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mtDNA Affinities of the Peoples of North-Central Mexico

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mtDNA haplotypes of representatives of the cosmopolitan peoples of north-central Mexico were studied. Two hundred twenty-three samples from individuals residing in vicinities of two localities in north-central Mexico were analyzed. A combination of strategies was employed to identify the origin of each haplotype, including length variation analysis of the COII and tRNA^{LYS} intergenic region, nucleotide sequence analysis of control region hypervariable segment 1, and RFLP analysis of PCR products spanning diagnostic sites. Analysis of these data revealed that the majority of the mtDNA haplotypes were of Native American origin, belonging to one of four primary Native American haplogroups. Others were of European or African origin, and the frequency of African haplotypes was equivalent to that of haplotypes of European derivation. These results provide diagnostic, discrete character, molecular genetic evidence that, together with results of previous studies of classical genetic systems, is informative with regard to both the magnitude of African admixture and the relative maternal contribution of African, European, and Native American peoples to the genetic heritage of Mexico. Phylogenetic analysis revealed that African sequences formed a basal, paraphyletic group.

Introduction

According to widespread popular belief, the present day peoples of Mexico are, by and large, descendants of Native American and European (Spanish) ancestors. Historical accounts also document African slavery in Mexico during the 16th–18th centuries (Beltrán 1944). Although records from this period are incomplete, estimates of the number of African slaves brought to Mexico are in the range of 200,000–500,000 (Beltrán 1944; Curtin 1969; Muhammad 1995). The actual number may be higher, since many slaves were imported illegally, without documentation, and since African ancestry was often not reported for census data (Beltrán 1944; Tjarks 1978; Muhammad 1995). The contributions of Africans to the genes and culture of the peoples of Mexico have been largely denied and forgotten in popular culture. Consequently, these Africans have been culturally and genetically assimilated to a greater extent than has been the case in other regions of the Americas.

Various classical genetic systems (blood groups, blood enzymes, and blood proteins) have been used to estimate the genetic composition of the peoples inhabiting Mexico (Crawford et al. 1974, 1976; Schanfield et al. 1978; Tiburcio et al. 1978; Lisker et al. 1986, 1988, 1990, 1994, 1995). Such studies have found that Native Amer-

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haplotypes among the general cosmopolitan population, to provide information regarding both Mexican history and prehistory.

Most Native Americans share common mtDNA mutations that define four primary haplogroups (A, B, C, and D), reflecting descent from Asian colonization of

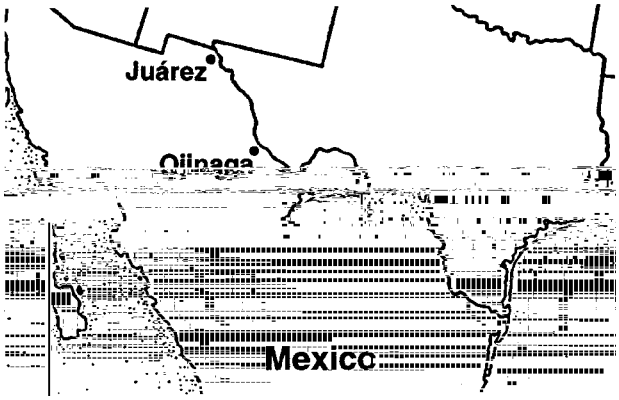

Figure 1 Locations of sample collection: Ciudad Juárez and Ojinaga, Chihuahua, Mexico.

Ten of these samples, identified by the presence of the *Hae*III site at np 663 as haplogroup A, also possessed the 9-bp deletion. Not 1 of these 10 samples had the *Hae*III site at np 16517, which is generally associated with both the deletion and haplogroup B, whereas all haplogroup B samples had the site present. Furthermore, HV1 sequence data were obtained for 7 of these 10 samples and were included in the phylogenetic analysis. The phylogenetic positions of these seven samples were within haplogroup A. These results confirm that the 9-bp deletion has arisen more than once, in two Native American haplogroups. Presence of the deletion in haplogroup A has been reported, in other studies, at low frequencies (Ballinger et al. 1992; Torroni et al. 1993, 1994*c*).

Of the 87 samples for which HV1 nucleotide sequence data were obtained, 63 had haplogroup A–, B–, or C–specific nucleotides at polymorphic positions, and, on the basis of restriction site analysis, one sample was identified as haplogroup D (table 3). Sixteen samples had Native American haplogroup A–specific nucleotides; Native American haplogroup B–specific nucleotides were present in 32 samples; and haplogroup C–specific nucleotides were present in 14 samples. One haplogroup B sample did not have a C at np 16189, and one haplogroup C sample did not have a C at np 16298; however, these samples were identified as being haplogroup B and haplogroup C, respectively, on the basis of the 9-bp deletion and restriction site analysis. All samples belonging to Native American haplogroups A, B, and C, which we ascertained on the basis of HV1 markers, had corresponding haplogroup restriction site markers. Samples identified as Native American did not have African or European HV1 or restriction site markers.

Non–Native American Haplotypes

Twenty-four samples did not possess Native American mtDNA markers. Twelve of 24 non–Native American samples were identified as European haplotypes (table

Table 3

Native American Haplogroups and HV1 Sequence Variation Observed for Individuals of North-Central Mexico

	Variable Nucleotide Position
	1111111111111111111111111111111111111111111111111
	6666666666666666666666666666666666666666666666666
	0011111111111112222222222222222222222333333333333333
	5[illegible] 112224677 0112223334456777[illegible] 000112223455666
	121367[illegible] 542617 [illegible] 47 23 34[illegible] 1 6604 04 14[illegible] 1[illegible] 3575267025
Reference Sequence[a]	[illegible]
Haplogroup A:	
C1	[illegible]
524I	[illegible]
C68	[illegible]
C70	[illegible]
D36	[illegible]
D37	[illegible]
O8	[illegible]
P13	[illegible]
P9	[illegible]
P4	[illegible]
5291	[illegible]
C12	[illegible]
C43	[illegible]
C47	[illegible]
C56	[illegible]
O21	[illegible]
Haplogroup B:	
O23	[illegible]
C4	[illegible]
P14	[illegible]
6032	[illegible]
C30	[illegible]
P20	[illegible]
C67	[illegible]
C42	[illegible]
N11	[illegible]
P15	[illegible]
N64	[illegible]
BB1	[illegible]
BB2	[illegible]
C39	[illegible]
P8	[illegible]
O32	[illegible]
P12	[illegible]
P19	[illegible]
524IV	[illegible]
5292	[illegible]
C31	[illegible]
C62	[illegible]
D30	[illegible]
C33	[illegible]
C53	[illegible]
C73	[illegible]
D16	[illegible]
C64	[illegible]
D20	[illegible]
D52	[illegible]
O39	[illegible]
C8	[illegible]
D27	[illegible]

(*continued*)

Table 3 Continued

	Variable Nucleotide Position
	111111111111111111111111111111111111111111111111
	666666666666666666666666666666666666666666666666
	001111111111111222222222222222222222333333333333333
	59 112224677 0112223334456777999 000112223455666
	1213679 542617 9 47 23 349 1 6604 04 149 19 3575267025
Haplogroup C:	
BB3	.. ..
P11	.. ..
O4A	.. ..
O4	....
P3	....
5299	....
O12	....
C9	....
P2	....
O2A	....
O3A	....
O9	....
P5	....
C10	....
Haplogroup D:	
C75	....

[a] Source: Anderson et al. (1981).

haplogroup D sample was the sister to haplogroup A. African sequences formed a basal, paraphyletic group. Native American haplogroup A was monophyletic. Two European haplotype lineages, C2 and C25, originated within the Native American haplogroup B clade. The positions of two others, C5 and D41, were unresolved in relationship to haplogroup B. Samples C2 and C25 had a C at np 16189, which is a definitive HV1 site for haplogroup B. Samples C5 and D41 both had the other haplogroup B definitive site, a C at np 16217. The position of European haplotype D33 was unresolved but was allied with Native American haplogroup C, because of the presence of one definitive HV1 marker, a C at np 16298. Other than these few exceptions, Native American clades were monophyletic and European lineages originated basal to haplogroup B. The phylogenetic position of the two unknown samples, D42 and Al3, was among the European samples. It is likely that these two samples are of European origin; however, further analysis is needed to confirm identity.

Discussion

A low frequency of African haplotypes in northern Mexico might be expected because of possible rare contact with African Americans from the United States. The historical and present African American population of the west Texas–Mexican border region is small, as has been African American emigration to Mexico from the United States. The discovery of a proportion of African haplotypes roughly equivalent to the proportion of European haplotypes cannot be explained by recent admixture of African Americans from the United States. This is especially the case for the Ojinaga area, which presently is, and historically has been, largely isolated from U.S. African Americans. In the Ojinaga sample set, the frequency of African haplotypes was higher than that of European haplotypes (table 2). The findings of a basal phylogenetic position and paraphyly of African haplotypes were generally concordant with other studies (e.g., Cann et al. 1987; Vigilant et al. 1991; Nei and Roychoudhury 1993; Chen et al. 1995).

We found that the frequencies of European haplotypes were lower than published estimates of European admixture in Mestizo populations (cosmopolitan communities) found, throughout Mexico, by classical genetic systems (Lisker et al. 1996). Other estimates ranged from 22.0% in the city of Tlaxcala to 86.3% in Monterrey (Crawford et al. 1974; Cerda-Flores and Garza-Chapa 1989). European-admixture estimates in our study are likely lower because of the maternal inheritance of mtDNA, as historically more Spanish males than Spanish females colonized Mexico.

The Mexican east coast is known to have greater African admixture, as is evident today in the physical appearance and culture of the populations residing there. This has also been seen in blood group marker studies, with east coast Mestizo communities having

Table 4

Non–Native American Haplotypes and HV1-Sequence Variation Observed for Individuals from North-Central Mexico

	Variable Nucleotide Position	Haplogroup
	111111111111111111111111111111111111	
	666666666666666666666666666666666666	
	001111111111112222222222222222223333333	
	[illegible] 12224667 [illegible] 11222356677 [illegible] 00122566	
	[illegible] 3146[illegible] 50227[illegible] 24723446150 614 4 103602	
Reference sequence[a]	[illegible]	
European:		
C5	....	H
O36	....	H
P16	....	H
D41	....	H
D60	. ...	H
C80	... [illegible]...	J
D58	... .	J
C2	....	K
C25	....	K
O6	....	V
D33	....	V
D40	. ...	U
African:		
O2S	(Sequence was not obtained)	L
C66	....[illegible]...	L1
D47	....[illegible]...	L1
N18	....	L2
P1	.. ..	L2
N16	....	L2
C59	... .	L3
O17	....	L3
C78	....	L3
C27	....[illegible]..	L3
Unknown:		
D42	....	...
AL3	....	...

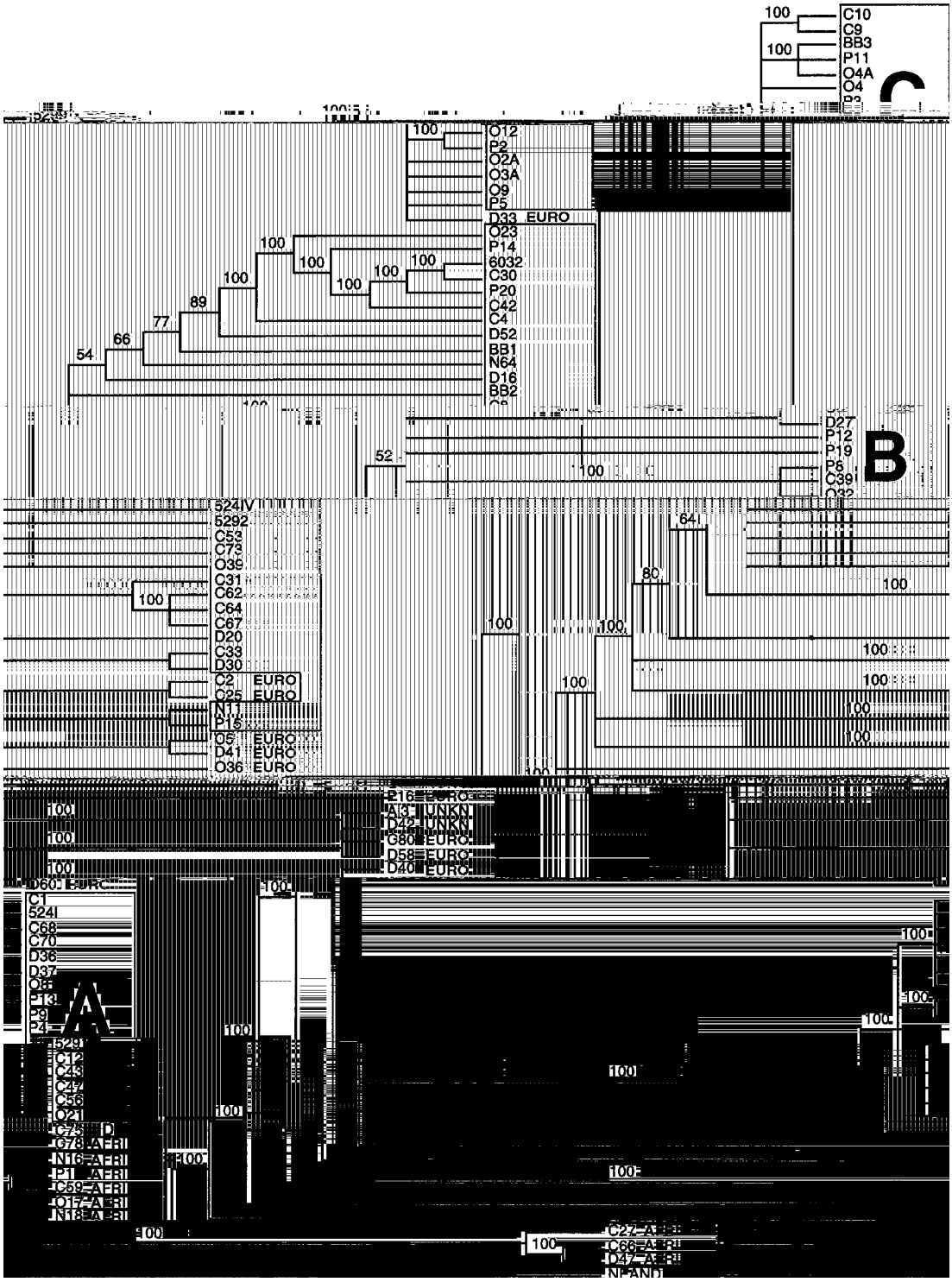

Figure 2 Majority rule consensus tree of 2,000 maximum parsimony trees generated from control region sequence data with a heuristic search with the tree bisection reconnection branch swapping algorithm of PAUP, rooted by using Neandertal as outgroup. Numbers on branches indicate the percentage of 2,000 trees with a depicted clade. This analysis was calculated multiple times, with the same result. Tree length is 146 steps; the consistency index (excluding uninformative characters) is 0.47. Boxes indicate Native American haplogroups. D = Native American haplogroup D; EURO = European haplotypes; AFRI = African haplotypes; and UNKN = unknown haplotypes. Because of high homoplasy, consistent character state changes do not define most major clades, yet this shortest, rooted network provides resolution of clades that is concordant with previous studies that made use of various genetic systems and with results of the restriction site analysis presented in table 1.

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