

**Amerindian mtDNAs and Admixture in Siberian Populations:
Examining Alternatives to Traditional Models of Ancient Human Migrations**

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KEY WORDS: AMERINDIANS, MIGRATION, ADMIXTURE, PALEOINDIAN AND
PALEOARCTIC TRADITIONS, "ESKIMO WEDGE THEORY", ARCHAEOLOGICAL AND
GENETIC CORRELATES, MTDNA ANALYSIS, ATHAPASKANS, SIBERIANS, NENANA
COMPLEX, LINGUISTICS, MYTH

Abstract The suggested presence in Northeast Asia of founding or nodal mitochondrial DNA haplotypes for each Amerindian haplogroup (Torrioni et al. 1993a) precludes an alternative explanation, that of admixture between Northeast Asians and Amerindians. This “reverse migration” out of the Americas provides a backdrop for the later formation of Sea Mammal Hunting Cultures, an idea Franz Boas identified as "Eskimo wedge theory" (Boas 1905 and 1910; also see Ousley and others in, *Human Biology*, June 1995). Presumably, as Boas believed, the removal of glacial barriers allowed human contact between the Longitudinal Hemispheres that was geographically un-encumbered and evidenced by widespread Holocene acculturation (also see Ackerman 1982; Dumond 1983; and Heizer 1943; and others) inasmuch as earlier Amerindian tribal populations existed before deglaciation. These assumptions provide an alternative explanation to mtDNA analyses, challenging the idea that Amerindian mtDNA Lineages (AAM1, CAM43, and DAM88) found in Siberians are ancestrally linked to the initial colonizers of the Americas. Rather, mtDNA analysis could be seen to support the Boas data in that the formation of contemporary Circumarctic Populations in Siberia may have been influenced by post-glacial Amerindian movements into Beringia, Siberia, and Northeast Asia. This study will examine this alternative explanation by proposing that Amerindian admixture, evidenced by the presence of common Amerindian mtDNAs in Siberians, links Circum-arctic Populations to the Americas. This is a "positional paper" according an Amerindian contribution to Eskimo and Athapaskan and, as well, Siberians Population formation since these groups share "distinct genetic affinities with Native Americans" (Torrioni et al. 1993b, pg. 591). This paper further accepts that mtDNA analyses concerning founding effects in the peopling of the Americas should be difficult to synthesize since "extensive genetic diversity" and "mutational-drift equilibrium" exists in Amerindian tribal populations (Ward et al. 1991; Chakraborty and Weiss 1991; and others).

Background

The issues defining the scope of Amerindian mtDNA studies have centered on several key questions. These include: (i) were there American Indians in the Americas *before* the beginning of the last glacial epoch (arising ~ 40,000 y.b.p.), (ii) did the earliest human settlers discover the Americas *during* the last glacial Ice Age, (iii) were the immediate ancestors of the Paleoindian Traditions the first humans in the Americas (beginning < 12,000) and, (iv) did Paleoindian Industries develop in pre-existing Amerindian populations following deglaciation and the diffusion of Upper Paleolithic-*like* industries from the north? Archaeological evidence now confirms the existence of South American human habitation in Chile 13,565 y.b.p., long before the advent of Paleoindian Industries (Dillehay 1989, 1997). This and other evidence of mid-Pleistocene New World habitation suggest that novel hypotheses -- those accepting an earlier than Clovis habitation -- should be tested. This paper will investigate genetic correlates encompassing Boas' "Eskimo wedge theory" with earlier Amerindian Paleoindian migrations north into deglaciated North America (Dixon 1993) and beyond into Northeast Asia.

Earlier studies have centered on linking common affinities between given *ancestral* Northeast Asians and *descendant* populations of Amerinds (Greenberg et al. 1986; Laughlin 1980; and Schurr et al. 1990). The Wallace Group propose that all Native American mtDNAs can be traced back into Siberia, and, before that, Northeast Asia, to single 'founder' haplotypes for each haplogroup defining Amerindians today (Wallace et al. 1985; Schurr et al. 1990). These haplogroups are defined in Torroni, Schurr et al. (1993a).

Each haplogroup was shown to be defined by a specific set of linked polymorphisms, as follows: haplogroup A by an *Hae*III np 663 site gain, haplogroup B by the 9-bp COII-tRNA^{Lys} intergenic deletion (Cann and Wilson 1983; Wrischnik et al. 1987) and an *Hae*III np 16517 site gain; haplogroup C by a linked *Hinc*II np 13259 site loss and an *Alu*I np 13262 site gain; and haplogroup

D by an *AluI* np 5176 site loss. Haplogroups C and D are almost always associated with *DdeI* np 10394 and *AluI* np 10397 site gains. (pp. 591-592)

The presence in Northeast Asia of proposed founding or nodal haplotypes for three-of-the four most common Amerindian haplogroups (A, C, and D) precludes any suggestion of admixture resulting from Amerindian migration(s) out the back door of the Americas during the Holocene. The Wallace groups interpretation of founding effects, as suggested in mtDNA analysis, seems consistent with earlier genetic, dental, and linguistic assessments (Zegura 1987, Turner 1987, Greenberg 1987). The main goal of this paper is to evaluate Boas's untested model highlighting today's view of pre-Clovis habitation and subsequent Amerindian gene flow leading to the formation of Northeast Asian Populations.

Archaeological Consequences and Genetic Correlates This paper tests principles adopted from Lewis Binford's (1983a) scientific identification in archaeology of evaluation and analysis through "Paradigm Growth and Theory Building." The shift in archaeological interpretations that has followed the verification of pre-Clovis human habitation has brought with it discussions of post-Glacial movements of once glacially isolated Amerindian populations north, into deglaciated North America (Hicks 1998; Dixon 1993). Further analysis could identify these mid-Pleistocene New World habitations as prime examples of what Binford refers to as "Black Swans" since they defy (archaeologically speaking), the standard criterion based on Old World discoveries. A scientific conundrum exists in that, for one reason or another, many archaeologists have been reluctant in accepting "earlier than Clovis" habitations (Lynch 1991; Dencauze 1984; Martin 1987). This is beginning to change with the publication of Dillehay's second volume on Monte Verde (see Fagan 1997). Anthropological inference must accompany the shift in archaeological assertions accompanying the abandonment of the "Clovis First" hypothesis.

Certainly, all swans are not white. By the same token, mid-Pleistocene New World human habitations should not be required to meet Old World criteria (Owen 1984). Binford -- in accepting an earlier than Clovis human habitation -- is willing to take his own persuasion even further by suggesting that northern Na-Dene speakers may have earlier roots in southern Dene speaking Amerindians (L.S. Binford, per. comm. 1997). Population movements defined by the "Clovis First" paradigm have left archaeological science -- and its related fields in anthropology -- insufficient momentum in resolving the implications an "earlier than Clovis" presence for mankind in the Americas offers (see Owen 1984).

The Old World genetic evidence documenting a recent expansion from a common origin (Johnson et al. 1983; Cann et al. 1987), can be seen to correlate archaeologically with the spread of modern humans, beginning less than 50,000 years ago (Sherry et al. 1994; Mellars 1991) even into Africa (Binford 1984). MtDNA analysis suggesting expanding population size, founding effects, and cladistic support for an out-of-Asia movement of today's human populations (Johnson et al. 1983), is not at odds with the archaeological evidence supporting the formation of a new, modern human occupation that, in terms of the European record, emanates from Western Asia (Leonova 1994; Mochanov 1980; Tang and Gai 1986). That is, the Russian Steppe and Northeast Asian Late Paleolithic predates the earliest Aurignacian of Europe demarcating the dawn of Upper Paleolithic Cro-Magnon habitations.

Conversely, the same archaeological correlation's assigned with the demic diffusion of an evolving Upper Paleolithic Industry in the Old World are surprisingly missing from evidence distinguishing the earliest archaeological record of New World's "pre-Clovis" Amerindians (Dillehay 1989; Adovasio and Carlisle 1986; Guidon and Delibrias 1986, Fagan 1997). The difficulties archaeologists have in applying the same criteria used in defining contemporary Pleistocene habitations of the Old World to the New have influenced attempts to bring meaning and/or widespread academic acceptance to what is indeed a limited archaeological production in mid-Pleistocene America (Owen 1984; Dincauze 1984; Jelinek 1992). This paper's intention, despite the archaeological standard's and a lacking Paleolithic criterion that have made it

difficult to interpret pre-Clovis occupations (and/or evaluate their anthropological implications, see Hrdlicka 1912; 1925; Lynch 1991), is to re-evaluate the significance of such a presence and to reconsider the possibilities of Amerindian movements *into* northeast Asia at the end of the last Ice Age (i. e. Boas 1905; 1910).

Introduction

The Meeting of Two Worlds The earliest presence of blade tools in Northeast Alaska has been attributed to the "Nenana Culture" linking them with the earlier "Dyuktai Cultural Traditions" of Northeast Asia (Mochanov 1980; Goebel, Powers, and Bigelow 1991; Hoffecker, Powers, and Goebel 1993; Reanier 1995). Siberian stone age technologies and Hunting Cultures have long been hypothesized to be antecedent (> 12,000) to later Paleoindian Traditions. The diffusion of these Old World industries -- south -- into pre-Clovis Amerindian populations will be considered here, against the backdrop of a subsequent movement of "Paleoindians Traditions" northward beginning 11,200 y.b.p. (Dixon 1993). Indications are that later "Paleoindian Traditions" with their diagnostic "fluting" may have been refined by Amerindians after the diffusion of earlier Upper Paleolithic-like industries found in Northeast Asia. Recently, a more direct route across the southern-enge of the Glacial Shelf that spaned the North Atlantic during the Last Ice Age has been proposed. The authors identify processural similarities in the manufacture of the Solutrean Willow Leaf Points of Europe and the Fluted Traditions that are unique to the Americas. The fluted "Paleoindian Traditions" are believed to be in situ developments emanating from Eastern North America (Stanford 1982) haveing spread to and Mid-Continental America following thier invention (Bryan 1991). A *demic* diffusion of "Paleoindian Traditions" north, following deglaciation, will be reconsidered since: "It is not at all improbable that [fluted points] were invented in America and reached the Arctic with the hunters who followed game northward with the retreat of the Glaciers (Krieger 1964)." Wormington held a similar opinion:

If the writer is correct in believing that the tradition of fluting developed in the southwest or in the Plains, the fluted specimens found in the extreme north may represent the spread of a trait through diffusion or by a later northward movement of people who employed this technique. In this case they would be more recent than those found farther south (Wormington 1957, pg. 210)(Reanier 1995 pp. 35-36)."

Again, Paleoindian movement north is best accomplished by accepting that there existed mid-Pleistocene Amerindians isolated primarily by glacial barriers (Mandrick 1992). It is thought that pre-existing Amerindian populations were primarily relying on simple bone and wood tool industries connected with a "pre-projectile point horizon" (Krieger 1958; Wormington 1957; Bonnicksen and Young 1980).

This positional paper addresses admixture between Siberians and Amerindians in northeast Asia (as evidence of Paleoindian migration north), and later (Boas's Eskimo wedge), during the formation of maritime Circumpolar People in coastal environments of Eastern Beringia between 10,600 and 6,000 years ago. These rarely discussed alternative directions of migration -- complemented by accepting a pre-Clovis occupation of the Americas -- suggest that movements of Amerindians into the north followed the retreat of glacial barriers after the *in situ* development of "Paleoarctic Traditions" in southeastern North America. Interior migrations can be traced to the Americas (north and east, out of unglaciated regions of North America), by boreally adaptive Athapaskans (Boas 1905; Dixon 1993) and in eastern North America by Algonquian speakers (Rogers 1985). These movements may have continued well into late-Holocene times (Ackerman 1982). Even more recent movements suggest acculturation during the Post-Paleoarctic interval in the Central Brooks Range (Schoenberg 1995).

This study proposes that distinct genetic affinities linking Amerindian mtDNAs with Siberians may have accompanied the formation of the today's Circumarctic Populations. As Boas suggests a separate "Eskimo wedge" divided Northeast Asian Amerindians from their

parent stock in the Americas. Boas alternative naturally follows today's scientific extenuation of a presence of pre-Clovis people and with it, the testing of the possibility of regional expansions into deglaciaded areas of the Northern Hemisphere by these first Americans. However, this (back migration) counters traditional scientific wisdom that today calls for a northeast Asian origin for Eskimos and Athapaskans (Greenberg et al. 1986; Torroni et al. 1993a; Shields et al. 1993). Boas's Historical interpretation provides an alternative measure from which to address the direction of human migration, bringing into question the once dominant "Clovis First" theory and the limitations often used to guide analogous genetic observations.

Other Data Stephen Ousley, in *Human Biology* (June 1995), identified numerous relationships shared between North Pacific groups, some stretching from Washington State in the Americas to the Island of Hokkaido in Japan. "Their common history is also expressed in Eskimo and Koryak mythology, belief, ritual, social structure, and funeral clothing (Arutiunov 1988b) (Ousley 1995 pg. 432)." Other affinities shared with Northeast Asians include; 1) GM haplotypes (Williams 1985); 2) archaeological signatures including the Anangula Blade Complex, which may be older in Alaska (Ackerman 1992; McCaryney 1984); Norton and Choris phased pottery (Ackerman 1992); "preparations and use of poisons (Heizer 1943)"...Nootka dugout canoes and Eskimo *uniaks* (Arima 1988; Rousselot et al. 1988); and socioeconomic organization where "Clans included speakers of different languages and dialects (Ousley pg. 433)."

Ousley (1995) further suggests a non-coastal sphere of influence for the Na-Dene; "In contrast, the Haida, Tlingit, and Tsimshian showed greater interior influences and were the result of later population movements to the coast (pg. 433);" while, "Leer (1991) uncovered unique syntactic elements in Aleut that were borrowed from northern Northwest Coast languages (Eyak, Haida, Tlingit), including intense contacts between Aleuts and peoples on the northern Northwest Coast (Ousley pg. 434)." Finally, Ousley (1995) indicates that "Although the archaeological record of northeast Siberia is poorly known, archaeological, ethnographic, and linguistic data suggests that cultural exchanges across the north Pacific were extensive (pg.

435)." The evidence of continuing contact could link "acculturated" coastal Amerindians to the formation of populations presently occupying Beringia, and earlier, to those that developed Paleoarctic Traditions "about 10,600 B.P. (Dixon 1993 pg. 65)." Also, coastal Athapaskans could be linked to *interior* Na-Dene speakers and they in turn, to an earlier movement north and west of populations using Paleoindian Traditions emanating from mid-Continental North America, as suggested earlier. Amerindian migration into Northeast Asia *as* proposed by Boas, occurred before the formation of the Inuit tribal system.

Material and Methods

Mitochondrial DNA studies and interpretations concerning the origins, affinities, and genetic diversity of the American Indians have been extensively reported (Bailliet et al. 1994; Torroni et al. 1993a, and 1994; Cann 1994; Merriwether et al. 1993, 1995, and 1996), and have expanded the data base and implications generated in earlier publications (Wallace et al. 1985; Schurr et al. 1990; Ward et al. 1991; Chakraborty and Weiss 1991; and others including Johnson et al. 1983). Other studies provide comprehensive mtDNA data sets by including those of the Circumpolar Populations of Siberia, Beringia, North America, and Greenland (Torroni et al. 1993b; Shields et al. 1993). These genetic studies seem to concur that Western Circumpolar People and Amerindian Tribal groups have distinct genetic affinities. Not surprising, but contrary to the "Clovis first" model, is the inference that the formation of the Circumpolar Populations (including the Eskimo and Athapaskans), appears to have occurred much more recently than the formation of individual Amerindian Tribal Groups, those inhabiting regions south of the deglaciated areas (Torroni et al. 1993b; Shields et al. 1993).

It should be noted that; the tenets of this paper provide many novel interpretations contrasting data collected by the aforementioned authors. Specific "Materials and Methods" undertaken and the compilation of the data -- referred to in this positional paper -- can be found in the original papers cited. I am deeply indebted to the subjects studied, to the authors who have

acknowledged their contribution and, to the researchers themselves who have compiled and analyzed the data used in this analysis. However, it has come to my attention that many of the ideas and opinions presented in this paper are not optimistically pursued by the original authors. Any inconsistencies that might be found in this paper, or interpretations that they may or may not share, should not be attributed to those researchers.

ASSUMPTIONS

MtDNA Data Cladistic analysis and assumptions used in this positional paper have been adopted from other studies (Johnson et al. 1983; Excoffier and Langaney 1989). The maternal heredity and high mutation rate of the mtDNA genome aids geneticists in determining the source for the initial movements of fully modern *Homo sapiens* providing strong support for archaeological assessments of a recent common origin for Modern Humans in the Old World. The presence of a distinctive allele (haplotype or lineage) in any given population can be measured against its potential to be identified as a regional founding haplotype. Alternatively, indications of admixture within a regional population can be measured by comparing the frequencies of specific mtDNA lineages within and outside the regional population being studied. Simply, the presence of an uncommon haplotype(s) in any given regional population could support evidence of migration and admixture suggesting an extra-regional origin for certain "rare" mtDNA lineages.

The inability of mtDNA analyses to confirm the "Out of Africa" hypothesis (Templeton 1993) or resolve the origins of modern humanity (Long 1993) should not reflect against the merits of mtDNA cladistical analysis and its documented ability to 1) define the initial and accumulated mtDNA sequences of indigenous populations that define their original regional expansions (i.e. Johnson et al. 1983; Excoffier and Langaney 1989; Templeton 1993); 2) discern

which mtDNA lineages were initially present from those that were generated during the initial regional expansions of modern humans into continental and regional areas of the world; 3) determine if the presence of admixture is a viable alternative to hypotheses suggesting that certain rare mtDNAs represent founding lineages; and 4) the maternal ancestry and regional source for the *admixing* (migrating) population (Pasarino et al. 1993).

“The author advocates thoughtfully planned experiments as the best investment. He [Weiss] writes: ‘Order can be found in the complexity if we know what to look for. I have tried to suggest that it is in the context of evolution that we are being led to such a synthesis (Weiss 1996 p. 1566) (Terwilliger 1997 p. 314).’”

This analysis, of Holocene Amerindian migration into Northeast Asia, offers one example of the interplay (and resulting complexity) Weiss seeks to interpret. In order to trace the origin of gene flow to its ancestral population it should be presumed that admixing haplotype(s) would 1) be found in higher frequencies in the ancestral group from which they presumably originated unless pre-existing populations do not exist (i.e., in Polynesia and Madagascar, or was derived following isolation, as we are testing for the New World); 2) be found in association with other regional mtDNAs and/or nuclear (nDNA, including HLAs) haplotypes also affirming an independent origin; and 3) not be equivocated as nodal mtDNAs, but rather, the result of "regional subdivision" since, presumably, they would not be a 'founding lineage' related to the original population expansion in the specific regional population under consideration.

Examples suggesting that gene flow can be used to trace the recent arrival of humans from an outlying area can be cited in the detection of the mtDNA Region V *9bp* deletion found in *coastal* New Guinea and *coastal* Melanesia where it appears as an admixed marker associated with the later arrival of Polynesians (Stoneking et al. 1989). By example, the *9bp* deletion does not appear to be a founding lineage in New Guinea, Australia, and Melanesia since it is virtually

absent in the interior aboriginal populations who presumably first settled Oceania. Type B mtDNAs encompassing the Region V 9bp deletion are, however, found in their highest frequencies in Middle and Equatorial Amerindians and have been detected in New World mummies dating to 6,000 y.b.p., predating the peopling of Polynesia.

Mutation rates, so often used to detect the age of a given population, have been shown to be highly variable and thus, unreliable for determining the age of specific population since selection and drift can greatly effect divergence times (Excoffier and Langaney 1989; Templeton 1993). Moreover, as Weiss seems to be asserting (op. cit. 1997), alternative, all inclusive models need to be addressed when traditional one dimensional models are unable to support a specific paradigm being tested. This has been called for, not only for the peopling of the Americas, but also, in the modern peopling of the Old World (Templeton 1993; Harpending 1994). As Eموke Szathmary (1993b) points out in the closing lines of her Invited Editorial of the New World mtDNA data: "Alternative models now need to be examined, and alternatives already exist. Perhaps these should be considered 'in an explicit and preferably numerical manner' (Madison 1991, pg. 362)(pg. 797)." Szathmary also (1993b pg. 794) summarizes the core anthropological issues and the theories being put to test in the Americas as "(a), contrasting models of occupation and (b), timing of human entry into the Americas." As she points out, "It is clear that uncritical use of hypotheses under dispute can be unwise" (ibid. 1993b, pg. 795). Further caution needs to be applied in testing mtDNA results based primarily against the three wave hypothesis in that; "If Greenberg and his supporters (e.g. see Ruhlen, in press) have lumped languages into "Amerind" inappropriately, then use of this linguistic category for testing of genetic hypotheses could produce spurious outcomes (ibid. 1993b pg. 795)."

Examining Alternatives

Shifting Paradigms The presence of proposed Amerindian "founding haplotypes" (rare Asian mtDNAs), in Siberian populations is presented by Torroni et al. (1993b) to "establish that all native American mtDNAs derived from four founding haplotypes" (1993a, pg. 584). There

have, however, been many other studies that challenge this finding (Ward et al. 1991; Chakraborty and Weiss 1991; Horai et al. 1993; Bailliet et al. 1994; and others including Cann 1994). Although the Wallace Group contended that a "dramatic founding effect" was evidenced by the increased frequency of rare Asian mtDNAs in Amerindians (they have since softened this opinion while noting that it now seems more complicated than initially believed; T. G. Schurr personal communication 1995), it should be noted that a total absence of any of the more common Asian markers was inconsistent with what was expected (Wallace et al. 1985, Schurr et al. 1990). Examinations of Amerindian mtDNAs continue to bear out that the more common Asian mtDNAs, found to be central to the Late Paleolithic radiation of Southeast Asian people (Ballinger et al. 1992), are surprisingly absent in Amerindian populations.

Amerindian admixture and a resulting reversal of gene flow provides an alternative explanation for the detection of A, C, and D lineages in Northeast Asians (see Table 1). This follows Boas's contention (the first phase of his "Eskimo wedge theory") suggesting an Amerindian *source population* for the easternmost Siberian populations as not a *founding population* for the first Americans as the Jesup expedition initially hypothesized. Recent studies distinguish the same groupings identified by Boas and his collaborators.

Based on the *HLA-DRB1* frequency data, the seven Siberian samples can be divided into two groups which correlate with the geographical distribution of the populations but not with their linguistic affiliations. The two populations in the interior of Siberia, the Evenks and the Kets, are on a different branch of the phylogenetic tree (Fig. 4) than the five eastern Siberian populations. The Evenks speak a language belonging to the northern Tungusic branch of the Altaic language family (Ruhlen 1988). The Ket language is of undetermined origin, a language isolate. The Udegeys speak a language of the southern Tungusic

branch, the Koryaks and Chukchi speak Paleo-Asiatic languages, the Siberian Eskimos speak Yupik, and the language of the Nivkhs is another isolate of unknown origin (Grahovac et al. 1998 pg. 41).

Post Ice Age movements of "regionally specific haplotypes" (A, C, and D lineages out of the Americas) could be assumed by accepting mid-Pleistocene Amerindian isolation coupled with the earlier loss of the effects of bottlenecks that is supported by the existence of mutational-drift equilibrium in Amerindian populations (Chakraborty and Weiss 1991). Chakraborty and Weiss report that no specific Amerindian lineage (let alone A, B, C, or D) can be distinguished as the oldest. The detection of mutational-drift equilibrium in Amerindian populations (if "relevant," see Templeton 1993 pg. 59), contrasts sharply with studies of Old World populations where disequilibrium and bottleneck are seen to support a recent expansion from a common ancestral population (Johnson et al. 1983; Cann 1987; Excoffier and Langaney 1989).

Re-interpretation

Table 1 identifies what have been termed "rare Asian mtDNAs" haplotypes (A, B, C, and D) that may simply link Northeast Asians with Amerindians. These mtDNA haplotypes found in Northeast Asians (haplotypes **A**AM1, **C**AM43, and **D**AM88) and (for group B haplotypes associated with the Region V *9bp* deletion), **B**AM13, found in association with most Polynesians, demonstrate affinities with Amerindian mtDNAs. If the presence in northeast Asia of these haplotypes are not evidence of 'founding lineages' for each Amerindian haplogroup (as I am suggesting), then an alternative explanation must be identified. This paper identifies such an alternative; that admixture between Northeast Asians and Amerindians accompanied the Holocene re-formation of Circumarctic Populations in Siberia, contrasting the disguise of affinities as "founding lineages" with evidence of "back migration" .

It must be first assumed that southern Amerindian tribal groups are older than the formation of populations living in deglaciated North America (a paradigm central to this hypothesis). This requires that Amerindians were south of North America's Wisconsin Glacial expanse prior to deglaciation (a perspective endorsed by nearly every genetic and linguistic study of Amerindians). Could recently derived Amerindian lineages have been carried out of the Americas by Athapaskans and early Sea Mammal Hunting Cultures, with this being evidenced by post-Ice Age admixture with Siberians? This hypothesis suggests that "regional subdivision" (again, see Templeton 1993) occurred in the Americas (suggested by the high mutation rate of mitochondrial DNA) and that this led to the presence of novel -- A, B, C, and D -- mtDNA sequences. Pre-Clovis habitation would have isolated the "differentiation of the distinctive Amerindian types ([as suggested from anthropometric data], see Ousley 1995 pg. 428)" accentuating the effects of the glacial barrier that separated New and Old World People. This isolation is further distinguished by the contexts of two separate archaeological records that remained unrelated until the end of the Last Glaciation (Hicks 1995).

Many, including Shields et al. (1993), have concluded that Circumarctic People are younger than Amerindian populations to the south.

Low sequence diversity, coupled with the broad geographic distances over which some Circumarctic populations (e.g., Alaskan Inupiaqs and West Greenland Eskimos) have become established, suggests that the establishment of these far-flung populations occurred during a relatively short period of time. By contrast, the mtDNAs of Bella Coola, Nuu-Chal-Nulth, and Yakima are broadly divergent, even though the present geographic distribution of these people is confined to a relatively small region. This suggests that these Amerind tribes are much older than the Circumarctic tribes and have undergone considerable localized genetic differentiation (Shields et al. 1993 pg. 558)."

In this it is suggested that the present Beringian Populations post-date the formation of the Amerindians to the south while scientists have yet to suggest that the Eskimo represent the ancestors of the Amerinds. One thing is certain, they do share common affinities with Amerindians including mtDNA haplotypes (Torroni et al. 1993a, and 1993b) and dental traits.

“In other words, the following populations were classified in the Sinodont pattern: Amur, Archaic Canada, Athapaskan, California, Eastern US/Canada, Gulf of Alaska, Hong Kong, Japan, Lake Baikal, NE Siberia, NW Canada/US, Southwest US; and in the Sundadont pattern: Burma, Early Malay, Early Mainland (SeA), Indomalaysia, Jomon, Nepal, Philippines, South China 1 and 2, South East Asia, Thai, Taiwan; and Europe was classified as a group alone (Haydenblit 1996 pg. 237 and 239).”

Torroni et al. (1993b) and Shields et al. (1993) have demonstrated that the only mtDNA lineages directly linking Northern Asians and Amerindians are those found in the more recently formed Circumarctic Tribes. Yet, these studies both ignore the possibility that there might be an alternative explanation, this being admixture resulting from a demic contribution *to* the formation of East Asian Circumpolar Populations *from* the Americas. We should remember here that the Circumarctic Populations are believed to be younger than the original Amerindian to the south. I quote Shields et al. (1993) again here;

"Moreover, lineages observed in distinct populations are intermingled among the branches of the tree, with no obvious clustering of lineages by the geographic location, or linguistic affiliation, of the tribe from which they were ascertained. For example, individual lineages of Chukchi, West Greenland Eskimos, Athapaskans, and Haida are scattered throughout the tree. This pattern is exactly what would be expected for populations which have recently undergone a

demographic expansion and which are in the early stages of evolutionary divergence" (Shields et al. 1993, pg. 558; emphasis added).

The consensus view surrounding Amerindian descentancy theories -- through which most all subsequent data is analyzed -- starts with the initial hypothetical given that Amerindians can be traced to founding populations in Asia (Acosta 1676; Greenberg et al. 1986; and others). This scenario limits, without merit, the possibility that Amerindians may have contributed to the formation of Northeast Asians following deglaciation. That is, the consensus view adopted by cladistical analysis -- perhaps through the sanctioning of archaeological conservatism by Clovis First proponents -- contends that the Eskimo and Athapaskans are, themselves, more recent descendants of the same Asian ancestors as the earliest Amerindians (Torroni et al. 1993a and 1993b; Greenberg et al. 1986).

Accepting the existence of mid-Pleistocene Amerindian pre-Clovis occupations could lend support to Boas's earlier hypotheses by linking mtDNAs with anthropometric, linguistic, archeological, and cultural affinities shared between Siberians and Native Americans (see Ousley 1995). This alternative proposes that i) Amerindians contributed to the formation of the Athapaskans and Eskimo and later, admixed, with Northeast Asian Circumarctic People following deglaciation; ii) admixture between Northern Amerindians (i.e. Eskimo and Athapaskans) and Northeast Asians occurred in Siberia and, to a lesser extent, Mongolia and Tibet. Simply, Ice Age Amerindian migrations into deglaciated North America are a viable explanation for the decreasing frequencies in northeast Asia of common Amerindian mtDNA lineages.

Never-the-less, it seems unlikely that several independent migrations from Asia , all carrying these specific "'supposed' founding" Amerindian Lineages (Torroni et al. 1993a)? Not Likely! Alternatively, if the four widespread Amerindian mtDNA haplotypes are not founding lineages then any evidence of founding effect(s) for the Native Americans is likely to remain undetectable (Chakraborty and Weiss 1991; Szathmary 1993). Moreover, if A B C and D

represent more recent mutations the regional specific frequencies of haplotypes A, B, C, and D *post-dates* the original or nodal Amerindian mtDNA diversity. The contention, that mutational-drift equilibrium exists in the first Americans would acquiesce to this perspective since any evidence of a founding effect in the peopling of the Americas has been erased. This kind of analysis suggests, rather, that A, B, C, and D haplogroups represent an Amerindian example of Templeton's "regional subdivision", a direct example of drift that, "could reflect the age since the last favorable mutation[s] arose in the population (1993 pg. 59-60)."

Founding Effects in Northeast Asian and American Circumpolar People

Despite the vast geographic area inhabited by Circumpolar People their overall genetic diversity is relatively low (Shields et al. 1993; Torroni et al. 1993b). In fact, there is a marked contrast between the diversities found in the Circumpolar People and those comprising much smaller geographic boundaries defining southern Amerindian tribal groups. Clearly, genetic diversity estimates indicate a much greater time depth for independent Amerindian Tribal Groups each predating the Holocene formation of Circumpolar Populations. Many linguists contend that Greenberg's "Amerind" represents more than a single language family (Campbell 1986; Nichols 1990). These findings conflict with the most basic assumptions supporting the "Clovis First" model (Hoffecker et al. 1993) and a recent origin for the diversity of Amerindian Tribes. If Amerindians are derived from northern Asian ancestral populations, these matriarchal northeast Asians need to predate the migrant populations comprising the Amerindians to the south. Just as scenarios advocating population extinction or replacement in pre-Clovis America have been entertained, so too must admixture in Siberia (for the earliest ancestors of pre-Clovis Amerindians) be anticipated, especially if 33,000 year old or older dates prove to be accurate. MtDNA analysis, suggesting Holocene population re-formation resulting from migrations back into Siberia, must be incorporated into hypotheses that accompany the gathering of new data (Bailliet et al. 1994; Merriweather 1994). Again I will turn to Szathmary for her own appraisal of the Shield et al. (1993) dating of the age of the Amerindian mtDNAs;

Would knowing the standard errors of the age estimates make a difference? Are the pre-Clovis time depths obtained on archaeological sites wrong? Would older mtDNA time depths be obtained were the mutation rate based on the coalescent applied to South America? Is the problem more that the mutation rate is derived from the coalescent? These questions clearly need to be addressed (1993b pg. 797).

Shields et al. (1993) seem to support a recent Asian ancestry for the contemporary Circumpolar Peoples while reluctantly pointing out that an Amerindian contribution cannot be ruled out. Admixture would provide an alternative to the three wave hypothesis by identifying an Amerindian origin (e.g., Szathmary 1993a), for both the Athapaskan and Eskimo/Aleut. The fact is, within-group divergence found in independent southern Amerinds is greater than those characterizing the Circumpolar Population despite smaller geographic distributions of the more ancient Amerindian Tribal Groups (Shields et al. 1994).

The Traditional Amerindian Migration Model Torroni et al. (1993b), in an attempt to identify Amerind phylogeny, hypothesize that corresponding rare Asian mtDNA *haplotypes* are the ancestral or nodal type for each Amerindian *haplogroup* it is affiliated with (**Table 1**). The criteria used to test the dominant paradigm (that is an Asian origin for the Eskimo, Athapaskans, and Amerinds), presumes that the founding haplotype for each Amerindian haplogroup should; 1) be widespread throughout the Americas; 2) be central to the branching order of their haplogroup in the phylogenetic analysis; and 3) be detected in East Asian or Siberian Populations (Torroni et al. 1993, pp. 581 and 582). Again, this model fails to address the alternative discussed here, that admixture from the Americas contributed to the formation of the Circumpolar Populations from Eastern Siberia to Greenland.

Surprisingly, two of the hypothesized haplogroup founder types either do not appear in Siberia (all group B haplotypes) or, as for type C, are difficult to discern cladistically as the haplotype central to the radiation of the Amerindian haplogroup containing it (see Torroni 1993a pgs. 583-4). As Torroni et al. (1993a) point out, "Contrary to the results of the parsimony analysis, the putative founding group C haplotype observed in east Asia was not AM32 but, instead, haplotype AM43, one that is identical to Asian haplotype AS65 found in 5.0% of the Taiwanese Han and other northeast Asians (Ballinger et al. 1992)," (Torroni et al. 1993a, pg. 583). Moreover, the group C mtDNA that is most parsimonious, AM32, is not proposed to be the founding haplotype because AM43 is the only group C haplotype found in Asia.

Two dramatic founding effects could be presumed: one following the migration(s) of the initial Amerindian Populations into the New World, the second during the formation of Circumpolar People. In hypothesizing an alternative explanation -- back migration and admixture -- I am identifying that the eastern-most Beringians and, as well, the original Amerindians, are missing any of the more common southeast Asian mtDNAs. The chances that *only* 'rare' Asian mtDNAs (equivalent to ~ 5.0 % of the total mtDNA diversity) would distinguish the formation of two or more migrating groups (or waves of migrations), is unreallistic. Holocene "back-migration" provides a less complicated alternative for the shared affinities and the direction of gene flow since Amerindians pre-date the Holocene formation of Circumpolar People.

Merriwether et al. 1995 suggest that it is implausible for the more common Asian specific haplotypes to all have been lost in the founding Amerindian population(s) and as well, the later populations comprising the Eskimo/Aleut/Inuit and Athapaskans (see Table 2). They suggest that separate migrations into the Americas for Eskimo and Athapaskans carrying the same "rare" Asian mutations as the Amerinds, themselves, is not tenable (1995).

"The fact that Native Americans all share variants of the same founding lineages indicates that they are likely to have come from the same source population, and

that it is unlikely that multiple migrations from the same area would continuously choose the same four lineages from a subset of the lineages available in the parent population. Clearly, examination of contemporary Asian and Siberian populations indicate that these four lineages are not the only lineages present (pg. 427)"

Merriwether et al. (1995) are perhaps the first to use mtDNA analysis to discreetly address the likelihood of Amerindian migrations into Siberia, creating an alternative to the formation of the Circumarctic Peoples that would support the Boas data and unpublished results of the Jesup Expedition.

"The current Native residents of Alaska and Siberia may be descendants of more recent migrations from the Siberian side of the Bering Strait (as suggested by Torroni et al., 1993b; and Shields et al., 1992, 1993), *or from migrations back into the area from within the New World* (Merriwether et al. 1995 pg. 424 *emphasis added*)."

If "regional subdivision" accrued in the Americas, it may be possible to hypothesize that A, B, C, and D lineages represent polymorphic events that took place in isolation within the Americas during the last Ice Age (see Table 3). Others have identified mtDNA subdivisions that are specific to regional populations of the Old World (Johnson et al. 1983; Ballinger et al. 1992; Passarino et al. 1993; van Holst Pellekaan et al. 1998). Similar evidence of founding effects, during the formation of the Circumarctic Populations, can be detected in accordance with mtDNA mutational divergence that may have occurred during the regional expansion of Amerindians into deglaciated areas of the Northern Hemisphere. For example;

The Siberian mtDNAs were also screened for the absence of the *RsaI* np 16329 site, a mutation found in 29.0% of the Na-Dene haplogroup A mtDNAs but not in those of Amerinds (Torroni et al. 1992, 1993). This marker was not observed in

any of the Siberian mtDNAs analyzed in the present study (tables 1 and 3), nor in the Alaskan and Siberian Eskimo, Aleut, and Chukchi mtDNAs analyzed by Shields et al. (1992). Consequently, this mutation appears to have arisen in the Americas after the ancestral Na-Dene separated from the modern aboriginal Siberians and Amerinds (pg. 598).

Whether a selection mechanism is at work, or not, in affixing the absence of the *RsaI* np 16329 in 29% of the Na-Dene, the evaluation suggests that novel mutations are useful in determining cladistic relationships in isolating private polymorphisms in adjacent peoples who share an earlier common origin (Torrioni et al. 1993a). The post-nodal position of an *HpaI* site at np 3592 further suggests that mutational events need not be initially conceived by maternal inheritance mechanisms but retained because of them, in that, "regional subdivision" can be Regional, and, as well, Population specific. Moreover, the occurrence of post-nodal mutations in isolated populations suggests that neutral and/or perhaps selective pressures influence the accumulation of 'localized' sequence diversity (Passarino et al. 1993; Cann et al. 1987).

Discussion

The Eskimo, Athapaskans, and Amerindians appear to make-up one specific group -- with distinct mtDNA affinities -- while all Old World modern human populations make up another. Others have found a similar lack of comparison between the distribution patterns of the mtDNAs of Amerindians and Old World populations. These differences include evidence in Amerindians of "mutation drift equilibrium," "extensive mtDNA diversity" on the "tribal level" (Ward et al. 1991), cladistic divination of an Asian Origin that is at least dramatic (Wallace et al. 1985) and, surprisingly evidenced by "a few Asians, if any" (Horai et al. 1993, pg. 23). Extensive independent Amerindian tribal diversity, equivalent to ~62% of all sub-Sahara Africa or ~81% of urban Japan, has been detected in the mtDNA of independent New World Tribal Peoples (the Vancouver Island Nu-Chal-Nulth were analyzed by Ward et al. (1991), a finding that supports an

antiquity well outside the limits initially hypothesized. All of these findings are fundamentally inconsistent with what was expected in determining a recent origin for the modern humans of the New World, and/or with it, a "Clovis First" peopling of the Americas (Scheilds et al. 1993; Martin 1974; 1987; Haynes 1967).

Pre-Clovis or paleoarchaic mid-Pleistocene American habitations defy any relationship to Old World Upper, Late, or even Middle Paleolithic-*like* industries (Adovasio and et al. 1980; Carter 1980; Dillehay 1989; Berger and Orr 1968; Mirambell 1978; Guidon 1986; MacNeish 1979; Krieger 1964; and others). However, we have learned from the discovery of an irrefutable mid-Pleistocene human occupation at Monte Verde, dated at $13,565 \pm 250$ BP is that it is unreliable to contend that sophisticated lithic tool industries or refined hunting technologies should be used as a criterion for substantiating earlier-than-Clovis human occupations of the Americas (as suggested by Hoffecker et al. 1993; Lynch 1991). Monte Verde's earlier dates of 12 -14 thousand years ago may pail in significance if an earlier "learned economy" detailing habitation at Chile's Monte Verde 33,000 years ago is established.

Perhaps the most important lesson to be gained from the verifiable evidence of early human occupation at Monte Verde, Chile, is that we should not wait for a majority of archaeologists to accept this and other occupations before determining, for ourselves, the anthropological significance and implications of a mid-Pleistocene Amerindian presence. The testable hypothesis that was endorsed here identifies that Amerindians were in the Americas before the formation of populations now living in deglaciated areas of North America. The hypothesis that awaits further testing contends that Amerindians contributed to the formation of North American Tribal groups, specifically, the Athapaskans and Eskimo, and that they, in turn, migrated beyond Beringia contributing to the formation of northeast Asian and Circumarctic Peoples? One line of agreement can be confirmed (even without widespread archaeological support), there are alternative routes of migration (out the Back Door of the Americas), when accepting a greater than "Clovis Only" modeling for the peopling of the Americas.

Contrasting Examples Differing interpretations of mtDNA data generated in studies of Amerindians have led to contrasting opinions (Cann 1994). The existence of 'mutational-drift-equilibrium' itself suggests an indefinite time frame for the Amerindian branch of the human mtDNA tree. Contrary to evidence in the Old World of "bottlenecks" (associated with the spread of modern humans Stoneking et al. 1987), is the evidence that this phenomenon -- bottlenecks -- is not observed in the radiation of New World populations (Horai et al. 1993; Chakraborty and Weiss 1991; Baillett et al. 1994).

"Furthermore, sequence differences in all pairwise comparisons of Native Americans showed a bimodal distribution that is significantly different from Poisson. These results suggest that the ancestral Native American populations underwent neither a severe bottleneck nor rapid expansion in population size, during the migration of people into the Americas" (Horai et al. 1993, pg 23).

This discovery seems inconsistent with the "Out of Africa, Eve hypothesis" and/or diversity levels found in Old World tribal people (Ward et al. 1991; Cann et al. 1984). The "bottleneck" phenomenon might find support in Templeton's (1993); "not necessarily out of Africa" argument. Certainly, further consideration, when it comes to the Amerindian data, is warranted .

New World mtDNA data sets and associated implications contrast sharply with mtDNA analysis of Old World Populations. Evidence of a recent expansion event are seen to correlate with the demic diffusion -- with profound changes found in the archaeological record -- that is seen to confirm a modern humans expansion throughout the Old World beginning ~ 50,000 years ago (Binford 1984; Sherry et al. 1994). Unfortunately, many New World archaeologists seem willing to agree only to disagree as to whether (or not) there were People in the Americas during the Pleistocene. An open endorsement of even Chile's Monte Verde was inevitable while the effects of acceptance awaits a prevailing theory to guide this observation (see Brian Fagan's "Book Review" of Monte Verde Vol. II in *Archaeology Magazine* March/April 1997).

Archaeological Theory

The Nenana Culture and the Origins of New World Hunting Technologies

Finally, European mtDNAs, initially assigned to post-Colombian admixture with Amerindians, are now thought to be evidence of pre-Columbian European admixture since they have now been found in ancient pre-Columbian Amerindian remains (Bailliet et al. 1994). These same markers are found in nearly 100% of the Europeans and 27% of the Siberians studied. The pre-Columbian presence of this 'European' mtDNA lineage brings into question possible contributions Europeans may have made to the formation of the Nenana Culture and a post-Glacial movement and admixture of Siberian People into pre-Clovis Native American populations.

Easton et al. (1996) confirmed our assumption, changed the letter "E" to "X," and reported X₆ and X₇ as two forms of founder haplotypes corresponding to the haplogroups that we formerly had designated as "E." Forster et al. (1996) also named as "X" one additional founder haplotype within what we formerly had called haplogroup "E." However, since the X haplotype of Forster does not correspond to X₆ or X₇, we propose to name it "X₈," and we recommend using the letter "X" instead of the letter "E," to avoid confusion with the haplogroups "E," reported by Torroni et al. (1994) in Tibetans. It is worth mentioning here that we have found the X₈ haplotype in 6 of 41 Sioux individuals studied (Bianchi and Baillet. 1997 pg. 245).

These markers X6, X7, and X8 may indicate another example of admixture, this between pre-existing Amerindians and Siberians following contact between New and Old World people, at the end of the Last Ice Age.

Perhaps new interpretations are called for in determining if mtDNA analyses support Carbon-14 dating of Amerindian-derived Paleoindian migrations into Alaska emanating from the North American High Plateau ~ 11,200 years ago. In deference to the Greenberg et al. (1986) model, this analysis attests to a northern movement of Amerindians into coastal and interior biomes following the melting of the Wisconsin Ice Sheets. The arrival of Paleoindian Traditions into deglaciated mid-continental North America virtually coincides (11,200 and 10,600) with the *in situ* development of Paleoarctic Traditions in the Bering Refume (Dixon 1993). These distinctive New World Traditions mark the arrival of the last permanent occupation of deglaciated North America. They are believed to post-date, in Alaska, the Nenana Culture who show clear Paleolithic relationships emanating with northeast Asian habitations before end of the last Ice Age. Post-Glacial movements of Amerindians north can also find links with *HLA* class II haplotypes (some shared, some generated by recombination), linking the present Indigenous Populations of northern North America and “eastern Siberia” with “clear genealogical relationship to Amerinds.”

We found a high number of *HLA* class II haplotypes in Siberian populations. More haplotypes have been found in Siberia than in any other population. Some of the haplotypes are shared with non-Siberian populations, but most of them are new, and some represent "forbidden" combinations of *DQAI* and *DQB1* alleles. We suggest that a set of "public" haplotypes was brought to Siberia with the colonizers but that most of the new haplotypes were generated in Siberia by recombination and are part of a haplotype pool that is turning over rapidly. The allelic frequencies at the *DRB1* locus divide the Siberian populations

into *eastern* and central Siberian branches; *only the former shows a clear genealogical relationship to Amerinds* (Grahovac et al. 1998 pg.27, *emphasis added*).

The identified haplotypes fall into two categories: those found in both Siberian and non-Siberian populations (public haplotypes) and those restricted to Siberian populations (private haplotypes). The bulk (83%) of the haplotype diversity in the Siberian populations is constituted by the private haplotypes. Why are so many HLA class II haplotypes present in the Siberian populations? Since most of the Siberian haplotypes are found exclusively within Siberia, they could not have been introduced from other populations; they must have been generated in situ, by intergenic recombination (Grahovac et al. 1998 pg. 40 *emphasis added*).

Could pre-Clovis isolation and Holocene back-migration with resulting admixture through gene flow leading to intergenic recombination have accelerated the process of regional sequence diversity as evidenced by an increase in private haplotypes in Siberians. Certainly, pre-Clovis people must predate “(83%) of the haplotype diversity in the Siberian populations [that] is constituted by the private haplotypes.”

Amerindian Concepts The Archaeological evidence presented here may have a valid correlation in the origins of the Sundance Ceremony and the subsequent movement of populations using "Fluted Technologies" from the mid-continental High Plains north. The "instructions" (the diffusion of Upper Paleolithic-like technologies and the ceremonies that went with them) were given to the Plains Indian Tribes through Sutai, "Horns Standing Up", following his return from the north. These "instructions" of how to perform the "Great Medicine

Ceremony" are represented in this story to have been given to him in the north by the Creator, "Maheo" through his helper, "Great Roaring Thunder."

"With *issiwun* [the sacred hat] you will control the animals---the buffalo, the antelope, the elk, the deer---who give themselves to the people for food. The Tsis-tsis-tas shall never be hungry again, but live in plenty (Josie Limply, as told to Richard Erdoes in, Erdoes and Ortiz pg. 36, 1984)."

This myth depicts archaeological support for the existence of an Amerindian population that were not auspicious hunters (Krieger's 1964 pre-projectile point stage), while citing that the capacity to successfully hunt large game animals was gained from knowledge contained in the north (perhaps by the Nenana Culture and/or Upper Paleolithic relatives of Kennewick Man). Moreover, there exists linguistic support that would link the deglaciated inhabitants of the north, the Na-Dene, with the Northern Plains Sioux, corroborating the interpretations of Boas and Sapir (1916) with analysis of the mtDNA data described in this paper.

"Jurgen Pinnow, while hesitant to strongly affirm Sino-Dene or Dene-Caucasian, has in fact supplied substantial evidence for the connection (Pinnow, 1976, pp. 98-105), and *views Na-Dene as a transitional link between Sino-Tibetan and American families such as Siouan* (personal communication 1993) (Bengston 1994, pg 211)."

Linking origin myths with linguistic, genetic, anthropometric, and archaeological data may help in defining viable relationships' those demonstrated by traditional scientific assessments (Greenberg et al. 1986; and others). New hypotheses based on properly interpreting myth and traditional indigenous knowledge may find substance in defining alternatives to the conventional wisdom. Certainly, human migrations incorporating the possibilities of movements of Amerindians north following deglaciation have not been adequately tested and/or refuted.

Finally, the difficulty or intransigence many archaeologists evince in accepting a pre-Terminal Glacial human habitation of the Americas should not limit the scope of hypothesis testing in concert with the development of "paradigm growth and theory building" (Binford 1983; 1991).

ACKNOWLEDGMENTS

I thank the editor of *American Journal of Physical Anthropology* for providing the forum for this work, Lewis R. Binford and Richard Rogers for their insightful opinions, and Theodore G. Schurr for his lively discussions and generous contribution of time concerning my interpretation and application of mtDNA data sets. I also would like to thank Lanning Kaufer and Larry Heitz who have helped make this paper easier to read.

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Table 1

Proposed Amerindian Admixture A-D in Old World Populations

<u>Asians</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>E</u>	<u>F</u>	<u>G</u>	<u>Other</u>
Tibetans*	11.1	5.6	3.7	16.7	7.4	14.8	5.6	35.1
Koreans*	7.7	15.4	0	23.1	7.7	15.4	15.4	15.3
New Guineans **	0	19.3	0	0.8	0	0.8	0	79.1
Malays*	0	3.1	0	0	0	21.4	0	64.3
Vietnamese*	0	14.3	0	0	0	32.2	0	53.5
Han (Taiwan)*	10.	35	5	5	0	5	0	40

Note; Lineage AM13 has been confirmed in Melanesian Coastal Populations alternatively suggesting trans-Pacific migration by Amerinds. The Polynesian Motif (type B) has diverged only one mutation from the ancestral Amerindian condition (**B**_{AM13}) (Stoneking et al. 1995).

* Sources Ballanger et al. (1992); ** Stoneking et al. (1990).

TABLE 2

Regional Tribal Frequencies of Amerindian mtDNA Lineages A, B, C, D,
and proposed admixture with Other Northeast Asian Populations.

<u>N. Eastern Siberians</u>	No.	A	B	C	D	Other	Source
Sel'kups [20]		0	0	35	0	65	2
Evenks [51]		3.9	0	84.3	9.8	2	2
Evens [43]		0	0	58.1	7	34.9	2
Yukagirs [27]		0	0	59.3	33.3	7.4	2
<u>Eastern Siberians</u>		A	B	C	D	Other	
Chukchi [24]		37.5	0	16.7	16.7	29.2	2
Koryaks [46]		23.9	0	21.7	8.7	45.7	2
Ngansans [49]		2	0	38.8	36.7	22.5	2
Eskimo [50]		80	0	20.0	0	0	2
<u>Alaskan Eskimo</u>		A	B	C	D		
<u>Other</u>							
Old Harbor [115]		61.7	3.5	0	34.8	0	6
Ouzinkie [41]		73.2	0	4.9	14.6	7.3	6
Gambell [50]		58	0	14	26	2	6

Savoonga [49]	93.3	0	0	2	4.1	6
<u>N. West Coastal Groups</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Other</u>	
St. Paul Aleut [72]	25	0	1.4	66.7	6.9	6
Bella Coola [32]	78.1	6.25	9.4	6.25	0	3
Nuu-chal-Nulth [40]	40.	6.7	13.3	26.7	13.3	3
Haida [38]	92.1	0	0	4	0	3

<u>Sub-Arctic Groups</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Other</u>	
Dogrib [154]	90.9	0	2	0	7.1	6
Chipewa [15]	26.7	13.3	33.3	0	26.7	1
Ojibwa [28]	64.3	3.6	7.1	0	25	1
Mohawk [18]	46.4	10.5	13.8	0.6	28.7	6

<u>Na-Dene Speakers</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Other</u>	
Tibetans*	11.1	5.6	3.7	16.7	62.9	8
Dogrib [154]	90.9	0	2	0	7.1	6
Haida [25]	92.1	0	7.9	0	0	1
Navajo [48]	58.3	37.5	0	0	4.2	1
Apache [25]	64	16	12	8	0	1

<u>Amerinds (combined)</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Other</u>	
Northern	39.1	19.1	20.9	8.7	12.2	1
Central	65.7	28.5	2.9	2.2	0.7	1
Southern	14.4	18.5	28.8	38.4	0	1

Populations; [] sample size; percentages of Regional-Specific Amerindian Lineages; and "other" types suggesting Holocene and/or post-Colombian European admixture in Amerinds. Data compiled from Merriwether et al. 1995. These sources; Torroni et al. (1993a)¹, Torroni et al. (1993b)², Ward et al. (1993)³, Schurr et al. (1990)⁴, Horai et al. (1993)⁵, Merriwether et al. (1995)⁶ Torroni et al. 1994a)⁷, and Ballanger et al. (1992)⁸;

Table 3

Regional Subdivision of Contemporary Amerindian mtDNAs

<u>North/Central Amerinds</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Other</u>	<u>Source</u>
Pima [30]	6.7	50	43.3	0	0	4
Alta Mixtec [15]	73.4	13.3	13.3	0	0	7
Zapotec [15]	33.3	33.3	33.3	0	0	7
Maya [27]	51.9	22.2	14.8	7.4	3.7	4
<u>Equatorial Amerinds</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Other</u>	
Columbia [20]	50	20	25	5	0	5
Yanomamo [24]	0	16.7	54.2	29.2	0	1
Ticuna [28]	17.9	0	32.1	50	0	4
Mataco [28]	10.7	35.7	0	53.6	0	1
<u>South Amerinds</u>	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Other</u>	
Aymara [172]	6.4	67.4	12.2	14	0	6

Atacemeno [50]	12	72	10	6	0	6
Chilean Mapuche [45]	4.4	22.2	40	33.3	0	5
Peheunche [100]	2	9	37	52	0	6

Populations; [] sample size; percentages of Regional-Specific Amerindian Lineages; and "other" types suggesting Holocene and/or post-Colombian European admixture in Amerinds. Data compiled from Merriwether et al. 1995. These sources; Torroni et al. (1993a)¹, Torroni et al. (1993b)², Ward et al. (1993)³, Schurr et al. (1990)⁴, Horai et al. (1993)⁵, Merriwether et al. (1995)⁶ and Torroni et al. 1994a)⁷.