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mtDNA Variation Indicates Mongolia May Have Been the Source for the Founding Population for the New World

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Summary

mtDNA RFLP variation was analyzed in 42 Mongolians from Ulan Bator. All four founding lineage types (A [4.76%], B [2.38%], C [11.9%], and D [19.04%]) identified by Torroni and colleagues were detected. Seven of the nine founding lineage types proposed by Bailliet and colleagues and Merriwether and Ferrell were detected (A2 [4.76%], B [2.38%], C1 [11.9%], D1 [7.14%], D2 [11.9%], X6 [16.7%], and X7 [9.5%]). Sixty-four percent of these 42 individuals had "Amerindian founding lineage" haplotypes. A survey of 24 restriction sites yielded 16 polymorphic sites and 21 different haplotypes. The presence of all four of the founding lineages identified by the Torroni group (and seven of Merriwether and Ferrell's nine founding lineages), combined with Mongolia's location with respect to the Bering Strait, indicates that Mongolia is a potential location for the origin of the founders of the New World. Since lineage B, which is widely distributed in the New World, is absent in Siberia, we conclude that Mongolia or a geographic location common to both contemporary Mongolians and American aboriginals is the more likely origin of the founders of the New World.

Introduction

There have been numerous studies of mtDNA variation in Asian populations that use either RFLP or D-loop sequence analysis (Horai et al. 1984, 1993; Harihara et al. 1986, 1988, 1992; Horai and Matsunaga 1986; Horai 1987, 1991*a*, 1991*b*; Hertzberg et al. 1989; Horai and Hayasaka 1990; Stoneking et al. 1990; Ballinger et al. 1992; Torroni et al. 1994*b*; Redd et al. 1995), however, most have concentrated on either southeast Asian or coastal populations (primarily Japan, Taiwan, and Korea). Many Siberian populations have been studied (Shields et al. 1992, 1993; Torroni et al. 1993*b*), especially those nearest to Alaska across the Bering Strait, because of their location with reference to the initial peopling of the New World. There have been few population studies of central and northern inland Asian populations.

Studies of mtDNA variation in the New World (Wallace et al. 1985; Schurr et al. 1990; Ward et al. 1991, 1993; Merriwether et al. 1992, 1993, 1994, 1995*a*, 1995*b*; Shields et al. 1992, 1993; Torroni et al. 1992, 1993*a*, 1994*a*, 1994*c*; Ginther et al. 1993; Horai et al. 1993; Merriwether 1993; Bailliet et al. 1994; Lorenz and Smith 1994; Torroni and Wallace 1995; Merriwether and Ferrell 1996) have led to several theories regarding the mitochondrial portrait of the peopling of the New World. Schurr et al. (1990) were the first to suggest that all Native Americans could apparently trace their roots back to one of four "founding lineage" haplotypes that entered the New World from Asia. Although Torroni et al. (1992, 1993*a*, 1993*b*, 1994*a*, 1994*c*) argue that just one variant of each of these founding lineages entered the New World, Bailliet et al. (1994), Merriwether and Ferrell (1996), and Merriwether et al. (1994, 1995*b*) demonstrated that at least two variants of three of the four founding-lineage haplotypes are present throughout the New World, Siberia, and Asia. Merriwether and Ferrell (1996) and Easton et al. (1996, in this issue) demonstrated the widespread presence in the New World, Siberia, and Asia of at least two additional founding lineage types not reported by Torroni et al. (1992, 1993*a*, 1994*a*, 1994*b*), designated X6 and X7 after their initial definition in the admixed Hispanic population of the San Luis Valley, Colorado (D. A. Merriwether, S. Huston, S. Iyengar, R. Hamman, M. I. Kamboh, and R. E. Ferrell, unpublished data) and the Mongolian population in this study. X6 and X7 were the sixth and seventh non-A, -B, -C, -D lineages observed in Native Americans and their hybrid populations. This brings the total number of Asian lineages shared between the New World and Asia to 9 (or 10, if the less widely distributed B2 lineage is counted as a founding lineage).

The New World founding haplogroups can be identi-

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Table 1

RFLP Sites That Define the Major Haplogroups Observed in Native American Populations

Type	*Hae*III 663	Deletion	*Hin*cII 13259	*Alu* 15176	*Dde*I 10394	*Alu*I 10397	*Hae*III 16517
A1	+	N	+	+	−	−	+
A2	+	N	+	+	−	−	−
B1	−	D	+	+	−	−	+
B2	−	D	+	+	−	−	−
C1	−	N	−	+	+	+	+
C2	−	N	−	+	+	+	−
D1	−	N	+	−	+	+	+
D2	−	N	+	−	+	+	−
X6	−	N	+	+	+	+	−
X7	−	N	+	+	+	+	+

NOTE.—A plus sign (+) signifies a restriction-site gain; a minus sign (−) signifies a restriction-site loss; N signifies nondeleted status for the region V 9-bp deletion region; and D signifies the region V 9-bp deletion.

fied by screening for a small number of RFLPs and one 9-bp intergenic deletion. The founding haplogroups and their subsets are defined in table 1. The lineages, called "A1," "A2," "B1," "B2," "C1," "C2," "D1," "D2," "X6," and "X7" can be distinguished unambiguously by using the seven markers in table 1. Of interest to New World scholars is where these founding lineages arose, now widely accepted to be somewhere on the Asian side of the Bering Strait. Shields et al. (1992, 1993) and Torroni et al. (1993*b*) demonstrated that only variants of lineages A, C, and D are found in Siberia and Alaska. Although Sukernik et al. (1995) recently reported three copies of a 9-bp deletion in the Yukagir of southern Siberia, all three individuals had the deletion on a lineage C background (presence of the *Hin*cII 13259 site loss and lacked the *Hae*III 16517 site gain commonly associated with the deletion in the New World), indicating that the Siberian deletion is not the same deletion commonly associated with lineage B in the New World. Sukernik et al. (1995) also note the presence of the New World–type 9-bp deletion in one northern Altai Tubular individual, in agreement with Shields et al.'s (1992) detection of the deletion in another Altai population. Altai is far west of Siberia and the Bering land-bridge region. Merriwether et al. (1994, 1995*b*) detected the 9-bp deletion in the Old Harbor Eskimo population of Kodiak Island, but at a frequency of $<5\%$, and in no other Alaskan population among 600 Alaskan Eskimos and Aleuts screened for the deletion.

One would expect that the "founding population," or at least the population directly descended from the founding population, should ideally possess all of the common widely distributed haplotypes found in the New World. While drift, selection, and migration will alter the variation in all descendants of the "ancestral" population, we still expect that the most closely related populations will share the greatest number of haplotypes. Chakraborty and Weiss (1991) and Merriwether et al. (1991) demonstrated that New World populations were at Hardy Weinberg equilibrium with regard to the frequencies of their mtDNA RFLP haplotypes. Siberia is therefore an unlikely source for the founding population, because no Siberian populations possess either the B1 or B2 variant of the 9-bp founding lineage, and most possess only a small subset of the other founding lineage haplotypes. Therefore, the search for the source of the founding population requires the examination of more-distant Asian populations. We seek to identify the region from which New World populations first arose, by identifying those contemporary Asian or Siberian populations, which are most closely related to New World populations. We report the analysis of mtDNA variation in a Mongolian population that meets many of the requirements of a founding population (or, more precisely, being descended from the same founding population).

Methods

DNA was extracted following Merriwether et al.'s (1994, 1995*b*) modifications of Boom et al.'s (1990) procedure. The PCR (Saiki et al. 1988) was carried out in a Perkin Elmer 9600 thermocycler using cycling parameters, conditions, and primers described by Merriwether et al. (1994, 1995*b*). Amplicons were digested with the appropriate restriction endonuclease following manufacturers' recommendations (New England Biolabs or Bethesda Research Labs), electrophoresed on 2% agarose gels stained with ethidium bromide, and visualized under UV light. A total of 14 polymorphic sites and 3 monomorphic sites were surveyed (see table 2) from six PCR-amplified regions of the mtDNA of each individual.

Table 2

Restriction Site Cut and Deletion Frequencies in the Mongolian Population of Ulan Bator

Site[a]	Number	Frequency
*Hae*III 663 (+)	2	.0476
Region V deletion	1	.0238
*Hin*cII 13259 (+)	37	.8810
*Alu*I 5176 (+)	35	.8333
*Dde*I 10397 (+)	27	.6429
*Alu*I 10394 (+)	24	.5714
*Hae*III 16517 (+)	26	.6190
*Dde*I 10360 (+)	42	1.0000
*Hae*III 16460 (+)	42	1.0000
*Ava*II 8249 (+)	1	.0238
*Rsa*I 16329 (+)	42	1.0000
*Hin*cII 12406 (+)	39	.9286
*Hpa*I 12406 (+)	39	.9286
*Ava*II 16390 (+)	42	1.0000
*Rsa*I 16303 (+)	37	.8810
*Eco*RV 16274 (+)	6	.1429
*Sau*96I 16517 (+)	23	.5476

[a] Plus sign (+) indicates the presence of the restriction site.

Samples

DNA was extracted from the cell pellets of 45 Native Mongolians from the capital city of Ulan Bator in north-central Mongolia.

Analysis

Haplotypes were created by combining the 14 RFLPs and the 9-bp deletion data for each individual. Swofford's (1989) PAUP 3.0s program was used to generate 1,000 replicates of heuristic searches, saving the 20 shortest trees from each search, to generate a population of parsimony trees. A consensus tree was created from all the equally parsimonious shortest trees found by the replicate searches.

Results

Table 2 shows the frequencies of each restriction site in the sample population. Table 3 shows the frequencies of each observed haplotype in the sample population, with the "short haplotypes" corresponding to the New World subset shown in figure 1 and with the "extended haplotypes" showing the frequencies of all the observed RFLP haplotypes. Figure 1 is a stacked histogram, which displays the frequencies of haplotypes found in the New World, Siberia, and Asia. The percentage of the bar to the right of each population name, which is filled in with a particular pattern, corresponds to the frequency of that haplotype in that population. For example, in the Malay population at the far left of the histogram, the bottom pattern is "solid black," corresponding to the frequency of haplotype A1 in this Malay population (21%). The next pattern up on the bar is a "dark gray," corresponding to the frequency of haplotype C1 in the Malays (44%), and the top pattern on the bar is "white," corresponding to the frequency of "other" haplotypes in the Malays (35%). The "stacked" patterns add up to 100% for each population. Note that many populations possess multiple founding lineage variants. Table 4 displays the data used to generate figure 1, including sample size and frequency for each haplotype in each population. Figure 2 shows a majority-rule consensus tree of the data, constructed using the parsimony method (PAUP 3.0s) from 500 equally parsimonious trees generated by 100 replicates of heuristic searches, saving the 20 shortest trees from each replicate, restarting each replicate with random sequence addition. Once again, the tips of the tree represent RFLP haplotypes consisting of one or more individuals. Haplotypes clustered together on the tree indicate that they

Table 3

mtDNA RFLP Haplogroup Frequencies in the Mongolian Population

Type	Number	Frequency
Short Haplotype Frequencies		
A2	2	.0476
B1	1	.0238
C1	5	.1190
D2	5	.1190
D1	3	.0714
X3	2	.0476
X4	3	.0714
X5	10	.2381
X6	7	.1667
X7	4	.0952
Extended Haplotype Frequencies		
A2	2	.0476
B1	1	.0238
C1	1	.0238
C3	3	.0714
C4	1	.0238
D1	4	.0238
D2	2	.0952
D3	1	.0476
D4	1	.0238
X4	2	.0238
X5	5	.0476
X6	3	.1190
X7	3	.0238
X8	1	.0238
X9	1	.0238
X10	1	.0238
X11	2	.0476
X12	1	.0238
X13	2	.0476
X14	1	.0238
X15	4	.0952

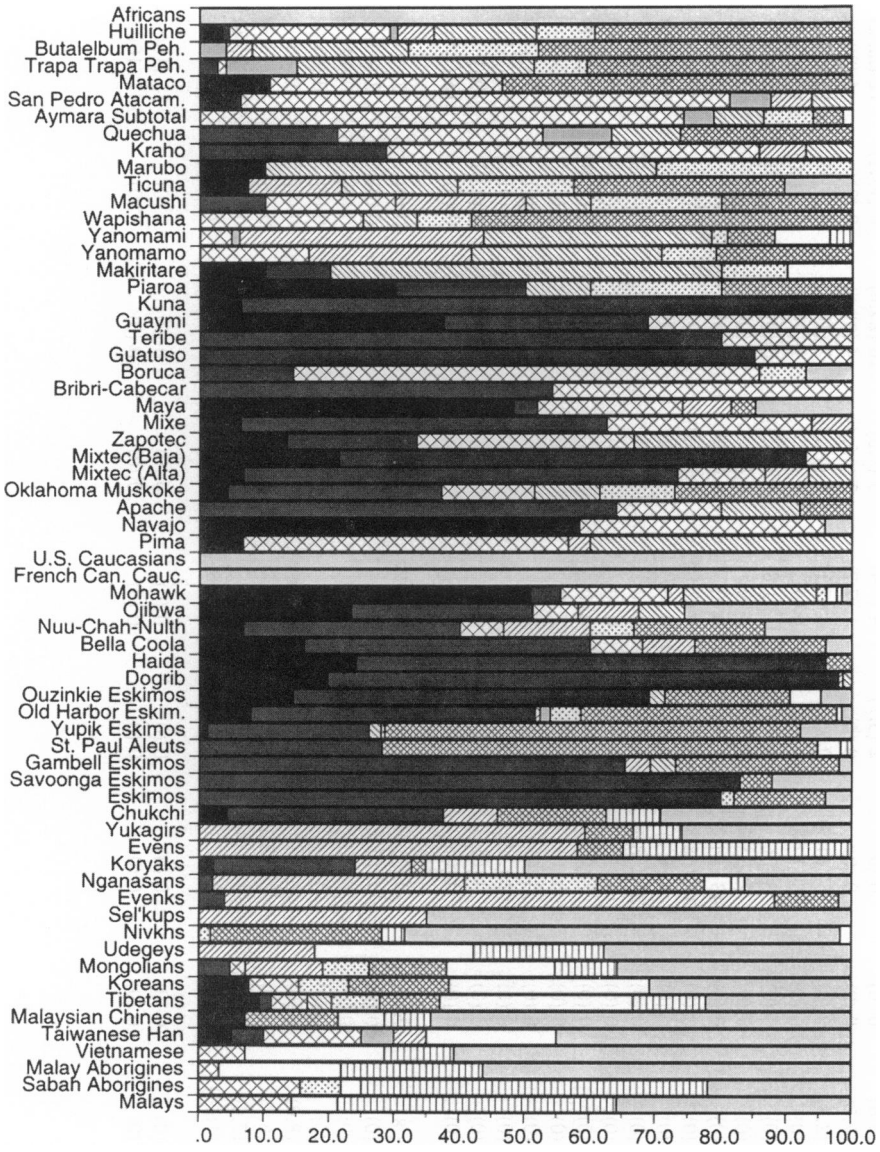

Figure 1 Frequencies of the New World founding lineage haplogroups in New World, Siberian, and Asian populations.

are more closely related to each other than to other haplotypes on the tree. The numbers at the nodes indicated the percentage of the time that bootstrap resampling of the data yielded each particular node. Only those nodes supported ≥50% of the time in the bootstrap replicate trees are displayed and labeled. All other nodes are collapsed back to the last node supported at by ≥50% of the bootstrap replicates. This is a means of estimating the strength of these nodes, or the confidence we might place on the node being correctly placed. The generally low bootstrap values are typical for parsimony trees for human within-population data, because of the relatively recent divergence of modern human populations (Merriwether et al. 1991).

Discussion

Contemporary Mongolians appear to be related to the same source population from which the New World Natives arose. Even a small sample of 45 individuals possessed seven of the nine major mtDNA haplogroups observed in the New World, and these seven accounted for 64% of all observed haplotypes. Mongolians represent the population geographically closest to the New World possessing such a large percentage of New World haplotypes. We find the Tibetans (A1, A2, B1, C2, D1, D2, X6, and X7) (Torroni et al. [1994*b*] describe the Tibetans in their study as "displaced Mongolians") and the Mongolians (A1, B1, C1, D1, D2, X6, and X7) have the largest number of founding lineage variants shared with the New World, with the Taiwanese Han (A2, B1, C2, D1, and X6) and the Koreans (A1, B1, D1, D2, and X6) sharing slightly fewer lineages. The Yukagir completely lack lineage A and have only three of the founding lineage variants (they have C1, D2, and X7, according to Torroni et al. [1993*b*]). We propose that

Table 4

Frequencies of the New World Founding Lineage Subtypes in the New World, Siberia, and Asia

Population	No.	A1	A2	B1	B2	C1	C2	D1	D2	X6	X7	Other
Malays	14	0 (0)	0 (0)	2 (14.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (7.1)	6 (42.9)	5 (35.7)
Sabah Aborigines	32	0 (0)	0 (0)	5 (15.6)	0 (0)	0 (0)	0 (0)	2 (6.3)	0 (0)	1 (3.1)	17 (53.1)	7 (21.9)
Malay Aborigines	32	0 (0)	0 (0)	1 (3.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	6 (18.8)	7 (21.9)	18 (56.3)
Vietnamese	28	0 (0)	0 (0)	2 (7.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	6 (21.4)	3 (10.7)	17 (60.7)
Taiwanese Han	20	1 (5.0)	1 (5.0)	3 (15.0)	1 (5.0)	1 (5.0)	0 (0)	0 (0)	0 (0)	4 (20.0)	0 (0)	9 (45.0)
Malaysian Chinese	14	1 (7.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (14.3)	1 (7.1)	1 (7.1)	9 (64.3)
Tibetans	54	5 (9.3)	1 (1.9)	3 (5.6)	0 (0)	0 (0)	2 (3.7)	4 (7.4)	5 (9.3)	16 (29.6)	6 (11.1)	12 (22.2)
Koreans	13	1 (7.7)	0 (0)	1 (7.7)	0 (0)	0 (0)	0 (0)	1 (7.7)	2 (15.4)	4 (30.8)	0 (0)	4 (30.8)
Mongolians	42	0 (0)	2 (4.8)	1 (2.4)	0 (0)	5 (11.9)	0 (0)	3 (7.1)	5 (11.9)	7 (16.7)	4 (9.5)	15 (35.7)
Udegeys	45	0 (0)	0 (0)	0 (0)	0 (0)	8 (17.8)	0 (0)	0 (0)	0 (0)	11 (24.4)	9 (20.0)	17 (37.8)
Nivkhs	57	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (1.8)	15 (26.3)	0 (0)	2 (3.5)	38 (66.7)
Sel'kups	20	0 (0)	0 (0)	0 (0)	0 (0)	7 (35.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	13 (65.0)
Evenks	51	0 (0)	2 (3.9)	0 (0)	0 (0)	43 (84.3)	0 (0)	0 (0)	5 (9.8)	0 (0)	0 (0)	1 (2.0)
Nganasans	49	0 (0)	1 (2.0)	0 (0)	0 (0)	19 (38.8)	0 (0)	10 (20.4)	8 (16.3)	2 (4.1)	1 (2.0)	8 (16.3)
Koryaks	46	1 (2.2)	10 (21.8)	0 (0)	0 (0)	4 (8.7)	0 (0)	0 (0)	1 (2.2)	0 (0)	7 (15.2)	23 (50.0)
Evens	43	0 (0)	0 (0)	0 (0)	0 (0)	25 (58.1)	0 (0)	0 (0)	3 (7.0)	0 (0)	15 (34.9)	0 (0)
Yukagirs	27	0 (0)	0 (0)	0 (0)	0 (0)	16 (59.3)	0 (0)	0 (0)	2 (7.4)	0 (0)	2 (7.4)	7 (25.9)
Chukchi	24	1 (4.2)	8 (33.3)	0 (0)	0 (0)	2 (8.3)	0 (0)	0 (0)	4 (16.7)	0 (0)	2 (8.3)	7 (29.2)
Eskimos	50	0 (0)	40 (80.0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (2.0)	7 (14.0)	0 (0)	0 (0)	2 (4.0)
Savoonga Eskimos	41	0 (0)	34 (82.9)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (4.9)	0 (0)	0 (0)	5 (12.2)
Gambell Eskimos	52	0 (0)	34 (65.4)	0 (0)	0 (0)	2 (3.9)	2 (3.9)	0 (0)	13 (25.0)	0 (0)	0 (0)	1 (1.9)
St. Paul Aleuts	57	0 (0)	16 (28.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	38 (66.7)	2 (3.5)	1 (1.8)	0 (0)
Yupik Eskimos	165	2 (1.2)	41 (24.9)	0 (0)	0 (0)	0 (0)	3 (1.8)	1 (.6)	105 (63.6)	0 (0)	0 (0)	13 (7.9)
Old Harbor Eskimos	128	10 (7.8)	56 (43.8)	1 (.8)	2 (1.6)	0 (0)	0 (0)	6 (4.7)	50 (39.1)	1 (.8)	0 (0)	2 (1.6)
Ouzinkie Eskimos	42	6 (14.3)	23 (54.8)	0 (0)	0 (0)	0 (0)	1 (2.4)	0 (0)	8 (19.1)	2 (4.8)	0 (0)	2 (4.8)
Dogrib	143	28 (19.6)	112 (78.3)	0 (0)	0 (0)	1 (.7)	2 (1.4)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Haida	25	6 (24.0)	18 (72.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (4.0)	0 (0)	0 (0)	0 (0)
Bella Coola	25	4 (16.0)	11 (44.0)	2 (8.0)	0 (0)	2 (8.0)	0 (0)	0 (0)	5 (20.0)	0 (0)	0 (0)	1 (4.0)
Nuu-Chah-Nulth	15	1 (6.7)	5 (33.3)	1 (6.7)	0 (0)	2 (13.3)	0 (0)	1 (6.7)	3 (20.0)	0 (0)	0 (0)	2 (13.3)
Ojibwa	43	10 (23.3)	12 (27.9)	3 (7.0)	0 (0)	4 (9.3)	3 (7.0)	0 (0)	0 (0)	0 (0)	0 (0)	11 (25.6)
Mohawk	128	65 (50.8)	6 (4.7)	21 (16.4)	0 (0)	3 (2.3)	26 (20.3)	2 (1.6)	0 (0)	2 (1.6)	1 (.8)	2 (1.6)
French Canadian Caucasians	28	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	28 (100.0)
U.S. Caucasians	147	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	147 (100.0)

Pima	30	2 (6.7)	0 (0)	15 (50.0)	0 (0)	1 (3.3)	12 (40.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Navajo	48	28 (58.3)	0 (0)	18 (37.5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (4.2)
Apache	25	0 (0)	16 (64.0)	4 (16.0)	0 (0)	0 (0)	3 (12.0)	0 (0)	2 (8.0)	0 (0)	0 (0)	0 (0)
Oklahoma Muskoke	70	3 (4.3)	23 (32.9)	10 (14.3)	0 (0)	0 (0)	7 (10.0)	8 (11.4)	19 (27.1)	0 (0)	0 (0)	0 (0)
Mixtec (Alta)	15	1 (6.7)	10 (66.7)	2 (13.3)	0 (0)	1 (6.7)	1 (6.7)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Mixtec (Baja)	14	3 (21.4)	10 (71.4)	1 (7.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Zapotec	15	2 (13.3)	3 (20.0)	5 (33.3)	0 (0)	0 (0)	5 (33.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Mixe	16	1 (6.3)	9 (56.3)	5 (31.3)	0 (0)	1 (6.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Maya	27	13 (48.2)	1 (3.7)	6 (22.2)	0 (0)	2 (7.4)	0 (0)	0 (0)	1 (3.7)	0 (0)	0 (0)	4 (14.8)
Bribri-Cabecar	24	0 (0)	13 (54.2)	11 (45.8)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Boruca	14	0 (0)	2 (14.3)	10 (71.4)	0 (0)	0 (0)	0 (0)	1 (7.1)	0 (0)	0 (0)	0 (0)	1 (7.1)
Guatuso	20	0 (0)	17 (85.0)	3 (15.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Teribe	20	0 (0)	16 (80.0)	4 (20.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Guaymi	16	6 (37.5)	5 (31.3)	5 (31.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Kuna	16	1 (6.3)	15 (93.8)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Piaroa	10	3 (30.0)	2 (20.0)	0 (0)	0 (0)	0 (0)	1 (10.0)	2 (20.0)	2 (20.0)	0 (0)	0 (0)	0 (0)
Makiritare	10	1 (10.0)	1 (10.0)	0 (0)	0 (0)	0 (0)	6 (60.0)	1 (10.0)	0 (0)	1 (10.0)	0 (0)	0 (0)
Yanomamo	24	0 (0)	0 (0)	4 (16.7)	0 (0)	6 (25.0)	7 (29.2)	2 (8.3)	5 (20.8)	0 (0)	0 (0)	0 (0)
Yanomami	83	0 (0)	0 (0)	4 (4.8)	1 (1.2)	31 (37.5)	29 (34.9)	2 (2.4)	6 (7.2)	7 (8.4)	3 (3.6)	0 (0)
Wapishana	12	0 (0)	0 (0)	3 (25.0)	0 (0)	0 (0)	1 (8.3)	1 (8.3)	7 (58.3)	0 (0)	0 (0)	0 (0)
Macushi	10	0 (0)	1 (10.0)	2 (20.0)	0 (0)	2 (20.0)	1 (10.0)	2 (20.0)	2 (20.0)	0 (0)	0 (0)	0 (0)
Ticuna	28	2 (7.4)	0 (0)	0 (0)	0 (0)	4 (14.3)	5 (17.9)	5 (17.9)	9 (32.1)	0 (0)	0 (0)	3 (10.7)
Marubo	10	1 (10.0)	0 (0)	0 (0)	0 (0)	0 (0)	6 (60.0)	3 (30.0)	0 (0)	0 (0)	0 (0)	0 (0)
Kraho	14	0 (0)	4 (28.6)	8 (57.1)	0 (0)	1 (7.1)	1 (7.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Quechua	19	0 (0)	4 (21.1)	6 (31.6)	2 (10.5)	0 (0)	2 (10.5)	0 (0)	5 (26.3)	0 (0)	0 (0)	0 (0)
Aymara Subtotal	66	0 (0)	0 (0)	49 (74.2)	3 (4.6)	0 (0)	5 (7.6)	5 (7.6)	3 (4.6)	1 (1.5)	0 (0)	0 (0)
San Pedro de Atacama Atacameno	16	1 (6.3)	0 (0)	12 (75.0)	1 (6.3)	1 (6.3)	1 (6.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)
Mataco	28	3 (10.7)	0 (0)	10 (35.7)	0 (0)	0 (0)	0 (0)	0 (0)	15 (53.6)	0 (0)	0 (0)	0 (0)
Trapa Trapa Pehuenche	74	0 (0)	2 (2.7)	1 (1.4)	8 (10.8)	0 (0)	27 (36.5)	6 (8.1)	30 (40.5)	0 (0)	0 (0)	0 (0)
Butalelbum Pehuenche	25	0 (0)	0 (0)	0 (0)	1 (4.0)	1 (4.0)	6 (24.0)	5 (20.0)	12 (48.0)	0 (0)	0 (0)	0 (0)
Huilliche	89	3 (3.4)	1 (1.1)	22 (24.7)	1 (1.1)	5 (5.6)	14 (15.7)	8 (9.0)	35 (39.3)	0 (0)	0 (0)	0 (0)
Africans	140	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	140 (100)

NOTE.—Numbers in parentheses are percentages. The original references for the sources of these data and the locations of these populations appear in table 2 of Merriwether and Ferrell (1996) and table 4 of Easton et al. (1996) (this issue).

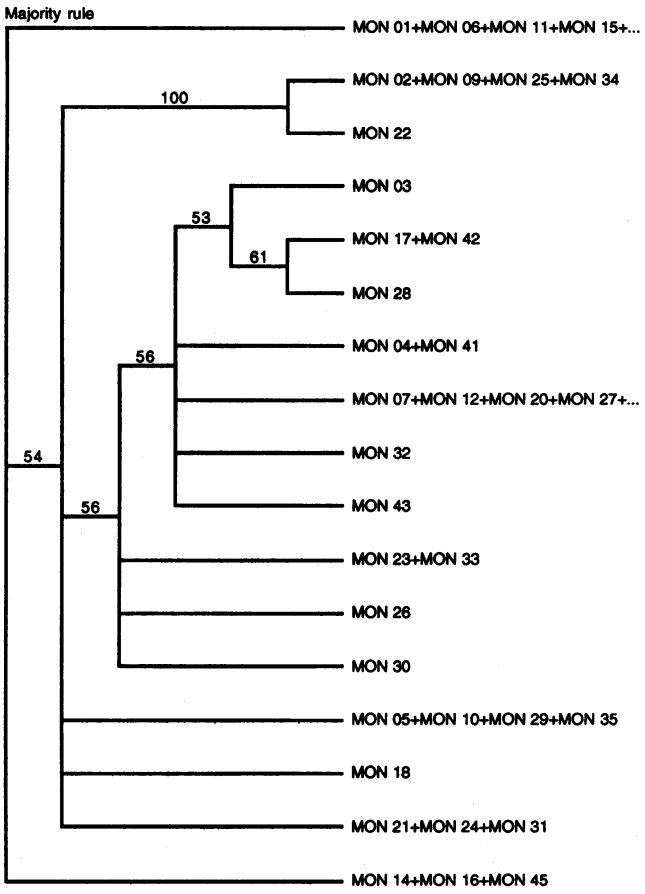

Figure 2 Majority-rule consensus tree of the Mongolian RFLP haplotypes.

Mongolia represents a better potential source for the founding population of the New World than other Asian regions studied to date, because our Mongolian population (and those directly descended from them, such as the Tibetans described by Torroni et al. [1994*b*]) have a larger number of the founding lineage haplogroups than the geographically more proximate Siberian populations. In particular, Siberian populations lack lineage B, which is common in Amerindians and present in Mongolia. The large amount of variation present in this small sample indicates that the population is either very old or consists of a mixture of a number of disparate groups. Samples are currently being collected from 13 different populations throughout Mongolia, to better define Mongolian variation and to further refine our search for the parental population to the New World. The wide range of mtDNA founding lineage haplotype variants found in the New World, the wide distribution of most of these variants, and the presence of multiple variants in many populations all point toward a single source population for peopling the New World. The presence of a large proportion of New World haplogroups in this small Mongolian sample indicates that Mongolia may represent the seat of the migration(s) that peopled the New World (or at least that the Mongolians and Amerindians appear to be descended from the same ancestral population). We acknowledge that sampling contemporary Mongolian populations of Ulan Bator and Tibet is not the same thing as sampling the true "ancestral" population and that population movements may have had as much impact on the geographical location of the present day Mongolians as they have on New World populations. However, these populations are closely related to the New World peoples and are therefore the most likely populations sampled to date to be descended from the same ancestral population as New World peoples. The fact that two separate populations classified as "Mongolians" share the highest number of haplotypes with the New World connects contemporary Mongolians and New World populations to a common founding population. Our larger sampling of Mongolian populations should strengthen this argument. This is in agreement with the data reported by Neel et al. (1994), who suggested that the "Mongolia/Manchuria/southeastern Siberia" region was the most likely source for the New World founding population on the basis of HTLV II virologic and mtDNA data.

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