; Wright, 1999). Wolpoff (Wolpoff, 1992: 56) wrote,

“Africans or African features should be identifiable in the earliest modern populations outside of Africa, unless the model has no prediction at all”.

The staunchest critic of the “Out-of-Africa” hypothesis should not have problems with an “Out-of-America” scenario.

Alternatively some late Pleistocene/early Holocene skeletal remains (Buhl woman from Idaho, 10,700 BP; Wizards Beach man from Nevada, 9,200 BP) resemble modern Native Americans (Wright, 1999: 55)⁵.

⁵ The Paiutes, who historically inhabited the territory in Nevada where the Spirit Cave man and the Wizards Beach man were found, have preserved myths about a family in which two children were born white, and the other two were born dark-skinned. They lived in peace until a certain time, when the father took the white siblings and separated from the mother who stayed with the dark-colored children. When in the XIX century the first Europeans entered the Paiute lands, some Indians, including Chief Truckee, took this event to mean a final reunion of the family and the completion of the mythological cycle (see, Hopkins, 1994: 6-7; Heizer and Hester, 1972: 50-52).

At the beginning of the creation myth of the Hopi, who have expanded from the Great Basin to the American Southwest, “white and red men of all nations” lived peacefully in the underworld. They were driven away from there by evil characters called Two-Hearts who caused their separation. The famous Hopi Prophecy holds that, with the return of the Chosen White Brother (Paahana), peace and harmony will be restored in America (Simmons, 1942: 379-380; Geertz, 1994). A Hopi medicine man, David Monongye, saw the “white brothers” in modern Indian hobbyists and hippies, since, according to the prophecy, the “white brothers” would wear long hair and would want to live like Indians (Hungry Wolf and Hungry Wolf, 1983: 17).

Struggling to explain the tight connection between the prototypical human skull morphology and the Native American lineage, Lahr (Lahr, 1996a: 246-247) resorted to the old argument about isolation as a factor in the preservation of ancient traits. However, in view of the extreme gracialization of Sub-Saharan Africans (especially the Khoisans), who supposedly did not move anywhere from the original habitat of humans, the retention of ancestral features among the Patagonians and Fueguians, who allegedly have traversed the whole planet and hence must have experienced heavy population and ecological fluctuations, this explanation cannot be regarded as relevant. Moreover the Eskimos cluster with the Khoisans in terms of gracialization (Lahr, 1996a: 263) suggesting that, first, it is this trait and not robusticity that is responsive to the factor of isolation and, second, that gracialization is accompanied by migrations and subsequent local adaptation. Despite Lahr's effort to infer the "Out-of-Africa" scenario from craniological data, the big temporal gap (80,000-100,000 BP for the Border Cave remains vs. 12,000 years BP for proto-Khoisan and proto-Negroid remains) that separates the earliest modern human skulls found in Africa and "archaic" specimens (Lahr, 1996a: 282-283) virtually excludes this possibility.

The structural discontinuity between modern and archaic skulls in Africa, which had been used by many as an argument against the "Out-of-Africa" model, was subverted by Lahr to show the contrary (Lahr, 1996a: 224). However, while the variability of Native American cranial morphology meets the criterion of neutrality of ancestral characteristics with respect to later specific regional developments, the undifferentiated character of the "archaic" African sample suggests that they bear no historical affinity to living humans. As her own discussion reveals (see especially, Lahr, 1996a: 34-37, 281-283 and further), Lahr's "Out-of-Africa" conviction was nurtured not by the craniological material but by general preferences and widely circulated interpretations of African genetic variability.

Contrariwise craniological evidence clearly shows a different pattern of human dispersal, namely from the Americas, that is congruent with such facts as the

Some vague allusions found in historical documents to the Aztecs initially confusing Cortéz with their legendary ruler, Quetzalcoatl, who purportedly had left their country in a boat, may have a certain amount of historical truth.

These stories may well be connected to the underlying idea of the Ghost Dance religion that had been initiated among the Paiutes in the last half of the XIX century and that subsequently spread across a vast territory in western North America (Mooney, 1965). Wowoka preached that, if Indians would perform certain rituals, the dead Indians would come back to life and the peace and harmony on the earth would be restored. In many indigenous cultural traditions (Lévy-Bruhl, 1925: 405-444; Lévy-Bruhl, 1966: 306-307), the whites were seen as the original inhabitants of the other world, i.e. the dead. Their sudden coming from overseas where allegedly no alive Indians could exist, the color of their skins and the mysterious objects that they possessed - all contributed to this Indian interpretation. Naturally enough, who else could live overseas as not the dead Indians themselves.

The fact that these traditions were recorded in several tribal groups, by several independent observers at different times and the fact that they display considerable variation on the plot level allows treating them not as a secondary reflection on the colonization but as a historical memory going back to the late Pleistocene/early Holocene times. It is noteworthy that all these traditions invariably come from one historico-cultural community, namely the Uto-Aztecan linguistic family. The Algonquins and the Iroquois, to be true, had a mythological cycle about two brothers, who lived in constant contradiction until one of them separated and ascended to the skies (Hennepin, 1699. Vol. 2: 50-51). This is interesting in view of the latest identification of "European" haplotypes at high frequencies in the Ojibwa (see n. 3).

proximity between American and Australian morphology (with Australian specific cranial features stemming from the factors of local evolution) and the full retention of ancestral features in recent South American populations. The following statement by Stringer and Bräuer (Stringer and Bräuer, 1994: 417) shows that what is expected but not found in Africa is unexpectedly found in America.

“...The earliest modern humans should resemble their proposed African *ancestors*...and not *modern* Africans, except where it can be shown that modern Africans have also retained such ancestral features” (italics in original, stress added).

Polymorphism so sharply pronounced in prehistoric American populations was also characteristic of early Australian and African remains that supports the thesis about relatively late local standardization of cranial morphology (Lahr, 1994) and the plasticity of human evolutionary development.

Odontology

Human dental characteristics are genetically determined (Dahlberg, 1951: 140) and exhibit patterned geographic variation. Being odontologically homogeneous and possessing a kind of “master dental plan” (Scott and Turner, 1997: 2), humans nevertheless display morphological and metrical traits that vary between individuals and populations. Modern human dental variation is largely known through a series of works by Christy Turner and Richard Scott (Scott and Turner, 1997, with references to earlier reports). Going along the lines of Howells’ craniological interpretations and arguing against Cavalli-Sforza’s assessment of African genetic variability as a function of time, Turner found African dentition less differentiated and specific than the Sinodont pattern characteristic of East Asians and Native Americans and suggested that modern Africans were relatively late colonists on the continent (Scott and Turner, 1997: 285, 302; Turner, 1992: 431-432). Typologically Africans and especially Caucasoids are situated at the opposite extreme from Sinodonts that figure as the primary outliers in tree diagrams (Scott and Turner, 1997: 288-292).

“To evolve Sinodonts out of Africans is as difficult as to evolve Sinodonts out of Europoids” (Turner, 1992: 431).

The Sinodont dental pattern marked by high frequencies of shoveling and double shoveling, enamel extensions and 3-rooted lower first molars is treated as the most complexly differentiated and specialized type (Turner, 1992: 427-428). It is immediately related to the Sundadont pattern found in Southeast Asia and Oceania, which is distinguished by less pronounced character of those features. Sundadonts represent a more generalized dental configuration and occupy an intermediary evolutionary niche between Sinodonts and Euroafricans on the scale of dental complexity and robusticity. Australians demonstrate conspicuous local peculiarities but nevertheless are grouped by Turner and others into the synthetic proto-Sundadont or Australaisan category. The generalized nature of the Sundadont pattern has led Turner to believe that it represents the ancestral human dental type (Turner, 1992: 429).

Although Turner subsumes all Native Americans under Sinodonts, his research demonstrates marked north-south clines in the America. 3-rooted lower first molars (3RM1) reach their highest frequencies in the American Arctic, Northeast Asia, China

and Mongolia, which was initially interpreted by him as an evidence for three migrations into the New World (Turner, 1971; Greenberg et al. 1986). North and South America display slightly higher frequencies of this trait than Southeast Asians and prehistoric Jomon (Japan) but cannot compete with the northern branch (Scott and Turner, 1997: 231-233). Alternatively double shoveling figures most prominently in North America, Northwest Coast and South America, with the Paraguayan Lengua having 61.3% and Peruvian Indians having 60.5% of this trait. Double shoveling gradually decreases in the American Arctic, Northeast Asia, China and Southeast Asia (Scott and Turner, 1997: 185-187).

Prehistoric American dentition, Turner (Scott and Turner, 1997: 279) acknowledges, is considerably different from the recent pattern. Haydenblit (Haydenblit, 1996) analyzed four prehistoric Mexican series (Tlatilco, 1300-800 BC, Cuicuilco, 800-100 BC, Monte Alban, 500 BC – 700 AD and Cholula, AD 550-750) and observed surprising structural variation that enabled him to refer to these series as “populations”. Among these populations, only 27% of traits are consistent with the Sinodont pattern and only Cholula can be classified as Sinodont. Powell (Powell, 1993) also reported Sundadont frequencies from prehistoric American remains.

The intensification of Sundadont traits among the Sinodonts, in contrast to their simplification in Africa and Europe, suggests that the early phases of dental evolution are associated with America. The ancestral pattern must have been characterized by more generalized and variable shoveling and lower molar features than in living Sinodont populations mostly clustered around Northeast Asia, China and northern North America but, without any doubt, more complex and robust dentition than in contemporary Caucasoid and African groups. It is possible that a proto-human dental plan was discriminate in terms of Sundadont and Sinodont features: e.g. it had low frequencies of 3RM1 but high frequencies of double shoveling.

The temporal convergence that seemingly exists between American and Australaisan dental features is in full accord with functionally related craniological data (see above). Historically Native Americans and Northeast Asians have intensified the principal characteristics of the proto-Sundadont (with Native Americans preserving a higher degree of morphological variation than is found in Asia (Lahr, 1996a: 322; Givens, 1968, among others)), Australians modified them in response to isolation, while Southeast Asians possibly preserved the dominant Sundadont frequencies but reduced the variability. The details of the evolutionary process that has led to the extant Australaisan and American variants of the ancestral dental pattern need further thorough investigation in the context of the “American hypothesis” under exploration here but, in keeping with the craniological and dental evidence, it is obvious that African (as well as Caucasoid) region is excluded as a potential homeland of modern humans.

Genetic Evidence for Human Evolution⁶

The Argument of Diversity

Genetic evidence remains largely controversial. Despite the repeated attempts on the part of some genetic laboratories to demonstrate the variability and specificity

⁶ For the presentation of the latest genetic information pertaining to the origins and migrations of modern humans, I have made extensive use of the collections amassed and annotated by Alvah Hicks (Hicks, 1996; Hicks, 1997; Hicks, 1997-1998).

of the African mitochondrial genetic makeup and argue for the dispersion of humans from Africa around 140,000-90,000 BP (see, Chen et al. 1995; Lahr, 1996a: 36-37; Tishkov et al. 1996; Watson et al. 1997), the validity of these criteria as evidence for greater time depth remains unproven.

Local studies (Workman and Niswander, 1970; Salzano, 1968; Crawford, 1998: 147, 150-151) have abundantly demonstrated that genetic diversity is dependent on a variety of stochastic factors such as group fission-fusion, intergroup isolation enforced by social hostility, population fluctuation, etc. Sub-Saharan Africa (with the sole exception of bilateral Khoisans) is a classic country of segmentary lineages, which are highly conducive to prescriptive marriage alliances. Lineage systems are strongly correlated with skewed, or Crow/Omaha kinship terminological patterns (see below) (Radcliffe-Brown, 1950), which indicate the rapid “fading away” of kinship ties and constant partitioning of kin groups (Lévi-Strauss, 1969).

“In the first generation, a person moves from being unrelated to a particular house to being an affine. After he has children, his generation then becomes related as fathers and father’s sisters to his child; for a woman, the next generation is made up of the children of men in the houses related affinally to the previous generation. The third generation, the oldest, is the grandfathers and grandmothers of the children of the marriage. In the fourth generation there is no relationship” (Kasakoff, 1984: 80).

Ancestors, whose importance in African societies is overwhelmingly stressed in religious beliefs, ritual practices and social institutions, may be seen as ideational counterparts of genetic haplotypes emphasizing the distinctiveness of every lineage.

African, New Guinean and South American materials (Sahlins, 1961; Meggitt, 1965; Århem, 1981) suggest that segmentary lineage structures function as an adaptive response to population density and land shortage that leads to predatory expansion. This accords with geneticists’ and craniologists’ speculations about the origins of African variability in significantly greater long-term effective population size (Rogers and Jorde, 1995: 23-24; Relethford and Harpending, 1994; Relethford and Jorde, 1999). In this case, the mtDNA coalescence time shows not the age of a regional population but the age of the last favorable mutation (Templeton, 1993: 59-60) correlated with a rapid demic expansion. Following the same line of argument, Ward et al’s report (Ward et al. 1991) on the phenomenal mitochondrial diversity (with the coalescence time of 78,000 years BP) in the Nuu-Chah-Nulth tribe from the American Northwest composed of unilineal kin groups may not necessarily indicate either the time of the peopling of the Americas, or the actual formation time of this group.

The above said does not mean that diversity has apriori nothing to do with the time depth of the existence of a group. Sometimes it does, sometimes it does not. It is reasonable to suppose that a group that has stayed the longest in a certain region will demonstrate higher diversity than its latest branches but the opposite is an equally plausible historical situation. It is therefore important to determine, first, what *kind* of diversity corresponds to what *kind* of historical events, and, second, what *kind* of diversity does not depend on the point of view. If geneticists argue that all non-African markers can be clustered in three principal lineages, while in sub-Saharan populations the situation is totally different, with very pronounced haplotypal variability and disequilibrium patterns (Tishkov et al. 1996), it may very well indicate a rather late mutation of the ancestral small number of haplotypes in Africa. For instance, non-Austroneasian-speaking New Guineans exhibit consistent homogeneity in terms of the number of mtDNA lineages (Stoneking et. al. 1990) but their presence

in Australasia is considered to be archaeologically attested from 40,000 years BP. Taking into account the overall genetic homogeneity of modern humans that comprise one long-term evolutionary lineage (Templeton, 1993: 69-70), it is doubtful that a proto-human population was characterized by an African-like mitochondrial diversity. As Excoffier and Langaney (Excoffier and Langaney, 1989: 82) pointed out ten years ago,

“...The most important goal may not be to identify one population or group of populations as being ancestral to others but to recognize which characteristics could be ancestral and what would have been the probable genetic pool of early populations”.

In continuation of their argument, they note that some Caucasoid populations have a genetic background close to that of an ancestral population and that most of the African mtDNA types have appeared only recently (Excoffier and Langaney, 1989: 82).

“Though Africans are genetically clearly differentiated from other populations of the world, they do not seem to constitute the latter’s direct ancestors” (Excoffier et al. 1987: 184).

A b-globin analysis showed that, while genetic diversity measured by numbers of segregated sites is the greatest in Africa, the diversity measured by pairwise sequence difference proves to be greatest in Asia (and especially in Mongolia) (Harding et al. 1997: 780).

Nuclear DNA Evidence

A series of studies on the non-recombining portion of the human *nuclear* Y chromosome, which is inherited exclusively through father’s line and does not recombine with the X chromosome (Hammer, 1994; Hammer, 1995; Hammer et al. 1997; Hammer and Zegura, 1996; Altheide and Hammer, 1997; Hammer et al. 1998) vividly demonstrated that a major component of African Y-chromosome diversity has its roots in Asia. For instance, the ancestral lineage 3 of a Y-linked polymorphism known as the “Y Alu polymorphic” (YAP) element was found at higher frequencies and with higher diversity in Asia than in Africa. Within haplotype 3, two haplotypes 3G and 3A are associated respectively with SRY₄₀₆₄-G and SRY₄₀₆₄-A alleles. The ancestral 3G haplotype was present only in Asian and New World populations, while the derivative 3A haplotype was present only in African groups and in one European individual (Altheide and Hammer, 1997: 463). The highest frequencies of the haplotype 3 were recorded among the Tibetans (50%). From the Tibetans, the ancestral YAP⁺/SRY₄₀₆₄-G/ahV haplotype was also obtained. The Mongolians are marked by the presence of two ancestral haplotypes, YAP⁻/SRY₄₀₆₄-G/ahV and YAP⁺/SRY₄₀₆₄-G/ahV (Altheide and Hammer, 1997: 465).

The researchers interpret this astonishing finding as evidence of “substantial” Asian contribution to African genetic pool and of a re-immigration of Asians into Africa (Hammer et al. 1998). Hammer et al. believe that this Asian contribution did not affect the ancestral African (and human) haplotype 1A. This allegedly ancestral haplotype was detected by comparing a portion of human Y chromosome with homologous DYS257 STS sequences from four species of great apes (Hammer et al. 1998: 432-433). This conclusion is not supported by the actual distribution of the haplotype 1A in human populations. Africans are the only carriers of this polymorphism, which is

moreover found among them inconsistently (absent in Pygmies, East Africans, West Bantu) and at low frequencies (20% in the Khoisans, 3% in West Africans, 4% in East Bantu, 5% in the Dama) (Hammer et al. 1998: 488). The most common African haplotypes are haplotypes 4 and 5 found in 57% of the populations: 50% in the Pygmies, 20% in the Khoisans, 66% in West Africans and 86% in East Africans. Haplotypes 4 and 5 are again restricted only to Sub-Saharan Africans, and, according to Altheide and Hammer (Altheide and Hammer, 1997: 463) they evolved from haplotype 3. The two most common world haplotypes are 1B and 1C. They are found at equal frequencies (33%) in Europeans. 1B is found at overwhelming frequencies in Asia and the New World: North Asians – 80%, Australasians 96%, East Asians 80%, South Asians 65%, Tanana 75% and Navajo 11%. 1C was recorded in Amerinds at 100%, in the Navajo at 89% and at low frequencies in other parts of the world including Africa (West Bantu – 7%, Dama 5%, etc.) (Hammer et al. 1998: 428).

In view of their ubiquitous distribution, 1B and 1C are the most likely candidates for the ancestral haplotype. 1C has the most consistent distribution pattern, which points to its evolutionary primacy. It gradually decreases from Amerinds to Na-Dene, shows a marked east-west cline in the Old World and mutates into 1B that is most common in the Old World but attains its highest values in North Asians and Australasians.

Hammer et al.'s thesis about an Asian admixture to the African paternal genetic pool is also unlikely on linguistic grounds. Any recent penetration of Asians into Africa would have left traces on the linguistic map of Africa and this is definitely not the case. One has to entertain a possibility that the initial dispersion of humans across the Old World was from east to west, or from Asia to Africa and Europe.

A well-pronounced east to west cline is revealed by a haplotype analysis of the myotonic dystrophy locus in the X chromosome (Tishkoff et al. 1998). In the vast majority of the world populations, the most frequent haplotypes are the one that is marked by the presence of the sites *Alu*(+), *HinfI*(+) and *TaqI*(+) (+++) and the one that is marked by the absence of these sites (- - -). The frequencies of the (- - -) haplotype are overwhelming in the Americas, with an increase trend from north to south (the Tucuna in South America show this haplotype at 100%). In the Old World, the highest frequencies of the (- - -) haplotype are found in Australians, Melanesians and Polynesians and then in Asia. Starting from the Middle East, the (+++) and intermediary haplotypes increase, with Africa having the highest frequency of the (+++) haplotype and the largest variation between the (+++) and the (- - -) extremes. Although Tishkoff et al. (Tishkoff et al. 1998: 1395) claim that the (+++) haplotype is ancestral and that Africans, therefore, should be considered the ancestral population, they note that the sequence of events (three mutations and recombination) leading to the (- - -) haplotype is unknown. This in fact means the opposite from what Tishkoff et al. infer, namely that the evolution went from the (- - -) haplotype via 4 intermediary conditions (+ - +, - - +, etc.) to the (+++) haplotype. The American Indian polymorphisms are more specific than the Old World ones, since they represent a unique consistency of representation of a single haplotype. It is more parsimonious to derive the (+++) haplotype and the intermediary haplotypes of the Old World from the New World, than vice versa. African polymorphisms display a marked inconsistency, with the (- - -) haplotype widely spread among the Ethiopian Jews, (+++) prevalent among the Yemenite Jews and Druze, (+-) prevalent in the !Kung San, (+++) prevalent in the Pygmies and (- - -) and (+++) equally distributed among the Bantu (Tishkoff, 1998: 1396). Taking into account that the Bantu represent a much later population than the Khoisans, it is unlikely that (+++) constituted the ancestral African condition.

Since it is certain that the dystrophy causing alleles are completely associated with a full-length allele, *Alu* (+), and that this disease is not found in the Americas, it is more than reasonable to assume that the mutation leading to the disease in question emerged after the early human population left America. The increase in mutation in North America in contrast to South America is a good illustration of this process.

Mitochondrial DNA Evidence

As far as the human mitochondrial DNA passed down exclusively through females is concerned, the New World genomes (Eskimos, Athabascans and Amerinds) are described as forming a distinct group opposed to the Old World genomes (Merriwether as quoted in Hicks, 1995: 4). This is defined principally on the grounds of the “mutation drift equilibrium” (see above) and the extensive mitochondrial diversity on the “tribal level” equivalent to ~62% of sub-Saharan Africa or ~81% of urban Japan observed in the Nuu-Chah-Nulth and the Maya (Ward et al. 1991).

A comparison between American Indian and North Asian genomes yields unexpected results. Instead of finding many of the typical Asian polymorphisms at low frequencies, which would be natural for an “Asian-derived” population, *all* laboratories report “rare Asian mutations at dramatically high frequencies”, namely “the rare Asian RFLP *HincII* morph 6, a rare *HaeIII* site gain, and a unique *AluI* site gain” (Schurr et al. 1990: 613). These mutations are conventionally designated as lineages A, C and D. The fourth lineage B marked by a 9-base-pair (9-bp) deletion in the non-coding region 5 is absent in North Asia completely. The fifth, E or now X₆, X₇, X₈, haplotype detected in some North American groups (Sioux, Ojibwa, Mohawk, Makiritare, Yanomami, and others) (Powledge and Rose, 1996: 64; Bianchi and Bailliet, 1997; Wright, 1999; Merriwether et al. 1995: 421, subsumed under “other lineages”; Easton, Merriwether et al. 1996: 218-219) is widely spread in North Asia and Europe. Some researchers argue that the percentage of unusual haplotypes in Native Americans may be higher than indicated by available data (Santos et al. 1996).

Although the vast majority of geneticists working on the Americas keep interpreting the similarities between Asia and America as proving migrations into the New World, this interpretation comes from a preconceived belief rather than is read from the data. For instance, Santos et al. (Santos et al. 1996: 318) interpreted the trimodal distribution of pairwise differences between sequences of different haplogroups previously identified as an evidence for the lack of both a bottleneck and a rapid population expansion in the Americas (Horai et al. 1993) in the way that a proportion of the differences observed today were already present at the beginning of the settling process. However they did not show on what grounds the “settling” assumption is based. Their further suggestion to examine the differences between haplogroups to determine whether population fluctuations have occurred in the Americas is nevertheless well taken.

The available analyses of the X lineage also demonstrate misinterpretations. Thus, Easton, Merriwether et al. (Easton, Merriwether et al. 1996), having started their article on the Yanomami genome with an axiomatic phrase “Modern *Homo sapiens* did not arise in the New World”, then introduced their finding of the X₆ and X₇ haplotypes in this tribal group. In order to evaluate whether or not a lineage can be considered a founding one, they resorted to Torroni et al’s (Torroni et al. 1993a) definition that holds the following. A haplotype can be regarded as founding if it is widespread in the Amerindian populations because it would have preceded tribal differentiation; if it is central to the branching of its haplogroup in the phylogenetic

analysis because new haplotypes would have originated from it; if it is present in Siberian and East Asian populations. Easton et al. continue by saying that haplotypes X₆ and X₇ are “widespread in Amerindian populations. These populations range from the far north of North America to well into South America, which is consistent with lineages X₆ and X₇ being founding lineages” (Easton et al. 1996: 221). However, what the authors call “widespread” is in fact a rather meager distribution, with the Mohawks showing X₆ at 1.6% and X₇ at 0.8%, Makiritare X₆ at 10%, Aymara X₆ at 1.5% and Yanomami X₆ at 7.4% and X₇ at 3.6% (Easton et al. 1996: 218-219). Their tables do not list Ojibwa and Sioux frequencies but they cannot be higher. No other group, including the Yanomamo, is known to possess these haplotypes. In contrast, in Siberia, East Asia and Southeast Asia, they are indeed widely spread and display frequencies from 2% in the Nganasan to 34.9% in the Evens, 42.9% in the Malays and 53.1% in the Sabah aborigines. Thus the first criterion set forth by Torroni et al. is not met, while the third one is irrelevant since, as it was pointed out earlier, common traits by themselves do not indicate the direction of derivation. The extremely weak distribution of the X haplogroup in the Americas, unlike its distribution in Asia, does not represent any pattern, and it is reasonable to assume that, in the Americas, it has evolved independently in several disperse and widely separated populations. Its presence in Asia is obviously much older but one can suppose that it had evolved in the same environment, as did the X haplogroup later in the American groups. The American data suggest that this environment was provided by the A, B, C and D haplotypes and that the Asian haplogroup X evolved against the Amerindian genetic background (comp.: Stone and Stoneking, 1998: 1166). The Yanomami case also illustrates the point made earlier in this paper that the haplotypic diversity (this group contains 8 haplotypes) may be a very recent phenomenon, which is contingent on a variety of factors including village fission-fusion fluctuations (see Crawford, 1998: 150-151 on the Yanomami).

American populations demonstrate surprisingly wide range of values in nucleotide diversity analyses ($\pi = 0.016$ in the Nuu-Chah-Nulth from the Pacific Northwest and the Maya from Mexico, and 0.009 in the Kuna of eastern Panama) and, in terms of diversity, approximate the Mongolians for whom $\pi = 0.018$ was obtained (Kolman et al. 1996: 1328; Ward et al. 1991). In terms of the number of restricted sites, Native Americans are markedly less diverse than Asians having 50 haplotypes encompassing 68 sites vs. 106 haplotypes encompassing 191 site in Asia (Wallace and Torroni, 1992: 408-409). Asians are in turn less diverse in sites than Africans.

This implies that the long-term effective population size was the smallest in the Americas, intermediary in Asia and the greatest in Africa. This is consistent with a “mutation drift equilibrium” condition of the Native American genome and a disequilibrium condition of the Old World genomes (Horai et al. 1993: 23; Merriwether et al. 1991: 552; Templeton, 1993: 59). It also fits well in the “weak” Garden of Eden model of human dispersion (see, Relethford and Harpending, 1994: 267). In contrast to the “strong” Garden of Eden model that implies that the dispersion took place roughly at the same time as the expansion in size occurred, the “weak” model holds that humans appeared in a single “limited region” followed by a dispersion throughout parts of the Old World with subsequent increase in size.

Mongolians, central Chinese and Tibetans are the *only* Asian (and in fact Old World) populations that contain all principal haplotypes found in the Americas, with Mongolians carrying 48% (A₂, B₂, C₁, D₁, D₂, X₆, X₇ haplotypes), central Chinese – 45%

and Tibetans – 31% of the New World haplotypes (Kolman et al. 1996: 1331)⁷. Kolman et al. logically continue to argue that these three groups occupying adjacent areas in east Asia represent the closest genetic relatives of Native Americans. They note that, whereas southeast Asians and Oceanians carry the B haplogroup at high frequencies but not haplogroups A, C or D, Siberians carry the other 3 (or 4 with X) haplogroups at low frequencies but completely lack haplogroup B (Kolman et al. 1996: 1331). The geographic and statistical scarcity of the New World haplogroups in Asia makes a multiple-migration scenario impossible, for it is

“extremely unlikely that the same four haplogroups would be drawn out of one geographic region [East Asia – G. D.] three independent times to form New World Esk-Aleut, Na-Dene and Amerind groups” (Kolman et al. 1996: 1331).

Kolman et al. therefore conclude that there was only one migration into the New World from the territory of Mongolia and China (Tibetans are recent migrants from northern China). The same reasoning was employed by Forster et al. (Forster et al. 1996: 939, 943) and Stone and Stoneking (Stone and Stoneking, 1998: 1166), who made the same inference concerning the number of the migrations. An analysis of 5 *Alu* sequences showed consistent clustering of Native Americans and especially the Maya with the Chinese (Novick et al. 1998: 25, 37).

Following Torroni et al. (Torroni et al. 1993b), Kolman et al. eliminate the possibility that Siberians were the New World founders and claim that *Siberia was colonized later than the Americas because the divergence of Siberian C and D haplotypes is estimated as 13,500 – 27,000 BP, whereas New World C and D haplotypes show the divergence of 18,750-37,500 BP* (Torroni et al. 1993b). Judging from the “elevated frequencies” of haplotypes A, C and D in Siberia (e.g. 58.1% of C₁ in the Evens, 59.3% of C₁ in the Yukagirs vs. 11.9% of C₁ in the Mongolians; from: Easton et al. 1996: 218), Kolman et al. (Kolman et al. 1996: 1332) have to admit “an historical relation” between Siberians and Native Americans supported by Szathmary’s (Szathmary, 1994) analysis of 15 blood groups and allozyme markers. *If an historical relation is known to exist between two populations, and one population, namely Native Americans, is known to have existed longer than the other, the simplest logical implication is that Siberians descended from Native Americans and migrated into their present habitats from the New World.* This agrees perfectly well with the genetic evidence demonstrating lower diversity in Siberians than in Amerindians (Merriwether, 1995). The conclusion that would seem so natural to Jefferson in the XVIII century and to the Jesupians in the early XX century today is simply a taboo. Evidently not prepared to break the taboo, Kolman et al. consider “long-term genetic exchange” between Siberia and America as an alternative explanation to “close genetic relationship”. One is left to fantasize how populations occupying vast territories separated by a strait would engage in such a “long-term genetic exchange”.

The sharpness of the argument in favor of the unity of the American lineage makes further speculations about the number of migrations into the New World irrelevant. Rogers et al. (Rogers et al. 1991) explained the differences in genetic and linguistic diversity in Amerinds, Na-Dene and Eskimo-Aleut as engendered by isolation in ice-free pockets. The most parsimonious conclusion is therefore that the Na-Dene and the Eskimo-Aleuts occupied these refuges from the south and not from the north.

⁷ According to Easton et al. (Easton et al. 1996: 218), the central Chinese (designated in their tables as “Taiwanese Han”) do not have the D haplogroup.

Now it remains to decide if the unity of the American lineage and its deep genotypic relationship with Mongolians, central Chinese and Tibetans means a migration *from* the Old World or a migration *into* the Old World. Mongolia also figures prominently in Merriwether's analysis of the external affinities of the New World natives. His team's conclusion was formulated in the following way:

"We conclude that Mongolia or *a geographic location common to both contemporary Mongolians and American aborigines* is the more likely origin of the founders of the New World" (Merriwether et al. 1996: 204, italics added).

Needless to say, "a geographic location common to both contemporary Mongolians and American aborigines" can be situated in America. The fact that Mongolians, central Chinese and Tibetans share with Native Americans the same set of haplogroups together with the lack of significant differences between both clusters in nucleotide diversity resist any automatic interpretation of the directionality of the population movement.

Taking into account that very few of common mtDNA mutations found in the Old World are present in Native Americans (Horai et al. 1993), it seems worthwhile to draw attention to the 9-bp deletion, or the haplotype B, that is considered a useful marker for Southeast Asian, Pacific and Native American populations. Unlike the other three haplotypes, the B lineage displays in multiple regression analyzes not a north-south cline but a radiation pattern, with zero frequencies in the extreme north (among the Eskimos and the Northern Athapascans) and extreme south (Tierra del Fuego) (Merriwether et al. 1995: 420; Fox, 1996: 866). In the Old World, the 9-bp deletion is found in one North Altai individual, in the Yukagirs (although against a lineage C background, i.e. with presence of the *HincII* 13259 site loss and the absence of *HaeIII* 16517 site gain) (Merriwether et al. 1996: 205), among the Mongolians (2.38%) (Merriwether et al. 1996), Chinese (7%), Japanese (19%), Koreans (15%), Ainu (1,5%), Malays (3%) (Fox, 1996: 867, percents read from a chart), Negritos, Coastal New Guineans, eastern and western Micronesians, Filipinos and Vedda, and in high frequencies among the Maori, Fijians, Samoans (90%), Cook Islanders, Tonga (100%), Nieu, Hawaiians (95%) (Harihara et al. 1992; Lum et al. 1994; Melton et al. 1995; Cann and Lum, 1996). The cases of a 9-bp deletion representing two independent origins – one from the Asian clade, the other from local development – were reported from Western Australia (Betty et al. 1996). A 9-bp deletion is further reported in the Pygmies (Mbuti 30%, Efe 30.3%), Malawian (26.7%), Lemba (26.9%), Sotho-Tswana (20.4%) and other Bantu and in the Nilo-Saharan Luo (1.7%) (Soodyall et al. 1996: 595). It was found in a single European individual but against a different haplotypic background (Soodyall et al. 1996: 603). Soodyall et al. argue for possible independent origin of the African and European deletion. There is evidence for this deletion in West Africans (Merriwether et al. 1995: 424), and the formation of the Bantu linguistic family is associated with West Africa. In other parts of the world, the deletion is also thought to have arisen multiple times but it nevertheless implies a "single ancient event" (Wallace and Torroni, 1992: 408; Santos et al. 1994: 971). The presence of a 9-bp deletion against a different lineage in the Yukagirs, who live between the areas of "classical" Asian deletion, suggest that this marker has a genetic foundation (comp.: Fox, 1996: 868). It is also possible that, by virtue of its ubiquitous distribution, the 9-bp deletion represents the most ancient human mutation.

Judging from the distribution of B haplotype, Native Americans and Southeast Asians show the same proximity as craniological and dental data indicate (see above).

However the conventional interpretation of this regularity as showing the migration of a population from Asia into the New World is not responsible to facts. Wallace and Torroni (Wallace and Torroni, 1992: 408) motivate it by pointing to the Han Chinese from Taiwan who display the deletion at 40%⁸. However there are many American Indian groups (Bribri, Kraho, Boruca and others) that show this haplogroup at even higher frequencies (Easton et al. 1996: 218-219).

One rather has to infer, following Hicks (Mother Tongue, 1996), a reverse scenario, namely from the New World into the Old World. Only this model can simultaneously account for the lack of the 9-bp deletion in the extreme north and south of the American continent, in Northeast Asia and its presence in sub-Saharan Africa and Southeast Asia, which otherwise looks puzzling (Cann and Lum, 1996).

One part of the early population migrated directly into the region of China and Mongolia where the northernmost presence of the marker is recorded⁹, where the three other principal New World haplogroups are found, and where the highest genetic diversity in world measured by pairwise sequence differences was established. Another group continued moving in the direction of Africa. The preservation of a 9-bp deletion at high frequencies in Polynesia points to a small group of endogamous colonists exclusively carrying this marker. The exportation of the B haplotype to the Americas from Polynesia (Cann, 1994: 10) is excluded, first, because, while Polynesia was peopled around 3,500 BP, a 9-pb deletion was identified in a 8,000-year-old South American mummy (Monslave et al. 1996) and in 8,000-year-old White River skeleton, Colorado (Powledge and Rose, 1996: 64), and second, because the even distribution of this marker in North, Central and South America, would not correlate with any known populational movement in the Americas around the IV millenium BP.

The interpretation set forth by Torroni et al. (Torroni et al. 1992; Torroni et al. 1993a; Torroni et al. 1993b) and supported by Starikovskaya et al. (Starikovskaya et al. 1998) and Schurr et al. (Schurr et al. 1999) that B haplogroup stands for a separate migration beginning somewhere from southeast Siberia and occurring after the other major three haplogroups were deposited in the New World should be dismissed. First of all, a D-loop sequencing analysis showed a high diversity of this group in the New World (Santos, 1996: 317). Second, common sense resists the idea of a group leaping over Siberia and leaving no genetic traces in Northeast Asian populations in order to spread evenly throughout North, Central and South America. The same doubt was expressed by some of the commentators:

“it was unlikely that the lineage could become extinct in all Siberian populations [unless they have moved from America – G.D.]; furthermore, how could it spread throughout the Americas if it arrived in a later migration? The lineage B remained something of an anomaly” (Powledge and Rose, 1996: 62).

Thus the patterns of distribution of the Native American haplotypes in Siberia, Southeast Asia and Oceania suggest that the profound correspondences between the Native American genome, on the one hand, and the genome of Mongolians, Chinese and Tibetans has to be interpreted as evidence for a migration into this region from the New World, and not vice versa. A migration from East Asia into America would

⁸ Easton et al. (Easton et al. 1996: 218) give only 20% of the haplogroup B (15% of B₁ and 5% of B₂) in the Taiwanese Han.

⁹ It could have left traces in the Old Harbor Eskimo population of Kodiak Island in which the deletion is reported at less than 5% (Merriwether et al. 1996: 205). No other group in the northern parts of North America has retained this marker.

have been conceivable if the frequencies of the common Native American haplotypes were *higher* among the East Asian populations. Meanwhile haplogroups A, B, C and D are significantly reduced in East Asians (see, Kolman et al. 1996: 1332), which correlates with the general decrease of typical American markers in Asia, Oceania and Australia. If East Asia were a springboard into America, then one would have observed the reduction of typical East Asian markers in Native American populations. However the opposite is true. Novick et al. (Novick et al. 1998: 37) noted that the close genetic proximity between all Native Americans and between Native Americans and East Asians looks anomalous and is not consistent with the (single) migration hypothesis. They argued, therefore, for multiple migrations from a single source, which is however unconceivable on the grounds mentioned by Merriwether, Kolman and others. The only realistic scenario is that East Asians represent an enclave of immediate descendants of Native Americans and recent migrants from the New World.

The only exception to the pattern of decrease of A, B, C and D haplogroups in the Old World is formed by the 9-bp deletion in Polynesia, where its frequencies exceed the frequencies recorded in Native Americans, but even this increase seems to have occurred against the background of radical reduction of the other three American haplogroups. Local increase in frequencies of a particular mtDNA is attested among the Sami: although the haplogroup V was acquired from neighboring Caucasoids, it is carried by 40.9% of the Sami, which is significantly higher than the general percentage of this marker in Europe and North Africa (Torroni et al. 1998: 1149). Also, in the Kuna of Panama, the A₂ lineage “edged out” virtually all other typical American Indian lineages and attained the frequency of 93.8% (Easton et al. 1996: 219). This process was accompanied by a significant reduction in sequence diversity (Batista et al. 1995; Kolman et al. 1996: 1328). In the traditional interpretation of the geographic distribution of the 9-bp deletion in Asia and America (Wallace and Torroni, 1992: 408), the “fixation” of the haplogroup B in Polynesia is also considered a secondary event.

The dominant interpretation set forth by Wallace et al. (1985) and Schurr et al. (1990) that the discrepancies between Asian and Native American genomes are due to a bottleneck and founder effect that affected the migrants into the New World stems from the deeply engrained belief in the Asian origins of Asian-American similarities. Seen objectively, the genetic data make this scenario difficult to imagine. The drastic reduction of the typical Amerindian markers in North Asian populations points to a bottleneck, while the emergence of those Asian markers that are not found in the Americas was caused by a founder effect (comp.: Hicks, (n.d.): 35-36).

From East Asia, an early population radiated further south into Australasia¹⁰ and, much later, back north into Siberia. This reverse migration into Siberia may be identified as the late Ugrian and Turkic expansion. Additional admixture from North America could lead to the formation of the Paleo-Siberian groups (a variant of the 9-bp deletion in the Yukagirs may reflect this).

The profound importance of the single-migration hypothesis in the genetic interpretations of the New World history lies not simply in establishing the unity of the Native American lineage but in endorsing the functional unity of the principal Native American haplotypes. It makes them a valid tool for measuring the correspondences between Native Americans and other populations. Through the A, B, C and D haplogroups, Native Americans are connected to the East Asians; through A, C and D

¹⁰ There is a study suggesting genetic affinities between Australian aborigines, on the one hand, and Siberians and East Asians, on the other (Jones, 1996). The linguistic part of it, however, makes little, if any, sense.

haplogroups, they are linked to Siberians; haplogroup B relates them to Southeast Asians, Oceanians, western Australians and West Africans. Finally American Indians (northern Amerinds and southern Na-Dene) are specifically connected to Caucasoids by means of the haplogroup X (Brown et al. 1998). Brown et al's idea that this lineage was brought to America relatively recently by a Caucasoid group from Near East constitutes an impossible scenario. An argument that excludes this possibility is that the haplogroup X is not found in Siberia. Moreover a Near Eastern group travelling all the way to North America can exist only in somebody's imagination.

The fact that a genetically unitary population shares all its principal markers with all other major world clusters in different configurations is unique. To compare, Sub-Saharan Africans have 4 small haplogroups marked by the absence of the 3952 *HpaI* site that are "relatively similar" to some Asian and European haplogroups. Among them, only two haplotypes (AF₂ and AF₇) are shared with Europeans (Chen, 1995: 142-143). None of the principal African lineages are found in the Americas or in Australia. The vast majority of African nuclear and mitochondrial haplotypes is *not* present outside of Africa, which contradicts the definition of a founding haplotype (Torrioni et al. 1993a) applied by several research teams to the relationship between New World and Asian genomes (see above). This circumstance constitutes an additional evidence against the "Out-of-Africa" evolutionary model (comp.: Hicks, 1996: 33).

In view of the fact that everywhere in the Old World, except for Polynesia, the New World markers are found at drastically reduced frequencies, their exportation from the Americas into the Old World, and not vice versa, should be postulated. Examples from other parts of the world amply illustrate this regularity. Thus, the well-established Paleolithic (re)expansion of Caucasoids from southwestern Europe northward caused by the climatic warming (Otte, 1990) is marked by a decrease in typical Basque frequencies like 49a,f/TaqI-Ht15, which is considered a "proto-European haplotype" (Semino et al. 1996; Torrioni et al. 1998; also Francalacci et al. 1996; also Chikhi, 1998); the Neolithic agricultural expansion into Europe from the Near East is marked by the decrease in typical Near Eastern gene frequencies like p12f2-8-kb (see, Semino et al. 1996).

In the same way as the Near East shows two missing ancestral haplotypes that link the western and the central European clusters (Richards, 1996: 194), Native Americans contain all those haplogroups that unite together Siberians, East Asians, Southeast Asians, Oceanians, Australians, Europeans and Africans. If non-human hominid lineages are absent in the Old World populations, Native American haplotypes account both for some of the rare and divergent Old World lineages and for some of those that are widely spread. Naturally enough, taking into account the geographic distance, the connections between the New World and the Old World haplotypes are weaker in Australia, Africa and Europe and stronger in Asia.

Alternatively each major population cluster in the Old World could not independently contribute to the formation of Native Americans. Such an idea would contradict the genetic evidence for the unity of the Native American lineage as well as common sense.

An early migration from the Americas is further supported by blood group distributions. Beginning from the area of the Great Lakes southward, the O allele is found at 95-100% (Mourant et al. 1958: 270; Crawford, 1998: 98). The Na-Dene linguistic community shows 80-85% of the O blood group. The next highest percentage is found in northern and western Australia (75-80%), while Sub-Saharan Africa is marked by a variation of 75 to 85%. The Eskimos display a 65-75% variation in this

blood marker. Taking into account the universal donor quality of the O blood group (Kabat, 1956: 4-5) and the unique consistency of its worldwide distribution, it is most parsimonious to view this distribution as a populational cline leading from the Americas into the Old World.

A study conducted among the Caddo-speakers in North America (Gray and Laughlin, 1960: 90) revealed that the reduction of the O-allele frequency and concomitant increase in A (45-48%) and B groups (4,3%) occurred among the Pawnee and the Wichita who had suffered rapid and severe reduction in size followed by gradual population increase, while the Caddo, who had undergone only a decrease in numbers, retained the O group at overwhelming frequencies (94,4%). If one follows Carson's argument (Carson, 1975; also Horai et al. 1993) that a genetic bottleneck is a consequence not of isolation but of fluctuation in population size, the study among the Caddoans links together the evidence of genetic bottlenecks in the Old World populations and their absence in the Americas (see above) to illustrate the process of human migration from the New World into the Old World. The genetic function of this process was the bifurcate mutation of the O-allele into the A- and B-alleles. All other explanations of the blood group homogeneity of Native Americans (like preservation as a result of isolation) will be at odds with facts and common sense.

Thus a wealth of craniological, odontological and genetic data contains consistent evidence for a relatively late dispersal of humans from a single source. Conspicuous geographic and typological clines indicate that this source of human evolution is located in the Americas. The "mutation drift equilibrium" detected in the genome of American populations and further illustrated by the overwhelming frequencies of the O blood allele found south of the last glacier's boundary suggest that the A, B, C and D haplotypes evenly distributed throughout the Americas and found at low frequencies in every other part of the world represent the ancestral human genetic pool.

Idenetic Evidence for Human Evolution

Culture talks to us and gives us messages from the past

Ernie Turner

Principal Analytical Categories

Kinship can be understood as involving several distinctive conceptual units. The *genotype* comprises a biologically inherited set of DNA molecules. The *phenotype* is an empirical biological and behavioral set of features only partly determined by individual genotype (Lewontin, 1982: 18). All phenotypic traits *recognizable* by any pair of kinsmen as important for their relationship can be called *idenotype*. The idenotype requires interaction between at least two phenotypes and constitutes any particular and strictly individual relationship between two persons. *Idenetics* encompasses what is usually referred to as systems of kinship and social classification.

The interaction between two phenotypes implies the workings of two basic kinship operations: the objectification of the self and the identification with the other. A *kinship system* is a set of relations between the whole variety of idenotypes realized within a given community and the latter's social institutions (rules of descent and marriage, corporate groupings, political apparatuses, economic organization, etc.).

A kinship system exists in three forms: idenological, classificatory and genealogical. The difference between the three lies in the nature of the construction of kinship categories. The idenological dimension involves disjunctive logic, i.e. the relationship between categories is not determined by any external system of reference. For instance, the fact that there can be no father without a son (children), no grandfather without a grandson (grandchildren) etc. cannot be accounted for by reference to such differential features of another order as gender, generation, age or linearity.

The classificatory dimension is based on adjunctive logic, i.e. a category can be built provided that at least one differential feature of another order provides a basis for the classification. However, while defining the criterion of possible belonging to the group, it leaves undefined the criterion by which certain elements are excluded from the group. For instance, a single feature “male” can account for a category that includes a certain number of actual male relatives (equally non-relatives); or two categories “male” and “first ascending generation” suffice to group together father, father’s brother, mother’s brother and their respective cousins and so *ad infinitum*.

The genealogical dimension exhibits conjunctive logic, i.e. a category can be fully and precisely described by reference to a bunch of differential features. For instance, the category “father” (without the category “son (children)” being included) can be exhaustively circumscribed as the one standing for “a male relative one generation above from me in the direct line¹¹”. Genealogically, then, every category is uniquely represented as a particular combination of differential features and is related to every other category, first, by means of its absolute difference in terms of its composition; and second, due to the finite number of the differential features that can be potentially involved.

A *kinship terminological system* (KTS) reflects those aspects of the kinship system that ensure a meaningful communication. It is a system of classification and as such it employs two basic operations: *merging* and *bifurcation*. In other words, two kinship categories can be either classed together or assigned to different classes. For instance, one kinship terminological system may merge father’s brother and mother’s brother in the class “uncle” and use separate terms for father’s father and son’s son, while another system may keep the first pair separately and conflate the second pair. The actual application of the two operations of grouping the relatives depends ultimately on which of the three dimensions of the kinship system (idenological, classificatory or genealogical) an actual terminological system is based.

In accordance with the Saussurian vision of the nature of a linguistic sign, a kinship terminological system represents a unity of the morphophonemic elements and the semantic principles of the grouping of kin categories. The two planes are relatively independent of one another, *viz.* the elements of each of the planes stand in closer relation to one another than to the elements of the other plane.

A KTS combines the features of a closed and an open system¹². On the one hand, it includes only those lexemes that can be uniquely defined by reference to the

¹¹ If one adds to this proposition the operator “and” to form a statement “a male relative one generation above from me in the direct line *and* a male relative one generation below me in the direct line (i.e. son)”, this will automatically transform the category into a disjunctive one.

¹² In the traditional systems theory, it was assumed that systems can be either closed or open. However, in the last two decades, the developments of the sociocybernetic approach associated primarily with Niklas Luhmann have sufficiently showed that higher order systems employ the principles of openness and closeness alike (see, Luhmann, 1984; Luhmann, 1990).

genealogical parameters. A KTS is contiguous with other lexical domains since a kinship term can be classificatorily (or metaphorically) extended to mean a different thing. For instance, *father* has a primary genealogical meaning but it can also mean “God”; or a non-kinship phrase “little one” can be used as a term of reference or address to a son. The contiguous relationship between lexical domains of a language is, thus, comparable with the relationship of cross-language borrowing.

On the other hand, paradigmatically a KTS forms a part of a wider class of linguistic items called *identitives*. Non-kinship identitives are divided into two subclasses. The first subclass includes *theonyms* (names of divine characters), *gamonyms* (affinal terms, from Greek *γάμος* “marriage, wedding”), *socionyms* (words like *tribesman*, *kinsman*, *in-law*, *human*; relational names like *servant*, *lord*, *master*, *boy*, *man*, *woman* etc.) and *ethnonyms*. The second subclass assembles *paronyms* (names of body parts and spiritual constituents of personality), *pronouns*, *numerals*¹³ and *anthroponyms* (personal names).

The unity of the class of identitives is regularly stressed in languages. For instance, in the Eastern Pomo language, kinship terms, pronouns and personal names are explicitly and uniquely marked by agent-marking affixes (McLendon, 1990: 533).

Kin terms and paronyms can be distinguished from other noun classes by specific markers of inalienable possession; some languages (e.g. Cayapó and other Gé dialects of Brazil, Maori of New Zealand or Finno-Ugric Mari) can employ a partial overlap of kin and body parts lexemes. Kin terms and paronyms may be built in morphologically similar ways. Comp. Germ. *Schenkel* “ankle” vs. *Oberschenkel* “thigh” and Dutch *overgrootvader* “great-grandfather” or Gurage (Afro-Asiatic) “grandmother” as “mother-above” (Leslau, 1979); Latin *testes* “head” vs. *testiculus* lit. “small head”, “testicle” and *avunculus* lit. “little grandfather”, “mother’s brother”, or Germ. *Vater*, *Grossvater*, Fr. *père*, *grand-père*, Eng. *father*, *grandfather*, with an inversion of the meaning of the modifiers. Finally their semantics can undergo similar historical transformations. Comp. OInd. *kákṣā* “armpit”, Avest. *kaša* “armpit”, Lat. *coxa* “thigh”, OIr. *coss* “leg”, Old High German *hāhsina*, Toch. *kektseñe* “body” (Gamkrelidze and Ivanov, 1984. Vol. 1: 98) and Lat. *avus* “grandfather”, OIr. *(h)aue* “grandchild”, Old High German *ōheim* “mother’s brother”.

In relative-age-sensitive KTS, children may be designated numerically according to their birth order (e.g. Ancient Chinese, many Southeast Asian languages, Guidar of Cameroon and others); also in Spanish, numerals are used in reference to cousins: *primo* “male cousin”, *prima* “female cousin”, *primo(a) segundo* “second cousin”.

Finally the Indo-Aryan ethnonym *ārya* and Modern Sinhalese *ayiyā* “older brother” are close cognates, while Russ. *plem’ánnik*, *plem’ánnica* “sibling’s children” is derivative of *plém’a* “tribe”.

The elements of the group of identives are usually unevenly distributed among languages: for instance, many indigenous languages have a meager set of numerals, their group identification can hardly be called ethnonymic, while the pronoun and kin term systems are extremely diversified. A language may also lack (or almost lack) gamonyms, affines being referred to by kin terms or personal pronouns.

¹³ In the case of numerals, which might seem least of all to be identitives, I can cite the Cayapó language as an example of the contrary. The Cayapo in fact do not have a numerical system in our sense of the word. For 1, they say *pudi* “alone”, for 2 – *amaikrut* “both”, for 3 – *amaikrut i keket*, for 4 – *amaikrut amaikrut*, for 5 – *amaikrut amaikrut keket*, for 6- *amaikrut amaikrut amaikrut* (Maria, 1914: 236).

Initial Typological Principles

Strictly speaking, kinship terminological studies are the oldest branch of knowledge that systematically deals with the problems of human populational history. In the course of the last 150 years, an enormous amount of cross-cultural material analyzed at a variety of interpretative angles has been accumulated, which makes the kinship perspective on human diversity the most richly documented. Unfortunately kinship studies are late participants in the current debate on human origins and prehistory, which made Colin Renfrew to complain, in 1992, that

“no adequate consideration has as yet been given to kinship structures” (Renfrew, 1992: 470).

Since this paper represents one of the few present-day attempts to bring kinship studies into the focus of global human history studies, it is worthwhile outlining the history of approaches to kinship terminologies.

In the period from 1859 to 1870, the “discoverer” of kinship, Lewis H. Morgan, amassed and analyzed hundreds of kinship terminologies to suggest the common origin of the “human family”, the uniformity of human evolution and the codependence of social and populational history (Morgan, 1871). Morgan believed that KTS characterized by “permanency, systematic character and continuity of changes” (Lévi-Strauss, 1963: 300) provide a more solid basis for studies in human prehistory than historical linguistics, which by that time had succeeded in establishing the family relation between various Indo-European tongues. Morgan identified and typologized the first set of horizontal categorical markers known as Bifurcate, Incorporating (Hawaiian or Generation) and Lineal patterns and demonstrated the principles of their historical ordering. He suggested that the similarities between North Asian and American Indian KTS grouped by him in a single “Turano-Ganowanian” type indicated the common origin of these populations and the migration of American Indians through Bering Strait.

Later scholars enriched Morgan’s historical typology of KTS with new markers (Bifurcate Collateral, Dravidian) and questioned his grouping of Asian and American populations in one kinship type. The limited number of available markers and their even distribution around the world has led students of kinship to abandon Morgan’s focus on populational determinants of kinship change and to confine themselves to the search of social contexts of kin classification (residence and marriage patterns, descent and kinship behavior, etc.). Nevertheless several studies on Oceania (Murdock, 1968), Siberia (Chlenov, 1978) and India (Dumont, 1953; Yalman, 1967; Trautmann, 1981) have confirmed Morgan’s conviction that the patterns of kin grouping are sensitive to large-scale populational processes.

In 1957, Gertrude Dole (Dole, 1957) reviewed the worldwide distribution of kinship patterns and postulated the Lineal (Primitive Isolating in her terminology) model found among the Eskimos, Khoisans, Andaman Islanders, Southeast Asian Negritos, some Fueguian groups and elsewhere as typologically and historically primary. Driven by the then predominant evolutionary view of human culture as unilinearly developing from simple to complex forms, Dole took the categorical simplicity of the Lineal model to be a reflection of great time depth. However subsequent research has abundantly demonstrated that, among the Eskimos, this pattern constitutes an exception rather than a rule and is a relatively recent development. Khoisan systems are also much more dialectally variable, with Lineal

configurations being a historical reduction of complexity. Finally the Lineal pattern is characteristic of all Indo-European KTS except for Hindi, Albanian and some South Slavic groups (Murdock, 1960: 6), and its emergence out of other forms is well documented.

During the past 30 years, it has been considered well established that, as far as horizontal markers are concerned, the Bifurcate pattern gives rise to Incorporating and Bifurcate Collateral, which are in turn replaced by the Lineal pattern (Kryukov, 1972).

Historical Primacy of Alternate Generation Equivalencies

Starting from the mid-1960s, the interest of kinship students has become more and more oriented on the identification and typologization of various vertical (intergenerational) categorical markers such as Self-Reciprocal terminology, the Crow/Omaha models (having long history of their own in kinship studies), the Sliding-Generation model and the Cumulative model (treated usually as part of horizontal complex and known as Descriptive). David Aberle (Aberle, 1967) made the first attempt at classifying various forms of alternate generation equivalence. Louis Dumont (Dumont, 1966: 238) hinted at the evolutionary primacy of alternate generation equivalence and circular genealogical time. He proposed to “reverse our inherited view” and see the evolutionary process as going from more complex forms of structural complementarity to more simple forms of specialization and individuation.

Dumont’s insights received extensive elaboration in a series of works by Nick Allen (Allen, 1986; Allen, 1989a; Allen, 1989b) devoted to the reconstruction of the original form of human social relations. According to his “tetradic model”, the earliest type of kinship system assimilated grandparents and grandchildren into one category creating “generation moieties”, grouped relatives horizontally in a Bifurcate fashion and involved bilateral exchange of marriage partners. James Matlock (Matlock, 1994) made a further contribution to this line of thought and demonstrated, in elaboration of an earlier paper by Robert Parkin (Parkin, 1988), that alternate generation merging in kinship systems historically precedes and determines the formation of the reincarnation complex of beliefs and practices. Matlock noted the presence of alternate generation assimilation among the !Kung Bushmen, its extensive use in Australian systems of social classification and wide distribution in the Americas (Matlock, 1994: 266-269, 274-278). Following the conventional view on human evolution, he attributed an alternate generation equivalence pattern to the first humans who spread from Africa 100,000-50,000 years BP (Matlock, 1994: 266).

Social structures similar or almost identical to Australian and highland New Guinean section systems were recorded in South America (Melatti, 1977; Kensinger, 1995; Dole, 1991: 382-383; Matlock, personal communication on the Panoan Matses) and among the northern Na-Dene (Riddington, 1969).

Moreover it turns out that alternate generation equivalence is only a special case of intergenerational Self-Reciprocal terminology (Dziebel, 1997a; Dziebel, 1998). In my sample including around 1000 KTS, 362 languages show intergenerational Self-Reciprocal traits. These traits appear in 144 American Indian languages, in 83 languages of Oceania, 51 language of Australia, 34 languages of South and Southeast Asia, 43 African languages, and 3 languages of Northern Eurasia. More importantly, however, 15 American Indian kinship terminologies (Kutenai, Luiseno, Serrano, Cahuilla, Kawaiisu, Tubatulabal, Kaibab Paiute, Ute, Apache, Atsugewi, Achomavi, Tarahumara, Cora, Mixe, Soke) exhibit the strongest form of intergenerational Self-

Reciprocity, namely the one that is marked by self-reciprocal terms for grandparents/grandchildren and parents' siblings/siblings' children differentiated also by parity (relative sex) and linearity. In the Old World, the strongest form of intergenerational reciprocity was reported only for 3 languages of Oceania and Australia (Wikmunkan, Yir-Yoront, Keraki) and 1 language of Northern Eurasia (Sami).

The distribution of intragenerational kinship patterns yields a similar picture. Murdock's Complexly Differentiated type is exclusively found in 40 American Indian languages (Cariban, Siouan, Tupi-Guarani, Coahuiltec, Seri, Warrau, Caddo, Sahaptin and Mackenzie Eskimo). The next most diverse pattern is reported for 6 families and 13 individual languages in the Americas, Austronesian family, Korean and Burushaski languages in Asia, Bantoid, Furian and Northern Khoisan languages in Africa. The Age-Sex and Relative Age types again demonstrate the highest frequency in the Americas (Murdock, 1968: 5-7).

Reconstruction of the Aspects of a Proto-Human Kinship Terminological System

The reconstruction of any proto-system requires attaining such a level of abstraction from which all extant systems are possible to deduce through a limited set of transformation rules (Gamkrelidze and Ivanov, 1984. Vol. 1; also Bright and Minnick, 1966: 387-388). As far as now can be envisaged, a proto-human KTS employed the following set of categorical markers:

- *8 self-reciprocal terms for grandparents and grandchildren* (one term denoted father's father and son's son, another term denoted father's father and son's daughter, the third term – father's mother and son's son, the fourth term – father's mother and son's daughter, the fifth term – mother's father and daughter's son, the sixth term – mother's father and daughter's daughter, the seventh term – mother's mother and daughter's son, the eighth term – mother's mother and daughter's daughter);
- *12 self-reciprocal terms for the relatives of the first ascending and first descending generations* (one term denoted father's older sister and younger brother's children, another term – father's younger sister and older brother's children, the third term – father's older brother and younger brother's children, the fourth term - father's younger brother and younger brother's children, the fifth term – father and son, the sixth term – father and daughter, the seventh term – mother and son, the eighth term – mother and daughter, the ninth term – mother's older sister and younger sister's children, the tenth term – mother's younger sister and older sister's children, the eleventh term – mother's older brother and younger sister's children, the twelfth term – mother's younger brother and older sister's children.); and finally
- *8 terms for siblings and cousins* (one term denoted man's older brother and older male cousin, another term – man's younger brother and younger male cousin, the third term – man's older sister and older female cousin, the fourth term – man's younger sister and younger female cousin, the fifth term - woman's older brother and older male cousin, the sixth term – woman's younger brother and younger male cousin, the seventh term – woman's older sister and older female cousin, the eighth term – woman's younger sister and younger female cousin).

All principal categorical kinship markers (Bifurcate, Incorporating, Bifurcate Collateral, Lineal in the horizontal plane, Crow/Omaha, Sliding-Generation, Cumulative in the vertical plane, Undifferentiated Sibling, Relative Age, Skewed Age, Age-Sex, Relative Sex and Brother-Sister in the intragenerational plane) appear to be

derivative of this proto-pattern. The overall direction of kinship terminological evolution can be defined as the transformation of idenology based on intergenerational self-reciprocity, relative age and relative gender into genealogy based on linearity/laterality and absolute gender (comp. Dumont's ideas quoted above). In very general terms, idenological classification suits a small-size group in which little weight is placed on the distinction between relatives and non-relatives, while genealogical classification gains importance with the increase in the size of a population.

None of the known KTS operates with the full set of idenological distinctions but the kinship nomenclatures of Greenberg's Amerind, Na-Dene and Eskimo-Aleut linguistic families display the highest degree of approximation to the ancestral human KTS. Essentially the same number of categories but without self-reciprocity is recorded in Coahuiltec and Seri in Mexico; intergenerational self-reciprocity is a family feature of Uto-Aztecan, Macro-Oto-Manguean, Keresouan, Kiowa-Tanoan, Penutian, Hokan and Panoan families as well as of Southern Athabaskan subgroup of Na-Dene; the sibling categorical diversity, as it was already noted above, is represented by Cariban, Siouan, Tupi-Guarani, Coahuiltec, Seri, Warrau, Caddo, Sahaptin and Mackenzie Eskimo KTS.

American Indian KTS also display the highest continent-specific degree of typological variability so that all kinship markers found in the Old World are equally found in the New World. In addition, American Indian KTS show the greatest typological density, i.e. the wide presence of intermediary categorical configurations like the Stitching-Generation, Pomo and Split-Reciprocal patterns. The degree of typological density is indicative of categorical equilibrium suggesting the lack of significant population fluctuations that could cause a disruption of the social matrix. The Na-Dene and Eskimo clusters exhibit a decrease in typological density in comparison to Amerind. The categorical equilibrium can be directly compared to the genetically detected mutation drift equilibrium in Native American populations (see above), which, in the words of Rebecca Cann (Cann, 1994: 9) "eliminate, once and for all, the idea that a severe bottleneck" took place in the prehistory of the Americas (on the lack of bottlenecks in the peopling of South America, see Lia et al. 1995, with b-globin haplotype analysis).

There is a continuity between all three big American populations, with Na-Dene maintaining stronger relationship to Amerind than to Eskimo-Aleuts, which apparently have a much more recent formation period. Both Na-Dene and Eskimo-Aleut seem to have been derived ultimately from the same population that is likely to have been Amerind. Only from this perspective, one can account for some unusual continuities between Eskimo-Aleuts, Na-Dene and Amerinds that other sources of information sometimes mark, e.g. genetically, the Eskimos appear more similar to some Indian groups than to others, and both Eskimos and Indians are closer to each other than to their Asiatic relatives (Szathmary and Ossenberg, 1978); the phenetic and q analyses cluster the Eskimos and northern Na-Dene separating them from southern Athabascans and Amerinds (Lorenz and Smith, 1996: 318); Aleuts appear closer to Athabascans and Amerinds than to the Eskimos in skull morphology (Ossenberg, 1992: 517); other craniological studies (Kozintsev et al. 1999: 202) showed that Eskimo-Aleuts and the Chukchi occupy "beyond any doubt" an intermediary position between Siberians and Amerindians; Turner's Great Northwest Coast dental group includes not only Na-Dene but also several Eskimo samples (Kachemak Bay, Kodiak Island and Alaska Peninsula) (Szathmary, 1986: 490).

The Evidence of Kinship Terminological Systems on the History of the Na-Dene

The formation of the Na-Dene population presents herein a special problem. According to the conventional schema (Greenberg et al. 1986: 479; Ives, 1990), Northwest Canada and southern Alaska are considered the homeland of the Na-Dene-speakers, with California, Oregon and Southwest subgroups branching off only about 1,000 years BP. This argument is based on the Age-Area hypothesis in linguistics, namely that the locality characterized by the greatest diversity is the center of dispersal (Dyen, 1965: 15; Dolgopolsky, 1987: 11-12; Rogers et al. 1991: 624-625). The Northwest indeed hosts the largest number of distinct subgroups of Athabaskan (Tanaina, Eyak, etc.) together with Tlingit and Haida share with Athabascans a linguistic taxon of a higher order, namely Na-Dene.

However the diversity argument, as the cross-disciplinary dialogue seems to indicate (see above), contains numerous pitfalls, since the rate of diversification is hard to predict on the basis of formal distribution as well as all the vicissitudes of a population's history. For instance, the greatest variation within Indo-European is observed in the Balkans, where four separate subgroups of the family were historically present (Greek, Paleo-Balkan, Albanian and Slavic), but the Indo-European homeland is located in Anatolia from where a rapid agricultural spread around 4,000-6,000 BP brought the early Indo-Europeans first into the Balkan area and then elsewhere (Gamkrelidze and Ivanov, 1984).

Na-Dene KTS yield a dispersion pattern significantly different from the one suggested by the prevailing view. The Southwest branch of Athabascans (Apache, Navaho and Kiowa-Apache) shows the greatest proximity to Amerind systems¹⁴ in terms of the preservation of strong forms of intergenerational self-reciprocity, with avo-, avunculo-, amito-, patruus- and materteroreciprocal traits (Opler, 1936) and represents the proto-Athabaskan KTS virtually unchanged. Other Athabaskan dialects vary significantly in the degree of the preservation of this proto-system, with ancient features found predominantly in coastal groups (Carrier, California Athabascans, Eyak). Chipewyan, Dogrib and Yellowknife in east-central Canada possess the systems weakly reminiscent of the proto-Athabaskan. Tlingit and Haida KTS are most transformed in this cluster exhibiting classical Crow patterns of cousin grouping related to their elaborate system of matrilineal clans. KTS strongly support a rapid south-north migration of early Athabascans along the Northwest Coast to Alaska, from where they later radiated into the inland part of Canada.

The area with the highest linguistic diversity figures not as the homeland of Na-Dene but as a district where this early group probably stayed the longest after their fast spread from the south and prior to their radiation in the eastern direction. Following Rogers et al. (Rogers et al. 1991), this long-term occupation of the Northwest Coast can be best understood in terms of the favorable ecological condition of this region as one of the refugia during the Wisconsin glaciation. The specific position occupied by the languages and KTS of the Haida and Tlingit was most likely

¹⁴ The Southern Athabascans are the unique carriers of B haplogroup among the Na-Dene (Lorenz and Smith, 1996: 318; Easton et al. 1996: 219). The Navajo are the only carriers of the X haplogroup among the Na-Dene that unites them with the Ojibwa, Yakima and other Amerinds. Brown et al.'s (Brown et al. 1998) hypothesis that the Navajo acquired this marker from an Amerind source remains unsubstantiated, since, in the area historically occupied by the Navajo, no traces of X haplogroup have been found. For the same reason, the fact that Navajo sequences are almost identical to those of the Ojibwa indicates not an admixture but a common origin.

determined by a rapid cultural change induced by their maritime economic specialization and the development of a clan system.

Both geneticists and linguists estimate the age of Na-Dene as being 10,000-12,000 years (Ives, 1990), which archaeologically corresponds to Clovis culture from the western, central and eastern parts of contemporary United States. It has long been ascertained that the fluted points characteristic of the Clovis complex is “an American invention”.

“...No one can say with any confidence where the fluting technique originated but that the old idea of its having reached North America from Asia via the Alaska steppingstone must be abandoned because it is not found in Asia” (Krieger, 1964: 55).

Some archaeologists (Clark, 1991; Dixon, 1993: 119; also Bryan, 1991: 21) suggest that the decrease in fluted points frequencies in American Northwest Coast and in Alaska marks a south-to-north population movement into the newly deglaciated areas of the New World. It seems important that fluted points are not found north of extreme southern Alberta but are present in the coastal ice-corridor area and in Alaska (Bryan, 1991: 21), which makes a good fit with the distribution of the older features of Athabascan KTS in outlining the route of a northward migration of the Na-Dene speakers.

Although the lack of a fluting tradition in Asia (Dikov, 1977; Dikov, 1993; Močanov, 1977) makes the speculations about late Pleistocene contacts between the Old World and the New World archaeologically largely unsubstantiated, the *loss* of fluting skills in the course of migration out of America is *more likely* to have occurred than their sudden emergence in the purportedly newly colonized areas. This supposition stems from the very complex and cumbersome nature of fluting, possibly involving an ideational component inferred from the presence of “unusually well made and scaled-up points” in burials (Storck, 1991). It is not unreasonable to hypothesize that an extensive and rapid colonization of unknown areas would favor a simpler and “purely” pragmatic tool-kit.

The demise of the prominent Clovis technological feature in the course of the migration into the Old World may be seen in some traces of fluting in Northeastern Siberia, namely in the Uptar site, where a fluted point of a smaller size without grinding on the edges and base have been recently discovered and dated 8,260 +/- 330 BP, i.e. later than the Clovis and Folsom periods (King and Slobodin, 1996)¹⁵. Apart from fluting, “Americanoid” tools (points with longitudinal crests, deep notches on both sides and fine, even retouch over the ventral surface) are not infrequent in Siberian Mesolithic and Neolithic archaeological complexes (Derevianko, 1969: 123-126).

Regarding a Siberian or an American origin of the Na-Dene and the Eskimos, geneticist Peter Forster expresses indifference,

¹⁵ The discoverers are obviously perplexed by such a late date for a Clovis-like point in the Old World, for, after stating that a radiocarbon date of 8260 +/- 330 years BP was obtained from scattered charcoals in the tephra and at the interface between the tephra and underlying sediments, they write: “...The chronological relation between Uptar and the technology of fluting bifaces in the Americas is unresolved. Although the Uptar materials may be Pleistocene in age, we cannot exclude the possibility that the site is younger than 11,200 to 10,900 years BP, which is the time frame for Clovis, the earliest reliably dated Paleoindian culture in the Americas” (King and Slobodin, 1996: 636).

“We call it a re-expansion. It’s a matter of taste whether you call it a separate migration” (quoted in Gibbons, 1996: 33).

Meanwhile the interdisciplinary evidence seems to be quite unambiguous: Na-Dene separated from the Amerind cluster and expanded north leaving traces of the Clovis technology on the Northwest Coast and in Alaska (comp.: Hicks, 1998).

A similar late Pleistocene movement from south to north into the deglaciated parts of eastern North America was proposed for the carriers of the Algonquin dialects (Rogers et al. 1990). This considerations bring back to life Boas’ ideas about the “Americanoid” character of Paleo-Siberian peoples (see above), although no traceable linguistic connection exists between the Na-Dene, on the one hand, and the Chukchi, Koryak, Yukagir or Itelmen, on the other. Alternatively, the Paleo-Siberian languages share with Algonquin the typologically very rare polysynthetic morphology, which makes a genetic relationship between these populations not unlikely.

A genetic relationship based on 36 etymologies has been recently established between Na-Dene and the Yeniseian languages (Ket, Yug, Kott, Pumpokol and Arin) in inland Siberia (Ruhlen, 1998). This list of cognates contains the only cases of sound correspondences between a group of New World and a group of Old World languages that have been detected to date. However I cannot share Ruhlen’s conviction that these etymologies point to the origin of the Na-Dene in Siberia; they rather demonstrate the opposite: the migration of the Yeniseians from North America. This is seen in the regularities of sound correspondences between Yeniseian and Na-Dene (the glottal stop shifts from the anlaut in Na-Dene to the medial position in Yeniseian; Na-Dene preserves the initial stop [q], while Yug changes it to a fricative [x]), in the semantic transformation from proto-Athabascan *q’əy “birch tree” to Ket qi?y “birch bark” (the opposite transformation from part to whole proposed by Ruhlen looks unnatural), and finally in the very distribution of the languages in question. The Kets also exhibit proximity to the Amerindian cluster by having avunculoreciprocal traits in their KTS (Dziebel, 1997a) and polysynthetic language morphology (Ivanov, 1982: 141). “Active” syntactic structure widely represented in Native American languages and unknown in living Old World languages is believed to underlie ergativity in Ket (Verner, quoted in Ivanov, 1982: 141).

Summary of Phenetic, Genetic and Idenetic Evidence

In partial accordance with genetic, craniological and odontological data, among the Old World systems, the closest relationship to the ancestral human KTS is maintained by Australasian nomenclatures. Australians and Trans-New-Guineans appear to be closer to each other than either of them to Austronesians, which finds support in a-globin haplotype analysis (Roberts-Thomson et al, 1996). Although Australian and Trans-New-Guinean KTS possess more ancient traits than those of Austronesians, these three populations cluster together as being closer to the ancestral model than Sub-Saharan African populations. Kinship systems favor the common-origin-type of interpretation of the proximities between Amerindians and Australasians (Bonatto et al. 1996) and not recent-contact explanation. KTS can provide an adequate explanation for the preservation of a 9-bp deletion in Polynesians. In comparison to Melanesian systems, Polynesian systems show a drastic reduction of categorical lineages (Incorporating model in all 5 generations), with local collapse of generations (Samoans in Kernan and Coult, 1965) that indicates a small founding group carrying one lineage, and strong tendency towards endogamy (Dole, 1969). This

is consistent with a biogeographic model of island colonization postulating high inbreeding coefficients, low fecundity and relatively high likelihood of lineage extinction (Keegan and Diamond, 1987).

In Sub-Saharan Africa, a clear divide separates the Khoisans, who are conspicuously closer to Australasians and American Indians, from Nilo-Saharans and Nigero-Kordofanians. However, as is the case in Australasia, all three Sub-Saharan populations cluster together as opposed to Afroasiatics. The KTS of the Ethiopian Gurage (Needham, 1969; Leslau, 1979) appears anomalous if seen against their Afroasiatic linguistic background and sits better with the sub-Saharan cluster. This unusual grouping accords with the early genetic results produced by Cavalli-Sforza's team (Cavalli-Sforza et al. 1988).

Thus all historical information that one can extract from the study of modern human populations (craniology, dentition, genetics, idenetics) makes a strong case in favor of the initial dispersal of humans from the Americas into the Old World, and not vice versa as conventional knowledge holds. The distribution of intergenerational kinship markers and the B haplotype in the Americas points to a population radiating from Central America and southern parts of North America, on the one hand, north into modern Canada and via Bering Strait into the Old World and, on the other, into coastal areas of South America. The distribution of fluted projectile points indicates a similar pattern: their near absence in the extreme north of North America, the absence of Clovis-type points south of Panama and the presence of fluted fish-tailed points in western South America (Bryan, 1991: 21, 24-25; Dillehay et al. 1992; Meltzer, 1995: 25).

It is worth recollecting that Boas considered this "middle ground" to contain cultural traits that constitute quintessential (and hence most ancient) pattern of Native American culture. He wrote,

"In a general survey of the ethnic conditions of the American Continent a peculiar uniformity of culture may be observed among the Indians living around the Gulf of Mexico and the Caribbean Sea, on the Great Plains, and in the eastern United States and in a considerable part of South America. All these tribes notwithstanding far-reaching differences among themselves, have so much in common, that their culture appears to us as specifically American. The extended use of Indian corn, of the bean and the squash, the peculiar type of ritualistic development, their social institutions, their peculiar angular decorative art, are among the most characteristic features common to this area. When we compare this culture with the cultures of Polynesia, Australia, Africa, or Siberia, the similarities appear clearly by contrast with the non-American types of culture, and the common American traits stand out quite markedly (Boas, 1910: 530).

Both genetic and kinship evidence agree that, in South America, the groups stretching along the western coast display a closer relationship to this hypothetical center of radiation than do the groups occupying the east-central territories. The KTS of the Panoans, Andeans, Caribs and Mapuche are specifically marked in terms of ancestral features. It is noteworthy that archaeologically the western coastal areas of South America have the most conspicuous record in the late Pleistocene and the early Holocene (Dillehay et al. 1992: 149). It seems therefore likely that the early settlers in South America moved from north to south on both sides of the Andes.

The earliest migrants into the Old World appear to have experienced a bottleneck followed by populational growth. KTS suggest that, at an early stage, two groups have formed in the Old World. One group, probably of a smaller size, headed to Australasia from East Asia splitting on the way into the ancestors of respectively

Australians, Trans-New-Guineans and Austronesians. The area from Siberia in the north to Australia in the south is marked by several “patches” of Amerindoid forms: south-central Siberia (Ket, Altai, Tofalar) uniquely demonstrates the survivals of the Bird-Nester mythological motif; East Asia (Mongolians, central Chinese, Tibetans) uniquely exhibits all the typical Native American haplogroups at low frequencies; while the mountain New Guinea and northern Australia (Keraki, Wikmunkan, Yir-Yoront) shows strong forms of intergenerational reciprocity, with relative age distinctions in the +/-1 generations, almost exactly reproducing some of Native American (Uto-Aztecan) terminologies.

The other group demically expanded in the southeastern direction and reached Africa possibly already in separate waves, the Khoisans representing the earliest inhabitants of the continent. The formation of the Na-Dene in North America was part of the same populational process. The model proposed here shares many similarities with the conventional model succinctly presented by Colin Renfrew (Renfrew, 1992). According to Renfrew, the “initial dispersal” (prior to 15,000 BP) encompassed the Amerind, the Australian, the Khoisan, the Nilo-Saharan and the Trans-New-Guinean groups. Agricultural and nomadic dispersals (after 10,000 BP) involved Afroasiatic and Altaic populations. From the point of view of KTS, Afroasiatic and Altaic clusters possess typologically very derivative patterns known as Sliding Generation and Cumulative. The borderline between these types passes rather neatly along the Ural Mountains. Finally the formation of the Proto-Indo-European population in Anatolia around 6,000 years BP and its later migration north and west (one of the latest waves in Renfrew’s interpretation) underlie the transformation of the Cumulative type into the Lineal type. The KTS of Siberian peoples were significantly altered in the course of post-glacial migrations and nomadic intrusions but the Sami have retained a nomenclature typologically very similar to American Indian patterns.

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