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Title

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Permalink

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Journal

Journal of California and Great Basin Anthropology, 26(1)

ISSN

0191-3557

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Publication Date

2006

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Genetics, Linguistics, and Prehistoric Migrations: An Analysis of California Indian Mitochondrial DNA Lineages

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The advent of mitochondrial DNA analysis makes possible the study of past migrations among California Indians through the study of genetic similarities and differences. Four scenarios of language change correlate with observable genetic patterns: (1) initial colonization followed by gradual changes due to isolation; (2) population replacement; (3) elite dominance; and (4) intermarriage between adjacent groups. A total of 126 mtDNA samples were provided by contemporary California Indian descendants whose maternal lineages were traced back to original eighteenth and nineteenth century sociolinguistic groups using mission records and other ethnohistoric sources. In particular, those groups belonging to three language families (Chumashan, Uto-Aztecan, and Yokutsan) encompassed enough samples to make meaningful comparisons. The four predominant mtDNA haplogroups found among American Indians (A, B, C, and D) were distributed differently among populations belonging to these language families in California. Examination of the distribution of particular haplotypes within each haplogroup further elucidated the separate population histories of these three language families. The expansions of Yokutsan and Uto-Aztecan groups into their respective homelands are evident in the structure of genetic relationships within haplogroup diagrams. The ancient presence of Chumashan peoples in the Santa Barbara Channel region can be inferred from the presence of a number of haplotypes arrayed along a chain-like branch derived from the founding haplotype within Haplogroup A. A distinctive Haplogroup D sequence, represented by four Chumash lineages, belongs to a rare subgroup, occurring primarily among groups scattered along the Pacific coast of North and South America. This distribution is consistent with the hypothesis that an early coastal expansion occurred during the initial peopling of the Americas.

THE HIGH DEGREE OF LINGUISTIC DIVERSITY in native California reflects significant migration events in prehistory. Many of the larger, more widely-spread language families of North America are represented by small groups distributed along the Pacific Coast, as well as by a relatively high number of compact language families descended from more ancient migrations (Golla 2000a, 2000b, in press). Linguist Johanna Nichols (1992) has described the Pacific coastal region as a "residual zone," because the high ecological diversity of the region allowed for microdifferentiation and preservation of stable linguistic communities adapted to relatively circumscribed territories. In southern California, groups

speaking various Uto-Aztecan languages are wedged between Yuman societies in the San Diego-Colorado River-Baja California area and Chumash and Yokuts peoples in the Santa Barbara Channel and southern San Joaquin Valley regions. It has been presumed by nearly all researchers that this "Shoshonean Wedge" was the result of a prehistoric expansion of Uto-Aztecan peoples from an inland region to the coast and then to the southern Channel Islands (Bright and Bright 1976; Kroeber 1953), although there is considerable disagreement when this migratory event may have occurred. The most often cited date is about 2,000 years ago (Moratto 1984:559); however, some researchers have suggested a much earlier

period, perhaps 5,000 years ago, noting the geographic distribution of certain distinctive items of material culture throughout much of the range known to have been occupied historically by Uto-Aztecan speakers (Raab and Howard 2002).

The coming of age of mitochondrial DNA (mtDNA) genetic research by human biologists has provided an important new means of examining past migrations in many parts of North America (see Eshleman and Smith, in press). Mitochondrial DNA is inherited only maternally, so over many centuries mutations gradually accumulate in daughter lineages, making it possible to reconstruct ancestral types and derived lineages and relate these to one another. All of the mtDNA lineages in the Americas are associated with five recognized "haplogroups" that originated earlier in prehistory among human populations in Asia (Eshleman, Malhi, and Smith 2003; Merriwether 2002; Schurr 2004; Torroni 2000). Observations of genetic affinities between ancient peoples and ethnographically documented groups have been matched with archaeological and linguistic evidence to reconstruct population movements that led to patterns observed at the time of European contact (Eshleman, Malhi, and Smith 2003; Eshleman et al. 2004; Kaestle and Smith 2001; Kemp et al. in press; Lorenz and Smith 1996, 1997; Malhi, Schulz, and Smith 2001; Malhi et al. 2002, 2003, 2004; O'Rourke, Hayes, and Carlyle 2000; Rubicz et al. 2003; Schurr 2004).

Over the past thirteen years, the two coauthors of this study have collaborated to study the mtDNA from 126 separate California Indian *matrilines* (direct female lineages). These lineages have been traced through genealogical methods to specific native groups, mostly in south-central and southern California, thus providing a new database that elucidates the mosaic of genetic relationships in the region. This paper will use the sequences of the principal mtDNA hypervariable segment (HVS1) of 121 of these lineages in its analysis. Earlier publications of portions of these data (Lorenz and Smith 1996, 1997) and subsequent unpublished additions have been used in a number of comparative studies of native North American genetic relationships (e.g., Eshleman 2002; Eshleman et al. 2004; Kaestle and Smith 2001; Kowta 2003; Malhi et al. 2002, 2003; O'Rourke, Hayes, and Carlyle 2000). Continuing genealogical research has revised the ethnolinguistic group affiliations

of some of these previously reported samples, and the accumulation of additional samples has augmented our database significantly. The expanded and refined database produced by our continuing efforts now provides us with a clearer picture of mtDNA diversity among California Indian groups than has heretofore been available.

LANGUAGE CHANGE IN CALIFORNIA PREHISTORY

At the time of European contact, California was made up of a veritable patchwork of local groups often called *tribelets* (Kroeber 1963). In some regions, especially in areas of higher population density supported by fishing economies, there existed different levels of sociocultural integration and hierarchical relations among these local groups (Bean 1978; Johnson 1988, 2000; Jorgensen 1980). Contributing to the cultural mosaic represented by different *tribelets* and regional differences in sociopolitical organization was a high degree of linguistic differentiation. Some 88 distinct languages were spoken between the southern tip of Baja California and Oregon (Goddard 1996a, 1996b; Laylander 1997; Mithun 1999). These have been classified into fourteen language families and seven isolate languages. A number of these families and individual languages traditionally have been grouped into two macro-units or superfamilies, Hokan and Penutian, although the reality of these larger taxonomic entities remains hypothetical and is a subject of current investigation and debate among specialists in comparative linguistics. One interpretation is that these macro-units appear to represent ancient language families that became dispersed and evolved into descendant families and isolated languages through linguistic processes (Golla 2000a). Linguists and archaeologists have been interested in explaining the distribution of languages in the Pacific Coast region and adjacent Great Basin and have devoted much effort to reconstructing linguistic prehistory and proposing likely cultural processes (e.g., Bettinger and Baumhoff 1982; Breschini 1983; Bright and Bright 1976; Golla 2000b; Hill 2002; Hughes 1992; Jackson 1989; King 1986; Krantz 1977; Levy 1997; Madsen and Rhode 1994; Moratto 1984; Nichols 1988; Whistler 1977, 1978, 1988).

It is often assumed that populations speaking related languages might share genetic lineages in common, because they once had belonged to the same group

prior to linguistic differentiation. There are a number of factors, however, that make the correlation of languages and population genetics less than straightforward (Moore 1994; Sims-Williams 1998). Although in general language families often do share similar genetic lineages in populations around the world (Cavalli-Sforza 2000; Cavalli-Sforza, Menozzi, and Piazza 1994), there are plenty of exceptions to this rule because language transmission can occur for reasons having nothing to do with the physical movement of large numbers of people (e.g., Nasidze and Stoneking 2001).

An extensive literature has developed in recent years regarding models of language spread and replacement (Bakker 2000; Bellwood and Renfrew 2002; Dixon 1997; Golla 2000b; Foley 2004; Jones 2003; Nettle 1999, 2000; Nichols 1992, 2000; Renfrew 1987, 1992, 2000). Based on our review of this literature, we propose that the following four general scenarios are likely to account for most of the linguistic changes that occurred in prehistoric California:

1. Initial colonization by Paleoindians followed by gradual changes through time due to isolation or differentiation along dialectal continua.
2. Population replacement through immigration, with one group forcing another to abandon its territory, because of greater numbers, technological advances, more effective subsistence strategies, or some aspects of sociopolitical organization that give the incoming group an advantage over the former inhabitants.
3. Elite dominance, whereby an incoming group establishes hegemony over the original inhabitants, without displacing them, initiating an adoption of the language spoken by the new political leadership.
4. Inter-marriage of adjacent groups over an extended period of time, leading to linguistically mixed communities that would shift from one language to another over several generations.

Furthermore, we expect each of these four scenarios to have resulted in different genetic patterns:

1. Ancient populations that retain their residence in one region over many millennia will exhibit group-specific markers and branching, chain-like patterns of mitochondrial DNA variation with all descendant lineages preserved within the group. Populations that bud off and migrate elsewhere usually only retain a subset of the range of variation present in the ancestral population. In addition, ancient groups in California may be linked to some of the first expansions that peopled the Americas if they are found to possess rare lineages held in common with other early migratory groups. Such rare, ancient lineages would not necessarily be present among later peoples who entered California subsequent to the original founding populations.
2. Population replacement will result in differences between mtDNA lineages found among peoples living in the region today and samples from prehistoric burials of earlier periods. A spreading population also produces a “star-like” pattern of descendant lineages from the ancestral type, resulting from genetic drift and isolation as descendant subsets of the group move into geographically separated areas. In cases of population replacement, remnant lineages may exist here and there, representing the earlier group, just like certain lexical, phonological, or grammatical features may become incorporated into the language of the incoming group.
3. Elite dominance will result in just the opposite genetic pattern from that occurring with population replacement. In cases of elite dominance, the genetic patterns will not change significantly from those found among prehistoric peoples in the region, although language change took place. As was the case in number 2 above, a certain linguistic substrate may survive of the earlier language spoken in the region.
4. Inter-marriage of adjacent groups will result in shared genetic lineages, even though the peoples themselves speak unrelated languages.

Depending on the origins of the respective groups prior to their settlement adjacent to one another, one might be able to detect differences between prehistoric patterns in the region and determine which lineages were once associated with each group prior to their intermarriage with one another.

Based on these different expected outcomes, one can examine the actual patterns of mtDNA variation among California ethnolinguistic groups in order to reconstruct past processes of cultural change and compare these to aspects of the archaeological record. It is important to point out, however, that informative as they potentially can be, mtDNA patterns present among California Indians were very dependent on the form of post-marital residence practiced by the different groups. Since mtDNA is only inherited maternally, groups that practiced patrilocal post-marital residence would be likely to share maternal lineages with adjacent groups, whereas groups in which matrilineal post-marital residence predominated would preserve mtDNA distinctiveness over many generations. Our ability to differentiate between the different cultural processes that led to language change and distinctive mtDNA patterns would be obscured in patrilocal cases where wives moved across linguistic boundaries to take up residence in their husband's local group.

Generally, two patterns of social organization prevailed in Native California: (1) group affiliation based on bilateral descent in Northern California, and (2) group affiliation based on patrilineal descent with concomitant patrilocal residence in Central and Southern California (Jorgensen 1980; Kunkel 1976). It has been recently argued that even in Northern California, the predominant form of social organization was "patrifocal," although greater flexibility in post-marital residence occurred there (Burton, Moore, and Romney n.d.). The principal exceptions to the overall patrifocal emphasis in aboriginal California societies were the Central and Island Chumash peoples, where a matrilineal residence pattern predominated (Johnson 1988; 2001). Given these differences in California Indian post-marital residence preferences, one would expect a greater degree of mitochondrial DNA distinctiveness among Chumashan groups than might prevail elsewhere in Native California, where patrilocal residence or bilateral kin groups occurred.

Golla (in press) has summarized our current understanding of California's linguistic prehistory—following more than a century of investigation—to reconstruct probable scenarios that resulted in the configuration of languages existing at the time of European contact. Some of these proposed reconstructions are amenable to testing using mitochondrial DNA research. The sample utilized for this study (see below) is most informative for Central and Southern California, because we have not yet had the opportunity to conduct research among Northern California's indigenous peoples. Only six lineages characterized here pertain to the region north of San Francisco (see "Sample Descriptions" below). Thus, Golla's hypotheses pertaining to the Algonquian, Athabaskan, Wintuan, Maidu, and Yukon families and the dispersed Northern Hokan languages are not amenable to testing using our dataset.

Three groups in the Central and Southern California regions, however, probably do possess large enough samples to begin to inform us about past genetic relationships among ethnolinguistic groups. These include the Chumashan family, the Uto-Aztecan family, and the hypothesized Yok-Utian branch of the Penutian superfamily. Also, a modest number of samples from central and southern Hokan peoples (Salinan, Esselen, and Yuman-Cochimí) permit comparisons with adjacent groups that possess larger numbers of samples. Golla has proposed that because of its linguistic distinctiveness and lack of established relationships to other language families of the Americas, the Chumashan family might well constitute one of the "basement" language families of California (Golla 2000c). In contrast to Chumashan peoples, the spread of Uto-Aztecan languages into California appears to have occurred during a later period of prehistory, perhaps beginning four millennia or more before present. One currently accepted scenario, based on linguistic evidence, derives their origins from a region in Mexico. The resultant dispersal of Uto-Aztecan languages northward occurred with the spread of maize agriculture into the American Southwest. As populations budded off from these agricultural communities into desert areas unfavorable for growing crops, the descendant groups returned to a hunting and gathering adaptation, spreading into the southern San Joaquin Valley and adjacent southern Sierra Nevada (Diamond and Bellwood 2003; Hill 2001, 2002). Both Salinan and Northern Chumash languages,

as well as those of some other Central California groups, show evidence of prehistoric lexical borrowings from “Old California” Uto-Aztecan languages prior to the differentiation and expansion of the Numic subfamily (Klar 1980; Nichols 1988; Turner 1987). The later movement into Southern California of Uto-Aztecan peoples has been proposed to have occurred about two millennia ago, and to have originated from a region in the vicinity of the southern San Joaquin Valley (Golla, in press; Moratto 1984).

Within the hypothesized Yok-Utian branch of the Penutian macro-unit, Golla has proposed two migrations: one that introduced Proto-Utian into the Sacramento-San Joaquin Delta region some four millennia ago, and a second migration within the Late Period that brought Yokutsan into the Central Valley. He proposes that the ancestral homeland of both these families and of the Penutian superfamily generally was likely to have been in the Plateau region and in portions of the Great Basin. This idea was tested in part by Kaestle and Smith (2001) in their research contrasting ancient Great Basin population samples with samples obtained from modern Numic peoples, using a subset of the data collected for this study for their characterization of Californian groups. Yokutsan languages show substratal influences from Salinan (Golla, in press), suggesting that some mitochondrial lineages from an absorbed earlier group may be present in Yokuts populations.

A number of predictions may be derived from this discussion pertaining to language changes in aboriginal California:

1. Chumashan populations will be genetically distinctive compared to neighboring groups, because of the likelihood of their ancient presence in the Santa Barbara region and their matrilineal residence pattern, which would tend to preserve mitochondrial DNA lineages within the region.
2. Presuming that the distribution of languages within the Hokan and Penutian superfamilies represent ancient population spreads in California, the descendant populations speaking different languages found within each of these superfamilies will harbor ancestral mtDNA lineages, even though they are widely separated geographically.¹
3. Yokutsan and Uto-Aztecan groups, being more “recent” arrivals into California, will share mtDNA lineages with other regions of origin as well as less common mtDNA lineages from groups absorbed during the process of expansion.
4. Inter-marriage between adjacent groups from different language families, especially those practicing patrilineal post-marital residence, will result in a certain amount of sharing of mtDNA lineages. Such adjacent groups that exhibit the highest degree of linguistic influences, through features such as phonological convergence or lexical borrowings, will tend to be indistinguishable from a standpoint of mitochondrial DNA lineages, reflecting inter-marriage.

SAMPLE DESCRIPTIONS

The research design for this study is unique among Native American mtDNA studies conducted to date in that extensive genealogical documentation has been undertaken using ethnohistorical records. This approach was necessary because the relocation of many California groups to the missions during the Spanish colonial period and the subsequent demographic decline caused by the introduced European diseases led to inter-marriage and coalescence of what had been independent tribal entities. Present-day descendants of California Indians may identify themselves with a particular tribal designation; however, genealogical research may reveal that the matriline of these individuals descends originally from a woman from a different native group who had married a man from the person’s current tribe. If the anthropologist did not undertake genealogical research, many of the mtDNA samples would be misassigned to incorrect ethnolinguistic units, thus obscuring original patterns of genetic differences and similarities that had once existed among California’s native groups. By using mission registers, Bureau of Indian Affairs (BIA) records, ethnographers’ notes, censuses, and other sources, a relatively high degree of precision is obtained in determining the origin of most of the lineages sampled. It should be emphasized, however, that in the end our

efforts have only achieved a small sampling of the diversity that must once have been present in aboriginal California. Inevitably, the demographic collapse of the nineteenth century resulted in the loss of many mitochondrial DNA lineages. Although a relatively high degree of confidence may be placed in our affiliation of specific mtDNA lineages with particular tribal groups, these may not be truly representative in cases where only a few lineages survive.

The first samples obtained for this study were collected primarily among Chumash, Salinan, Yokuts, and Kitanemuk descendants in 1992. Sampling and documentation of lineages has been ongoing since that date. From 1992–1998, hair follicle samples were the principal means employed to obtain the mitochondrial DNA. Beginning in 1998, buccal swabs became the preferred method. All samples were stored in a freezer before being processed in the lab. In addition to California Indian samples collected, an even greater number of mtDNA samples from people of Mexican American and early colonial Spanish-Mexican families were obtained and will be discussed in a separate publication.²

Initial interviews with donors were conducted regarding knowledge of their ancestry, with particular attention to their female lineage. Based on this information, genealogical research was conducted using various ethnohistoric sources. Usually a person was able to supply information on the name and place of birth of their mother and maternal grandmother, often with additional details on those individuals' dates of birth, marriage, and death. Because California Indian families have had to supply genealogical data to the BIA for enrollment purposes in the twentieth century, beginning with the California Indian Jurisdictional Act of 1928, they often can provide information about earlier generations as well. Genealogical data supplied by families were checked against information provided on the original applications for the 1928–1933 enrollment and/or county birth and death records, church baptismal and marriage records, census records, and so forth. The goal in genealogical research was to link California Indian descendants of today with their ancestors baptized at the different missions. The mission records were then searched to determine insofar as possible the original native *ranchería* (town or village) where the earliest female ancestor in the direct matriline had been born.

In certain cases, especially for Chumash and other Central California Coast lineages, the research was conducted in reverse; that is, mitochondrial DNA lineages could be traced from known ancestors listed in mission records to families living in the region today. These individuals were then approached about their participation in the study. So rather than working backwards through the records, these people were contacted because we had followed their lineages forward through documentary research from mission times to the present. In sum, mission register research produced a total of 46 mitochondrial DNA lineages in which the town or village could be determined where someone's female ancestor had been born more than two centuries previously. It should be emphasized that our study differs from most other studies reported in the literature in that we are sampling lineages that have been determined to be derived from independent matrilineages as far back as can be traced through historical records. Other studies have used samples from tribal populations without extensive knowledge of genealogies, from medical clinics where degrees of relatedness were undocumented, or from prehistoric cemeteries of unknown familial background. Thus measures of frequency or diversity calculated from these different sampling strategies are not directly comparable to each other or to the findings reported here.

Table 1 classifies the 126 mitochondrial DNA lineages sampled in this study according to linguistic groupings, and Figure 1 shows the geographic distribution of these samples. Inevitably, not all of the ethnolinguistic affiliations could be determined precisely for all of the female ancestors of the matrilineages that gave rise to these samples. In particular, the ethnolinguistic affiliations of eleven lineages could not be determined with a high degree of confidence, even though in some cases these descended from women mentioned in records from particular missions. In these instances, usually the woman's name could not be matched with certainty to a particular baptismal entry, so her forebears were unknown. In other cases, the women were described to be of California Indian ancestry in BIA records of the 1928–1933 enrollment and/or ethnographic records, but tribal affiliations were unmentioned. Finally, there were a few cases of Indian children being raised in non-Indian households, so their parents' names and tribal affiliations were unknown. If there was no documentation at all to

substantiate a person's claim of possessing a California Indian genetic inheritance through a direct female lineage, such samples were omitted entirely from this analysis. In some of these last cases, it is expected that such evidence may eventually be discovered, but to avoid clouding the results, it was deemed better to proceed with the analysis of only those samples where little doubt existed.

For the most part, the samples in this study were categorized according to the most recent linguistic classification of Goddard (1996a, 1996b) and Mithun (1999), with some minor revisions based on the classification used by Golla (in press). Except for Uto-Aztecan and Chumashan, sample sizes were relatively small for most language families, so language families within the Hokan and Penutian superfamilies were grouped together within these macro-units for purposes of comparative analysis. It has long been assumed that the Hokan and Penutian superfamilies represented population spreads at separate times in prehistory, and our working hypothesis was that distinguishing genetic traces of these ancient migrations might be possible. Grouped according to maximal linguistic relatedness, our mtDNA dataset is represented by four principal divisions (Chumashan, Hokan, Penutian, and Uto-Aztecan), with single samples obtained from each of two groups along the northern coast (Yurok and Coos). Because the quality of this genetic record is dependent on the reliability of the ethnic affiliation of each of the samples, we have included descriptive information on the particular lineages sampled within each group.

Origins of the Chumash Samples

The Chumashan family is composed of at least six languages in three branches: Northern (Obispeño), Central (Purisimeño, Ineseño, Barbareño, and Ventureño), and Island (Cruzeño) (Klar, Whistler, and McLendon 1999). This family was formerly included in the Hokan macro-unit (Heizer and Elsasser 1980; Kroeber 1953), but it has since been determined to constitute an isolated language family with an ancient presence in California (Mithun 1999; also see Golla, in press). Samples from 21 mtDNA lineages, representing the territories of all six Chumashan languages, were obtained for this study. Nineteen of these could be documented as descending from women who resided in specific native towns and villages (Fig. 2). These comprise all but one of the known surviving Chumashan

Table 1

DISTRIBUTION OF CALIFORNIA INDIAN MITOCHONDRIAL DNA SAMPLES ACCORDING TO RECOGNIZED LINGUISTIC DIVISIONS

Linguistic Group	Documented Lineages	Number of Haplotypes	Number of Haplotypes Unique to Group	Not Sequenced
Chumashan Family				
Northern (Obispeño)	3	1	0	1
Central				
Purisimeño	2	2	0	0
Ineseño	5	3	0	0
Barbareño	4	4	2	0
Ventureño	6	6	5	0
Island (Cruzeño)	1	1	0	0
Chumashan Totals	21	13	10	1
Hokan Superfamily (Proposed)				
Achumawi/Atsugewi	1	1	0	0
Esselen	1	1	0	0
Salinan	6	5	3	0
Yuman-Cochimi Family				
Ipai	7	6	4	0
Tipai	1	1	0	0
Yuma	1	1	1	0
Cochimi	1	1	0	0
Hokan Totals	18	15	8	0
Penutian Superfamily (Proposed)				
Wintuan Family				
Wintu	2	2	1	0
Southern Patwin	1	1	0	0
Utian Family				
Sierra Miwok	4	4	1	0
Southern Costanoan	4	4	3	0
Yokutsan Family				
Nim Yokuts	13	8	5	1
Buena Vista Yokuts	3	2	0	0
Penutian Totals	27	17	10	1
Uto-Aztecan Family				
Tubatulabal	4	4	2	0
Numic Branch				
Kawaiisu	5	3	1	0
Mono	4	4	3	0
Takic Branch				
Gabrielino	2	2	0	0
Kitanemuk	3	3	1	0
Serrano/Vanyumé	4	3	2	0
Cahuilla	5	5	3	0
Cupeño	2	2	0	0
Luiseño	18	9	4	2
Uto-Aztecan Totals	47	25	13	2
Other Pacific Region Groups				
Coos	1	1	1	0
Yurok	1	1	0	0
Uncertain Tribal Ancestry	11	9	5	1
Other Groups Totals	13	11	6	1
Total California Indian Sample	126	67	—	5

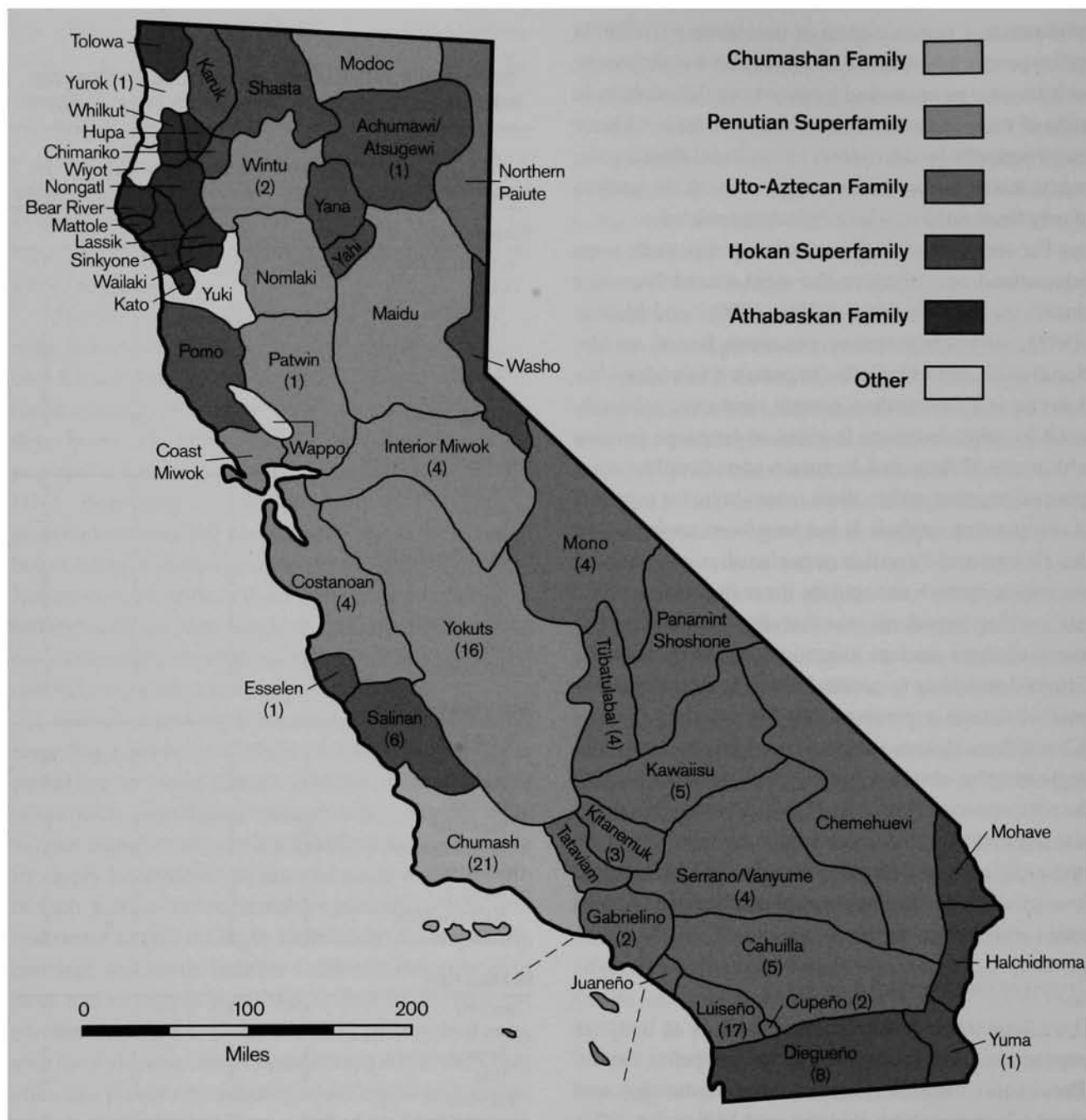


Figure 1. Map showing linguistic affiliations and distribution of samples obtained for mtDNA analysis.

mitochondrial DNA lineages.³ Five additional lineages were traceable to forebears living in the vicinities of the Chumash missions in the mid-nineteenth century; however, attempts to trace the tribal origin of these matrilineages has not yet been successful. One cannot be certain whether these lineages originated among Chumash populations or from Yokuts or other California Indian women who had moved into the area from elsewhere. Thus, the mtDNA

samples derived from these five lineages have been omitted from the Chumashan totals and included in the “Uncertain Tribal Ancestry” category in Table 1 and our subsequent analyses.

The samples derived from the 21 documented Chumash matrilineages include three Northern Chumash lineages, two Purisimeño lineages, five Ineseño lineages, four Barbareño lineages, six Ventureño lineages, and

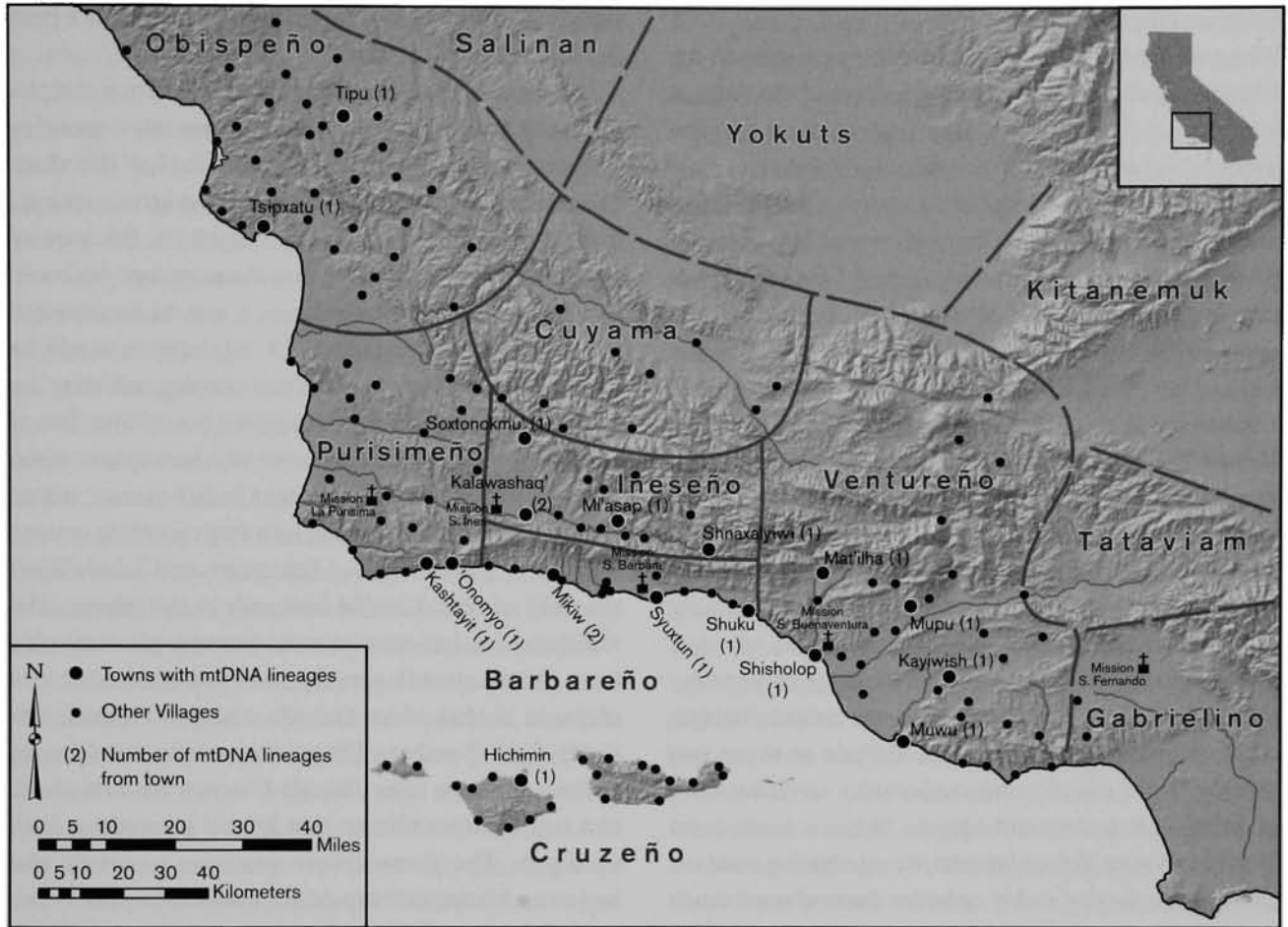


Figure 2. Origins of mtDNA lineages from Chumash towns and villages.

one Cruzeño lineage. The Northern Chumash samples include one from a woman born in *Tipu* in the upper Salinas River watershed, one from a woman from *Tsipxatu* at Avila Beach, and one from a woman listed as being from Mission San Luis Obispo in the applications of her descendants in the 1928–1933 California Indian enrollment. Potentially, this last mentioned individual could also have been a Yokuts woman, because many people from Valley Yokuts tribes were baptized at San Luis Obispo; however, her mention among John Harrington's Obispeño field notes has led us to include her among the Northern Chumash lineages until such time as her identity in mission records can be established with certainty.

All but one of the Central Chumash samples and the single Cruzeño sample are traceable through their direct female lineages back to their original ancestral towns and villages. The two Purisimeño lineages descend

from women born at *Kashtayit* (Santa Anita Creek) and *'Onomyo* (Gaviota) along the western Santa Barbara Channel coast. The five Ineseño matrilineal lines descend from two women born at *Kalawashaq'*, one woman from *Soxtonokmu*, one woman from *Mi'asap*, and one woman from *Shnaxalyiwi*. The four Barbareño lineages descend from two women from *Mikiw* (Dos Pueblos), one woman from *Syuxtun* (Santa Barbara), and one woman from *Shuku* (Rincon). Five Ventureño samples descend from women born at *Shisholop* (Ventura), *Mat'ilha* (Matilija), *Mupu* (Santa Paula), *Kayiwish* (Cayegues), and *Muwu* (Mugu). A sixth Ventureño lineage descends from a woman named María Tarango, who was reported by John Harrington to have spoken the Ventureño Chumash language, but whose identity in the mission records has proven elusive. The Cruzeño matriline stems from a woman born at *Hichimin* on Santa Rosa Island who was baptized at Mission Santa Inés.

Origins of the Hokan Samples

With two exceptions, all of the samples pertaining to the Hokan superfamily were from speakers of the Salinan language of Central California (six samples) and the Yuman-Cochimí family of Southern California and Baja California (ten samples). These two Hokan language areas were separated by Chumashan and Uto-Aztecan peoples at the time of European contact. One sample was obtained from an individual who descended through her direct female line from a woman baptized at Mission San Carlos from the Excelen tribelet, from which the name Esselen was derived. The single sample from a Northern Hokan lineage was obtained from a descendant of a woman who was from the Pit River area, with little else known regarding her background. In the absence of solid genealogical evidence, this lineage has been presumed to be either Achumawi or Atsugewi in origin, with the caveat that it could also be descended from a woman who had moved into the Pit River area from a neighboring group.

Salinan Samples. Samples from six Salinan lineages were obtained for this study. In addition to these, two samples from people whose ancestors were baptized at Mission San Antonio appear to have come from Northern Valley Yokuts women, despite having survived among people who today consider themselves Salinan or Northern Chumash. These two samples are described below in the Yokuts section. Using California Indian enrollment records and/or mission records, four of the six Salinan lineages could be traced to ancestral villages where the direct female ancestor had been born. These were: Lima in the upper San Antonio valley, Isley in the coastal district of Lamaca, Monet along the upper Nacimiento River, and Sicipats in the northern Carrizo Plain.⁴ The last mentioned sample could potentially be from a Northern Chumash lineage.⁵ The two remaining lineages descend from Salinan families whose direct female lines could be traced back to *neofitas* at Missions San Antonio and San Miguel who were married in the decades following the secularization of the missions. Unfortunately, the baptismal records for neither woman could be certainly identified. Either or both of these two matrilineal lines could therefore potentially be of Northern Yokuts origin, because of the large number of people from the San Joaquin Valley who were recruited to these missions after the Salinan population had been proselytized. Other than these six matrilineal lines, no other

potential Salinan mitochondrial DNA lineages have been determined to exist today.

Yuman-Cochimí Samples. Seven of the ten samples gathered from the descendants of peoples speaking Yuman-Cochimí languages came from the Ipai (Northern Diegueño), a group that often intermarried with its Takic (Luiseño and Cupeño) neighbors. Because of this intermarriage and because these groups practiced patrilocal post-marital residence, it was to be expected that some mitochondrial DNA haplotypes would be shared between Yuman and Takic peoples, reflecting the movement of women across linguistic boundaries. Two of the Ipai samples were from people who belong to Luiseño groups today. Their direct female lines, however, traced back through the Mission San Luis Rey records to women from the Ipai rancherías of Bataquitos and Tahui (*Tawí*) who had married Luiseño husbands at the mission. The remaining five Ipai samples came from people descended from the nineteenth century reservation communities of Santa Ysabel, Mesa Grande, and San Pascual. The single Tipai (Southern Diegueño) sample was from an individual whose direct female line was traceable back to a woman from Mission San Miguel in northern Baja California. The Yuma sample was from a woman who had moved from southern Arizona sometime prior to her marriage at Mission San Diego. Her descendants later intermarried with the Luiseños.⁶ The Cochimí sample was obtained from an individual of California Spanish descent whose direct female lineage descended from a neophyte woman at Mission Santa Gertrudis in Baja California in the latter part of the eighteenth century.

Origins of the Penutian Samples

About 60 percent of our 29 samples within the Penutian stock derive from ancestors who spoke Yokutsan languages; however, a few samples pertain to the Wintuan family and some were Miwok-Costanoan in origin. The specifics regarding these lineages are provided below.

Wintuan Samples. The Wintuan family consists of Wintu, Nomlaki, and various Patwin languages. Two Wintu samples, one Namtipom and the other Winnemum, were documented using the California Indian enrollment records. The Southern Patwin sample was obtained from an individual whose female ancestor was baptized at Mission San José from the original Napa tribelet. This woman subsequently married a Costanoan man, and

their descendants today are affiliated with an “Ohlone” (Costanoan) group.

Miwok-Costanoan (Utian) Samples. Four Miwok and four Costanoan lineages have been sampled for this study. The Miwok samples are all from the interior region, apportioned as follows: one Northern Sierra Miwok, one Central Sierra Miwok, and two Southern Sierra Miwok. The four Costanoan samples are all from southern groups. These include two lineages descending from women baptized at Mission San Carlos (one Ensen, one Tucutnut) and two lineages descending from women mentioned in the Mission San Juan Bautista records. One of the San Juan Bautista samples descended from a woman born in the Mutsun tribelet of Paigssin (Paicines); the other has not yet been determined. The last mentioned sample could conceivably be of Yokuts origin instead of Mutsun, because the female ancestor of this lineage has not been identified with absolute certainty in the mission records.

Yokuts Samples. Whistler and Golla (1983) have divided the Yokutsan family into three principal branches: Poso Creek (Palewyami), Buena Vista (Tulamni and Hometwoli), and Nim Yokuts (Foothill and Valley tribes). Our samples do not include Palewyami lineages, but otherwise they are fairly well distributed among groups located throughout the San Joaquin Valley region. People from the various Yokuts tribes were baptized at many California Missions, from San José in the north to San Fernando to the south. Six of our Yokuts samples could be traced back to ancestors baptized at the missions (two at San Juan Bautista, three at San Antonio, and one at Santa Inés). The remaining Yokuts samples were obtained from people whose lineages could be documented through the California Indian enrollment records and genealogical data collected by various ethnographers (e.g., Gayton-Spier n.d.; Harrington 1985).

The Buena Vista Yokuts samples came from one Tulamni and two Hometwoli (*Taneshach*) lineages. One of the Hometwoli lineages survives today among Chumash descendants, resulting from a marriage between a *Taneshach* woman and an Ineseño man. The two other lineages from the Buena Vista group survive among Yokuts descendants who settled at the Tejón Indian community. The Nim Yokuts samples were relatively evenly divided between northern and southern groups. Five Northern Valley lineages could be traced to women from particular groups or rancherías: Silelamne (near

Livingston), Zucuy (unlocated), Chauyat (unlocated), Chawchila, and Chukchansi.⁷ Two other Northern Valley lineages, one at San Juan Bautista and one at San Antonio, could not be traced to named groups, reflecting the tendency for some missionaries to designate Yokuts individuals generally as “Tulareños,” without regard to their specific origin. The Southern Valley and Foothill lineages were descended from women from Nutunutu, Tachi (3), Yawdanchi, and Yawelmani (2) groups. The donors of most of the Southern Valley and Foothill Yokuts samples are members of federally recognized Yokuts tribes.

Origins of the Uto-Aztecan Samples

The largest number of samples collected for this study originated among groups speaking Uto-Aztecan languages. Linguists classify California’s Uto-Aztecan languages into three major branches: (a) Tubatulabal, a single language; (b) Numic; and (c) Takic (Goddard 1996b; Mithun 1999:539). Most of our samples (33) descend from women who spoke languages in the Takic group, but samples were also obtained from people whose female ancestors spoke Tubatulabal (4) and two of the Numic languages (9). The Takic languages in southern California are regarded as having been introduced relatively late in prehistory.

Tubatulabal and Numic Samples. Tubatulabal and several Numic languages are spoken by neighboring groups in the southern Sierra Nevada region. There has been considerable intermarriage among these groups, who practiced patrilocal post-marital residence, so that mitochondrial DNA lineages would be expected to be shared among them to a certain extent. Moreover, it is difficult to trace female lineages back beyond the mid to late nineteenth century, because the native peoples of this region were generally not drawn into the mission system and therefore names and villages of origin were not recorded for earlier generations. California Indian enrollment records, genealogical data in ethnographic fieldnotes (e.g., Harrington 1985, 1986), the Kelsey census of non-reservation Indians in 1905 (Kelsey 1971), and U.S. census records provided the principal means of tracing female lineages.

Four lineages were determined to be Tubatulabal in origin: three directly traceable to women born in the upper Kern River watershed, and one reported as

Bankalachi from Tulare County. Nine Numic samples were collected in the course of our investigation. Three of these were Western Mono (Monache), one was Mono from the eastern side of the Sierra Nevada (Owens Valley Paiute), and five were Kawaiisu. Two of the Kawaiisu samples descended from women from Kelso Valley, one was from a woman from the Paiute Mountain area, and two were from women from the vicinity of Tehachapi.

Takic Samples. Takic languages are divided into two subgroups: Serran (Serrano-Vanyumé, Kitanemuk, Tataviam, Gabrielino) and Cupan (Cahuilla, Cupeño, Luiseño). Our samples included 9 lineages from Serran groups and 28 lineages from Cupan peoples. The three Kitanemuk samples came from families belonging to the Tejón Indian community. Two Vanyumé lineages descended from women baptized at Mission San Fernando from the *ranchería* of Topipabit, located in the Victorville Narrows. The two Serrano lineages came from women who were affiliated with Morongo Reservation near Banning. One of these was from a family who had come from the Mission Creek area near Morongo Valley. The direct female ancestor of the remaining Serrano lineage has not been determined with certainty and conceivably could be of Cahuilla derivation instead. The two lineages included in the Gabrielino group descend from women affiliated with Mission San Gabriel and Mission San Fernando, respectively. The Gabrielino lineage is traceable through the mission records to a woman from Quinquina, San Clemente Island.⁸ The Fernandeano sample has not been successfully associated with a female ancestor baptized from a native *ranchería*, and could conceivably have descended from a Tataviam speaker.⁹

In the Cupan division, five samples are traceable to Cahuilla ancestors, using California Indian enrollment records and ethnographic information. Two matrilineages were traceable to female ancestors living on the Cahuilla Reservation near Anza, and thereby are probably from the Mountain Cahuilla group; one is traceable to an ancestor at Soboba Reservation; one to an ancestor baptized at Mission San Gabriel from the Pass Cahuilla *ranchería* of Peatopa (*Pihatapa*); and the last to a Desert Cahuilla woman born near Indio, who had moved to Morongo with her Serrano husband. One of the two Cupeño samples was initially thought to be Luiseño, but when traced through San Luis Rey mission records proved ultimately to have descended from a woman from

Cupa. The second descended from a well-known Cupeño family documented by Strong (1929:194).

The largest number of samples obtained from descendants of speakers of any single language was seventeen obtained from Luiseño Indians. Because the original baptismal, marriage, and burial records for Mission San Luis Rey have been lost for more than a century and a half, a combination of ethnohistoric sources was used to trace the lineages of those who provided samples. The most important documents for providing data on Luiseño genealogies were the two surviving *padrones* (census books) of Mission San Luis Rey, the 1852 California State Census, nineteenth century parish books, BIA heirship records, and California Indian enrollment records (Johnson and Crawford 1999; Johnson and O'Neil 2001). Using these various sources, ten matrilineages could be traced to source *rancherías* listed in the *padrones*, five could be traced to late nineteenth century reservation communities, and two were of undetermined origin (Figure 3.). Most of the Luiseño samples where direct female lines could be traced were derived from groups originally located in the vicinity of Palomar Mountain (three from Cuqui, two from Toulepa, one from Temecula, one from Pimixga, and one from Aguanga). Only two matrilineages descended from women who lived closer to the coast, both from the *ranchería* of Topome (*Topomai*) on the Santa Margarita River, which was the largest of the Luiseño polities.

RESULTS AND OBSERVATIONS

The comparison of mtDNA haplogroup frequencies provides a low-resolution means of differentiating between populations of dissimilar ancestral origins. For most samples, restriction analysis had been conducted prior to sequencing to determine mitochondrial haplogroup affiliation. Much more information was obtained by analyzing sequences obtained from the principal non-coding, hypervariable segment (HVS1) of the mtDNA molecule. When two individuals possess identical HVS1 sequences, they are said to belong to the same "haplotype" and share a common ancestor within a particular haplogroup. The techniques used in sequencing for this study were those described by Lorenz and Smith (1997) and Lorenz et al. (2005). After sequences were obtained, these were checked backwards and forwards

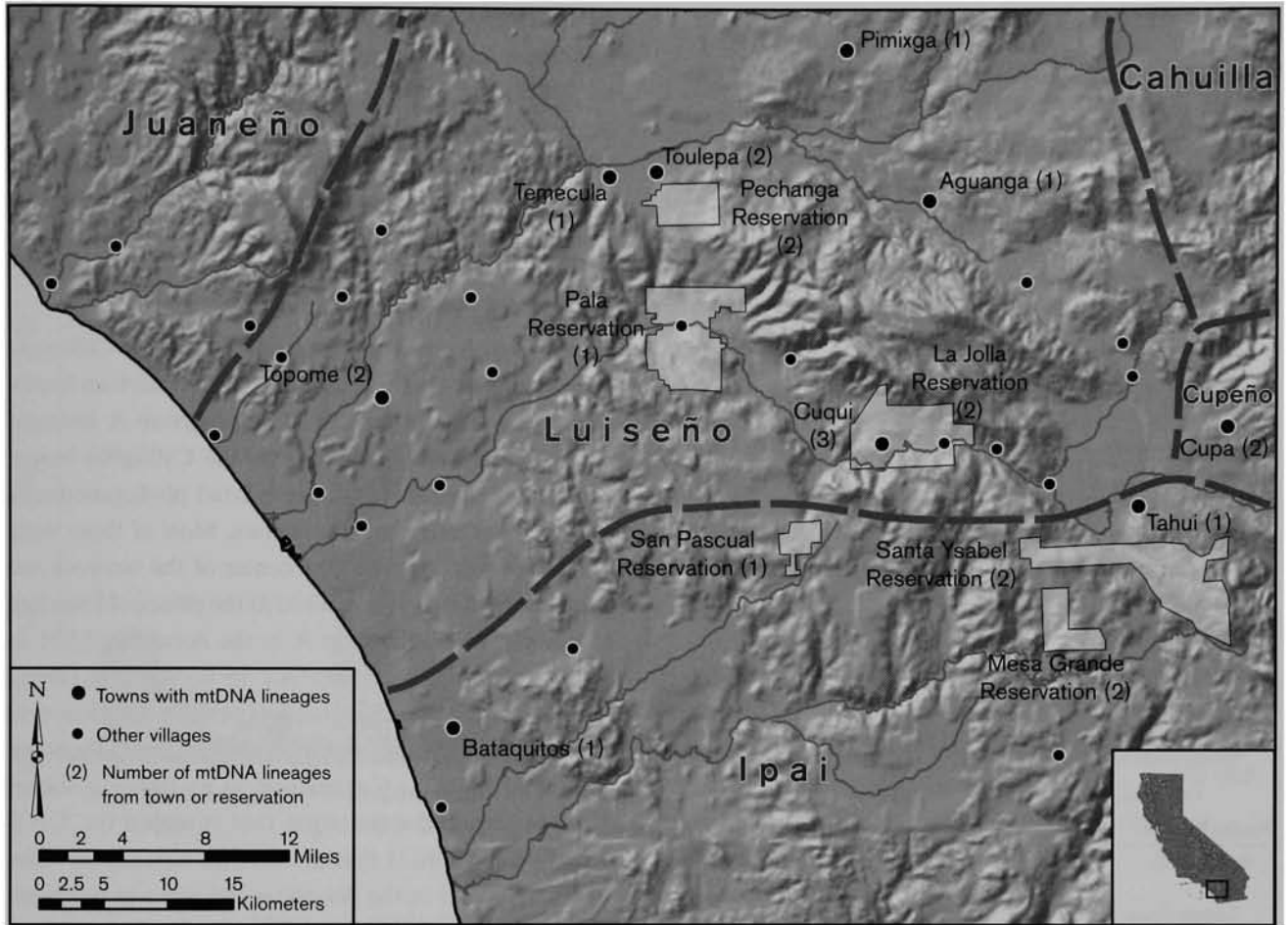


Figure 3. Origins of mtDNA lineages from Luiseño, Cupeño, and Ipai communities.

in many subsequent trials in order to be sure the results were accurate. In a number of instances, more than one individual from the same matriline had provided mtDNA samples, and so this provided a further check on our sequences.¹⁰ Our tables for each haplogroup report all variable nucleotide positions (np) between np 16051 and np 16362 that deviated from the Cambridge Reference Sequence. These variable positions thus serve as distinctive markers to study phylogenetic relationships among various California Indian lineages.¹¹

Comparative Haplogroup Frequencies

Table 2 summarizes the haplogroup frequencies observed in individual ethnolinguistic groups with totals for the language families and superfamilies used for broader comparisons.¹² All of our samples fell within the four predominant haplogroups found among American Indians (A, B, C, and D). There were no instances of Haplogroup X

discovered among the lineages we sampled.¹³ Our results indicate that there are clear differences between three of the principal language families present in central and southern California in terms of haplogroup frequencies (Figure 4). Haplogroups A and D predominate among the Chumash, haplogroups B and D prevail among the California Penutians, and haplogroups B and C are in the great majority among Uto-Aztecan groups. The California Hokan sample, heavily weighted by its Yuman component, also has a high proportion of haplogroups B and C. The similarity in haplogroup distribution between Yuman and Uto-Aztecan groups appears to be the result of extensive intermarriage between the Ipai and Luiseño, each of which comprise a plurality of samples within their respective groups. The most striking contrast is between Chumashan and Uto-Aztecan peoples. Comparing just these two groups in a 2 x 2 contingency table, the association of A or D lineages with the Chumash and

Table 2

**DISTRIBUTION OF CALIFORNIA INDIAN MITOCHONDRIAL DNA
LINEAGES ACCORDING TO HAPLOGROUPS**

Linguistic Group	Haplogroup			
	A	B	C	D
Chumashan Family				
Northern (Obispoño)	0	0	0	3
Central				
Purisimeño	1	0	0	1
Ineseño	3	0	0	2
Barbareño	1	0	1	2
Ventureño	5	0	1	0
Island (Cruzeño)	1	0	0	0
Chumashan Totals	(11)	(0)	(2)	(8)
Hokan Macro-Unit				
Achumawi/Atsugewi	0	1	0	0
Esselen	1	0	0	0
Salinan	3	2	0	1
Yuman-Cochimi Family				
Ipai	0	2	5	0
Tipai	0	0	1	0
Yuma	0	1	0	0
Cochimi	0	0	1	0
Hokan Totals	(4)	(6)	(7)	(1)
Penutian Macro-Unit				
Wintuan Family				
Wintu	0	2	0	0
Southern Patwin	0	1	0	0
Utian Family				
Sierra Miwok	0	3	0	1
Southern Costanoan	0	1	2	1
Yokutsan Family				
Nim Yokuts	1	8	0	4
Buena Vista Yokuts	0	0	1	2
Penutian Totals	(1)	(15)	(3)	(8)
Uto-Aztecan Family				
Tubatulabal	0	2	1	1
Numic Branch				
Kawaiisu	0	3	1	1
Mono	0	3	0	1
Takic Branch				
Gabrielino	0	1	0	1
Kitanemuk	0	0	2	1
Serrano/Vanyumé	0	2	1	1
Cahuilla	0	2	3	1
Cupeño	0	1	1	0
Luiseño	1	4	13	0
Uto-Aztecan Totals	(1)	(18)	(21)	(7)
Other Pacific Region Groups				
Coos	0	0	1	0
Yurok	0	0	1	0
Uncertain Tribal Ancestry	0	5	5	1
All California Indian Samples	17	44	40	25

B or C lineages with Uto-Aztecan groups is statistically significant and relatively strong ($\chi^2 = 32.03$, $p < 0.001$; $\tau = 0.478$). It would appear, therefore, based on the evidence of haplogroup frequencies alone, that these two groups had distinctively different population histories. This becomes even more evident in the analysis of individual sequences reported below.

Haplogroup A Lineages

Haplogroup A was the least common among California Indian samples in our database. A total of thirteen haplotypes were present among 17 Haplogroup A lineages (Table 3). Figure 5 illustrates how the California Indian lineages in Haplogroup A are related phylogenetically to each other in a network diagram. Most of these were of Chumashan origin. At the center of the network are found those samples recognized as the principal founding haplotype for Haplogroup A in the Americas (A01 in Fig. 5), called subhaplogroup "A2" by Forster et al. (1996). Several of the Chumash haplotypes are distinctive in that they are differentiated from the presumed founding haplotype by a T → C transition at np 16093; a subset of these acquired a mutation that reversed the C → T transition at np 16111 that characterize virtually all other "A2" haplotypes in the Americas and some in northeast Asia (Schurr 2004:14; Tanaka et al. 2004:1841). Those Chumash A haplotypes with the T → C transition at np 16093 form a branching chain (see Figure 5). According to the expectations of our model of *in situ* development combined with matrilineal residence, this pattern implies a stable presence of Chumashan peoples within the region over many millennia, whereby mutations resulting in new haplotypes became fixed within the population.

Non-Chumash lineages among our Haplogroup A samples were distributed as follows: Salinan (3), Esselen (1), Yokuts (1), and Luiseño (1). The Esselen and one of the Salinan lineages represent the founding haplotype in Figure 5. This Salinan lineage originates from the coastal region called Lamaca in the Mission San Antonio records, which was adjacent to the Esselen. Another Salinan sample, one mutation removed from the founding haplotype, was descended from a woman baptized at Mission San Miguel who had lived in a village presumably located in the Carrizo Plain, and could well be of Chumash origin.¹⁴ The single certain Yokuts sample and the single Luiseño sample represent

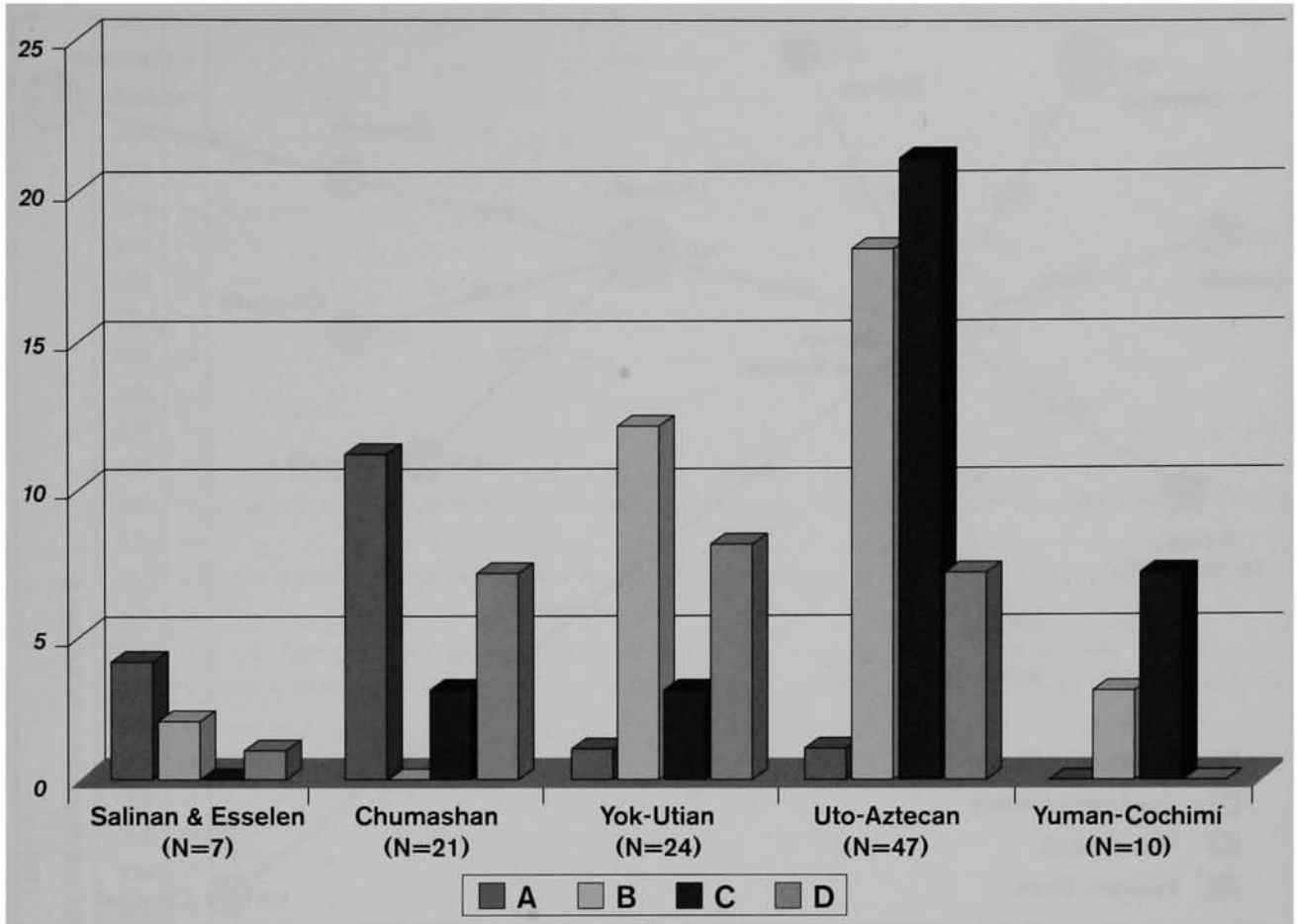


Figure 4. mtDNA Haplogroup distribution in Central and Southern California.

Table 3

CALIFORNIA INDIAN HVS1 SEQUENCES FOR HAPLOGROUP A

Sample	Ethnolinguistic Group	Documented Origin	Haplotype	16083	16111	16129	16163	16183.1	16189	16209	16221	16223	16257	16263	16278	16290	16301	16311	16319	16327	16362
				T	C	G	A	-	T	T	C	C	C	T	C	C	C	T	G	C	T
CRS				T	C	G	A	-	T	T	C	C	C	T	C	C	C	T	G	C	T
JJ039	Esselen	Excelen	A01	.	T	T	.	.	.	T	.	.	A	.	C
JJ133	Salinan	Isley, Lamaca district	A01	.	T	T	.	.	.	T	.	.	A	.	C
JJ135	Chumash	Snajalayegua (<i>Shnaxalyiwí</i>)	A02	x	T	T	.	.	.	T	.	C	A	.	C
JJ136	Chumash	Nomgio (<i>Ónomyo</i>)	A02	.	T	T	.	.	.	T	.	C	A	.	C
JJ010	Chumash	Sotonocmu (<i>Soxtonokmu'</i>)	A03	C	T	T	.	.	.	T	.	.	A	.	C
JJ070	Chumash	Calahuasa (<i>Kalawashaq'</i>)	A03	C	T	T	.	.	.	T	.	.	A	.	C
JJ091	Chumash	Cheumen (<i>Hichimín</i>), S. Rosa I.	A03	C	T	T	.	.	.	T	.	.	A	.	C
JJ002	Chumash	Mupu	A04	C	C	.	.	T	.	.	.	T	.	.	A	.	C
JJ153	Chumash	Matilija (<i>Mat'ilha</i>)	A05	C	.	.	.	C	C	.	.	T	.	.	.	T	.	.	A	.	C
JJ036	Salinan	Sicpats	A06	.	T	T	.	.	T	T	.	.	A	.	C
JJ040	Chumash	Ventureño (village not identified)	A07	C	T	T	T	.	.	.	T	.	.	A	.	C
JJ058	Yokuts	Tachi	A08	.	T	.	C	C	C	.	.	T	.	.	.	T	.	.	A	.	x
JJ085	Chumash	Miquigui (<i>Mikiw</i>)	A09	C	T	A	T	.	.	.	T	.	.	A	.	C
JJ168	Chumash	Cayegues (<i>Kaywísh</i>)	A10	.	T	T	T	A	.	T	T	.	A	.	C
JJ221	Luiseno	Pimixga (<i>Piimichnga</i>)	A11	.	T	T	.	.	.	T	.	.	A	T	C
JJ253	Chumash	Sisolop (<i>Shisholop</i>)	A12	C	T	.	.	.	T	.	.	A	.	C
JJ123	Salinan (or Yokuts?)	Mission S. Miguel (or S. Antonio?)	A13	.	T	C	.	T	.	.	.	T	.	.	A	.	C

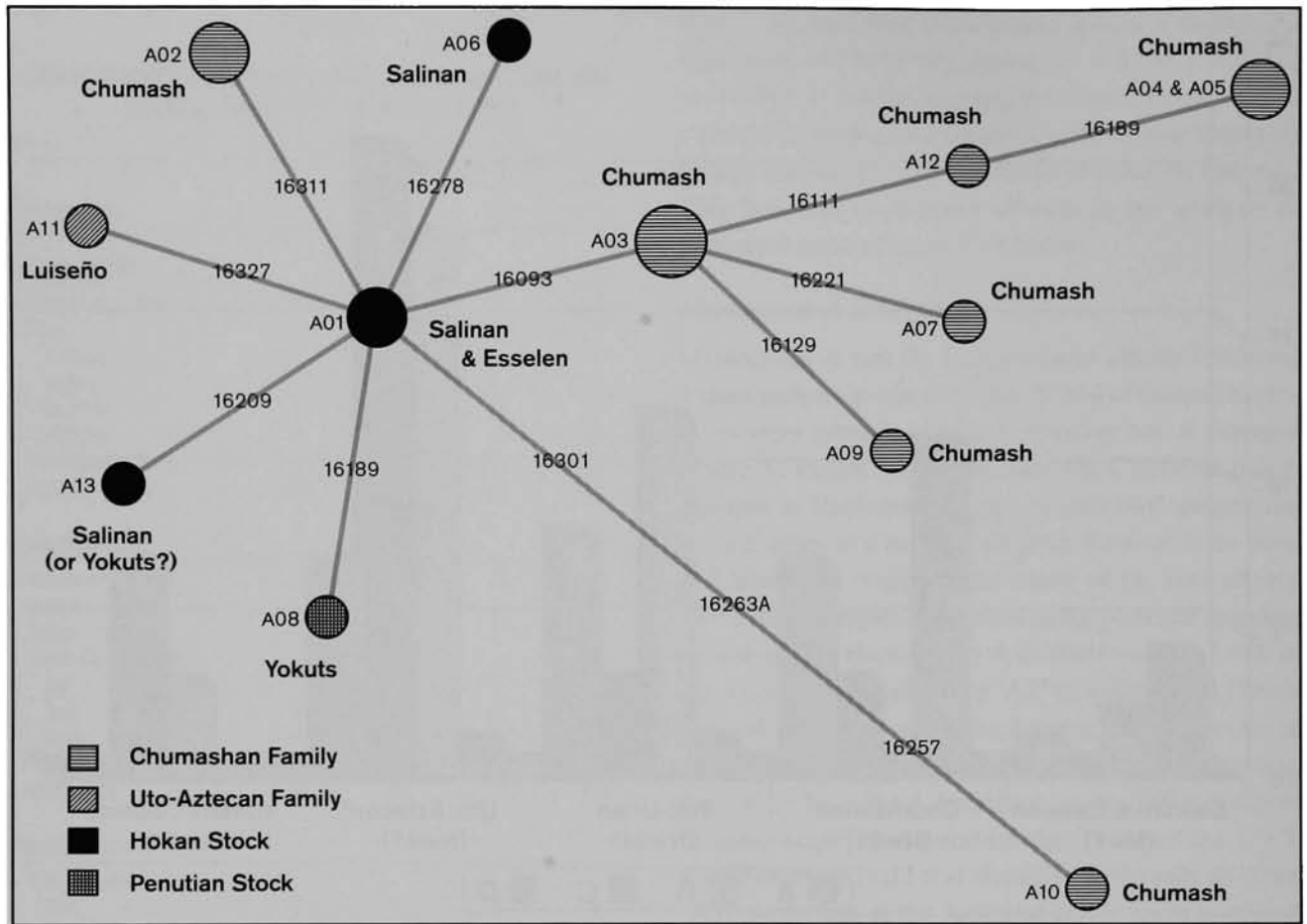


Figure 5. Haplogroup A network diagram for California Indian mtDNA lineages based on HVS1 sequences.

the only Haplogroup A lineages from Yokutsan and Uto-Aztecan groups in our database. Both Yokutsan and Uto-Aztecan peoples are believed to have spread into their ethnographically documented territories sometime between about four and a half millennia to about one and a half millennia before present (Golla, in press; Moratto 1984). Our migration model predicts that during this process, some lineages from the previously existing populations would be incorporated into the incoming groups, which were otherwise likely to be characterized by different haplotypes. We interpret the isolated A haplotypes found among Yokuts and Luiseño populations to be instances of this acquisition of older lineages during the process of population replacement.

Haplogroup B Lineages

The greatest number of lineages among our California Indian samples was characterized by Haplogroup B, slightly more than Haplogroup C. This in part has to

do with the large number of Uto-Aztecan samples in our database (Table 2), which conforms to the general predominance of haplogroups B and C among populations in the greater Southwest (Carlyle et al. 2000; Malhi et al. 2002, 2003; Merriwether 2002; Lorenz and Smith 1994, 1996). Haplogroup B also had the greatest sequence diversity of any haplogroup in our database. A total of 24 haplotypes occur among the 42 sequences obtained for Haplogroup B (Table 4).¹⁵ The founding haplotype proposed for Haplogroup B among North American Indian populations (Forster et al. 1996) is represented by two samples, each from groups that spoke languages within the proposed Penutian superfamily: Patwin and Sierra Miwok (Haplotype B03 in Figure 6). This founding haplotype is more prevalent elsewhere in the Americas (Malhi et al. 2002). Our two Wintu samples each represent a haplotype one mutational step removed from the founding lineage (Haplotypes B05 and B15 in Figure 6). One of these exhibits an HVS1 sequence that

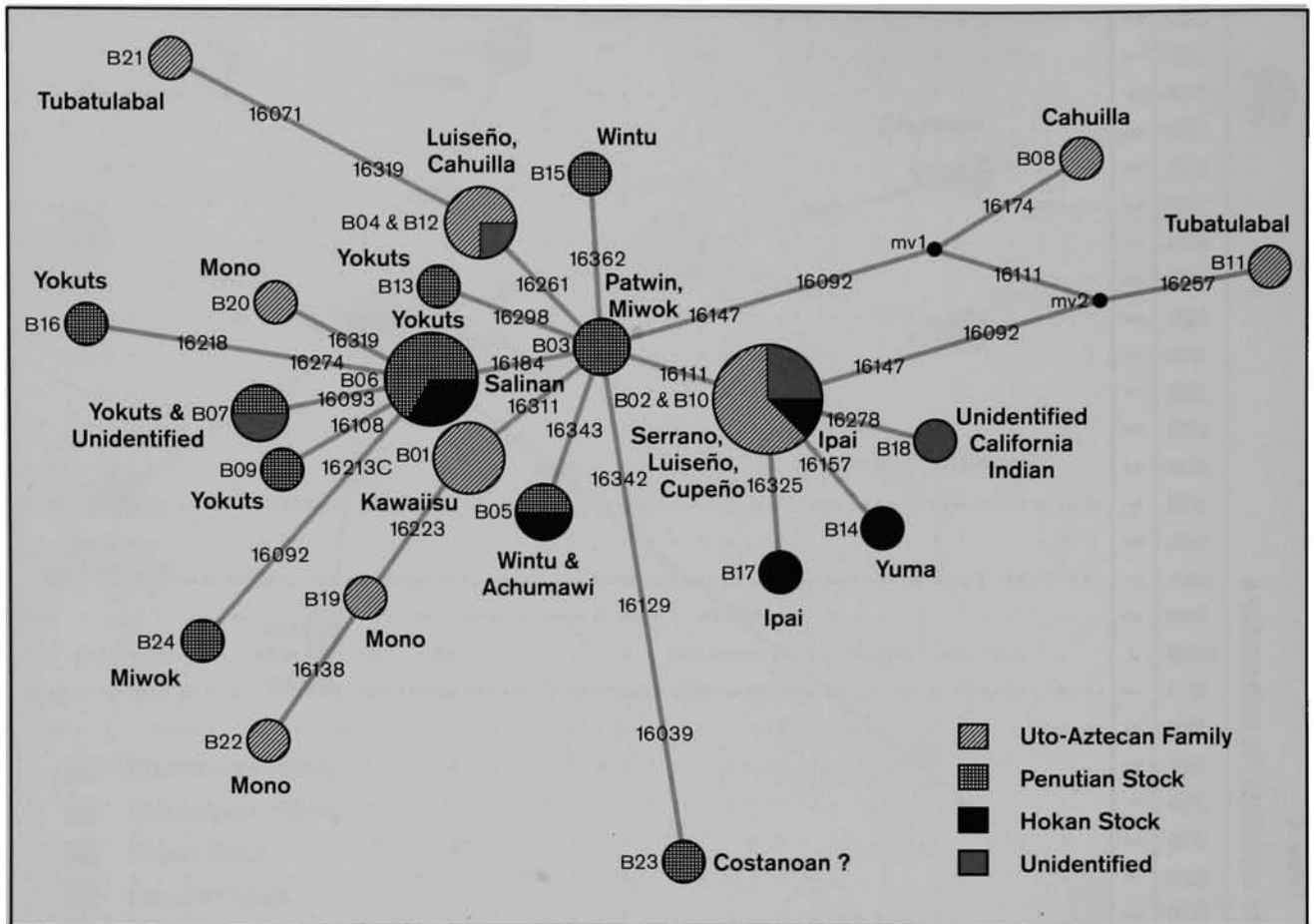


Figure 6. Haplogroup B network diagram for California Indian mtDNA lineages based on HVS1 sequences.

is shared with the single Achumawi/Atsugewi lineage represented in our sample, illustrating some degree of intermarriage among Northern California groups belonging to different linguistic phyla.

Twelve Haplogroup B samples distributed in six haplotypes share a unique mutation that resulted in a transposition of two nucleotides within the “poly-C” region. Instead of an A at np 16183 and a C at np 16184, these two nucleotides reversed position so they contain an A→C transversion at np 16183 and a C→A transversion at np 16184 (Table 4). Haplotype B06 contains only this transposition to distinguish it from the founding haplotype B03. Five other haplotypes branch from B06, each containing one or two subsequent mutations (Figure 6). This star-like pattern is commonly associated elsewhere in the world with migration events in prehistory. All of the sequences containing the np 16183/16184 transposition are from Yokuts lineages or their immediate neighbors (Salinan, Sierra Miwok, and

Western Mono), and so the resultant star-like pattern is consistent with the hypothesized Yokutsan expansion within the San Joaquin Valley region and adjacent Sierra Nevada foothills. The shared presence of the colonizing haplotype (B06 in Figure 6) among Yokuts, Sierra Miwok, and Salinan lineages probably derives from intermarriage between the Yokuts and their neighbors.

The non-Penutian portions of our Haplogroup B lineages are all associated with Uto-Aztecan and Yuman groups. It is probably significant that there is no overlap at all between the haplotypes represented by California Penutians and those present among California Uto-Aztecan (and Yuman) groups, implying separate population histories in geographically separated regions. It is difficult to discern phylogenetic patterns associated with particular Uto-Aztecan or Yuman subgroups because of the reticulations previously mentioned and because of past intermarriage between these groups, who all practiced patrilineal residence. Nonetheless,

there are certain preliminary observations that can be made. Although the frequently mutating np 16111 makes discernment of phylogenetic relationships problematic, it is perhaps not coincidental that the three B haplotypes found among the Yuman lineages in our database all appear on the same branch among those containing this mutation (Figure 6).¹⁶ Also, there are suggestive indications of at least one unique lineage among the linguistically and geographically isolated Tubatulabal, one which is characterized by four mutations that distinguish it from the founding B haplotype. Although the np 16111 mutational “hot spot” somewhat obscures its phylogenetic position in Figure 6, this Tubatulabal lineage is most likely related to a Desert Cahuilla lineage with which it shares two markers (a T→C transition at np 16092 and a C→T transition at np 16147).¹⁷ This provides a modicum of support for the notion, based on linguistic studies (Golla 2000b), that the Tubatulabal group was descended from a common Takic/Tubatulabal ancestral population

Four of the six Numic samples in Table 4, three Kawaiisu and two Western Mono, are on a distinctive branch of their own, containing three haplotypes. Indeed, there is greater differentiation between these particular Numic lineages than an examination of their HVS1 sequence alone suggests. All three diverge from other Haplogroup B samples by not exhibiting the defining 9-base pair deletion, even though they otherwise possess the distinguishing markers for Haplogroup B in their HVS1 sequences. These samples were initially categorized as “other” in our restriction enzyme analysis, which was unexpected because of the unquestioned Native American pedigree of those who provided the samples to us. Subsequent examination of the HVS1 sequences for these individuals revealed their Haplogroup B affiliation.

Haplogroup C Lineages

Haplogroup C comes a close second to Haplogroup B in terms of its large proportion and diversity of lineages within our database. Table 5 lists these 38 sequences, and Figure 7 illustrates the phylogenetic distribution of the 20 haplotypes identified within our California Indian database. The long-recognized founding haplotype for Haplogroup C is clearly apparent at the center of the diagram in Figure 7 (Haplotype C02); it occurred among the Luiseño and Kawaiisu, as well as in two Southern

California Indian lineages of uncertain origin. One of the interesting patterns revealed by the network diagram is the widespread phylogenetic relationships revealed between neighboring Luiseño and Ipai populations, even though they belonged to separate language families. All five Ipai samples in Haplogroup C occur on three separate “branches” that include either a shared haplotype with their Luiseño neighbors or are one mutational step differentiated from them. This pattern is predictable based on the documented intermarriage between these groups and the long prehistory of Uto-Aztecan and Yuman populations that were adjacent to one another in the Greater Southwest. Linguistic evidence of phonological convergence between Takic and Yuman groups is entirely consistent with the genetic data (Hinton 1991).

Two of the western Takic groups, the Kitanemuk and the Vanyumé (Desert Serrano), have unique haplotypes that warrant comment. One of the Kitanemuk sequences (Haplotype C19) shares the T→C transitions at np 16189 and np 16311 that also have been identified among Northern Paiute populations in the Great Basin (Kaestle and Smith 2001; Malhi et al. 2003, 2004), suggesting a past interaction or shared history with Numic peoples, who lived to the northeast of the Tehachapi Mountains where the Kitanemuk homeland was located. The single Vanyumé sample (Haplotype C10), with four mutations not shared with any other Haplogroup C lineage, is quite unusual. Two different individuals belonging to the same matriline participated in our study in order to double-check this distinctive pattern, and both sequences were identical. The earliest female ancestor of this lineage was a woman baptized at Mission San Fernando, who had been born about 1750 in the village of Topipabit, located along the Mojave River near the Victorville Narrows. Most recently, mtDNA samples obtained from the teeth of two Late Period burials from a prehistoric cemetery near Palmdale have yielded precisely the same HVS1 sequence, demonstrating that this lineage has a prehistoric presence in the Western Mojave Desert region (Kemp, Eshleman, and Malhi 2005).¹⁸ Its unique phylogenetic position within Haplogroup C may suggest a greater antiquity for this haplotype (C10) in the desert region, perhaps predating the arrival of Uto-Aztecan populations.

Although Haplogroup C lineages were overwhelmingly a Uto-Aztecan and Yuman-Cochimí phenomenon among our samples, a few Haplogroup C haplotypes

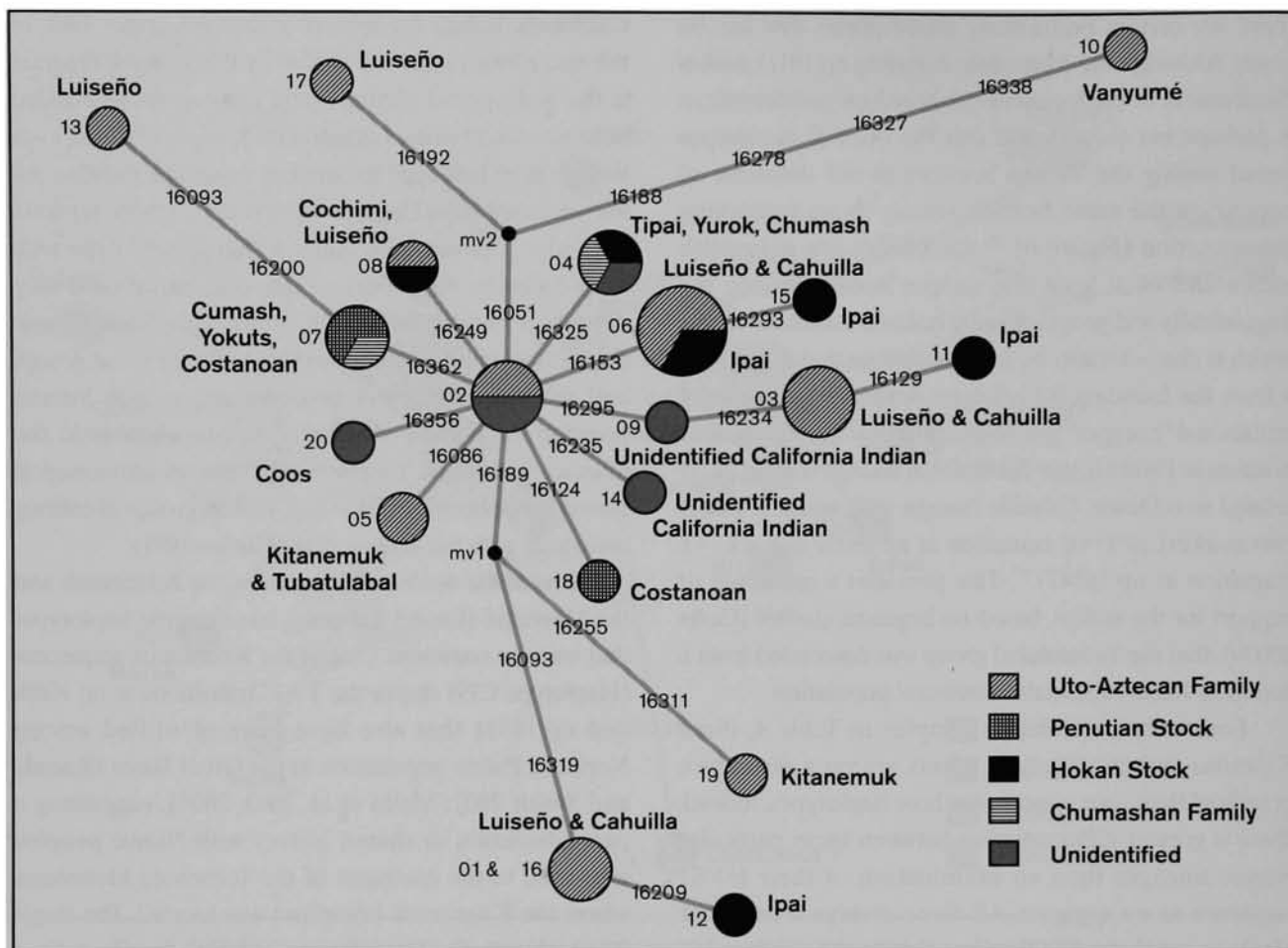


Figure 7. Haplogroup C network diagram for California Indian mtDNA lineages based on HVS1 sequences.

were found among such disparate groups as the Yurok of Northwestern California, the Coos of the Oregon Coast, the southern Costanoans, the Hometwoli Yokuts, and the coastal Chumash. One might suppose that the southern Valley Yokuts and Chumash samples might be derived from intermarriage with their Takic neighbors to the south; however, it is more difficult to explain the presence of the same haplotype (C07) among the southern Costanoans. One possibility would be that this particular haplotype derives from an "Old Uto-Aztecan" presence in the San Joaquin Valley prior to the Yokuts migration into the same territory, as has been proposed by Nichols (1988) and Moratto (1984:556). The presence of the C07 haplotype among the southern Costanoans, southern Valley Yokuts, and Ventureño Chumash could thereby result from intermarriage with the original Uto-Aztecan members of this lineage. This is but one among several conceivable hypotheses that could explain this

haplotype's dispersed distribution, and ancient DNA data from the regions in question will be necessary in order to test its likelihood.

The haplotype represented by our single Yurok sample (C04 in Figure 7) is present in both a Barbareño Chumash lineage and a Tipai lineage from northern Baja California, all from populations completely unrelated linguistically and widely separated from one another along some 1000 kilometers of coastline. This haplotype is defined by the lack of a T→C transition at np 16325, which furthermore has a broadly occurring distribution in the Northwest, Northeast, and Southwest regions of North America (Malhi et al. 2002:910–911). Although not currently recognized as a founding haplotype within Haplogroup C (Forster et al. 1996), it also is present among Asian populations and is centrally located in some network diagrams that cover the North American continent (Malhi et al. 202:910).The

Table 6

CALIFORNIA INDIAN HVS1 SEQUENCES FOR HAPLOGROUP D

Sample	Ethnolinguistic Group	Documented Origin	Haplotype	16129	16142	16179	16223	16241	16261	16291	16301	16304	16319	16325	16342	16362
CRS				G	C	C	C	A	C	C	C	T	G	T	T	T
JJ006	Yokuts	Hometwoli (<i>Taneshach</i>)	D01	.	.	.	T	C	.	C
JJ025	Yokuts	Tulamni	D01	.	.	.	T	C	.	C
JJ043	Yokuts	Silelamne	D01	.	.	.	T	C	.	C
JJ047	Yokuts	Yawdanchi	D01	.	.	.	T	C	.	C
JJ054	Yokuts	Nutunutu	D01	.	.	.	T	C	.	C
JJ060	Tubatulabal	South Fork, Kern River	D01	.	.	.	T	C	.	C
JJ098	Chumash	Tipu (Northern Chumash)	D01	.	.	.	T	C	.	C
JJ196	Chumash?	Mission San Luis Obispo?	D01	.	.	.	T	C	.	C
JJ280	Mono	Owen's Valley Paiute	D01	.	.	.	T	C	.	C
JJ363	Gabrielino	Quinquina (San Clemente Island)	D01	.	.	.	T	C	.	C
JJ059	Miwok	So. Sierra Miwok	D02	A	.	.	T	C	.	C
JJ163	Unidentified		D02	A	.	.	T	C	.	C
JJ017	Kitanemuk	Tejón region	D03	.	.	.	T	C	.	C	.	C
JJ048	Kawaiisu	Tehachapi region	D03	.	.	.	T	C	.	C	.	C
JJ001	Chumash	Miasap (<i>Miasap</i>)	D04	.	.	.	T	G	.	.	T	.	.	.	C	C
JJ067	Chumash	Siujtu (<i>Syuxturn</i>)	D04	.	.	.	T	G	.	.	T	.	.	.	C	C
JJ076	Chumash?	Calahuasa? (<i>Kalawashaq'</i>)	D04	.	.	.	T	G	.	.	T	.	.	.	C	C
JJ165	Chumash	Castait (<i>Kashtayit</i>)	D04	.	.	.	T	G	.	.	T	.	.	.	C	C
JJ050	Cahuilla	Wavaaikikum, Desert Cahuilla	D05	.	.	.	T	A	C	.	C
JJ075	Costanoan	Ensen	D06	.	T	.	T	C	.	C
JJ093	Chumash	Sucu (<i>Shuku</i>)	D07	.	.	.	T	.	T	T	.	.	.	C	.	C
JJ145	Vanyumé	Topipabit	D08	.	.	.	T	C	.	.
JJ155	Yokuts	Mission San Juan Bautista	D09	.	.	T	T	C	.	C
JJ416	Salinan	Lima	D10	.	.	.	T	.	.	T	.	.	.	C	.	C

reported hypervariability of np 16325, however, prevents geneticists from rejecting the competing hypothesis of convergence through independent mutations (Malhi et al. 2002:915).

Haplogroup D Lineages

Haplogroup D is represented by 24 sequences distributed in 10 haplotypes within our database (Table 6). Ten of these samples (41.7 percent) belong to the widely recognized founding Haplogroup D lineage occurring among American Indians (Forster et al. 1996). This haplotype (D01) was present among the Yokuts (five lineages), Northern Chumash (two lineages), Tubatulabal, Mono (Owen's Valley Paiute), and Island Gabrielino. With one notable exception, which we will discuss in further detail below, most of the remaining haplotypes are arranged about the basal Haplogroup D lineage in a star-like pattern just one or two mutational steps removed from the founding type (Figure 8). Virtually all of those haplotypes that are a single mutation removed from the founding D haplotype are found in groups living

adjacent to Yokutsan peoples, leading us to propose that intermarriage accounts for the incorporation of Haplogroup D lineages into neighboring Uto-Aztecan populations, which are otherwise dominated by haplogroups B and C. However, the Island Gabrielino, Desert Cahuilla, Barbareño Chumash, and Salinan lineages (belonging to haplotypes D01, D05, D07, and D10, respectively), are likely to be independently derived and not accounted for by intermarriage with the Yokuts. The Island Gabrielino and Desert Cahuilla lineages, in particular, and perhaps the Vanyumé lineage as well (Haplotype D08 in Figure 8), may represent older matrilineal lineages incorporated among Uto-Aztecan groups during their expansion into California, as in the explanations previously proposed for the presence of Haplotype A11 among the Luiseño (Figure 5) and Haplotype C10 among the Vanyumé (Figure 7).

One highly differentiated lineage within Haplogroup D is readily apparent in Figure 8. Considerable light has recently been shed on this haplotype, which occurs prominently among western coastal and Santa Ynez

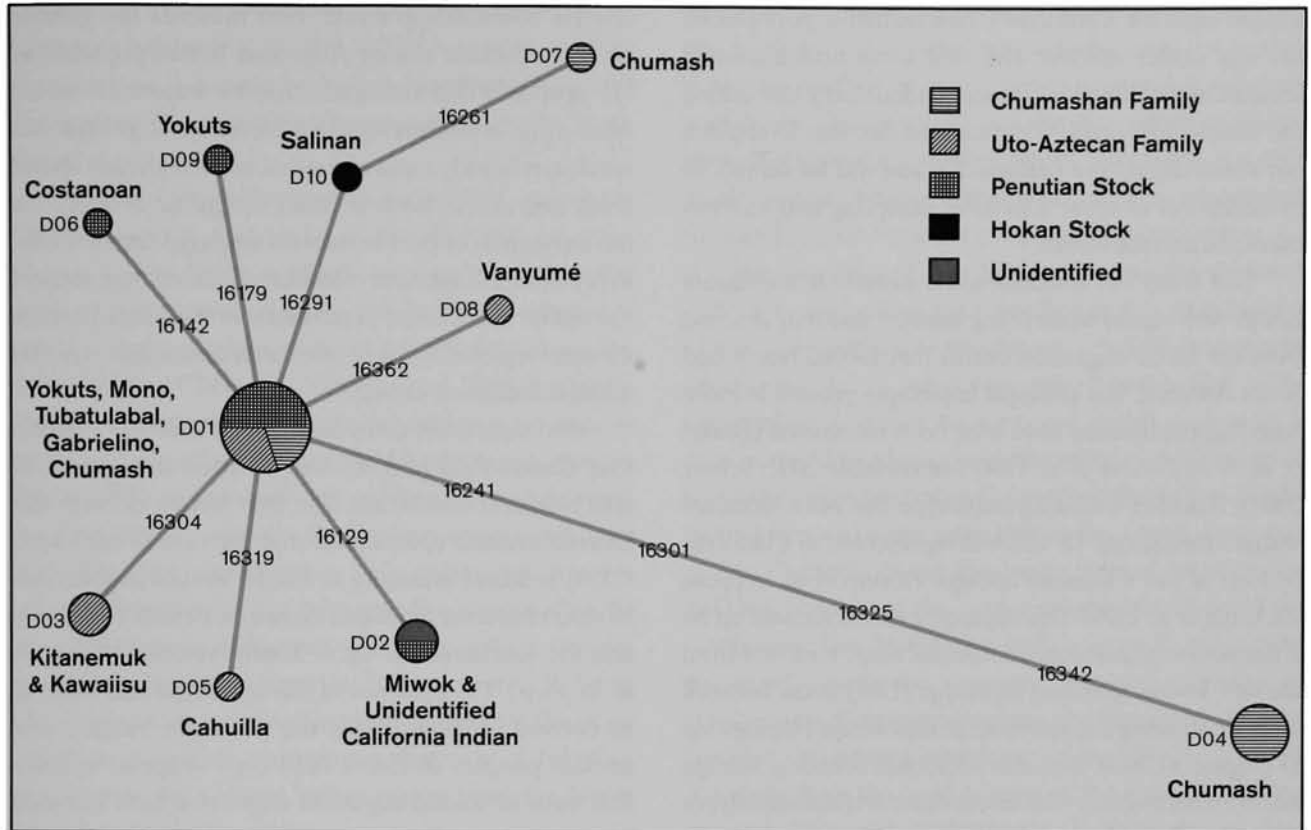


Figure 8. Haplogroup D network diagram for California Indian mtDNA lineages based on HVS1 sequences.

Valley Chumashan groups (our Haplotype D04). Four samples exhibit the exact same pattern, which differs from the previously recognized founding haplotype by possessing transitions A→G at np 16241, C→T at np 16301, and T→C at np 16342, as well as lacking the T→C transition at np 16325 (Table 6). A closely related haplotype had previously been discovered by Rickards and her colleagues (1999) among the Cayapa Indians of coastal Ecuador; it was proposed by these researchers that it represented an additional founding haplotype among American Indians. A sequence identical to that occurring among the Chumash was recently discovered by Kemp from an mtDNA sample obtained from a human tooth from an Early Holocene burial excavated by James Dixon in On Your Knees Cave (Dixon 1999:117–119; Kemp et al. in press). This finding supports the identification of this haplotype as being another founding lineage for the Americas. Other closely related lineages have now been identified among Mexican populations, the Mapuche Indians of southern Chile, and prehistoric peoples of Tierra del Fuego, among others (Kemp et al. in press).

DISCUSSION

Mitochondrial DNA lineages are useful for phylogenetic studies because they descend only from a single parent, one's mother, and therefore can be compared to each other to determine the closeness of genetic ancestry. The simple branching diagram or “cladogram” that can be used to graph mtDNA phylogenies is not necessarily a good model to depict the real world of how language change occurs or how different peoples come together to form descendant groups (Moore 1994). Nonetheless, when insights derived from linguistic prehistory and archaeology are used in conjunction with genetic analyses, a new synthesis becomes possible regarding past processes that resulted in changes in population composition and ethnogenesis. Earlier in this paper, we proposed that distinctively different genetic and linguistic patterns would result from different types of population interactions associated with migration events in prehistory. Our interpretations of the results of the mitochondrial DNA HVS1 sequences are based on these earlier predictions. We must recognize, however, that our

sample sizes for California's various native populations are still rather modest, and that some undetermined amount of genetic diversity was undoubtedly lost during the nineteenth-century population decline. Therefore, our observations are preliminary and will be subject to modification as more extensive sampling and analysis takes place in the future.

Our study has revealed some extremely interesting results with regard to surviving lineages that may descend from the initial migration events that settled North and South America. The principal haplotypes present in those founding populations have long been recognized (Baillet et al. 1994; Forster et al. 1996; Merriwether 2002; Schurr 2004). Another founding haplotype has been detected within Haplogroup D, which is represented in California by four of our Chumash lineages (Kemp et al. in press; Rickards et al. 1999). This haplotype (D04) showed up on a distinctive branch four mutational steps removed from the well-known founding haplotype (D01) in the network diagram showing lineage relationships within Haplogroup D (Figure 8). Now that this additional founding lineage has been discovered, what about other original haplotypes that might have lingered on among California's native peoples? A quick glance at Figure 7 shows that at least one other lineage is isolated on a distant branch in its respective haplogroup diagram: C10 (Vanyumé). This haplotype is even farther removed in the number of HVS1 mutations from the previously recognized founding haplotype for Haplogroup C than is the uncommon Chumash haplotype D04 within Haplogroup D. One must consider, therefore, the possibility that this Vanyumé lineage represents an additional rare survival remaining from very early migrations that led to the peopling of California.

Dixon (1999) has recently summarized the accumulating evidence that favors a Pacific coastal migration route by Paleoindian populations into the American continents by the end of the Pleistocene. Some anthropologists have proposed that the great diversity of languages and language families present along the Pacific Coast of North America derives from such initial colonization (Gruhn 1988, 1992; Rogers 1985). On the basis of a sophisticated linguistic analysis, Nichols (1992, 2000, 2002) has suggested that by whatever route the continent was initially populated, a subsequent coastal migration accounts for certain rare features in languages distributed along the Pacific Coast of the Americas. Fix (2002) has demonstrated that a

coastal colonization model best matches the genetic diversity present among American Indian populations. He proposes that transportation by watercraft would encourage intermarriage outside of local groups and result in relatively rapid expansion beyond already settled areas (see also Erlandson 2002). Linguistic evidence for the uniqueness of the Chumashan language family (Golla, in press) and the genetic evidence presented here support the notion that coastal populations in the Santa Barbara Channel region could well have been descended from this initial colonization event.¹⁹

Two significant clues exist in our mtDNA samples that Chumashan peoples had an ancient presence in south-central California. The first has to do with the aforementioned observation that the rare D haplotype (D04) is found primarily in Pacific coastal populations in discontinuous locations between British Columbia and the southernmost tip of South America (Kemp et al. in press). The presence of this haplotype and some of its derived lineages among the Mapuche, Yahgan, and ancient peoples of Tierra del Fuego suggests that the first wave of coastal migration might well have included women representing this mtDNA founding lineage. Its presence among some interior groups in Mexico and among prehistoric peoples in Illinois could well derive from subsequent expansions of coastal peoples into the interior of the North American continent.

The second clue regarding the greater antiquity of Chumashan groups derives from the distribution of Haplogroup A, which is largely limited to Northwest Coast and California groups inhabiting coastal regions (Eshleman et al. 2004). Haplogroup A lineages are present in their greatest abundance and diversity among Chumashan peoples, and the branching chain of Chumash haplotypes illustrated in Figure 5 is evidence of a lengthy and stable population throughout much of prehistory. Although both the rare D haplotype (D04) and the Haplogroup A lineages could be derived from the same coastal migration, we must also consider the alternative hypothesis that they resulted from two independent populations becoming established and coalescing in the highly productive Santa Barbara Channel region. Indeed, Nichols favors this scenario, based on her interpretations of a statistical analysis of the distribution of rare linguistic features among American Indian languages (Nichols 2002:287–290). Furthermore, Klar (2002) reports

evidence of a non-Chumashan substrate in the Cruzeño language. Analysis of ancient mtDNA samples will be necessary to determine whether Haplogroup A and Haplogroup D lineages have equal antiquity in the Santa Barbara region.

Haplogroup A lineages characterized our single Esselen sample and three of our Salinan samples, suggesting that these could well have persisted from the same early colonization along the Pacific shoreline that resulted in the establishment of a population along the Santa Barbara Channel (Eshleman et al. 2004; Eshleman and Smith, in press). The linguistic evidence for ancient contact between Esselen and the Chumashan languages (Shaul 1988), and the presence of Haplogroup A lineages from prehistoric burials in the Big Sur region (Eshleman 2002:122), could signify that a Salinan language was not initially spoken in the coastal region. It is possible that the three Haplogroup A lineages among our Salinan samples may have previously existed in the region prior to being absorbed during a Salinan expansion towards the coast under pressure from an incoming migration of Yokutsan groups into the Central Valley region from the Great Basin (see Golla, in press).

Similarly, rare instances of Haplogroup A lineages among the Yokuts and Luiseño samples were likely derived from earlier populations that were incorporated into expanding groups who arrived later in these respective regions (see also Eshleman and Smith, in press). The Yokuts Haplogroup A haplotype (A08) is particularly interesting because it is identical to a sequence reported from a prehistoric burial in Esselen territory, thus further suggesting an original coastal connection for this haplotype (Eshleman 2002:122). Haplogroup A lineages also have been identified among prehistoric populations living in marginal areas, such as the San Clemente Islanders and the Pericú of the southern tip of Baja California (Endicott et al. 2004; Potter 2004). This pattern is fully consistent with the expectations of an initial coastal migration hypothesis, in which this haplogroup became established early among peoples with a maritime subsistence base and then persisted in certain coastal locations despite later population expansions.²⁰

Based on an earlier subset of the data reported more fully here (Tables 2–6), Eshleman et al. (2004) noted a perceived similarity in haplogroup distributions between the Takic and Yuman groups of southern California and

certain Great Basin and Plateau groups, and Eshleman and Smith (in press) further note that the Takic distribution is similar to that of more ancient central California populations. The examination of specific haplotypes among these populations, however, shows that there is much greater genetic distance between them than was suggested by overall similarities in their haplogroup distributions.

The migration of Uto-Aztecan groups into southern California appears to have resulted in the introduction of new genetic lineages into the area, as well as language replacement. At least one non-Yuman and non-Chumashan language once existed in this region, as is demonstrated by a lexical and phonological substratum of undetermined affiliation in Gabrielino (Bright and Bright 1976). Here and there, especially in the desert areas and on San Clemente Island, there exist hints of the surviving mtDNA lineages of the earlier inhabitants of southern California. The distinctive Haplogroup C haplotype discerned among the Vanyumé; the rare presence of Haplogroup D lineages among the Vanyumé, Desert Cahuilla, and Island Gabrielino; and the sole Haplogroup A sample from the most interior of the Luiseño villages, are probable survivals from the pre-Takic period. The fact that these lineages all persisted in relatively marginal areas suggests that the dryer, desert regions served as refugia for peoples who otherwise came to speak the language of a dominant incoming group who co-opted more favorable habitats.

Eshleman and Smith (in press) and Golla (in press) have given thorough consideration to the evidence pertaining to the timing and spread of language families included within the Penutian macro-unit (see also Moratto 1984). Our data for Wintuan (3 samples) are still too sparse to come to meaningful conclusions regarding the spread of this language family in Northern California, other than to note that at least one Wintu lineage is shared with the linguistically unrelated Achumawi/Atsugewi. Our sample is likewise too small to test the hypothesis that the Miwok-Costanoan (Utian) family may have had a longer presence in California than the Yokutsan family; however, we did find a genetic pattern that supports the reconstruction of a relatively late expansion of Yokuts peoples in the San Joaquin region with concomitant absorption of older mtDNA lineages and intermarriage with neighboring groups (see also Eshleman and Smith, in press).

Mitochondrial DNA research is coming into its own as another means of exploring the prehistory of California's indigenous societies. Although our database undoubtedly under represents the genetic diversity once present among the native peoples of Central and Southern California, the high-resolution genealogical data do give us confidence regarding the patterns that have been revealed to date. A collaborative approach utilizing the analytical techniques of human genetics and taking advantage of California's rich ethnohistorical, ethnographic, and linguistic record has yielded and will continue to yield insights into the prehistoric past of the diverse peoples who inhabited the Pacific coast region.

NOTES

¹Prediction 2 has been investigated elsewhere (Eshleman et al. 2004) with regard to a wider geographical region extending beyond California.

²These non-California Indian samples were often from family members or friends of donors who accompanied California Indian participants in the study. Some samples descended from the Spanish-Mexican population of the Colonial Period were derived from mtDNA lineages initially believed to be California Indian, but later determined to have originated ultimately from a female ancestor who had immigrated to the region and whose female descendants had married a man who possessed California Indian ancestry. For example, one sample initially believed to be Gabrielino was subsequently determined to have descended from a woman born in Loreto, Baja California, whose female lineage had likely originated in Sinaloa (Northrop 1987). That woman's great granddaughter married a Gabrielino Indian man at Mission San Gabriel. So although the family was accurately identified as Gabrielino in the 1928–1933 California Indian enrollment records, the surviving mitochondrial DNA lineage was of Mexican Indian origin.

³Further research will be necessary to locate contemporary descendants of the single remaining Chumash mtDNA lineage known to exist that has not yet been sampled for our study. This matriline descends from a woman born on Santa Cruz Island and baptized at Mission San Buenaventura.

⁴See Milliken and Johnson (2005) for a discussion of village locations.

⁵Sicpats may be the same *ranchería* (village) called "Gmimu" in Mission San Luis Obispo's registers. Both words apparently meant 'carrizo place' in the Salinan and Northern Chumash languages respectively (Milliken and Johnson 2005:123). Thus, the Sicpats sample potentially could represent a Northern Chumash lineage, even though it may be traced back to a woman baptized at Mission San Miguel, which was founded in southern Salinan territory.

⁶The available records pertaining to the sample classed as "Yuma" here are conflicting with regard to tribal affiliation. At least one record was seen that implied that the woman from southern Arizona may have been Papago instead.

⁷The Chukchansi sample might be of Choinimni origin instead.

⁸The Island Gabrielino sample comes from the same matriline to which Felicitas Montañó belonged; she was one of John Harrington's Gabrielino consultants (McCawley 1996:17).

⁹After Gabrielino, the Tataviam language had the next greatest number of speakers at Mission San Fernando. People from these two groups comprised 40 percent and 25 percent respectively of those baptized at the mission (Johnson 1997:252; Johnson and Earle 1990).

¹⁰When more than one sample was obtained from the same matriline, only one was included in our analysis to avoid duplication.

¹¹The HVS1 sequences reported in this article have been submitted to the National Center for Biotechnology Information for inclusion in the GenBank database (accession numbers DQ383516–DQ383636). They are cross-referenced to the sample numbers appearing in Tables 3–6.

¹²The haplogroup affiliations of more than 100 of the 126 samples were determined through RFLP analysis. The remaining samples were assigned to haplogroups based on whether they possessed the diagnostic HVS1 markers for those particular haplogroups. HVS1 sequences were obtained for 122 samples out of the total of 126.

¹³Smith et al. (1995) reported that a HVS1 sequence from a single Pomo individual belonged to Haplogroup X; however, genealogical documentation was not obtained pertaining to this person's direct maternal ancestry. Further research will be necessary to determine if Haplogroup X lineages exist among the Pomo and whether they might yet be detected among other California native groups.

¹⁴See Note 5 above.

¹⁵The number of haplotypes may be slightly less than Table 6 indicates. The difficulty in determining the number of Cs in the "poly-C" region between np 16180 and np 16193 in the mtDNA sequence introduces some uncertainty in the assignment of haplotypes. We have reported the length variants in this HV1 C-stretch in our tables according to the recommendations of Wilson et al. (2002a, 2002b), but have eliminated positions np 16182 through 16183.2 from consideration in creating the network diagrams in our figures, because the sequence variability reported at these locations appears not to be phylogenetically meaningful in all cases.

¹⁶The C→T transition at 16111 causes reticulation in the network diagram in Figure 6. This nucleotide position appears to be something of a "hot spot" in the mitochondrial genome, with evidence of having undergone mutation within Haplogroup A also, among our California samples.

¹⁷The T→C transition at np 16092 also appears in an Ópata sample and two Hispanic lineages, also typed to Haplogroup B, in our larger database of Mexican American populations (to be reported elsewhere). It has also been reported for a sample collected in Chihuahua (Green, Derr, and Knight 2000). So the origin of this mutation may predate the entry of Uto-Aztecan peoples into California. The C→T transition at 16147, however, appears only among our samples from California.

¹⁸See Eshleman and Smith (in press) for additional examples of shared lineages between modern individuals and prehistoric burials elsewhere in California.

¹⁹Lacking California evidence, Oppenheimer (2003:304) has opined that Paleoindian populations belonging to mitochondrial Haplogroup B may have expanded southward in an early migration along the Pacific coast. The data reported in our study, however, suggest that the earliest peoples more likely would have belonged to mitochondrial DNA haplogroups A and D.

²⁰See Dixon (1999:34–43) for a model of the different stages of colonization of the Americas, spreading out from an initial coastal zone of occupation.

ACKNOWLEDGEMENTS

The authors especially thank David Glenn Smith for his support and encouragement pursuing this research and bringing this project to fruition. This study has benefited from discussions pertaining to linguistic and genetic prehistory with C. Melvin Aikens, Thomas Blackburn, Bernard Comrie, Phillip Endicott, Jason Eshleman, Stuart Fiedel, Michael Glassow, Victor Golla, Brian Kemp, Kathryn Klar, Ripan Malhi, Sally McLendon, Randall Milliken, Marianne Mithun, Amiee Potter, Theodore Schurr, Phillip Walker, and Kenneth Whistler, among others. A number of people have assisted us with making contact with California Indian descendants who have participated in our study, including Gary Breschini, Shelly Davis-King, Doreen Dishman, Cindy Ehlers, Janet Eidsness, Marta Mantzouranis, Jeff Norman, Steve O'Neil, Sheila Ruiz Harrell, and Tanis Thorne. Dan Reeves prepared Figure 1 and earlier drafts of figures 2 and 3 accompanying this paper, and Daniel Johnson assisted with creating figures 5–8. Terry Jones arranged for Brian Codding to prepare the final versions of figures 2 and 3, for which we are grateful. Jan Timbrook, Linda Agren, and Ray Corbett of the anthropology staff at the Santa Barbara Museum of Natural History, and Ra Thea, a UCSB student intern, helped with the logistics of collecting, storing, and shipping DNA samples. Andrea Vosbikian and Whitney Jackson assisted with lab work at Coriell Institute for Medical Research. Finally, we would be remiss if we did not thank and acknowledge the many California Indian descendants who willingly participated in our research and who directed us to others who also have been included. It goes without saying that this study could not have been conducted without them.

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