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Y Chromosome Markers and Trans-Bering Strait Dispersals

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ABSTRACT Five polymorphisms involving two paternally inherited loci were surveyed in 38 world populations (n = 1,631) to investigate the origins of Native Americans. One of the six Y chromosome combination haplotypes (1T) was found at relatively high frequencies (17.8–75.0%) in nine Native American populations (n = 206) representing the three major linguistic divisions in the New World. Overall, these data do not support the Greenberg et al. (1986) tripartite model for the early peopling of the Americas. The 1T haplotype was also discovered at a low frequency in Siberian Eskimos (3/22), Chukchi (1/6), and Evens (1/65) but was absent from 17 other Asian populations (n = 987). The perplexing presence of the 1T haplotype in northeastern Siberia may be due to back-migration from the New World to Asia. A. J. Phys. Anthropol. 102:301–314, 1997.

Although there is general agreement that the first human inhabitants of the Americas came from Asia, the exact geographic source, number of migrations, and timing of these population movements remain controversial (Crawford, 1992; Merriwether et al., 1995; Szathmary, 1993a). In 1986, Greenberg, Turner, and Zegura published a widely cited multidisciplinary synthesis which focused on the apparent congruence of the then available data from linguistics, dental anthropology, and genetics. They pointed out possible correspondences in the archaeological record, and concluded that today's indigenous New World populations could be divided into three distinct groups reflecting three separate migrations of dentally Sinodont Asian peoples from Siberia to the Americas (the "three-wave," "tripartite," or "three-migration model"). The first migration purportedly consisted of the Paleoindian ancestors of the Amerind speakers who currently inhabit North, Central, and South America. The North American NaDene-speaking Indians and the Aleut-Eskimo speakers were claimed to represent the de-

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scendants of the other two migrations. Although the order and chronology of the latter two migrations were problematic, all three lines of evidence pointed to a more recent entry for these two groups of Native Americans than for the initial Paleoindian occupation which was posited to have occurred at least 12,000 years ago.

Subsequent synthetic work relying on traditional serogenetic and protein polymorphism loci supported the three-migration model (Cavalli-Sforza et al., 1994) while mitochondrial DNA (mtDNA) based studies have presented a variety of competing scenarios ranging from one to six separate waves of Asian migrants to the New World (Bailliet et al., 1994; Cann, 1994; Forster et al., 1996; Horai et al., 1993; Kolman et al., 1996; Lorenz and Smith, 1994; Merriwether et al., 1995; Schurr et al., 1990; Shields et al., 1993; Szathmary, 1993b; Torroni et al., 1992; Torroni et al., 1993a,b, 1994c; Weiss, 1994). The most recent and most comprehensive reviews of all the pertinent mtDNA data champion a one-migration model (Merriwether et al., 1995) or a one-migration/reexpansion model (Forster et al., 1996), and point to Mongolia and North China (East-Central Asia) as possible alternatives to Siberia for the geographic homeland of these migrants (Kolman et al., 1996; Merriwether et al., 1996). Indeed, Laughlin's witty and incisive commentary published with the Greenberg et al. (1986) paper actually presented a single-migration model as a more parsimonious interpretation of the data discussed therein. Also, viral distribution data implicate Mongolia/Manchuria and/or extreme southeastern Siberia as the ancestral homeland of the Amerinds (Neel et al., 1994). Unfortunately, biparental nuclear DNA restriction fragment length polymorphism (RFLP), minisatellite, microsatellite, and nucleotide sequence data are still of insufficient quantity and geographic distribution to provide a meaningful test of the competing hypotheses for the early peopling of the Americas. A promising new data source involves paternally inherited polymorphisms from the nonrecombining male-specific portion of the Y chromosome (Bianchi et al., 1996; Hammer and Zegura, 1997; Jobling and Tyler-Smith, 1995; Lell et al., 1996; Pena et al., 1995; Santos et al., 1996a,b,c; Torroni et al., 1994a; Underhill et al., 1996).

The most compelling Y chromosome results so far also point to a single origin for all the linguistically diverse Native Americans. Underhill et al. (1996) presented data for STS SY103 at the *DYS199* locus where a polymorphic C-T transition occurs exclusively in the western hemisphere and may have originated approximately 30,000 years ago. This temporal estimate is generally consistent with recent dates for the initial peopling of the Americas from autosomal (32,000 BP: Cavalli-Sforza et al., 1994) and mtDNA (20,000–29,000 BP: Forster et al., 1996; Torroni et al., 1994c) data. Since the only Asian samples in the Underhill et al. (1996) study were from China, Cambodia, and Japan, one purpose of our study is to extend the geographic search for the T variant in Asia to include the major candidate source regions for the early peopling of the Americas. We also present Y chromosome haplotype data combining information from the *DYS199* and *DYS287* (YAP: Hammer, 1994) loci for numerous representative populations from around the world (Table 1), including nine Native American groups (n = 206).

MATERIALS AND METHODS

Subjects and DNA extraction

We analyzed a total of 1,631 males from 38 populations. Our DNA sources for these populations are indicated in Table 1. Additionally, buccal cell DNA was prepared at the University of Arizona (where the sampling protocol was approved by the Human Subjects Committee) from 10 Tibetan monks, 26 southern Chinese students, and 42 Navajos associated with Navajo Community College. D. Davidson provided buccal cells from 20 Tibetans living in Salt Lake City. Blood samples from 43 Taiwanese were donated by L.L. Hsieh. Buccal cell DNA for the above samples was isolated according to the procedure of Richards et al. (1993), while whole blood DNA was extracted using the procedure of Lahiri and Nurnberger (1991). Siberian samples were collected from traditional settlements of indigenous people. These DNAs were isolated by the Laboratory of Human Molecular and Evolutionary Genet-

TABLE 1. DSY199 and DYS287 combination haplotype frequencies (%) in 38 world populations[2]

Continent/ region	Population	N	Haplotype 1T	1C	3C	4C	5C
Asia	Siberian Eskimos	22	13.6	86.4			
	Chukchi	6	16.7	83.3			
	Evens	65	1.5	98.5			
	Koryaks	12		100.0			
	Yukaghirs	14		100.0			
	Yakuts	20		100.0			
	Siberian Evenks	78		100.0			
	Manchurian Evenks[a,1]	41		100.0			
	Oroqen[a]	23		100.0			
	Buryats	81		100.0			
	Altai	31		96.8	3.2		
	Forest Nentsi	41		100.0			
	Tundra Nentsi	51		100.0			
	Komi	15		100.0			
	Selkups	170		100.0			
	S. Chinese	26		100.0			
	Taiwanese	43		97.7	2.3		
	Mongolians[b]	195		97.4	2.6		
	Tibetans	30		46.7	53.3		
	Japanese[c]	116		52.6	47.4		
Americas	Alaskan Eskimos	4	75.0	25.0			
	Tanana	12	42.0	58.0			
	Navajos	55	49.1	50.9			
	Cheyenne	45	17.8	77.8		4.4	
	Havasupai	10	50.0	50.0			
	Pima	24	41.7	58.3			
	Pueblos	18	50.0	50.0			
	Zapotecs	15	60.0	33.3		6.7	
	Wayus[d]	23	34.8	60.9			4.4
Europe	British[e]	32		96.9		3.1	
	Germans	32		93.8		6.3	
	Greeks[f]	42		66.7		33.3	
	Italians[e,f]	39		87.2		12.8	
Australia	Aboriginal People[g]	31		100.0			
Oceania	Papuans[h]	36		100.0			
Africa	Egyptians	37		51.4	2.7	37.8	8.1
	Gambians[i]	48		14.6	16.7	12.5	56.3
	Bantus[j]	48		35.4	12.5	2.1	50.0

[1] Consult lettered citations for information on previously described samples: [a] Omoto et al. (1996); [b] Nakatome et al. (1996); [c] Hammer and Horai (1995); [d] Ijichi et al. (1993); [e] Ciminelli et al. (1995); [f] Mitchell et al. (1993); [g] Perna et al. (1992); [h] Stoneking et al. (1990); [i] Hill et al. (1991); [j] Spurdle and Jenkins (1992).
[2] Blanks in the table represent entries with a value of 0.0.

ics of the Institute of Cytology and Genetics, Novosibirsk, Russia. Other DNA samples were collected from 195 Mongolians, 41 Manchurian Evenks, 23 Chinese Oroqen, 30 Cheyenne, 24 Pima, 13 New Mexico Navajos, and 12 Tanana by various coauthors and their associates.

DNA samples were provided by other investigators as follows: 21 British, 39 Italians, and 30 Egyptians by A. Novelletto; 7 Egyptians by Y. Gad; 42 Greeks and 11 British by J. Mitchell; 32 Germans by G. Rappold; 116 Japanese by S. Horai; 10 Havasupai and 15 Cheyenne by T. Markow; 15 Zapotecs by W. Klitz; 23 Wayus from Colombia by K. Tajima, S. Sonoda, and V. Zaninovic; 12 Evens, 12 Koryaks, and 4 Inupiaq Eskimos by G. Shields; 31 Australian Aboriginal People, and 36 Papua New Guineans by M. Stoneking; 48 Gambians by A.V.S. Hill; and 48 Bantu speakers from South Africa by T. Jenkins.

PCR, SSCP, and site-specific oligonucleotide (SSO) hybridization

The STS 103 (*DYS199*) was amplified according to the conditions of Vollrath et al. (1992). Single-strand conformation polymorphism (SSCP) analysis was carried out as described by Sheffield et al. (1993). Rapid genotyping at the *DYS199* locus was performed by site-specific oligonucleotide (SSO) hybridization (Stoneking et al., 1991). The sequences of the SSO probes are: *DYS199*-C,

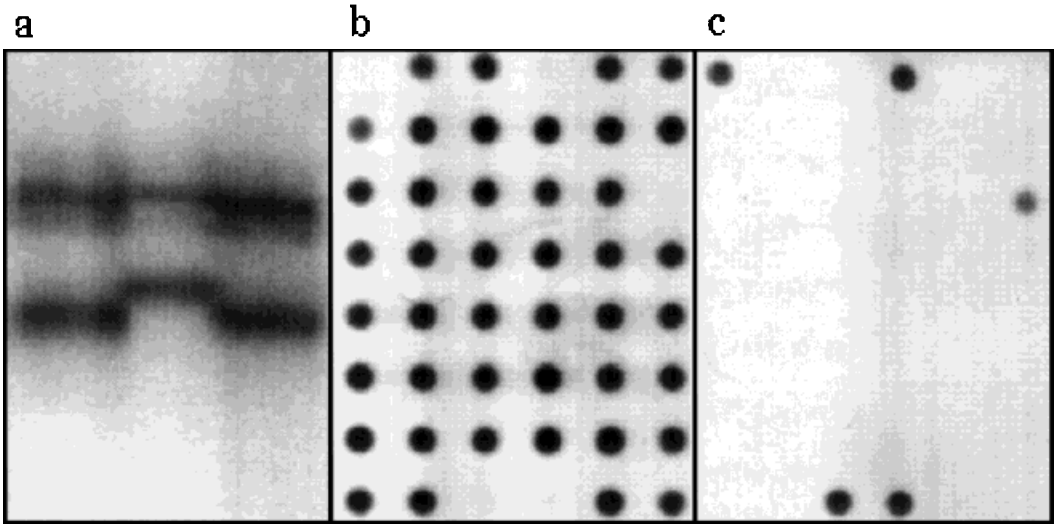

Fig. 1. Detection and rapid genotyping of alleles at the *DYS199* locus. **a:** Single-strand conformation polymorphism analysis of the *DYS199* STS PCR product from three males. **Lanes 1** and **3** contain samples with the *DYS199*-C allele and **lane 2** contains a sample with the *DYS199*-T allele. **b:** SSO hybridization with *DYS199*-C allele probe. Forty-eight DNA samples (eight rows × six columns) were hybridized with the *DYS199*-C probe. A dot indicates the presence of the C allele. **c:** SSO hybridization with *DYS199*-T allele probe. Five of the 48 samples in the 8 × 6 grid contain the T allele.

5′-GACTGACAATTAGGAAGAG-3′; and *DYS-199*-T, 5′-CTCTTCCTAATTATCAGTC-3′. The probes were labeled with [γ-^{32}P]-ATP (Amersham, Cleveland, OH) to a specific activity of at least 10^8 cpm/μg DNA. Approximately 200 ng (5 μl) of each amplified DNA sample was added to denaturation buffer (0.4 NaOH, 25 mM EDTA) and dotted on a nylon membrane (Amersham). The DNA was fixed to the membrane by UV irradiation with a Stratalinker™ UV crosslinker (Stratagene, La Jolla, CA). Membranes were prehybridized in hybridization solution (5 × SSPE, 5 × Denhardt's, 0.5% SDS) for 30 min at 50°C. Labeled SSO probes were then added directly to the hybridization solution to a concentration of 2 pmol/ml, and hybridization was carried out for 2 h at 50°C. Membranes were rinsed in wash solution (2 × SSPE, 0.1% SDS) at room temperature, washed at 50°C for 30 min, and exposed to film for 2–48 h. The *DYS287* (YAP) locus was scored according to the method of Hammer and Horai (1995) and the polymorphic nucleotide sites in the YAP region (Hammer, 1995) were scored by SSO hybridization (Hammer et al., 1997).

Data analysis

For each individual, the combination of sequence variants observed at the YAP locus and the *DYS199* locus is referred to as a Y chromosome haplotype (Hammer, 1995). All numerical analyses were performed using haplotype frequencies. Kinship (R) matrix and Fst (with sample size correction) analyses were performed using the computer program Antana (Harpending and Rogers, 1984) according to procedures developed by Harpending and Jenkins (1973). The genetic map is the result of a standard PCA eigenvector/eigenvalue decomposition of the R matrix.

RESULTS

Variation at the *DYS199* locus

A C-T transition at the *DYS199* STS locus was detected as a single-strand conformation polymorphism (Orita et al., 1989) by M. Kaplan and A. Chakravarti at the Laboratory of Molecular Systematics and Evolution (Fig. 1a). This same polymorphism was independently discovered by way of a novel mutation detection method based on hetero-

duplexed DNA strands (Underhill et al., 1996). We typed a total of 1,631 males at this locus using site-specific oligonucleotide (SSO) hybridization (Fig. 1b,c) and identified the T allele in 40% (83/206) of the North, Central, and South American samples (Table 1). Although the nine Native American frequencies appear to be quite heterogeneous (Fig. 2), due to the small size of some of our samples (i.e., Inupiaq Eskimos where n = 4), the differences among most pairwise combinations are not statistically significant ($P > 0.05$, Fisher's exact test). The Eskimos and the Central American Zapotecs have the highest frequencies (60–75%), followed by the four samples from the North American Southwest (42–50%), the Alaskan Tanana (42%), and the South American Wayus (35%). The Cheyenne, with the lowest frequency (18%) of all Native American samples, are significantly different in frequency from all other New World samples except the Wayus and Tanana ($P < 0.05$, Fisher's exact test). Other than the frequency similarities among the four groups from the American Southwest (Havasupai, Pueblos, Navajos, and Pima), there do not appear to be any clear trends (i.e., correlations between frequency and latitude or frequency and linguistic affiliation).

The mean *DYS199*-T frequency in our study (40%) is lower than the average frequency of 83% in a smaller sample of North, Central, and South American populations reported by Underhill et al. (1996). This rather large and statistically significant difference may be due to the high frequency of the T allele (31/32) seen in their two Brazilian samples (the Karitiana and Surui). Kidd et al. (1991) reported heterozygosity reductions of 27.1% for the Karitiana and 18.7% for the Surui compared with European heterozygosity values. These reductions may reflect the close level of genetic relationship within these populations as well as the confounding effects of genetic drift.

The *DYS199*-T allele was absent in 1,332 males representing 26 populations from Europe, Asia, Africa, and Oceania. Although the T allele was completely absent in the three Asian populations surveyed by Underhill et al. (1996), we found it in five of the 1,080 male Asians surveyed in our study (Fig. 2). All five of these T alleles were from northeastern Siberia: three from Siberian Eskimos (3/22), one from a Chukchi (1/6), and one from an Even (1/65).

Variation at the *DYS287* locus

The present report represents the first survey of the YAP element in Siberian, North American, and East-Central Asian populations. Previously, chromosomes carrying the YAP element (YAP^+) were found at high frequencies in Africa (46–86%), at very low to moderate frequencies in Europe (4–11%), but were not found in South Asia or Oceania (Hammer, 1994; Spurdle et al., 1994a,b). This also represents the first discovery of Asian YAP^+ chromosomes outside Japan (Hammer and Horai, 1995). Although YAP^+ chromosomes were found at very low frequencies in the southwestern Siberian Altai (3.2%), Mongolian (2.6%), Taiwanese (2.3%), and New World populations (1.9%), YAP^+ chromosomes were relatively frequent in Tibetans (53%). In contrast, the YAP element was absent in 14 indigenous populations from other regions in Siberia (n = 639).

The entire set of 1,631 individuals was also genotyped at three polymorphic nucleotide positions within the YAP region (Hammer, 1995). The combination of the four polymorphic sites yields five YAP haplotypes (Fig. 3). Haplotype 1 is the most geographically widespread and is found at the highest frequency worldwide (88%). All of the YAP^+ chromosomes from Asia are haplotype 3, whereas, all of the YAP^+ chromosomes from Europe are haplotype 4. Both of these haplotypes, as well as haplotype 5 are found in Africa (Table 1). In the New World, two males with haplotype 4 were identified in the Cheyenne and one in the Zapotecs, whereas, a single Wayu male carried haplotype 5. Because haplotype 5 is almost completely restricted to Africa (Hammer et al., 1997), the presence of this haplotype in the Americas is most likely due to admixture between Amerindians and people of African descent. The presence of haplotype 4 in the Americas could also be due to recent gene flow between Amerind and African-American or European-American populations. Given their apparent absence in Asia, it is not likely that males carrying haplotypes

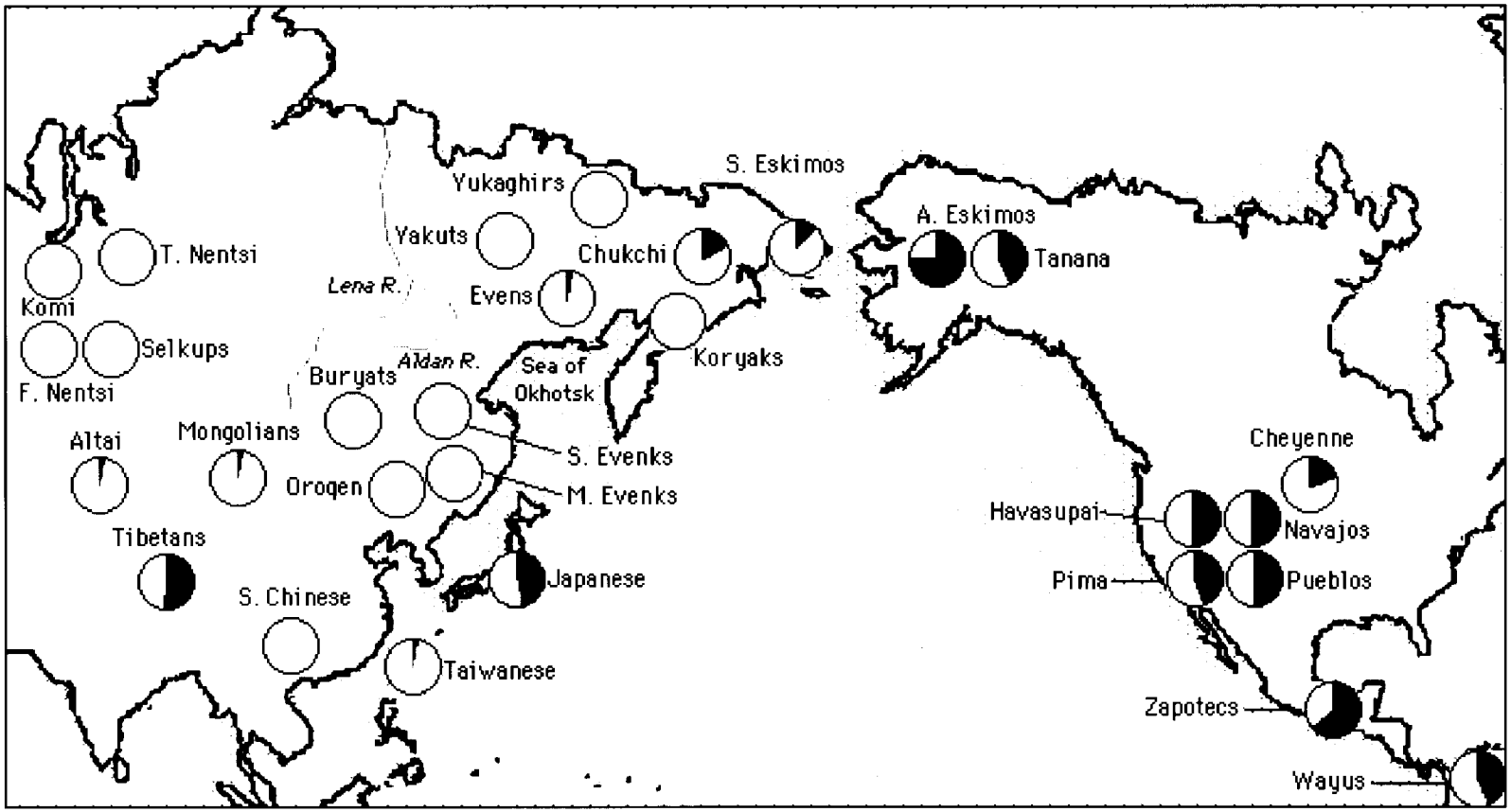

Fig. 2. Geographic map showing the frequencies of the *DYS199*-T (black), the *DYS199*-C (open), and YAP$^+$ (grey) alleles in the 20 Asian and nine New World samples in this survey. The Even and Yakut individuals were collected from a wider geographic area than depicted. The position of the pie chart indicates the approximate geographic center of the sample distribution. S. Evenks, Siberian Evenks; M. Evenks, Manchurian Evenks; F. Nentsi, Forest Nentsi; T. Nentsi, Tundra Nentsi; S. Eskimos, Siberian Eskimos; A. Eskimos, Alaskan Eskimos.

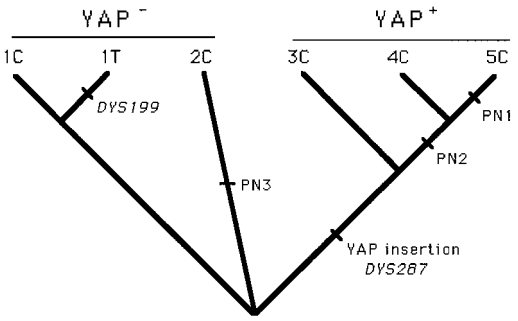

Fig. 3. Evolutionary tree for six *DYS199-DYS287* combination haplotypes. Mutational changes are indicated by a bar across a branch of the tree. Mutational changes at nucleotide sites PN1–3 yielding YAP haplotypes 1–5 were described previously (Hammer, 1995). Haplotypes carrying the YAP element are referred to as YAP^+ and those lacking the YAP element are referred to as YAP^- (the probable ancestral state for *Homo sapiens*). Letters refer to the *DYS199*-C allele (C) and the *DYS199*-T allele (T).

4 or 5 migrated across the Bering Strait. Thus, the four Native American YAP^+ haplotypes found in the present survey were eliminated from subsequent population structure analyses.

DYS199-DYS287 combination haplotypes

Figure 3 presents a hypothesis for the evolution of the six *DYS199-DYS287* combination haplotypes. Haplotype 2C shown in Figure 3 is absent in this data set. The *DYS199* C-T transition occurred on YAP haplotype 1C giving rise to 1T. Underhill et al. (1996) proposed that this C-T mutation originated as long ago as 30,000 years BP. The common ancestral YAP haplotype was estimated to have existed approximately 188,000 years ago (Hammer, 1995). We use these chronological reference points as a justification for preferring the topology in Figure 3 to alternatives such as a tree with a trichotomy for haplotypes 1C, 1T, and 2C.

The five haplotypes are unevenly distributed in the 38 populations surveyed. Although half of these populations are either fixed or nearly fixed for haplotype 1C, the overall Fst is 0.38. This Fst estimate is concordant with expectations based on the fourfold lower effective population size of the Y chromosome relative to autosomes (Hammer, 1994). Worldwide values of Fst for a variety of genetic data sources as well as for craniometric data sets cluster around 0.10 (Relethford, 1995).

The first axis of the genetic map depicted in Figure 4 reflects differentiation at the *DYS287* locus and accounts for 32% of the total variance. The population relationships on the second axis (accounting for 28% of the total variance) are determined primarily by differentiation at the *DYS199* locus. Because of the tight clustering of many of the Eurasian and Oceanic samples at the bottom right of the 38 population map (not shown), we have combined 20 of these populations into five composite groups for the sake of clarity in Figure 4.

DISCUSSION

New World versus Old World origin of the *DYS199*-T allele

The results presented here confirm both the presence of the *DYS199*-T allele in the Americas and its general absence in many parts of Asia (Underhill et al., 1996). Our survey extends the search for haplotype 1T to an additional 206 Native Americans from nine populations and 1,080 Asians from 20 populations, including the geographically critical regions of Mongolia (n = 195), Siberia (n = 670), and Tibet (n = 30). The only Asian populations found to possess the 1T haplotype were limited to northeastern Siberia: Siberian Eskimos, Chukchi, and Evens. This pattern was also recently found in a smaller survey of 121 Asians in which the *DYS199*-T allele was detected in four Siberian Eskimos (22%) and four Coastal Chukchi (17%), but was absent in the remaining samples (Lell et al., 1996). On the basis of their distributional data, Lell et al. (1996) concluded that the *DYS199*-T allele arose in Siberia prior to the migration of Asians into the Americas. However, it is known that the Bering Strait has not been a significant obstacle to movement by Eskimos in either direction (Forsyth, 1992; Krupnik, 1989). Indeed, close kinship has existed among the inhabitants of St. Lawrence Island, Alaskan Eskimos, and Siberian Eskimos for hundreds of years. Therefore, a reasonable alternative hypothesis is that the 1T haplotype originated in the New World (i.e., in eastern Beringia) and that Eskimo males migrating westward across the Bering Strait carried

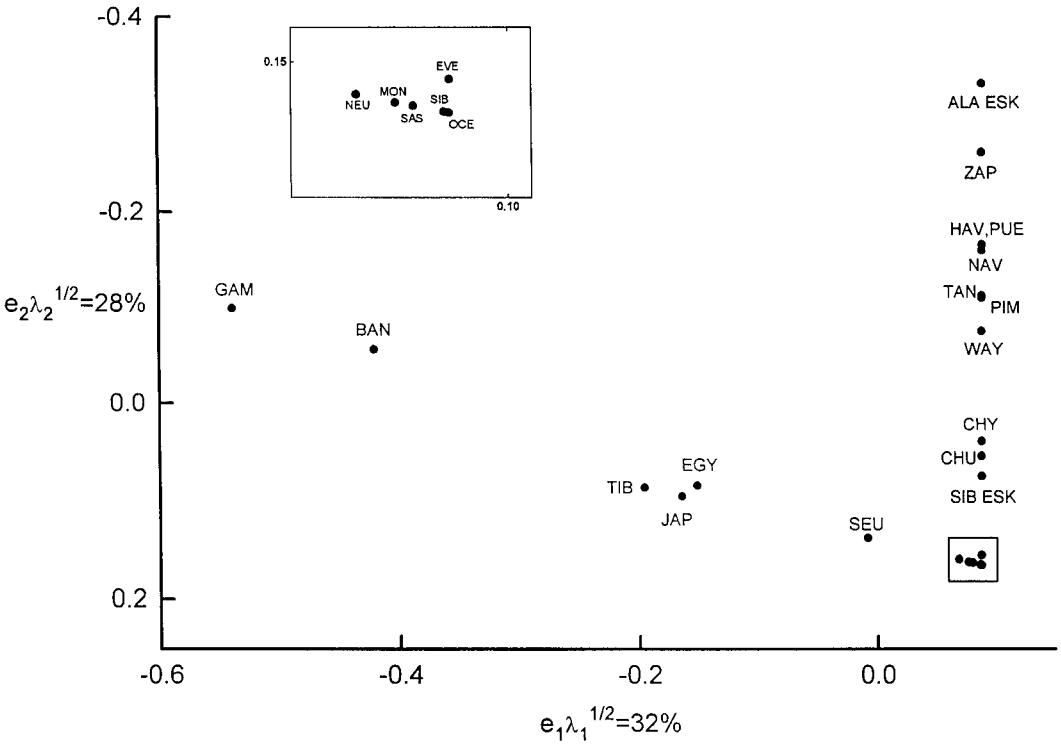

Fig. 4. Genetic map of 18 populations and five composite populations based on a principal components decomposition of the kinship (R) matrix derived from the *DYS199* and *DYS287* haplotypes. The discrete population codes are as follows: ALA ESK (Alaskan Eskimos), TAN (Tanana), NAV (Navajos), CHY (Cheyenne), HAV (Havasupai), PIM (Pima), PUE (Pueblos), ZAP (Zapotecs), WAY (Wayus), SIB ESK (Siberian Eskimos), CHU (Chukchi), EVE (Evens), MON (Mongolians), TIB (Tibetans), JAP (Japanese), EGY (Egyptians), BAN (Bantu speakers from South Africa), and GAM (Gambians), while the composite population codes are as follows: SIB (Siberians: Koryaks, Siberian Evenks, Manchurian Evenks, Oroqen, Buryats, Altai, Selkups, Forest Nentsi, Tundra Nentsi, Komi, Yakuts, Yukaghirs), SAS (S. Asians: S. Chinese, Taiwanese), NEU (N. Europeans: British, Germans), SEU (S. Europeans: Italians, Greeks), and OCE (Oceanians: Australian Aboriginal People, Papua New Guineans). Large rectangle at top left of figure is an enlargement of the smaller rectangle at bottom right.

this Y chromosome haplotype from Alaska to Siberia. Although the Eskimos and Evens are not known to have had direct contact, they both have had contacts with the Chukchi. The Coastal Chukchi are believed to have interacted with Alaskan Eskimos during times of trade and may have been involved in taking Eskimo women and children as slaves (Gurvich, 1988). Thus, backmigration and gene flow may explain the occurrence of the 1T haplotype in the Chukchi and Evens as well.

Although it is not possible to test the two competing hypotheses with current genetic data, we use supplemental ethnohistorical data to aid in determining the more plausible scenario. In our data set, the 1T haplotype was present in three Siberian Eskimos from Sireniki, a Chukchi individual from the Kolyma River Region, and an Even individual from the northern coast of the Sea of Okhotsk. For much of their known history, the Evens inhabited the taiga and boreal forest area encompassing the Yana, Indigirka, and Middle Aldan River Basins (where they were nomadic reindeer breeders and fur hunters/trappers living in small, widely scattered settlements). During the 1700s, a group of Evens moved eastward to the Okhotsk Sea, arriving at the Kamchatka Peninsula by the 1840s (Levin and Vasil'ev, 1964). This historical information would be consistent with the Asian origin model if the 1T haplotype had existed in the ancient

Even population from the Aldan River Basin and was carried to the Okhotsk coast during the recent range expansion (Fig. 2). However, we did not detect the 1T haplotype in 53 inland Evens from three different villages in northern and central Yakutia. Moreover, we did not find the 1T haplotype in several villages of the closely allied Evenks from the Trans-Baikal Region. These results support the hypothesis of a late introduction of the 1T haplotype into the maritime Even population after the migration to the Okhotsk coast in accord with the back-migration/gene flow model. Similarly, the 1T haplotype could have arisen in the ancestral Chukchi population; nevertheless, its apparent absence in the closely related Koryaks is also more consistent with the back-migration/gene flow model. Another less likely explanation for the Asian and American occurrences of the 1T haplotype is independent (parallel) mutation. Further data collection from northeast Siberian populations may help solve the puzzle posed by the occurrence of the 1T haplotype in these three Siberian groups.

The Y Alu polymorphism in Asia and the New World

We found the YAP element at very low frequencies in New World populations from North America (Cheyenne), Central America (Zapotec), and South America (Wayus). This observation is consistent with surveys of other Native American populations where the YAP element was identified in a single Mayan (Seielstad et al., 1994), in two Mixe individuals from southern Mexico (Lell et al., 1996), and in 5% of 105 Amerinds from southern South America (Bianchi et al., 1996). In each of the latter reports, an A to G transition at the *DYS271* locus was also investigated. The G allele has been found to be associated with a subset of YAP^+ chromosomes (Seielstad et al., 1994), and specifically, with YAP haplotype 5 chromosomes (Hammer et al., 1997). The *DYS271*-A allele was present on both Mixe and on four of the five southern South American Amerind YAP^+ chromosomes, while the G allele was present on the Mayan and on a single southern South American Amerind Y chromosome. Therefore, we infer that YAP haplotype 5 chromosomes occur in the latter two populations. This is consistent with our previous discovery of YAP haplotype 5 in a Mayan from Belize and in the Wayu individual from Colombia reported here. Because this haplotype is limited almost entirely to the African continent (Hammer et al., 1997), the presence of YAP haplotype 5 in these Central and South American populations is most likely due to admixture between Amerindians and people of African descent. In contrast, we cannot infer which YAP^+ haplotype (3 or 4) was carried by the two Mixe and four South American Amerinds in the studies mentioned above. In our present survey of Native American populations, we found three probably admixed individuals with YAP haplotype 4 (two Cheyenne and one Zapotec) and no individuals with YAP haplotype 3. This leads us to conclude that YAP^+ chromosomes did not arrive in the New World via Asia and the Bering Strait. Further characterizations of YAP^+ chromosomes from other Native American populations are needed to determine if New World YAP^+ chromosomes can be traced to Asian source populations.

This communiqué also reports the first discovery of Asian YAP^+ chromosomes outside Japan. YAP^+ chromosomes are present at relatively high frequencies in both Tibet and Japan, and at very low frequencies in southwestern Siberia, Mongolia, and Taiwan. All Asian YAP^+ chromosomes are haplotype 3C. Our data support the hypothesis of an East-Central Asian origin of the acient Jomon people, the original inhibitants of the Japanese archipelago (Hammer et al., 1996). In contrast, YAP^+ chromosomes were not found in the other Siberian locales surveyed. These results and those portrayed in Figure 4 make a major Tibetan/Japanese paternal contribution to the early New World gene pool unlikely, thereby compromising one of the four candidate source regions in Asia (Mongolia, Tibet, Taiwan, and Korea) found to possess all four founding mitochondrial DNA lineages (Kolman et al., 1996; Merriwether et al., 1995). Specifically, our results do not support the hypothesis of a Tibetan contribution to the Native American gene pool (Merriwether et al., 1995; Torroni et al., 1994b). In this regard, there are three important caveats to bear in mind. First, it is

possible that the frequency of the YAP element increased markedly in Tibet since the putative New World founders left Asia. Second, perhaps the founders carried no YAP^+ chromosomes to the New World by chance. Third, the possibility remains that maternal and paternal lineages in the New World will be traced to different source populations. This could occur by stochastic processes that can act more efficaciously on the reduced effective population sizes of maternal and paternal lineages relative to autosomal markers, or by selective processes that differentially affect mtDNA and Y chromosomes (i.e., war, polygamy, etc.), or it could represent actual demographic processes such as sex-biased migration.

The *DYS199* polymorphism in relation to other Y chromosome polymorphisms

The utilization of Y chromosomal data to address issues involved in the competing scenarios for the peopling of the Americas has been a relatively recent undertaking (Hammer and Zegura, 1997). Torroni et al. (1994a) published the first Y chromosome polymorphism data on Native American populations (Mixtec, Zapotec, and Mixe) based on the p49a/f RFLP (Ngo et al., 1986) system. The p49a/f probes yielded 11 combination haplotypes, six of which were shared with other geographic regions. One of these six, haplotype 18, exhibited by far the highest frequency (45.2%) in the New World populations, and was suggested as the best candidate for a founding haplotype. Haplotypes 13 and 63 were the next most common (12.9%) and, like haplotype 18, were previously identified in either "Caucasian" and/or African populations (Torroni et al., 1994a). Recently, the *DYS199* polymorphism was examined in the same three Native American populations with the T allele occurring at frequencies ranging from 48% to 86% (Lell et al., 1996). Every instance of p49 haplotype 18 was found to be associated with the *DYS199*-T allele, while p49 haplotype 63 carried both the C and T alleles.

Information from the *DYS199* locus has recently been combined with allelic data from two other Y-linked polymorphic systems. The first involves the microsatellite locus, *DYS19*, which exhibits five common length alleles (A–E) in most European, African, and Asian populations (Hammer et al., 1997; Santos et al., 1996b). In contrast, only alleles A–C have been identified in Native American populations (Hammer et al., 1997; Santos et al., 1996b; Underhill et al., 1996). Underhill et al. (1996) found that the *DYS199*-T allele co-occurred with the *DYS19*-A allele in 30 of 36 Native American Y chromosomes examined. Pena et al. (1995) and Santos et al. (1996a,c) have studied covariation at the *DYS19* locus and sequence variation in the alphoid centromeric region. Their polymerase chain-reaction (PCR)-based assays can detect 23 alphoid heteroduplex (αh) patterns and 46 αh/*DYS19* combination haplotypes in human populations. In a survey of 15 South American Indian tribes (n = 110, including two Central American Mayans), they found that 78% of the Y chromosomes had both the αh pattern II and the *DYS19*-A allele. This IIA haplotype was also found in 18 of 47 North American Mvskokes. These data led Santos et al. (1996c) to conclude that they had identified a major founder Y chromosome haplotype for North and South Amerindians (neither Na-Dene nor Aleut-Eskimo-speakers were included in their data base). Recently, Bianchi et al. (1996) studied the *DYS199* polymorphism in the same South American Amerind samples and found that the T allele was associated with the IIA haplotype.

We can infer from the above studies that many Native American populations are characterized by a high frequency of a single paternal lineage characterized by the *DYS199*-T allele, p49 haplotype 18, αh pattern II, and the *DYS19*-A allele. It becomes important to examine this set of markers and newly discovered Y chromosome polymorphisms in Asian populations to search for candidate source population(s) for this Native American paternal lineage, as well as to test hypotheses concerning the origin of the *DYS199*-T allele. To date, there have been limited surveys of these loci in Asian populations. However, it is interesting to note that in the few published studies, the *DYS19*-A allele is rare and the IIA haplotype has not been observed in Asian populations

(Gomolka et al., 1994; Hammer and Horai, 1995; Santos et al., 1996a,b).

One of the inherent advantages of using paternally transmitted polymorphisms to study the origins of Native American populations is that they are contained within the largest nonrecombining block in the human genome. Even if there are few known informative polymorphisms at present, there is great potential for discovering new ones. Once the ancestral state at each of several Y-linked polymorphisms is determined, it becomes possible to trace the evolution of Native American Y chromosome haplotypes to specific ancestral lineages, and to infer the geographic center of origin of these lineages. This approach has been labeled "intraspecific phylogeography" (Avise, 1994). By identifying Asian haplotypes ancestral to Native American Y chromosome haplotypes (and by defining their geographic distributions), it may be possible to infer the geographic homeland of specific male lineages in the New World. Likewise, by searching for haplotypes derived from the founding Native American haplotypes, it may be possible to trace the movements of populations in the New World and, perhaps, back to Asia. For example, if the *DYS199*-T allele originated in Asia, it may be feasible to identify Y chromosome haplotypes in Asia that represent precursors to this Native American haplotype. On the other hand, if the T allele originated in the New World and migrated back to Asia, one would predict that derived Y-linked markers will be associated with this haplotype in Asia.

Implications for the debate on the peopling of the Americas

In the genetic map (Fig. 4), all the Native American populations are part of a single, elongated cluster. The Chukchi and Siberian Eskimos fall closest to the New World populations while the Evens and the five populations in the rectangle are less closely connected to this grouping. The mean frequencies of the 1T haplotype in Greenberg's (1987) three major New World linguistic groups are: 36% in the Amerinds (n = 135), 48% in the NaDene (n = 67), and 70% in the Eskimos (n = 10). Since the frequencies of this haplotype do not differ significantly among the three linguistic groups ($P > 0.05$, Bonferroni test), and because there is a general absence of the 1T haplotype in most of the Asian regions surveyed, these data are not consistent with the most parsimonious interpretation of Greenberg et al.'s (1986) tripartite model. One interpretation of the current corpus of *DYS199* data is that this polymorphism originated in a single population that was ancestral to populations that now speak Amerind, Na-Dene, and Eskimo-Aleut languages. Regardless of whether the *DYS199*-T allele originated in the New World or in Asia, the substantial sharing of the T allele among representatives of these three linguistic groups is unexpected under the scenario of three linguistically and genetically differentiated Asian populations migrating separately to the New World. An alternative hypothesis posits a much more recent origin of the *DYS199* polymorphism coupled with admixture among populations from the three linguistic divisions. This hypothesis would require extensive gene flow over the vast geographic range of Native American populations, especially in North America, the only place where all three language groups overlap. Another hypothesis based on admixture involves an ancient polymorphism originating in Beringia with subsequent gene flow among Beringian populations. This admixture may include not only those populations already on Beringia, but also any subsequent dispersals from Asia filtering through Beringia. Eventually, one or more of these Beringian populations spread to the Americas.

A first step toward resolving these complex and interconnected issues would include a more refined estimate of the age of the *DYS199*-T allele. Specifically, information about the age of this polymorphism would be helpful for distinguishing among the latter two admixture-based hypotheses. Underhill et al. (1996) attempted to estimate the time at which the C to T transition occurred based on the ratio of *DYS19* microsatellite alleles associated with *DYS199*-T allele in Native American populations. Using two separate estimates of the average rate of human microsatellite evolution, they calculated that the *DYS199*-T allele could

have originated as early as 30,000 years ago or as recently as 2,100 years ago. Therefore, one way to achieve a more accurate age estimate for this polymorphism would be to measure the frequency of mutations at the *DYS19* microsatellite locus directly using multigenerational pedigree data.

Because of the above-mentioned limitations, as well as current deficiencies in the number of populations and Y-linked polymorphisms sampled, we feel that it is too early to make any firm conclusions about the number and timing of migrations into the New World. Although our results are compatible with the single-wave hypothesis of Merriwether et al. (1995) based on mtDNA data, claims that the current Y chromosome data support a single origin of all linguistically diverse Native American populations may be premature (Underhill et al., 1996). The paucity of Y chromosome polymorphisms sampled in Asian and Native American populations means that we have little or no information about the number and affinities of paternal lineages comprising any given population. As pointed out by Forster et al. (1996), any study that attempts to determine the timing and number of prehistoric migrations involved in the settlement of the American continents should be based on extensive sampling of both Native American and Asian populations, and enough polymorphism information to identify putative founder haplotypes.

CONCLUSION

The concordance in results from various data sources found in 1986 (Greenberg et al., 1986) predicated on the principle of consilience of induction (Gould, 1989) no longer seems to be the case for the Americas. Although our results do not specifically address the timing and number of migrational waves into the New World, it is becoming apparent that there are inconsistencies with a simple tripartite model. This is also the case with mtDNA data sets (Forster et al., 1996; Merriwether and Ferrell, 1996). The main challenge lies in explaining the different patterns of diversity seen in the multilocus biparental nuclear data, single locus autosomal data (especially *GM*), mtDNA data, Y chromosome data, morphological data, archaeological data, and linguistic data. A complicating factor for all genetic reconstructions is the possibility of extensive gene flow among the early migrants to the Americas (either before departing from Asia, while on Beringia, and/or at some time in the New World). The resolution of this conundrum awaits new data from a number of disciplines including genetics (*sensu lato*). In this vein, our major contribution to the debate centers on our belief that the present haplotype system (in conjunction with additional informative markers and samples) can provide a sound hypothesis-testing framework for the eventual unraveling of the early paternal population history of the peopling of the Americas.

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