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mtDNA Diversity in Chukchi and Siberian Eskimos: Implications for the Genetic History of Ancient Beringia and the Peopling of the New World

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Summary

The mtDNAs of 145 individuals representing the aboriginal populations of Chukotka—the Chukchi and Siberian Eskimos—were subjected to RFLP analysis and control-region sequencing. This analysis showed that the core of the genetic makeup of the Chukchi and Siberian Eskimos consisted of three (A, C, and D) of the four primary mtDNA haplotype groups (haplogroups) (A–D) observed in Native Americans, with haplogroup A being the most prevalent in both Chukotkan populations. Two unique haplotypes belonging to haplogroup G (formerly called "other" mtDNAs) were also observed in a few Chukchi, and these have apparently been acquired through gene flow from adjacent Kamchatka, where haplogroup G is prevalent in the Koryak and Itel'men. In addition, a 16111C→T transition appears to delineate an "American" enclave of haplogroup A mtDNAs in northeastern Siberia, whereas the 16192C→T transition demarcates a "northern Pacific Rim" cluster within this haplogroup. Furthermore, the sequence-divergence estimates for haplogroups A, C, and D of Siberian and Native American populations indicate that the earliest inhabitants of Beringia possessed a limited number of founding mtDNA haplotypes and that the first humans expanded into the New World ~34,000 years before present (YBP). Subsequent migration 16,000–13,000 YBP apparently brought a restricted number of haplogroup B haplotypes to the Americas. For millennia, Beringia may have been the repository of the respective founding sequences that selectively penetrated into northern North America from western Alaska.

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Introduction

Archaeological records of Kamchatka, Chukotka, and Alaska that date back to 15,000 years before the present (YBP) suggest that the latest inhabitants of the Bering land bridge were living in rich unglaciated lowlands and perhaps were occupying these areas of ancient Beringia as two distinct populations. One was apparently an inland population of mammoth and bison hunters, whereas the other consisted of small groups of fishing and sea mammal–hunting populations who were scattered along the coast of southern Beringia. The submergence of most of the Bering land bridge and subsequent formation of the Bering Strait ~10,000 YBP separated Chukotka and Alaska and may have affected the overall divergence of these groups, because of the dislocation of interior and coastal populations (Young 1988; Hoffecker et al. 1993; Dikov 1994; King and Slobodin 1996). Eventually, a few distinct populations evolved in the northern Pacific Rim, and presumably these are reflected genetically in the Paleoasiatic-speaking Chukchi, Na-Dené–speaking Indians, and Eskimo-Aleuts (Krauss 1988). The aboriginal inhabitants of Chukotka—the Chukchi and Siberian Eskimos—are likely the survivors of these rapid environmental changes and, hence, are of great importance for understanding the evolution of both Siberian and Native American populations.

The utility of the unique genetic properties of mtDNA, including its maternal inheritance and high mutation rate, have been helpful in addressing long-standing questions about the timing and origins of the first Americans, the number of subsequent demic expansions across Beringia, the chronology and routes of these expansions, and the sizes of the founding populations (Wallace et al. 1985; Ward et al. 1991; Neel et al. 1994; Wallace 1995; Forster et al. 1996). Our first survey of mtDNA variation in the Chukchi and Siberian Eskimos involved partial haplotype analysis and showed that the "reindeer" Chukchi exhibited three (A, C, and D) of the four mtDNA haplogroups (A–D) observed in Native Americans but lacked the COII/$tRNA^{Lys}$ intergenic 9-bp de-

letion associated with haplogroup B (Torroni et al. 1993*a,* 1993*b*). In contrast, Siberian Eskimos showed mtDNAs from only two of these haplogroups (A and D), and appeared to be the only aboriginal Siberian group lacking "other" haplotypes—that is, mtDNAs that are not within haplogroups A–D (Torroni et al. 1993*b;* Sukernik et al. 1996). When native Siberian mtDNAs were subjected to high-resolution restriction analysis, most of these "other" haplotypes were shown to be ethnic-, tribal-, or region-specific haplotypes that clustered into additional haplogroups. This was seen most clearly in the Udegeys of the Sikhote Alin and in the Nivkhs of the lower Amur/Sakhalin Island region (Torroni et al. 1993*b*).

Similarly, previous analyses of restriction-site variation in Native American mtDNAs had revealed that nearly all of these mtDNAs clustered within haplogroups A–D. Each of these haplogroups was widespread, although they were unevenly distributed among the different tribes and linguistic groups in the New World, and each haplogroup traced back to only one or two founding mtDNA haplotypes that had originated in Asia (Wallace 1985; Schurr et al. 1990; Torroni et al. 1992, 1993*a*). As a result, the variation that had accumulated within each haplogroup since the first humans arrived in the Americas was quantified and was found to give divergence times, for haplogroups A, C, and D, of 34,000–26,000 YBP. Since haplogroup B was not found in eastern Siberia but was prevalent in the Americas, it has been proposed that haplogroup B represents an independent population expansion into the New World (Torroni et al. 1992, 1993*b,* 1994*b*).

However, the results of other studies are at odds with this interpretation of a limited number of Asian founding mtDNA lineages populating the Americas and an "early" entry into the New World (Ward et al. 1991, 1993; Shields et al. 1993; Merriwether et al. 1995). On the basis of the low diversity and small mean pairwise sequence differences of mtDNA noncoding control region (CR) sequences within and between Chukchi, Siberian Eskimos, Alaskan Na-Dené Indians, and Alaskan and western Greenland Eskimos, Shields et al. (1993) estimated that the average date for the ancestry of these mtDNA lineages is 7,100–5,100 YBP. In contrast, the mean pairwise sequence differences within the Amerindian tribes—the Nuu-Chah-Nulth and the Yakima—gave estimated date of 13,200–12,100 YBP, implying a "late" entry of ancient Native Americans into the New World (Shields et al. 1993). However, the small sample sizes of the Chukchi and of the Siberian and Alaskan Eskimos (seven, six, and five individuals, respectively) that Shields et al. (1993) used for the analysis of CR sequences could have influenced these results considerably.

It is apparent that the Chukchi and Siberian Eskimo mtDNAs merit additional analysis and that such data would also be extremely helpful in the reconstruction of the evolutionary history of Beringia. In the present study, we have further characterized the mtDNA variation in Chukotkan populations, via high-resolution restriction analysis and CR sequencing, and have attempted to trace their origins by comparing the resulting RFLP haplotypes and CR lineages with those present in other Siberian and Native American populations.

Subjects and Methods

Populations

Chukchi.—When the first Russians reached the mouth of the Anadyr River in 1648, the Paleoasiatic-speaking Chukchi were reindeer and mountain-sheep hunters who wandered within specific hunting areas in eastern Chukotka and numbered <2,000 individuals (Dolgikh 1960). By the end of the 19th century, shortly after the transition from a hunting-fishing subsistence to a reindeer economy, the Chukchi had considerably increased in their population size and had spread widely in Chukotka, pushing and assimilating adjoining Yukagir tribes in the west, the Koryaks living south of the lower Anadyr region, and the Eskimos residing along the entire coast of the Chukchi peninsula (Gondatti 1897; Bogoras 1910). With the passage of time, some Chukchi families (present-day coast Chukchi) settled on the coast and adopted a way of life similar to that of Siberian Eskimos living in adjoining villages (Bogoras 1910).

Siberian Eskimos.—By the turn of the 20th century, the territory inhabited by Siberian Eskimos had been reduced to three small enclaves on the northeastern and southern coast of the Chukchi peninsula. These were populated by three Yupik-speaking tribes—the Naukan, Chaplin, and Sireniki Eskimos (Rudenko 1947; Menovshchikov 1959; Arutiunov et al. 1982; Krauss 1994). At that time, Naukan Eskimos inhabited the mountain terrace located southeast of Uelen, the settlement of coastal Chukchi. They spoke their own dialect of Siberian Yupik and occasionally intermarried with the nearby Eskimo tribe of Little Diomide Island (fig. 1). The Chaplin Eskimos were living in a number of settlements scattered along the coastline between Arakamchechen Island and Provideniya (Plover) Bay. They were isolated from the Naukan Eskimos by geographic distance, and Chukchi settlements were interspersed between them. Marital exchanges between Chaplin Eskimos and St. Lawrence Island Eskimos, who spoke the same dialect of Siberian Yupik, were common in historical times (Menovshchikov 1959). The Sireniki tribal group lived in a few settlements located west of Provideniya Bay. The decimation of the Siberian Eskimos by the turn of the 20th century, presumably because of in-

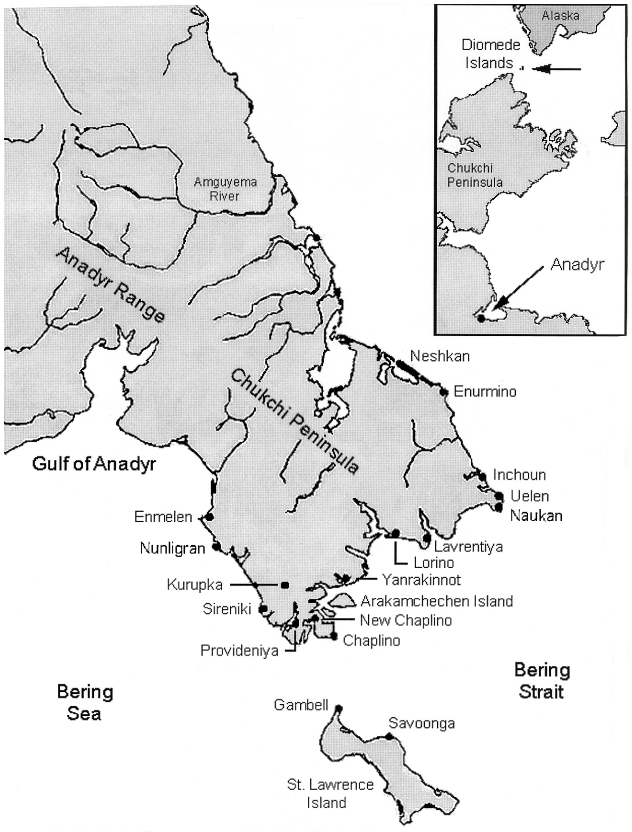

Figure 1 Map of eastern Chukotka, encompassing territories and villages where Chukchi and/or Siberian Eskimos analyzed in this study were born or derived. The inset map shows an expanded view of the Bering Strait area.

fectious diseases brought by European whalers and traders into coastal Chukotka, was augmented by the arbitrary relocation of the inhabitants of Naukan and Old Chaplino and other villages during the late 1950s. By 1985, there remained only 96, 161, and 156 Eskimos of Naukan, Chaplin, and Sireniki tribal-group origin (Sukernik et al. 1986).

Sample Collection and Preparation

In October 1994 and April 1995, blood samples from 66 Chukchi and 79 Siberian Eskimos were collected in New Chaplino, Sireniki, Provideniya, and Anadyr, of the Chukotkan Autonomous Territory (fig. 1). Genealogical information was used to select unadmixed, unrelated individuals as potential blood donors. After informed consent was obtained, blood specimens were collected from participants, by venipuncture, into two sets of 10-ml ACD Vacutainer tubes (Becton-Dickinson). These samples were shipped to Emory University for subsequent molecular-genetic analysis. mtDNAs were extracted from the platelet-rich plasma fractions by means of published methods (Torroni et al. 1992).

Of the entire Chukchi sample drawn from New Chaplino, Provideniya, Sireniki, and Anadyr, 55 individuals either had been born or had derived from the coastal villages of Neshkan, Enurmino, Inchoun, Uelen, Lorino, Yanrakinnot, Nunligran, and Enmelen and adjacent tundra camps (Kurupka) of the Chukchi peninsula, whereas 11 Chukchi either had been born or had derived from the Amguyema/Anadyr River area of interior Chukotka, the homeland of the reindeer Chukchi (fig. 1). In fact, the Eskimo sample assigned to the Chaplin tribe consists of individuals who either had been born or had derived from at least six tiny villages that had been scattered along the southeastern tip of the peninsula before being abandoned or closed during the 1940s and 1950s. Similarly, the Sireniki sample consisted of the Eskimos who had been born in Sireniki and a few other nearby but no longer existing villages. The Naukan Eskimos were represented by several individuals presently living in Sireniki, Provideniya, and New Chaplino.

Molecular-Genetic Methods

High-resolution RFLP analysis.—The entire mtDNA of each sample was PCR amplified in nine partially overlapping segments, by means of the oligonucleotide primers and PCR conditions described by Torroni et al. (1993*b*). Each PCR segment was subsequently digested with 14 different restriction enzymes: *Alu*I, *Ava*II, *Bam*HI, *Dde*I, *Hae*II, *Hae*III, *Hha*I, *Hinc*II, *Hinf*I, *Hpa*I, *Hpa*II, *Mbo*I, *Rsa*I, and *Taq*I. The resulting restriction fragments were resolved by electrophoresis in 1.0%–2.5% NuSieve plus 1.0% SeaKem agarose (FMC) gels and were visualized by ethidium bromide staining.

CR sequencing.—A total of 401 bp (from nucleotide position [np] 16000 through np 16400) encompassing the CR hypervariable segment I (HVS-I) from 65 Chukchi and 77 Eskimo mtDNAs were dideoxy sequenced. For each mtDNA, the HVS-I was read in both directions by direct double-stranded sequencing of PCR products, by an ABI 377A automated DNA sequencer (Applied Biosystems). Double-stranded PCR segments were amplified by primers that allowed the amplification of the entire CR (1,121 bp): forward (heavy strand) primer 5′-CTACGCCAATCACTTTATTG-3′ and reverse (light strand) primer 5′-CTGTTAAAAGTGCATACCGCC-3′. The PCR fragments were purified by Centricon-100 microconcentrators (Amicon) and sequenced by a *Taq* DyeDeoxy Termination Cycle Sequence Kit™ (Perkin-Elmer), by primers complementary to both the mtDNA light (5′-ACCATTAGCACCCAAAGCTA-3′) and heavy (5′-TGATTTCACGGAGGATGGT-3′) strands. Alignments and comparisons of the CR sequences were performed by the Sequencer 3.0 software tool (Gene Codes).

Phylogenetic and Statistical Analyses

Maximum parsimony (MP).—The phylogenetic relationships both among the Chukchi and Siberian Eskimos and among the other previously studied native Siberian (Shields et al. 1993; Torroni et al. 1993*b;* Schurr et al., in press) and Native American mtDNA RFLP data (Torroni et al. 1992, 1993*a;* Shields et al. 1993; Ward et al. 1993) were inferred by means of PAUP (version 3.1.1; Swofford 1994). Heuristic searches were performed by the tree bisection + reconnection (TBR) algorithm, with all MP trees being rooted from three African haplotypes: AF71 (Chen et al. 1995), TYPE-5, and HYPANC (Cann et al. 1987), which are characterized by the *Hpa*I np-3592 site gain and other unique RFLPs defining 60%–100% of the sub-Saharan African mtDNAs (macrohaplogroup L [Johnson et al. 1983; Cann et al. 1987; Scozzari et al. 1988; Vigilant 1990; Chen et al. 1995]). In addition, both strict and 50%-majority-rule consensus trees were derived from the MP trees, to determine the consistency of the branching arrangements.

Neighbor-joining (NJ) trees.—The phylogenetic relationships of the CR sequence data were analyzed by the NJ method (Saitou and Nei 1987). This method was used because it is known to reconstruct correct phylogenetic trees with a high probability when it analyzes closely related samples (Saitou and Imanishi 1989). In this analysis, genetic distances were estimated on the basis of sequence data, by three different models in DNADIST (Felsenstein 1993)—including the Kimura two-parameter method (Kimura 1980), DNAML (Felsenstein 1993), and the method of Jukes and Cantor (1969)—and unrooted trees based on these distances were obtained by the NJ method. To test the reliability of the branching order of the NJ trees, the CR sequence data were bootstrapped over 1,000 replicates by SEQBOOT, and the bootstrapped data sets were used to generate genetic distances by DNADIST (Felsenstein 1993). These sets of distances were then used to generate consensus trees by CONSENSE (Felsenstein 1993), in which the percentage of support for the branches represents the bootstrap value for the nodes of the trees.

Sequence-divergence estimations.—Intragroup sequence-divergence estimations based on restriction-analysis data were calculated by the maximum-likelihood procedure of Nei and Tajima (1983). When the divergence (radiation) times of the haplogroups were calculated, an mtDNA evolution rate of 2.2%–2.9%/million years (MYR) was used (Torroni et al. 1994*b*).

Results

Haplotype Distribution

RFLP analysis of 145 Chukchi and Eskimo mtDNAs revealed a total of 17 distinct haplotypes defined by 27 polymorphic sites (table 1). Of these 17 haplotypes, 7 were found to belong to haplogroup A, 6 to haplogroup D, 2 to haplogroup C, and 0 to haplogroup B. In addition, two haplotypes detected in four Chukchi individuals were identified as belonging to haplogroup G, a predominant mtDNA lineage in the Koryaks and Itel'men of Kamchatka (Schurr et al., in press).

Table 2 outlines the distribution of these haplotypes, within and between Chukotkan samples. Haplogroup A haplotypes SIB41 and SIB56 were found to be the most frequent in all Chukchi and Eskimo subdivisions, with the exception of the Naukan, in which SIB56 was miss-

Table 1

Chukchi and Siberian Eskimo mtDNA RFLP Haplotypes

Haplogroup and Haplotype	Polymorphic Restriction Site(s)[a]
A:	
SIB41	+663e
SIB53	+663e, −3337k
SIB54	+663e, −9052n/−9053f
SIB55	+663e, −1004o
SIB56	+663e, −11362a
SIB57	+663e, −11362a, +16517e
SIB58	+663e, −5003c
C:	
SIB26	+10394c, +10397a, −13259o/+13262a, +16517e
SIB59	+1117j, −4990a, +10394c, +10397a, −13259o/+13262a, +16517e
D:	
SIB40	−5176a, −10180l, +10394c, +10397a, +13717a, +14923c, +15437e
SIB48	+795e, −3315e, −5176a, +8683a, +10394c, +10397a
SIB49	−3315e, −5176a, +8683a, +10394c, +10397a
SIB50	−3315e, −4990a, −5176a, +8683a, +10394c, +10397a
SIB51	−3315e, −4990a, −5176a, +8683a, +10394c, +10397a, +16517e
SIB52	−3315e, −5176a, +8683a, +10394c, +10397a, +16517e
G:	
SIB46	+4830n/+4831f, +10394c, +10397a, +15494c, +16517e
SIB47	+4643k, +4830n/+4831f, +10394c, +10397a, +10135a, +15494c, +16517e

[a] The following sites were found to be present or absent in all samples contrary to the published sequence (Anderson et al. 1981), except when polymorphic: −4769a, +7025a, +8858f, −13702e, −14199o, +14268g, and −14368g. The restriction enzymes are designated as follows: a = *Alu*I; c = *Dde*I; e = *Hae*III; f = *Hha*I; g = *Hinf*I; j = *Mbo*I; k = *Rsa*I; l = *Taq*I; n = *Hae*II; and o = II. A plus sign (+) indicates a site gain relative to the published sequence, and a minus sign (−) indicates a site loss relative to the published sequence. A virgule (/) between sites indicates either simultaneous site gains or site losses for two different enzymes or a site gain for one enzyme and a site loss for another because of a single inferred nucleotide substitution. Haplotypes SIB26, SIB40, and SIB41 have been defined in Siberian populations by Torroni et al. (1993*b*), whereas SIB46–SIB59 denote newly defined haplotypes in these groups.

Table 2

Distribution of Chukchi and Siberian Eskimo RFLP Haplotypes

	Chukchi		Siberian Eskimos			
Haplogroup and Haplotype	Chukchi Peninsula	Interior Chukotka	Chaplin	Sireniki	Naukan	Total
A:						
SIB41	25	1	18	8	1	53
SIB53	0	0	10	2	0	12
SIB54	0	0	3	0	0	3
SIB55	3	0	0	1	2	6
SIB56	13	2	9	5	0	29
SIB57	0	0	1	1	0	2
SIB58	0	1	0	0	0	1
C:						
SIB26	4	3	0	0	1	8
SIB59	0	0	0	1	0	1
D:						
SIB40	0	1	0	0	4	5
SIB48	0	0	0	1	0	1
SIB49	1	1	0	0	0	2
SIB50	4	0	4	3	0	11
SIB51	1	0	0	0	0	1
SIB52	0	0	1	3	0	4
G:						
SIB46	4	1	0	0	0	5
SIB47	0	1	0	0	0	0
Total	55	11	46	25	8	145

ing, probably because of the restricted sample size of this group. SIB53, which was observed in two of the three Eskimo subdivisions, did not appear in the Chukchi. The most common haplogroup D haplotype in the Chukchi and the Eskimo was SIB50, with related haplotypes occurring infrequently in either one or the other subdivision(s).

Interestingly, the frequencies of haplogroups A and D mtDNAs in the Siberian Eskimos were nearly identical to those obtained in a previous analysis of sera mtDNAs from the same tribal groups (Torroni et al. 1993*b*). The only difference was the small proportion of haplogroup C mtDNAs (2.5%) revealed in the most recent Eskimo sample. On the basis of what is known of the family histories, it is likely that the presence of haplogroup C mtDNAs in Siberian Eskimos is attributable to gene flow from the Chukchi. On the other hand, haplogroup C mtDNAs were detected in Alaskan Eskimo populations (Merriwether et al. 1995), making it possible that a low frequency of haplogroup C mtDNAs are part of the ancestral genetic stock of the Eskimos.

In both Chukotkan populations, the high frequencies of haplogroup A haplotypes were found to be consistent with those observed in the Eskimos from St. Lawrence Island and southern Alaska and were similar to the frequency of this lineage in the Na-Dené (Haida and Dogrib) and Amerindian tribes from the Northwest Coast of North America (Bella Coola and Nuu-Chah-Nulth) (fig. 2 and table 3). When partial haplotypes are taken into account, the apparent genetic uniformity of Siberian and Alaskan Eskimos can be seen, since these populations have predominantly haplogroups A and D mtDNAs, with haplogroup A mtDNAs occurring at the highest frequency. Although also having only haplogroups A and D mtDNAs, the Aleuts differed from the Eskimos in that they have haplogroup D mtDNAs at a higher frequency.

Neither the Chukchi nor the Siberian Eskimos had haplogroup Y mtDNAs, which are common in the Nivkhs and are also present in the Koryaks and Itel'men (table 3). Thus, the high frequency of novel haplotypes from haplogroups A and D in the Chukchi and Siberian Eskimos, along with both the low frequency of haplogroup G mtDNAs and the absence of haplogroup Y mtDNAs, clearly differentiates Chukotkan populations from the rest of the northern-Asian mongoloid groups.

Evidence of Restriction-Site Heteroplasmy

Although many examples of mitochondrial heteroplasmy are currently known in healthy individuals (Bendall et al. 1996; Howell et al. 1996; Ivanov et al. 1996; Parsons et al. 1997), it has typically been detected via CR sequencing. For this reason, the finding, in the Eskimo samples, of a heteroplasmic point mutation causing a restriction-site polymorphism was noteworthy. The

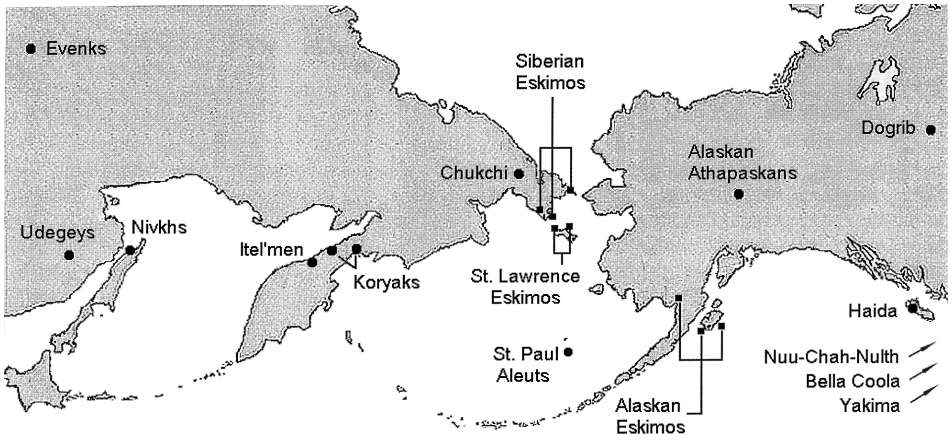

Figure 2 Northern Pacific Rim/Bering Sea region, with approximate locations of populations for which mtDNA haplogroup distribution is indicated in table 3.

mtDNAs of three Siberian Eskimos with the same haplotype, SIB54, were found to be heteroplasmic for the polymorphism that distinguishes them from SIB41. The two different forms, SIB41/SIB54, could be detected by restriction digestions with both *Hae*II and *Hha*I, with one form having the *Hae*II np-9052 and *Hha*I np-9053 site losses and the other lacking them. Multiple restriction digestions of these samples were performed, to confirm that this heteroplasmy was not artifactual. In addition, all three of the mtDNAs with SIB54 had identical CR sequences (i.e., 01), the only one present in SIB41 haplotypes from Siberian Eskimos. Thus, haplotype SIB54 appears to have arisen recently as a germ-line point mutation in the coding region of a Siberian Eskimo haplogroup A mtDNA.

CR Sequence Variation

Direct sequencing of 65 Chukchi and 77 Siberian Eskimo mtDNAs revealed a total of 22 different sequences, as defined by 27 variable nucleotide positions. These data have provided further insights into the variation of haplogroups A, C, D, and G (tables 4 and 5).

All Chukotkan CR sequences specific to haplogroup A exhibited the np 16111 C→T (16111T) transition, which characterizes both Na-Dené and Amerindian haplogroup A mtDNAs but which was not observed in those from Asian populations (Torroni et al. 1993*b;* Horai et al. 1996). Aside from the 16111T mutation, either the C→T transition at np 16192 (16192T) or the A→G transition at np 16265 (16265G) further subdivided Siberian haplogroup A mtDNAs and differentiated Chukotkan haplogroup A sequences from related mtDNAs observed in the Koryaks and Itel'men of Kamchatka (Schurr et al., in press).

Although the greatest CR sequence diversity was observed among haplogroup A mtDNAs, several unique CR sequences were also found within haplogroups C, D, and G. In haplogroup C, two distinct sublineages were observed, the first being represented by CR sequences 17 and 18, the second by CR sequence 19. Both sublineages shared the np 16298 T→C transition (16298C), which defines haplogroup C mtDNAs in both Asia and the New World (Torroni et al. 1993*a,* 1993*b*). However, the first sublineage also contained additional variants (transitions 16124 T→C, 16318 A→T, and 16327 C→T), which do not appear in haplogroup C mtDNAs from other Siberian or Native American tribes (Ward et al. 1991, 1993; Shields et al. 1993; Torroni et al. 1993*a,* 1993*b*). In contrast, the second sublineage was distinguished by the presence of transitions 16093 (T→C), 16189 (T→C), 16261 (C→T), and 16288 (T→C). Interestingly, the mutation at np 16189 (T→C) created a homopolymeric stretch of C's within the 14-bp hypervariable domain (16180–16193), which has been observed in both Asian and Native American mtDNAs from different haplogroups (Horai et al. 1993). The second sublineage appears to be region—rather than tribal—specific, since, aside from appearing in the Chukchi (table 5), it was also detected among Koryak and Itel'men haplogroup C mtDNAs (Schurr et al., in press).

Four different CR sequences were observed within haplogroup D. The 16362 T→C transition is characteristic both of CR sequences of haplogroup D and of those of haplogroup A (Torroni et al. 1993*a,* 1993*b*). Additional nucleotide substitutions differentiated Siberian haplogroup D mtDNAs, revealing two different sublineages (table 4). The first sublineage, represented by CR sequence 13, was distinguished by the 16093C, 16173T, and 16319A substitutions and was linked with only one haplotype, SIB40. This sequence, which was detected in

Table 3

mtDNA Haplogroups in Siberia and the Northern Pacific Rim

Population (No.)	Frequency in Haplogroup (%)							Reference(s)
	A	B	C	D	G	Y	Other[a]	
Tungusic:								
Evenks (51)	3.9	.0	84.3	9.8	.0	.0	2.0	Torroni et al. (1993*b*)
Udegeys (45)	.0	.0	17.8	.0	8.9	.0	73.3	Torroni et al. (1993*b*)
Linguistic isolate:								
Nivkhs (57)	.0	.0	.0	28.1	5.3	64.9	1.8	Torroni et al. (1993*b*)
Paleoasiatic:								
Itel'men (47)	6.4	.0	14.9	.0	68.1	4.3	6.4	Schurr et al. (in press)
Koryaks (155)	5.2	.0	36.1	1.3	41.9	9.7	5.8	Schurr et al. (in press)
Chukchi (66)	68.2	.0	10.6	12.1	9.1	.0	.0	Present study
Eskimo-Aleut:								
Siberian Eskimos (79)	77.2	.0	2.5	20.3	.0	.0	.0	Present study
St. Lawrence Eskimos (99)	76.0	.0	7.0	14.0	.0	.0	3.3	Merriwether et al. (1995)
Old Harbor Eskimos (115)	61.7	3.5	.0	34.8	.0	.0	.0	Merriwether et al. (1995)
Ouzinkie Eskimos (41)	73.2	.0	4.9	14.6	.0	.0	7.1	Merriwether et al. (1995)
St. Paul Aleuts (72)	25.0	.0	1.4	66.7	.0	.0	6.9	Merriwether et al. (1995)
Na-Dené:								
Haida (38)	92.1	.0	7.9	.0	.0	.0	.0	Ward et al. (1993)
Haida (25)	96.0	.0	.0	4.0	.0	.0	.0	Torroni et al. (1993*a*)
Dogrib (154)	90.9	.0	2.0	.0	.0	.0	7.1	Merriwether et al. (1995)
Dogrib (30)	100.0	.0	.0	.0	.0	.0	.0	Torroni et al. (1992)
Amerind:								
Bella Coola (32)	78.1	6.3	9.4	6.3	.0	.0	.0	Ward et al. (1993)
Bella Coola (25)	60.0	8.0	8.0	20.0	.0	.0	4.0	Torroni et al. (1993*a*)
Nuu-Chah-Nulth (63)	44.4	3.2	19.0	22.2	.0	.0	11.1	Ward et al. (1991)
Nuu-Chah-Nulth (15)	40.0	7.6	13.3	26.7	.0	.0	13.3	Torroni et al. (1993*a*)

[a] Haplotypes that belong to the haplogroups listed but that may have different haplogroup affiliations.

four Naukan Eskimo individuals and one reindeer Chukchi individual, had been observed previously in two North American Eskimos (Shields et al. 1993). The second sublineage was represented by three CR sequences (14–16) and was distinguished by the 16129A and 16271C transitions. These sequences occur multiple times in association with haplotypes SIB48–SIB52 in the Chukchi and Siberian Eskimos but not in the Na-Dené Indian and Amerindian tribes of the Pacific Northwest (Ward et al. 1991, 1993; Shields et al. 1993; Torroni et al. 1993*a*), thereby implying their recent origin within the restricted area.

Haplogroup G mtDNAs were found to harbor three distinct CR lineages (20–22). All three sequences had the unique variant 16017C. Along with the *Hae*II np-4830 site gain and the *Hha*I np-4831 site gain, the 16017C mutation clearly defines mtDNAs belonging to haplogroup G (Schurr et al., in press).

Phylogenetic Analysis of RFLP Haplotypes

One of numerous MP trees derived from the mtDNA RFLP data is presented in figure 3. This tree was generated by the TBR algorithm, in which 59 Siberian (SIB01–SIB59) and 31 Native American (AM01, AM02, AM05, AM06, AM09, AM13–AM20, AM22–AM26, AM33–AM38, AM43, AM61–AM63, AM70, AM86, and AM87) complete haplotypes clustered together into haplogroup branches A–D, G, and Y.

For haplogroup A, the most common Chukotkan haplotype, SIB41, has only the *Hae*III np-663 site gain and appears to be the only haplogroup A mtDNA shared among the populations of both Siberia and northwestern North America and, thus, dispersed throughout the northern Pacific Rim. SIB41 is identical to AS56 in central and eastern Asia (Ballinger et al. 1992; Torroni et al. 1994*a*) and AM01 in the New World (Torroni et al. 1992, 1993*a*) and thus defines the nodal position for haplogroup A in the MP tree. On the other hand, the Na-Dené Indians and Amerindians of northern North America show sets of related mtDNAs belonging to haplogroup A that are distinct from those in the Chukchi and Eskimos, supporting the inference of an early and permanent separation between Siberian and North American populations (Torroni et al. 1992, 1993*a*). Furthermore, the terminal haplotypes are specific for individual Siberian, Na-Dené, and Amerindian populations, a distribution that suggests a distant divergence time for haplogroup A, with minimal gene flow between these linguistically divergent groups since their common origin.

Table 4

CR Sequences Identified in Chukchi and Siberian Eskimos

Haplogroup and and CR Sequence	Polymorphic np[a]																											
	0 1 7 T	0 8 5 C	0 9 3 T	1 1 1 C	1 2 4 T	1 2 9 G	1 7 2 T	1 7 3 C	1 7 6 C	1 8 9 T	1 9 2 C	2 2 3 C	2 4 5 C	2 6 1 C	2 6 5 A	2 7 1 T	2 8 8 T	2 9 0 C	2 9 4 C	2 9 8 T	3 1 1 T	3 1 8 A	3 1 9 G	3 2 7 C	3 5 3 C	3 6 2 T	3 6 6 C
A:																												
01	–	–	–	T	–	–	–	–	–	–	T	T	–	–	–	–	–	T	–	–	–	–	A	–	–	C	–
02	–	–	–	T	–	–	–	–	T	–	T	T	–	–	–	–	–	T	–	–	–	–	A	–	–	C	–
03	–	–	–	T	–	–	–	–	–	–	T	T	–	–	–	–	–	T	–	–	C	–	A	–	–	C	–
04	–	–	–	T	–	–	–	–	–	–	T	T	–	T	–	–	–	T	–	–	–	–	A	–	–	C	–
05	–	–	–	T	–	–	–	–	–	–	T	T	–	–	–	–	–	–	–	–	–	–	A	–	–	C	–
06	–	–	–	T	–	–	–	–	–	–	T	T	–	–	–	–	–	T	–	–	–	–	A	–	T	C	–
07	–	–	–	T	–	–	–	–	–	–	–	T	–	–	–	–	–	T	–	–	–	–	A	–	–	C	–
08	–	–	–	T	–	–	–	–	–	–	–	T	–	–	G	–	–	T	–	–	–	–	A	–	–	C	–
09	–	–	–	T	–	A	–	–	–	–	–	T	–	–	G	–	–	T	–	–	–	–	A	–	–	C	–
10	–	–	–	T	–	–	–	–	T	–	–	T	–	–	G	–	–	T	–	–	–	–	A	–	–	C	–
11	–	–	–	T	–	–	–	–	–	–	–	T	T	–	G	–	–	T	–	–	–	–	A	–	–	C	–
12	–	T	–	T	–	–	–	–	–	–	–	T	–	–	G	–	–	T	–	–	–	–	A	–	–	C	–
D:																												
13	–	–	C	–	–	–	–	T	–	–	–	T	–	–	–	–	–	–	–	–	–	–	A	–	–	C	–
14	–	–	–	–	–	A	–	–	–	–	–	T	–	–	–	C	–	–	–	–	–	–	–	–	–	C	–
15	–	–	–	–	–	A	–	–	–	–	–	T	–	–	–	C	–	–	–	–		–	–	–	–	C	T
16	–	–	–	–	–	A	–	–	–	–	–	T	–	–	–	C	–	–	T	–	–	–	–	–	–	C	T
C:																												
17	–	–	–	–	C	–	–	–	–	–	–	T	–	–	–	–	–	–	–	C	–	T	–	T	–	–	–
18	–	–	–	–	C	–	–	–	–	–	–	T	–	–	–	–	–	–	–	C	C	T	–	T	–	–	–
19	–	–	C	–	–	–	–	–	–	C	–	T	–	T	–	–	C	–	–	C	–	–	–	–	–	–	–
G:																												
20	C	–	–	–	–	A	–	–	–	–	–	T	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
21	C	–	C	–	–	A	–	–	–	–	–	T	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
22	C	–	C	–	–	A	C	–	–	–	–	T	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–

[a] Numbered according to the published reference sequence, which is given below the vertical three-digit numerals (Anderson et al. 1981); the prefix "16" has been deleted.

Table 5

Distribution of CR Sequences within RFLP Haplogroups

Haplogroup, Haplotype, and CR Sequence	No. in		
	Chukchi	Eskimos	Total
A:			
SIB41:			
01	19	22	41
02	0	1	1
03	3	0	3
05	1	0	1
06	0	1	1
07	2	1	3
SIB53:			
01	0	12	12
SIB54:			
01	0	3	3
SIB55:			
03	3	3	6
SIB56:			
08	11	12	23
09	1	2	3
10	1	0	1
11	1	0	1
12	1	0	1
SIB57:			
08	0	2	2
SIB58:			
04	1	0	1
C:			
SIB26:			
17	1	0	1
18	2	1	3
19	4	0	4
SIB59:			
17	0	1	1
13	1	4	5
D:			
SIB40:			
16	0	1	1
SIB49:			
15	2	0	2
SIB50:			
14	4	7	11
SIB51:			
14	1	0	1
SIB52:			
15	0	4	4
G:			
SIB46:			
20	2	0	2
21	1	0	1
22	2	0	2
SIB47:			
21	1	0	1
Total	65	77	142

For haplogroup C, the nodal haplotype is SIB26. It is identical to the Asian haplotype AS65 and to the Native American haplotype AM43 (Schurr et al. 1990; Ballinger et al. 1992; Torroni et al. 1993*a*). SIB59, which occurred in one Sireniki Eskimo, differed from SIB26 by having two additional mutations not previously seen in other haplogroup C mtDNAs.

For haplogroup D, the nodal haplotype is SIB13. This is identical to AS25 in central and eastern Asia (Ballinger et al. 1992; Torroni et al. 1993*a*) and to AM88 in the New World (Torroni et al. 1992, 1993*a*). Interestingly, SIB13 was not observed among the Chukchi and Eskimos, who exhibited a set of haplotypes distinct from those seen in other Siberian populations. Furthermore, the most divergent haplotype in the Chukotkan groups, SIB40 (fig. 3 and table 1), which assumed a terminal position in the cluster, occurred in the Chukchi and Naukan Eskimos, as well as in the Koryaks of northeastern Kamchatka (Schurr et al., in press), suggesting that it belonged to a common gene pool of the latest inhabitants of western Beringia.

For haplogroup G, the putative nodal haplotype is SIB08. Haplotypes SIB46 and SIB47, the novel mtDNAs observed solely in the Chukchi, differed from SIB08 by two or three mutations. Since haplogroup G haplotypes have been found neither in the Eskimo populations residing on either the Siberian or the American side of the Bering Strait nor in the Na-Dené Indians and Amerindians, it is unlikely that the bearers of these mtDNAs ever reached Beringia and entered the New World. The haplotypes from haplogroup Y (SIB01-SIB07) and the "other" category (SIB17 and SIB20–SIB25) are also found in Siberia but not in the Americas (Torroni et al. 1993*a,* 1993*b;* Schurr et al., in press).

Both Siberian and Native American branches of haplogroups A and C mtDNA lineages do not share any derivative haplotypes (fig. 3). This finding supports the hypothesis that only the nodal, or founding, haplotypes were brought from Siberia to the Americas, with the two haplogroups subsequently diverging through the accumulation of new mutations (Wallace et al. 1985; Schurr et al. 1990; Torroni et al. 1992, 1993*a,* 1993*b*).

Phylogenetic Analysis of CR Sequences

The NJ tree in figure 4 clearly differentiates CR sequences from haplogroups A–D and G. For haplogroup C, the Chukotkan sequences (CHU17–CHU19) formed their own subbranch within the larger cluster of Native American mtDNAs. Similarly, for haplogroup D, most of the Chukotkan sequences (CHU14–CHU16) were separated from comparable Alaskan/Northwest Coast mtDNAs, forming a distinct branch. Because of its having several mutations in common with haplogroup A sequences, CHU13 appeared in this haplogroup, although as an outlier relative to other sequences in this cluster. Haplogroup G sequences also formed a distinct branch. The presence of the Yakima92 CR sequence within this haplogroup results from both haplogroups D and G mtDNAs having the 16129A mutation in com-

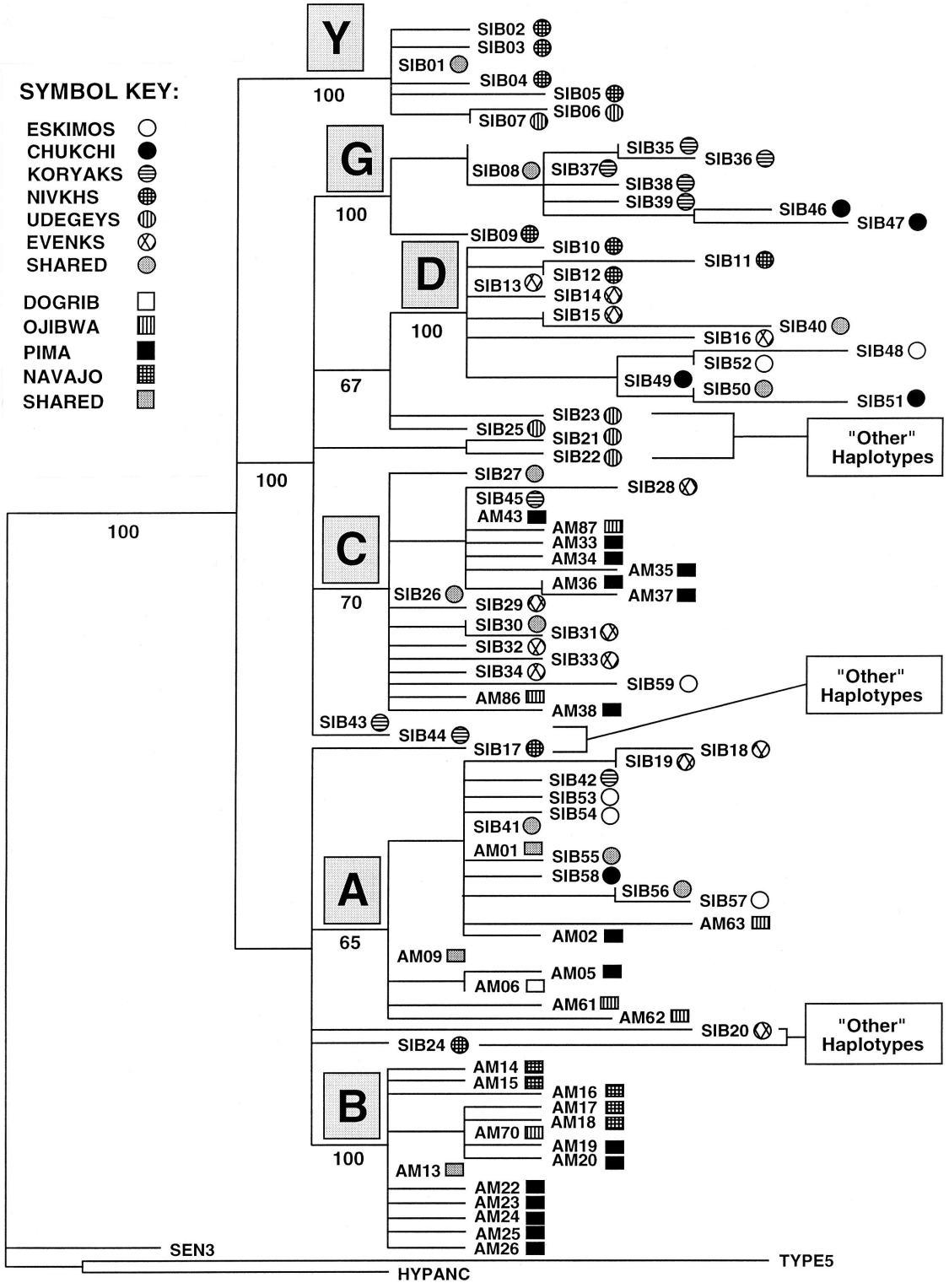

Figure 3 MP tree, showing phylogenetic relationships of Chukchi, Siberian Eskimo, selected Siberian, and northern Native American RFLP haplotypes. The tree is 144 mutational steps in length; has consistency and retention indices of .785 and .889, respectively; and represents 1 of 3,000 MP trees that were generated by the TBR branch-swapping algorithm. It was rooted by use of three African haplotypes, AF71 (Chen et al. 1995), TYPE-5, and HYPANC (hypothetical ancestor) (Cann et al. 1987). The haplogroups observed in native Siberian populations are indicated by the large uppercase letters in boxes, and the haplotypes appearing in each population are identified by circles or squares as defined in the "Symbol Key," with haplotype designations corresponding to those given by Torroni et al. (1993*a*, 1993*b*). "SHARED" haplotypes are those observed in more than one population. The horizontal branch lengths are proportional to the number of mutational events that separate the haplotypes. The numbers located under the major branches of the MP tree indicate the percentage of support for each branch in the 50%-majority-rule consensus tree.

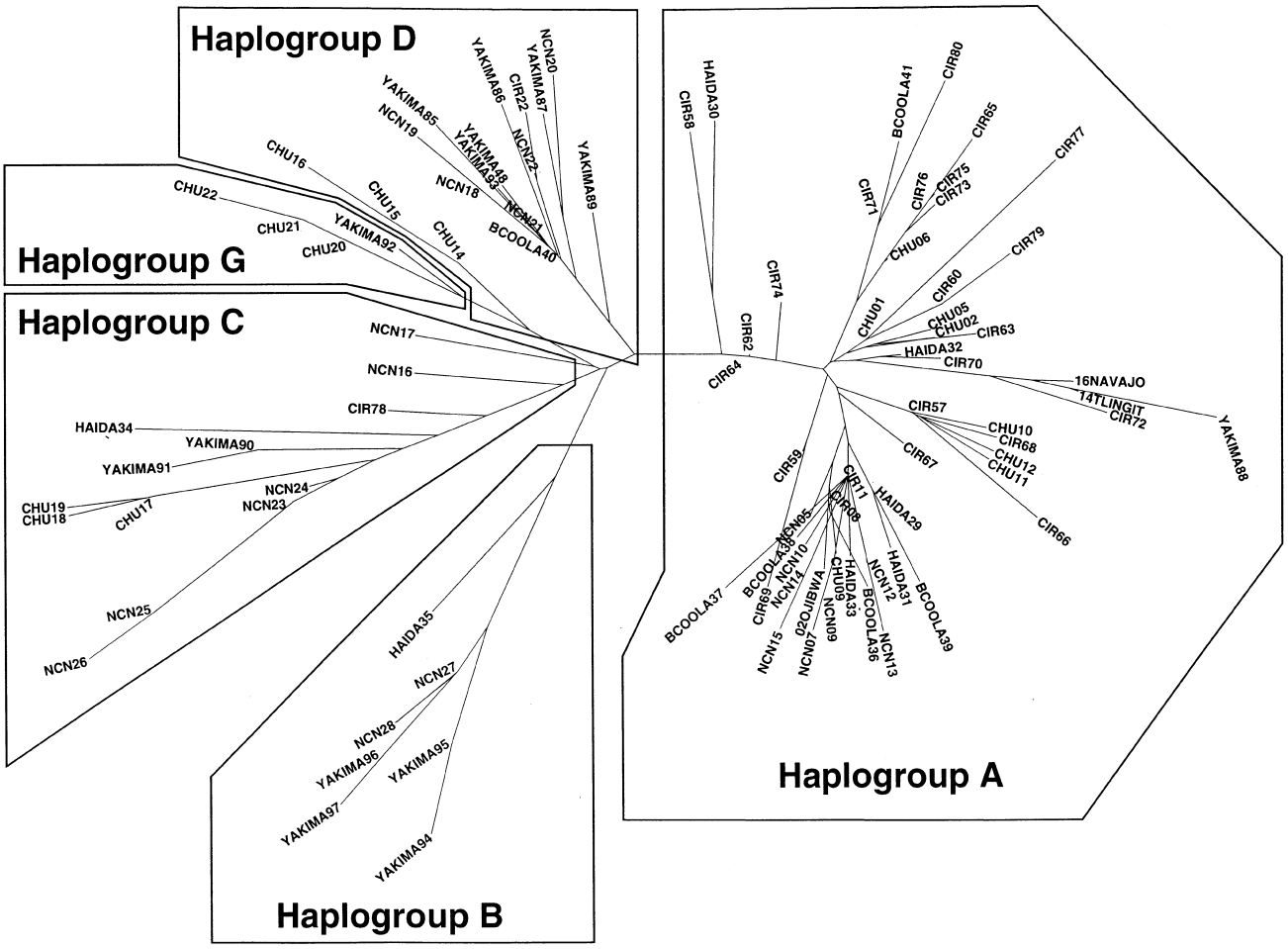

Figure 4 NJ unrooted tree of CR sequences from Chukchi, Siberian and Alaskan Eskimo, Na-Dene, and Northwest Coast Amerindians. The five groupings are clusters of related CR lineages affiliated with haplogroups and the populations in which they are found. The abbreviation "CHU" (Chukotkan) differentiates the novel Chukotkan CR lineages defined in the present study versus those described elsewhere either by the abbreviation "CIR" (circumpolar) or by tribal name with the number situated either before (Torroni et al 1993*a*) or after (Ward et al. 1991, 1993; Shields et al. 1993) the name of the tribe. The "CIR" lineages are as defined in the footnote to table 6.

mon. However, the Yakima92 CR sequence lacks the 16017C mutation, which defines haplogroup G (table 4), indicating that it belongs to a different mtDNA lineage.

For haplogroup A, the relationship between Siberian and Native American sequences is presented in figure 5. Aside from the 16111T mutation, which delineates a Chukotkan/New World set of haplogroup A mtDNAs, this mtDNA lineage is further subdivided by the 16192T variant, which is found solely in mtDNAs of the Chukchi, Eskimos, and Na-Dené Indians. Hence, it appears that 16192T delineates a "northern Pacific Rim" subbranch of haplogroup A, which presumably arose in the last inhabitants of Beringia.

Within the 16192T cluster, a Na-Dené–specific cluster was also observed. It was characterized by the 16233G and 16331G transitions, the latter also causing the *Rsa*I np-16329 site loss, which defines Na-Dené RFLP haplotypes AM05 and AM06 (Torroni et al. 1992, 1993*a*). Since these haplotypes are shared between different Na-Dené tribes, including the Tlingit of the Pacific Northwest, the Dogrib of Canada, and the Navajo and Apache of the U.S. Southwest (Torroni et al. 1992, 1993*a*) (fig. 3), it is most likely that the 16331G mutation arose in the common founding population prior to the split of the Athapaskan-speakers from their common roots with Tlingit populations, which, on the basis of linguistic analysis, is thought to have occurred in southern Alaska ~5,000 YBP (de Laguna 1988).

Another cluster, encompassing many of the Haida haplogroup A CR sequences and one Bella Coola haplogroup A CR sequence, was defined by the presence of the 16355T mutation in the absence of the 16331G transition. This mutation differentiates the Haida from other

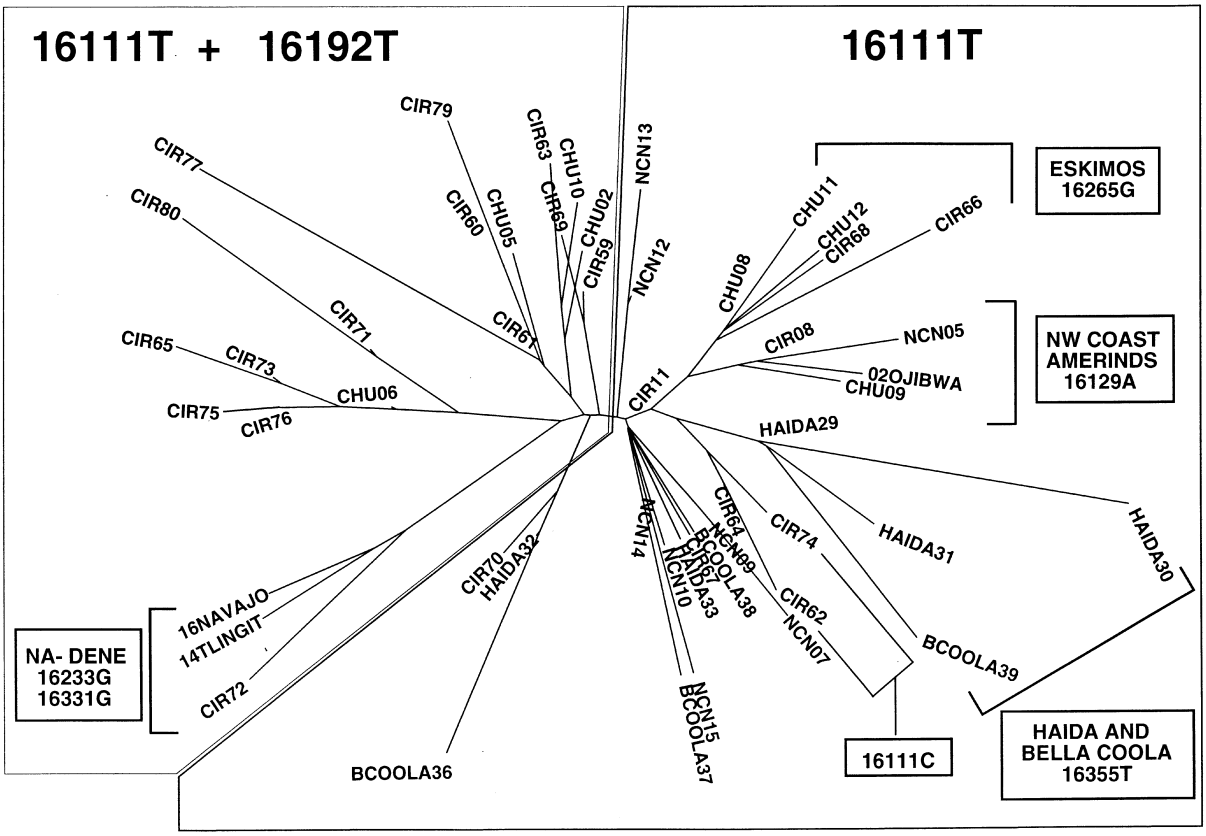

Figure 5 NJ unrooted tree of haplogroup A CR sequences from Chukchi, Eskimos, Na-Dene, and Northwest Coast Amerindians. All samples are as defined in the legend to figure 4. The two groupings are major subgroups of related CR sequences within this haplogroup, with the defining nucleotide polymorphisms indicated therein. Note that the boxes for the 16111T and 16192T polymorphisms overlap, in that all sequences with the 16192T polymorphism also have the 16111T polymorphism (but not vice versa). However, three CR sequences (CIR62, CIR64, and CIR74) exhibit a C rather than a T at np 16111 (Shields et al. 1993). This nucleotide difference appears to have resulted from a secondary T→C transition in 16111T mtDNAs, since all three of these CR sequences also possess the 16223T, 16290T, 16319A, and 16362C polymorphisms that are characteristic of haplogroup A mtDNAs; CIR74 also has the 16192T mutation.

Na-Dené populations and reveals its relatedness to Northwest Coast Amerindians (Torroni et al. 1992, 1993*a;* Shields et al. 1993) (fig. 5).

The haplogroup A CR lineages having the 16265G variant formed a distinct cluster of exclusively Eskimo mtDNAs. In fact, every Eskimo population analyzed for CR sequence variation contained mtDNAs with this variant (Shields et al. 1993; present study). The 16265G mutation appears to have arisen in ancestral Eskimos shortly before the split and subsequent spread of the Inupiaq-speakers into northern Alaska, the Canadian Arctic, and Greenland during the past millennia (Harper 1980; Krauss 1988).

Finally, the haplogroup A CR sequences that harbored the 16129A mutation delineated a North American Amerindian cluster that encompassed mtDNAs from the Haida, Nuu-Chah-Nulth, and Bella Coola, as well as the Ojibwa. The presence of Chukotkan CR sequence 09 (CHU09) within this cluster is due to its having the 16129A mutation, although otherwise it belongs in the Eskimo 16265G cluster.

These findings at the phylogenetic level were also reflected in the distribution of shared CR sequences among northern Pacific Rim tribal groups, as summarized in table 6. The putative founding CR sequence for haplogroup A, 07, is identical to CIR11 in the Nuu-Chah-Nulth (Ward et al. 1991). This CR sequence occurs in the Chukchi and Siberian Eskimos, as well as in all of the major linguistic groups of Native Americans residing in the northern Pacific Rim (Ward et al. 1991; Shields et al. 1993; present study). However, the remaining CR sequences from haplogroup A occurred in either the Haida and Northwest Coast Amerindians, the Na-Dené Indians other than Haida, or the Siberian Eskimos and Chukchi. The same separation of CR sequences was seen for both haplogroups C and D. Thus, the emergence of distinct sublineages within the haplogroups shared by the Chukchi and Eskimo, in one case, by the Na-Dené

Table 6

CR (HVS-1) Sequences Shared between Northern Pacific Rim Populations

	No. of Shared Circumpolar (CIR) HVS-1 Sequences[a]														
	Haplogroup A							Haplogroup B		Haplogroup C	Haplogroup D				
Population	08	11	57	59	60	61	69	01	27	34	21	22	58	Total	Reference
Chukchi	...	2	11	...	1	19	6	...	...	...	...	...	1	40	Present study
Chukchi	...	1	...	...	...	2	...	...	...	...	...	...	...	3	Shields et al. (1993)
Siberian Eskimos	...	1	14	...	...	37	3	...	...	...	...	...	4	59	Present study
Siberian Eskimos	...	...	1	...	...	2	...	...	...	...	...	...	...	3	Shields et al. (1993)
Inupiaqs	...	...	1	...	2	...	1	...	...	...	...	...	1	5	Shields et al. (1993)
Western Greenland Eskimos	...	...	2	1	1	7	...	...	...	...	...	...	1	12	Shields et al. (1993)
Alaskan Athapaskans	...	6	...	...	3	2	...	...	...	...	...	...	...	11	Shields et al. (1993)
Dogrib	...	1	...	...	...	...	...	...	...	...	...	...	...	1	Torroni et al. (1993*a*)
Haida	1	20	...	...	...	...	...	...	...	3	2	...	...	26	Ward et al. (1993)
Tlingit	...	1	...	...	...	...	...	...	...	...	...	...	...	1	Torroni et al. (1993*a*)
Navajo	...	1	...	...	...	...	...	...	...	...	...	...	...	1	Torroni et al. (1993*a*)
Nuu-Chah-Nulth	2	5	...	...	...	...	...	3	1	...	3	3	...	17	Ward et al. (1991)
Bella Coola	8	3	...	...	...	...	...	2	...	3	5	2	...	23	Ward et al. (1993)
Yakima	...	1	...	...	...	...	...	...	9	...	2	...	...	12	Shields et al. (1993)

[a] Numbers and abbreviations of HVS-1 sequences are adopted from Ward et al. (1991, 1993) and Shields et al. (1993). The CIR sequences represent the CHU sequences described in table 4, as follows: CIR61 = 01, CIR69 = 03, CIR60 = 04, CIR11 = 07, CIR57 = 08, and CIR58 = 13.

populations in another, and by the Amerindians of the Northwest Coast in a third is suggestive of a profound temporal and geographic separation of the founders of different linguistic groups inhabiting the exposed areas of former Beringia.

Discussion

This analysis has elucidated the range and nature of mtDNA variation in the Chukchi peninsula. The Chukchi and Siberian Eskimos harbored mtDNAs from three haplogroups (A, C, and D) of the four common among aboriginal Americans but none from haplogroup B. Furthermore, the Chukchi, but not the Siberian Eskimos, had mtDNAs from Asian haplogroup G, indicating their genetic affinities with the Koryaks and Itel'men of Kamchatka.

Diversity of Haplogroup A mtDNAs

Both RFLP and CR sequence analysis of haplogroup A mtDNAs in northeastern Siberia revealed a distinct geographic pattern. The haplogroup A CR variant 16111T differentiated the Chukotkan and American mtDNAs from those in the rest of Asia (Ward et al. 1991; Horai et al. 1993; Shields et al. 1993; Torroni et al. 1993*a;* present study). Hence, the 16111T polymorphism defines the founding haplogroup A mtDNA sequence(s), which originated among the earliest inhabitants of Beringia prior to their migration into the New World.

Aside from this ubiquitous polymorphism, other variable CR nucleotides revealed considerable substructure within haplogroup A. Along with the *Alu*I np-11362 site gain, the 16265G polymorphism demarcated a specific set of haplogroup A mtDNAs that are unique to the Chukchi and Eskimo populations. Likewise, the 16192T mutation defined a northern Pacific Rim branch of haplogroup A, encompassing mtDNAs from the Chukchi, Eskimos, and Na-Dené Indians, and appears to have arisen in the last inhabitants of Beringia. Several additional CR sequence clusters of haplogroup A were observed in the Northwest Coast populations, including at least one cluster that appears only in Amerindian groups. Thus, the occurrence of distinct CR lineages and sublineages of haplogroup A in contemporary populations of the northern Pacific Rim may reflect the genetic history of human populations that existed in Beringian and southern Alaskan refugia at the end of the last glacial maximum (Rogers et al. 1991). Therefore, the Chukchi, Eskimo, and Na-Dené Indian populations are likely to be the remnants of the progenitors of the first Americans, who brought haplogroups A, C, and D to the New World, even though they currently retain much lower haplogroup A diversity than is seen in the Amerindians.

The clear affinity between the mtDNAs from aboriginal Chukotkan populations and those of Native Americans, as compared with those of modern mongoloid populations of northern Asia, is also supported by parallel studies of Y-chromosome polymorphisms. Specifically, it has been shown that a C→T transition at np 181 of the DYS199 locus is broadly distributed among all Native American populations (Underhill et al. 1996; Lell

et al. 1997) but in Siberia is found only among the Chukchi and Siberian Eskimos (Lell et al. 1997). An apparently higher affinity between the Chukchi and the northern Athapaskans, relative to the adjacent Yukagirs and Evens, was also made evident in the comprehensive analysis of variation at the GM locus (Sukernik 1992). Thus, both the mtDNA and nuclear-DNA data reveal the genetic differentiation between Chukotkan populations and adjacent Siberian groups, as well as their close genetic linkage to Native Americans.

Divergence Time for mtDNA Lineages in Siberia and the Americas

Geological data and environmental history suggest that the most propitious time for the first entry of humans into the New World from Beringia occurred 35,000–30,000 YBP, when deglaciation was sufficient to form the so-called Alberta corridor from western Alaska to the Great Plains. During the last glacial maximum (~23,000–16,000 YBP), the glacial coalescence prevented further human dispersal from the Alaskan portion of Beringia southward. With the global climate change that brought the Ice Age to an end, the Alberta corridor opened again, presumably permitting a second wave of human immigrants into the New World (Butzer 1991; Wright 1991).

To determine whether mtDNA variation correlates with this geological time frame, we estimated the divergence times for the major Siberian and American haplogroups (table 7). To obtain these estimates, previously reported data (Torroni et al. 1992, 1993*a,* 1993*b*) were combined with more recently analyzed data sets (Torroni et al. 1994*b;* Huoponen et al. 1997; Schurr et al., in press; present study). In these estimates, it was assumed that all nonshared mtDNA variation at the RFLP level evolved independently in Siberia and the Americas, since only the founding haplotypes of the various haplogroups were shared by Siberian and Native American populations. This assumption was validated by the starlikeness of each haplogroup in the respective RFLP haplotype MP trees, both in the present study (fig. 3) and in the work of Torroni et al. (1993*a,* 1993*b*), and, more recently, by Forster et al. (1996) and Bonatto and Salzano (1997), in their analysis of CR sequence variation within Native American populations. However, it was also understood that the assessment of dates for the mtDNA "most-recent common ancestor" (MRCA) could have broad confidence intervals (Templeton 1993; von Haeseler et al. 1996).

As seen in table 7, the sequence-divergence estimates for Siberian haplogroups C and D were comparable to those for the analogous mtDNA lineages in Native Americans, being within the range of 40,000–20,000 YBP. These results confirmed the antiquity of haplotypes in haplogroups C and D in northern Asia and the Americas, as well as the ancient genetic links between populations inhabiting these regions. By contrast, the divergence time for haplogroup A in Siberia was much smaller than that for this haplogroup in the Americas, primarily because Siberian haplogroup A consisted al-

Table 7

Sequence Divergence and Divergence Time of Native Siberian and Native American mtDNA Haplogroups

Haplogroup and Region	No. of Haplotypes[a]	No. of Individual mtDNAs/ Haplogroup	Sequence Divergence (%)	Divergence Time[b] (YBP)
A:				
Siberia	10	119	.028	12,727–9,655
America	46	189	.079	35,909–27,241
B:				
America	30	99	.039	17,727–13,448
C:				
Siberia	14	123	.043	19,545–14,828
America	31	72	.122	55,545–42,069
D:				
Siberia	13	47	.111	50,455–38,276
America	16	62	.057	25,909–19,655
G:				
Siberia	11	106	.024	10,909–8,276
Y:				
Siberia	7	58	.014	6,364–4,828

[a] Data are from Torroni et al. (1992, 1993*a,* 1993*b,* 1994*a,* 1994*b*), Huoponen et al. (1997), Schurr et al. (in press), and present study.

[b] Estimated on the basis of an mtDNA evolutionary rate of 2.2%–2.9%/MYR (Torroni et al. 1994*b*).

most solely of Chukchi and Siberian Eskimo haplotypes. The relatively low sequence diversity of haplogroup A mtDNAs in the Chukchi and Siberian Eskimos has also been observed in North American Eskimos and Na-Dené Indians (Shields et al. 1993).

In fact, our three estimates of the genetic divergence of haplogroup A in Siberian and Native American populations—that is, in the Chukotkan groups (0.029%; 12,727–9,655 YBP), the Na-Dené Indians (0.021%; 9,545–7,241 YBP [Torroni et al. 1992]), and the Amerindians (0.079%; 35,909–27,241 YBP)—show very clearly the extent of diversity that has developed between these populations, not just within the haplogroup itself. Thus, even if these estimates are upper limits on the actual divergence times for these populations, the relative temporal differences, in their origins, that are implied by these data will not change much in more-refined calculations. This is especially true because only the founding haplotype (SIB41+AM01) is shared among them, every other haplotype being unique to one of these population sets (Torroni et al. 1992, 1993*a,* 1993*b,* 1994*a,* 1994*b;* present study). Therefore, it appears that the ancient founding populations that gave rise to the Chukchi, Eskimo-Aleuts, and Na-Dené Indians underwent a more recent bottleneck (13,000–7,000 YBP) followed by the expansion of selected haplogroup A haplotypes—and that this fluctuation in effective population size reduced diversity and, hence, the apparent time back to the MRCA (von Haeseler et al. 1996). This interpretation is consistent with the environmental history of the northern Pacific Rim, as well as with more recent historical events.

Haplogroup B also had a divergence time (17,700–13,500 YBP) that was considerably more recent than those of Amerindian haplogroups A, C, and D (table 7). This estimate correlates with the last exposure of the Bering land bridge (16,000–13,000 YBP), when the Alberta corridor was open again or when the coastal route could be traversed (Wright 1991). However, recent analyses of CR sequence variation in Native Americans indicate that haplogroup B may be as diverse as haplogroups A, C, and D (Bonatto and Salzano 1997; Stone and Stoneking 1998). Given the general concordance of divergence estimates for RFLP and CR sequence data for the other three haplogroups, the reason(s) for the disparity between them in relation to haplogroup B may be explained, in part, by the different methodologies used in these studies. On the other hand, the relatively recent divergence times of Siberian haplogroups G and Y, as well as their absence in the New World, indicate that they reached the southwestern periphery of Beringia substantially after the migration(s) that populated the Americas.

Proposed Dual Origin of Paleoindians

A number of models for the peopling of the New World that are based on mtDNA variation have been advanced in the past several years. Some researchers have proposed that all four mtDNA lineages were brought together in the initial colonization of the Americas (Kolman et al. 1995; Merriwether et al. 1996), although they have differed somewhat in their estimates (30,000–15,000 YBP) of the time when this event occurred. Others have suggested that each haplogroup found in Native Americans represents a separate, temporally distinct migration from Asia to the New World, all of which arrived 21,000–14,000 YBP (Horai et al. 1993). In contrast, we have postulated that ancestral Paleoindians had a bipartite origin, with haplogroups A, C, and D being brought during the initial ancient migration to the Americas and with a restricted number of haplogroup B mtDNAs being brought during an additional, more recent migration (Torroni et al. 1993*b*). The results of the study generally support our original supposition and allow us to make several inferences about the process of the peopling of the New World.

First, the average divergence time for haplogroups A, C, and D in the Americas indicated that humans first expanded into the New World 39,000–29,700 YBP (table 7), dates that coincide with the opening of the Alberta corridor (Wright 1991). These sequence-divergence values were averaged because they were the only ones present in both the Americas and Siberia (table 7). Since considerably distant divergence times (40,000–25,000 YBP) for these same three mtDNA lineages also have been obtained in recent studies of CR sequence variation in Native Americans (Bonatto and Salzano 1997; Stone and Stoneking 1998), the ancient expansions of haplogroups A, C, and D is now well substantiated. Thus, ancient Paleoindians appear to have been present in the Americas well before the dates associated with the Clovis lithic tradition (Haynes 1992).

Second, the recent divergence time (17,700–13,500 YBP) for haplogroup B, as well as the predominance of the founding haplotype, AM13, in Native American populations (~69%; Torroni et al. 1992, 1993*a,* 1994*a,* 1994*b*), imply that haplogroup B arrived in the New World later than the other three haplogroups, whose founding haplotypes appear far less frequently among all Native American groups. In addition, as noted in several studies, haplogroup B haplotypes are virtually absent in northeastern Siberia and most of northern Asia (Shields et al. 1992; Torroni 1993*b;* Sukernik et al. 1996; Schurr et al., in press), with the most proximal modern populations harboring haplogroup B mtDNAs being located in southeastern Siberia and the adjacent Mongolia/Manchuria region (Kolman et al. 1996; Merriwether et al. 1996; Sukernik et al. 1996). These observations sug-

gest that, ~40,000 YBP, haplogroup B mtDNAs were absent in the early modern humans from the upper Lena/Baikal region, the putative homeland of the first wave of ancestral Amerindians (Goebel and Aksenov 1995) but apparently reached Beringia at a temporally distinct and later period, although prior to the most recent submergence of the Bering land bridge.

If one accepts that haplogroup B arrived in the New World more recently, our mtDNA data are consistent with recent archaeological findings that suggest that there were two waves of Paleoindian migration into South America. The first migration resulted in both the occupation of the Amazon basin ~16,000–10,500 YBP, by a population subsisting on fruit and nut gathering, fishing, and hunting of small animals (Roosevelt et al. 1996), and the peopling of southern Chile, by 13,500 YBP, by a population using similar mixed-subsistence strategies (Dillehay 1997). The second migration apparently brought a big game–hunting culture that was associated with a lithic technology of bifacially flaked projectile points (Clovis culture) and that appeared south of the North American ice sheet 11,500 YBP (Bonnichsen et al. 1991; Haynes 1992). These Clovis hunters may have swamped the earlier hunter-gatherers of North and Central America, whereas, in South America, the earlier culture(s) survived.

Intriguingly, the low frequency of haplogroup B in the Amerindian tribes of the Northwest Coast, its high frequency in those inhabiting Mesoamerica, and its absence in populations of extreme southern South America (Torroni et al. 1993*a,* 1994*b;* Fox 1996; Lorenz and Smith 1996; Merriwether et al. 1996) roughly parallel the distribution of Clovis sites. This distribution may imply that haplogroup B entered the New World shortly prior to the Clovis innovation and expanded along with Clovis hunters. However, even if the Clovis tradition is shown to represent a New World innovation, rather than arising from a distinct migration from Asia (Bryan 1991; Stanford 1991), the distribution of haplogroup B in the Americas may still suggest that an independent, possibly coastal, migration to the New World occurred after the Americas were initially settled.

Conclusions

Our comprehensive analysis of mtDNA variation on both sides of the Bering Strait and further inland into eastern Siberia and the New World has permitted us to draw several conclusions. First, ~34,000 YBP, ancient Beringia harbored a population(s) that contained haplogroups A, C, and D and gave rise to the first Americans. Second, ~16,000–13,000 YBP, a later migration brought haplogroup B, presumably from southeastern Siberia. Third, the ancestors of the Chukchi and Eskimos, as well as those of the Na-Dené Indians and Northwest Coast Amerindians, are the products of substantial genetic differentiation of populations that were occupying different glacial refugia during the end of the last glacial maximum. This is clearly shown by the diversity in haplogroup A CR sequences, as well as by the latters' association with different Native American linguistic groups.

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