

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

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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

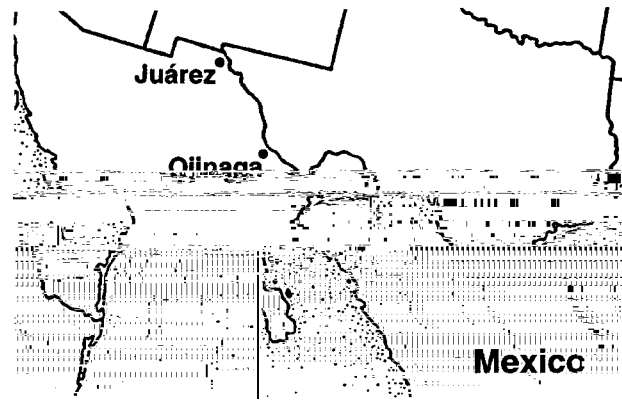


Figure 1 Locations of sample collection: Ciudad Juárez and Ojinaga, Chihuahua, Mexico.

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, 1994c).

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									
	1	2	3	4	5	6	7	8	9	10
	11	12	13	14	15	16	17	18	19	20
	21	22	23	24	25	26	27	28	29	30
	31	32	33	34	35	36	37	38	39	40
	41	42	43	44	45	46	47	48	49	50
	51	52	53	54	55	56	57	58	59	60
	61	62	63	64	65	66	67	68	69	70
	71	72	73	74	75	76	77	78	79	80
	81	82	83	84	85	86	87	88	89	90
	91	92	93	94	95	96	97	98	99	100
Reference Sequence ^a	A	A	A	A	A	A	A	A	A	A
Haplogroup A:										
C1
524I
C68
C70
D36
D37
O8
P13
P9
P4
5291
C12
C43
C47
C56
O21
Haplogroup B:										
O23
C4
P14
6032
C30
P20
C67
C42
N11
P15
N64
BB1
BB2
C39
P8
O32
P12
P19
524IV
5292
C31
C62
D30
C33
C53
C73
D16
C64
D20
D52
O39
C8
D27

(continued)

Table 3 Continued

	VARIABLE NUCLEOTIDE POSITION									
	1	2	3	4	5	6	7	8	9	10
	11	12	13	14	15	16	17	18	19	20
	21	22	23	24	25	26	27	28	29	30
	31	32	33	34	35	36	37	38	39	40
	41	42	43	44	45	46	47	48	49	50
	51	52	53	54	55	56	57	58	59	60
	61	62	63	64	65	66	67	68	69	70
	71	72	73	74	75	76	77	78	79	80
	81	82	83	84	85	86	87	88	89	90
	91	92	93	94	95	96	97	98	99	100
	101	102	103	104	105	106	107	108	109	110
	111	112	113	114	115	116	117	118	119	120
	121	122	123	124	125	126	127	128	129	130
	131	132	133	134	135	136	137	138	139	140
	141	142	143	144	145	146	147	148	149	150
	151	152	153	154	155	156	157	158	159	160
	161	162	163	164	165	166	167	168	169	170
	171	172	173	174	175	176	177	178	179	180
	181	182	183	184	185	186	187	188	189	190
	191	192	193	194	195	196	197	198	199	200
	201	202	203	204	205	206	207	208	209	210
	211	212	213	214	215	216	217	218	219	220
	221	222	223	224	225	226	227	228	229	230
	231	232	233	234	235	236	237	238	239	240
	241	242	243	244	245	246	247	248	249	250
	251	252	253	254	255	256	257	258	259	260
	261	262	263	264	265	266	267	268	269	270
	271	272	273	274	275	276	277	278	279	280
	281	282	283	284	285	286	287	288	289	290
	291	292	293	294	295	296	297	298	299	300
	301	302	303	304	305	306	307	308	309	310
	311	312	313	314	315	316	317	318	319	320
	321	322	323	324	325	326	327	328	329	330
	331	332	333	334	335	336	337	338	339	340
	341	342	343	344	345	346	347	348	349	350
	351	352	353	354	355	356	357	358	359	360
	361	362	363	364	365	366	367	368	369	370
	371	372	373	374	375	376	377	378	379	380
	381	382	383	384	385	386	387	388	389	390
	391	392	393	394	395	396	397	398	399	400
	401	402	403	404	405	406	407	408	409	410
	411	412	413	414	415	416	417	418	419	420
	421	422	423	424	425	426	427	428	429	430
	431	432	433	434	435	436	437	438	439	440
	441	442	443	444	445	446	447	448	449	450
	451	452	453	454	455	456	457	458	459	460
	461	462	463	464	465	466	467	468	469	470
	471	472	473	474	475	476	477	478	479	480
	481	482	483	484	485	486	487	488	489	490
	491	492	493	494	495	496	497	498	499	500
	501	502	503	504	505	506	507	508	509	510
	511	512	513	514	515	516	517	518	519	520
	521	522	523	524	525	526	527	528	529	530
	531	532	533	534	535	536	537	538	539	540
	541	542	543	544	545	546	547	548	549	550
	551	552	553	554	555	556	557	558	559	560
	561	562	563	564	565	566	567	568	569	570
	571	572	573	574	575	576	577	578	579	580
	581	582	583	584	585	586	587	588	589	590
	591	592	593	594	595	596	597	598	599	600
	601	602	603	604	605	606	607	608	609	610
	611	612	613	614	615	616	617	618	619	620
	621	622	623	624	625	626	627	628	629	630
	631	632	633	634	635	636	637	638	639	640
	641	642	643	644	645	646	647	648	649	650
	651	652	653	654	655	656	657	658	659	660
	661	662	663	664	665	666	667	668	669	670
	671	672	673	674	675	676	677	678	679	680
	681	682	683	684	685	686	687	688	689	690
	691	692	693	694	695	696	697	698	699	700
	701	702	703	704	705	706	707	708	709	710
	711	712	713	714	715	716	717	718	719	720
	721	722	723	724	725	726	727	728	729	730
	731	732	733	734	735	736	737	738	739	740
	741	742	743	744	745	746	747	748	749	750
	751	752	753	754	755	756	757	758	759	760
	761	762	763	764	765	766	767	768	769	770
	771	772	773	774	775	776	777	778	779	780
	781	782	783	784	785	786	787	788	789	790
	791	792	793	794	795	796	797	798	799	800
	801	802	803	804	805	806	807	808	809	810
	811	812	813	814	815	816	817	818	819	820
	821	822	823	824	825	826	827	828	829	830
	831	832	833	834	835	836	837	838	839	840
	841	842	843	844	845	846	847	848	849	850
	851	852	853	854	855	856	857	858	859	860
	861	862	863	864	865	866	867	868	869	870
	871	872	873	874	875	876	877	878	879	880
	881	882	883	884	885	886	887	888	889	890
	891	892	893	894	895	896	897	898	899	900
	901	902	903	904	905	906	907	908	909	910
	911	912	913	914	915	916	917	918	919	920
	921	922	923	924	925	926	927	928	929	930
	931	932	933	934	935	936	937	938	939	940
	941	942	943	944	945	946	947	948	949	950
	951	952	953	954	955	956	957	958	959	960
	961	962	963	964	965	966	967	968	969	970
	971	972	973	974	975	976	977	978	979	980
	981	982	983	984	985	986	987	988	989	990
	991	992	993	994	995	996	997	998	999	1000

^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 A13, 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 parafyly 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

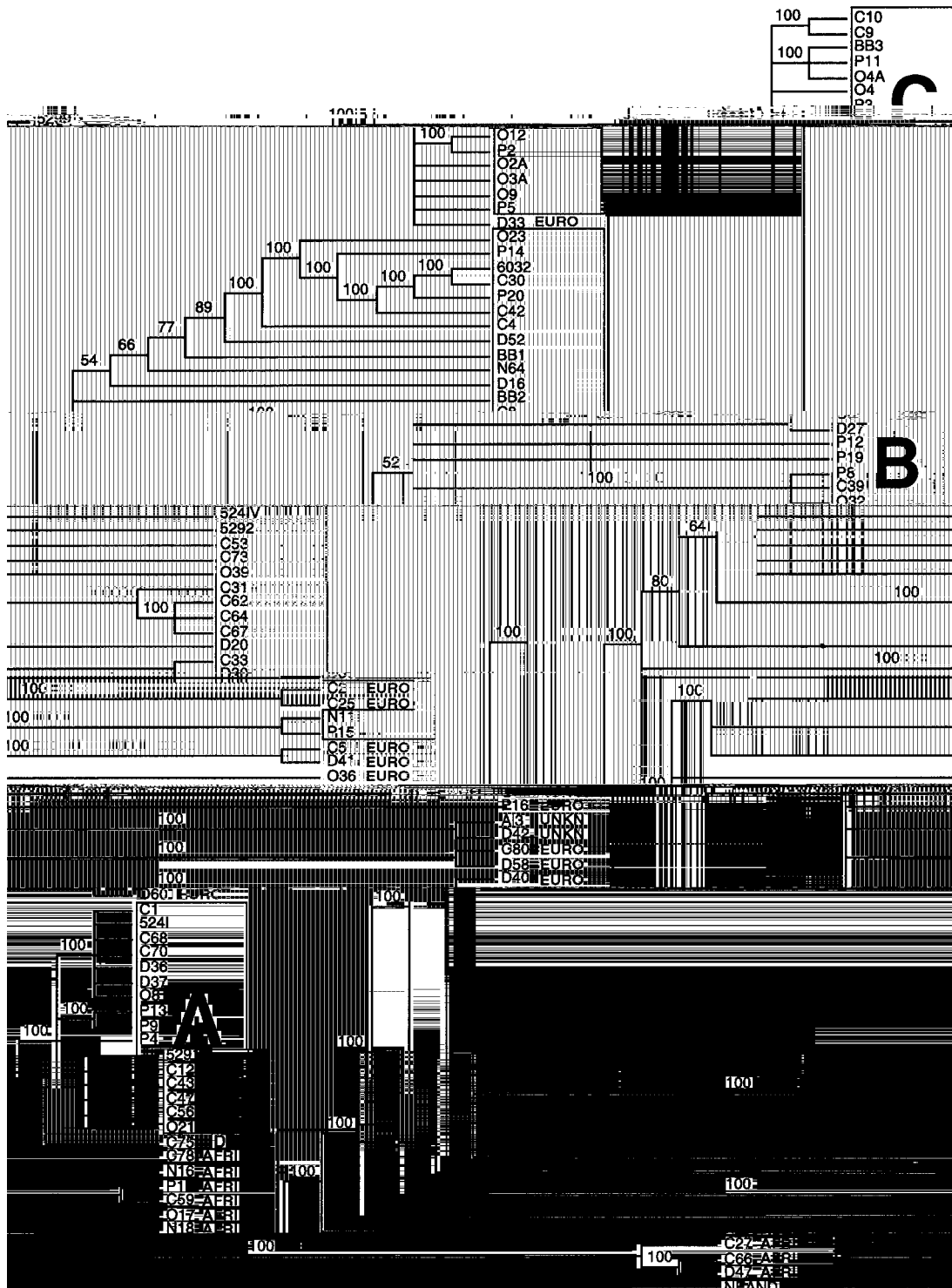


Figure 2 Majority rule consensus tree of 2,000 maximum parsimony trees generated from control region sequence data with a heuristic search with the tree bisection reconnection branch swapping algorithm of PAUP, rooted by using Neandertal as outgroup. Numbers on branches indicate the percentage of 2,000 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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