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The Mitochondrial DNA Affinities of the Prehistoric People of San Clemente Island: An Analysis of Ancient DNA

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Native American mitochondrial DNA belongs to one of five haplogroups defined by lineage-specific markers. Haplogroup frequency distribution is non-random among cultures. At historical contact, the Gabrielino occupied the southernmost California Channel Islands and the adjacent Los Angeles Basin. The Chumash thrived on the northern Channel Islands and Santa Barbara mainland. The Gabrielino were linguistically, culturally, and possibly genetically distinct from the Chumash. Haplogroup frequencies were determined for two prehistoric populations from San Clemente Island (Eel Point and the Nursery Site) to investigate Uto-Aztecan migration onto the southern Channel Islands. Analysis included three measures of genetic distance and phylogenetic analysis, as well as Fisher's exact tests. The Eel Point and Nursery Site frequency distributions were compared to one another, and to extant Uto-Aztecan and Great Basin/California populations. Results suggest that the prehistoric occupants of Eel Point and the Nursery Site were not closely related to one another or to the Chumash.

At the time of historic contact, Southern California was occupied by numerous distinct cultures that spoke various languages within the Hokan, Penutian, and Uto-Aztecan stocks. Two California coastal groups are the central focus of the following discussion and research—the Chumash and the Gabrielino. The Chumash spoke languages once thought to belong to the Hokan language stock; however, it is now accepted that Chumash is an ancient linguistic isolate (Mithun 1999). The Gabrielino spoke a Takic language within the Northern Uto-Aztecan stock.

The ethnographically-described Chumash and Gabrielino thrived in the Santa Barbara and Los Angeles Basin regions, as well as on the northern and southern California Channel Islands, respectively. Both groups had well developed maritime economies with similar technologies and subsistence patterns. Their resource utilization was necessarily similar, as the environmental contexts for both groups were comparable, although there were slight differences in aridity and prevailing ecosystems (Arnold 1992; Erlandson 1997; Masters and Gallegos 1997; Raab 1997; Walker 1986). Despite geographic proximity and similar cultural ecologies at the time of European contact, the Chumash and Gabrielino spoke mutually unintelligible languages and had distinct and separate cultural features in their religious and sociopolitical organization. Additionally, although ethnographic data clearly describe active trade and intermarriage between the Chumash and Gabrielino, there also existed trade networks and interaction spheres for both groups that recognized separate cultural boundaries (Byrd and Raab 2007; Raab 1997; Raab et al. 1994; Vellanoweth 1995). These features, in conjunction with the limited skeletal data, suggest cultural and genetic distinctions between the Chumash and Gabrielino, as well as population movements in conjunction with language movements in the Los Angeles Basin, on the southern Channel Islands, and in the Great Basin.

Kroeber (1925) proposed that linguistic and archaeological evidence supported a model of early

Holocene settlement and occupation of southern and central California by homogenous Hokan-speaking populations (Kroeber 1925; Moratto 1984). By A.D. 1750, the Chumash, once thought to speak a language within the Hokan stock, occupied the larger Santa Barbara Channel area. In the San Diego area, from the coast to the Colorado River, there were Yuman tribes speaking languages that fell within the Hokan superfamily. The area between these two regions was occupied by Northern Uto-Aztecan peoples (Fig. 1). This area included the Los Angeles Basin, Orange County, the Mohave Desert, the Owens Valley, Kern County, the southern San Joaquin Valley, and the Great Basin.

Within the Northern Uto-Aztecan language family, four linguistic subdivisions existed: Takic, Hopic, Numic, and Tubatulabalic (Koerper 1979; Lamb 1958; Moratto 1984; Sutton 1988). At the time of historic contact, Takic peoples occupied the Los Angeles coastal plain, the southern Channel Islands, and Orange and San Diego counties, while Numic speakers inhabited the Great Basin (Koerper 1979; Kroeber 1925; Miller 1991; Moratto 1984; Raab and Yatsko 1992; Titus 1987). Gabrielino was the name given by the Spanish to the Takic-speaking populations inhabiting the San Gabriel Mission area, the Los Angeles Basin, and the southern Channel Islands at the time of historic contact.

The California Channel Islands lie off the coast of the Santa Barbara mainland and the Los Angeles basin. Populations inhabiting these islands shared cultural features and genetic ties with the mainland populations.

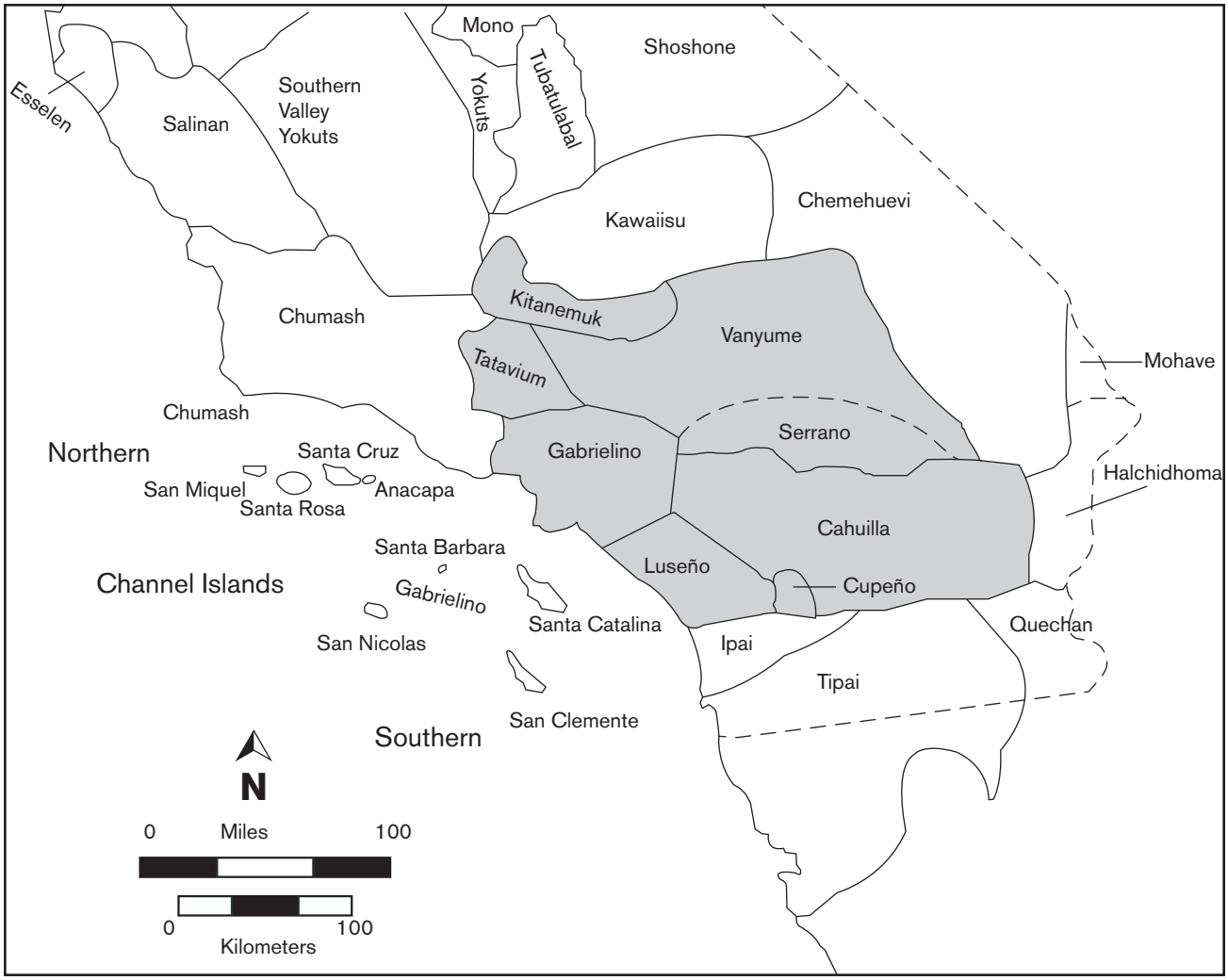

Figure 1. Geographic locations of southern California ethnolinguistic groups at time of historic contact. Map reproduced with permission of Pacific Coast Archaeological Society, adapted from Sutton (2009:32). Shaded area indicates Takic languages.

At the time of European contact, the islands were divided between two cultural spheres, with the Chumash occupying the northern islands (Anacapa, Santa Cruz, Santa Rosa, and San Miguel), and the Gabrielino the southern islands (Santa Catalina, San Clemente, San Nicolas, and Santa Barbara). King (1990) has reconstructed the origins of the historic island Chumash through cultural developments extending back into the early Holocene, while a more complex picture of population replacement is evident in the southern islands and adjacent mainland (Kroeber 1925; Miller 1991; Moratto 1984; Raab and Yatsko 1992; Titus 1987).

Kroeber (1925) argued that "Shoshonean" (Uto-Aztecan) groups expanded from a homeland in the southern Great Basin and intruded into the Los Angeles Basin area, splitting apart and displacing the Hokan-speaking occupants by what has been called the "Shoshonean Wedge" (Kroeber 1925; Miller 1991; Moratto 1984; Raab and Yatsko 1992; Titus 1987). Kroeber envisioned this expansion as involving a series of migrating waves, with the initial and most significant movement occurring approximately 1,500 years ago (Koerper 1979; Kroeber 1925; Moratto 1984). Drover and Spain (1972), however, have suggested an early date of 6,435 ± 130 years B.P. for a Uto-Aztecan occupation of the Los Angeles Basin (Koerper 1979). Others have suggested Uto-Aztecan intrusions as late as A.D. 700, but Koerper (1979) found no evidence to support a Uto-Aztecan intrusion later than 2,000 years ago at a site (ORA-119-A) in Orange County (Koerper 1979; Warren 1968). Moratto (1984) dated the intrusion of Uto-Aztecan peoples to between 3,000 and 2,000 years ago, and Lamb (1958) argued that the expansion of the Northern Uto-Aztecan family occurred about 3,000 years ago, when it broke up into its four subdivisions. Swadesh (1964) proposed an earlier date, based on glottochronology, arguing that Gabrielino and Tubatulabal have been separated for about 3,900 years. Sutton (1988) suggested that a significant populational event, beginning between 3,000 to 2,500 years ago, was reflected in the Antelope Valley archaeological record. At the time of European contact, the Antelope Valley was inhabited by the Takic-speaking Kitanemuk. Sutton (1988) speculated that the patterning demonstrated by Antelope Valley archaeological data resulted from either an expansion of Takic speakers into the area, or population growth occurring in groups already occupying the area. The Fremont Valley, north of the Antelope Valley, was claimed ethnographically by the Numic-speaking Kawaiisu (Fig. 1). Archaeological data from the Fremont Valley are limited, but those available suggest an extended occupation with some antiquity (Sutton 1988). As the above review shows, the precise patterning and time when Uto-Aztecan intrusions occurred remain matters of continuing debate.

Current models of population replacement in the Los Angeles Basin and on the southern Channel Islands are based on interpretations of human osteological data that demonstrate subtle shifts in skeletal morphometrics and paleopathologies (Kerr 2004; Titus 1987; Titus and Walker 2000). These data support a model of population replacement on San Clemente Island, California during the Late Holocene.

Two temporally-separated prehistoric cemetery populations excavated from San Clemente Island, California, have played a prominent role in the limited number of biological anthropology studies conducted on the southern Channel Islands. Skeletal remains excavated from these two cemeteries are considered to represent two separate populations, based on radiometric dating and geographic separation (Potter 1998; Titus 1987; Titus and Walker 2000). The two sites, Eel Point and the Nursery Site, have been argued to both predate and postdate the Uto-Aztecan intrusion onto the island (Fig. 2). The Eel Point site dates to the late Middle or early Late Holocene, while the Nursery Site dates to the Late Holocene. Burials from the Eel Point site have been argued to have been more closely related biologically to Hokan or Chumash peoples, while the later individuals at the Nursery Site were more closely related to the Uto-Aztecan Gabrielino (Titus 1987; Titus and Walker 2000).

MITOCHONDRIAL DNA IN THE AMERICAS

Mitochondrial DNA (mtDNA) data indicate that native North, Central, and South American populations tend to fall into five groups containing related mtDNA lineages that are characterized by coding-region restriction site markers or the presence of a 9-base-pair deletion (Table 1). In addition, each coding region marker is associated with mutations within the Hypervariable Segment I (HVSI) region of the non-coding D-loop (Baillet et al. 1994; Bonatto and Salzano 1997; Carlyle et

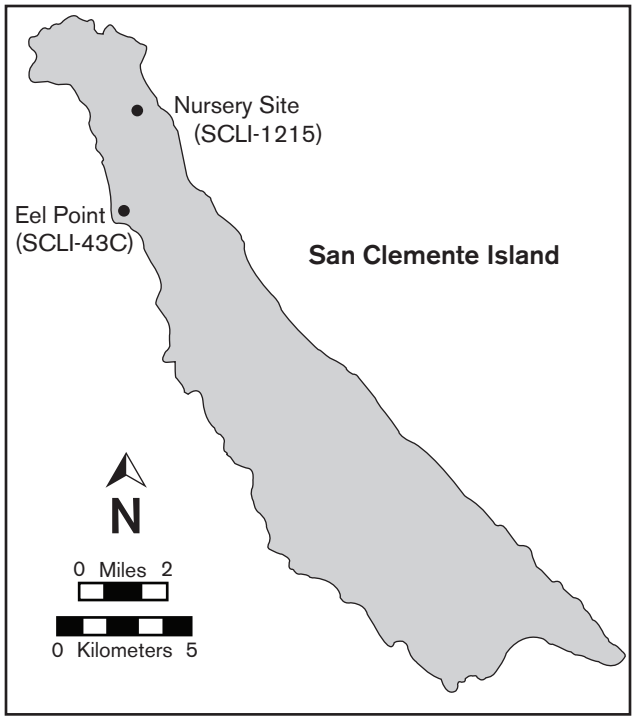

Figure 2. Eel Point and the Nursery Site, San Clemente Island

al. 2000; Eshleman 2003; Eshleman et al. 2004; Forster et al. 1996; Kaestle 1998; Lorenz and Smith 1994, 1996; Malhi and Smith 2002; Malhi et al. 2003; Parr et al. 1996; Schurr et al. 1990; Torroni et al. 1992; Torroni et al. 1993; Wallace et al. 1985; Ward et al. 1991). These lineage groups have been termed Haplogroups A, B, C, and D. More recently, a fifth cluster, Haplogroup X (previously thought to represent recent European admixture), has been identified in prehistoric samples (Smith et al. 1999; Stone and Stoneking 1993). The haplogroups and their markers are summarized in Table 1.

We report here the results of an analysis of mtDNA extracted and amplified from two prehistoric cemetery populations excavated on San Clemente Island, California. The mtDNA data are used to examine the genetic relatedness of the cemetery populations to one another through a direct comparison of haplogroup frequencies. The mitochondrial DNA haplogroup affiliation of each individual was determined. The results of the mitochondrial DNA analysis of the prehistoric remains were then compared to published extant data in order to investigate a model of Northern Uto-Aztecan expansion and suggest genetic affinities with additional cultures of diverse ethnolinguistic affiliation.

Table 1

NATIVE AMERICAN MITOCHONDRIAL DNA HAPLOGROUPS AND ASSOCIATED MARKERS

Haplogroup	Restriction Site	HV I SNPs
Haplogroup A	+*Hae* III np 663	T np 16,223, 16,290; A np 16,319; C np 16,362
Haplogroup B	9 bp deletion between base pairs 8,281and 8,291	C np 16,189, 16,217
Haplogroup C	+ *Alu* I np 13,262	C np 16,298; T np 16,223, 16,327
Haplogroup D	– *Alu* 5,176	T np 16,223
Haplogroup X	– *Dde* I np 1,715 – *Dde* I np 10,394	T np 16,223, 16,278; C np 16,183, 16,189

Although mtDNA haplogroup frequency distributions are not sufficient measures of population-specific genetic affinities, genetic distance analysis may be a preliminary step in elucidating prehistoric affinities. With a caveat based upon the limitations of frequency-based distance analysis and the effects of small sample size, these data and comparisons are used to (1) tentatively identify the extant California/southwestern Arizona, Pacific Northwest, and Great Basin populations with which the Eel Point and Nursery Site individuals may have had the closest maternal genetic affinities; (2) determine if there is evidence of genetic continuity on San Clemente Island; and (3) consider whether there is support for a close genetic relatedness between the two San Clemente Island cemetery populations. The mitochondrial DNA of the San Clemente Island people is used to try to resolve questions about the pattern and timing of Uto-Aztecan migration onto the southern Channel Islands.

MATERIALS AND METHODS

Cemetery Populations Studied

San Clemente Island, the southernmost Channel Island, lies approximately 61 km. off the Los Angeles Coast. It is the fourth largest Channel Island and covers approximately fifty-eight square miles (Potter 1998; Raab et al. 1994; Salls 1992). The island is currently a Naval Reserve, inaccessible to the general public, with archaeological materials being managed by the United States Navy (Raab et al. 1994; Salls 1992).

The Eel Point site (CA-SCLI-43A, -B, and -C) is located on the western coast. Field schools conducted by UCLA archaeologists during the 1980s produced a series of 24 radiocarbon dates (Salls 1988), as well as a large collection of fish bones and artifacts. Radiocarbon dates for the three loci span a period from 8,210 ± 60 cal years B.P. (Beta-95897) to 580 ± 60 cal years B.P. (Beta-77956). The Eel Point site, with its almost 10,000 years of occupation by indigenous peoples, has contributed greatly to our current understanding of southern California maritime cultural change (Erlandson 1994; Porcasi 1995; Potter 1998; Raab and Yatsko 1992; Raab et al. 1994; Salls 1988). Additional excavations, led by Raab and Yatsko in 1994, 1996 and 2003, have produced a body of data—including radiocarbon dates, faunal analyses, and analyses of cultural remains—that have further refined the cultural chronology for the site (Raab 1997; Raab and Larson 1997; Raab and Yatsko 1992).

The Nursery Site has an inland location and represents a period of extended occupation from 5,500 to 450 years B.P. Excavations conducted by UCLA archaeologists in 1984 revealed the first evidence on the island of house pits and related features (Raab 1997; Rigby 1985). Further excavations were conducted during a summer field school led by Raab and Yatsko in 1990 (Raab 1997).

The Eel Point burials were excavated by UCLA archaeologists in 1983, and represented 11 individuals. Another 22 burials were excavated from the Nursery Site in the years 1984, 1985, and 1987 (Potter 1998; Titus 1987; Titus and Walker 2000). The direct radiometric dating of human bone from one burial and cultural materials associated with another placed both cemeteries in the Late Holocene, with Eel Point Locus C dated to 3,040 ± 70 cal B.P. and the Nursery Site dated to 1,490 ± 30 cal B.P. (Potter 1998). Twelve radiocarbon dates for Eel Point Locus C ranged from 4,500 ± 350 years B.P. to 1,090 ± 25 years B.P., but most clustered around 3,000 years B.P. A bone collagen sample from a burial at Eel Point Locus C was dated to 3,040 ± 70 B.P. (Titus 1987).

Analysis

DNA extraction was completed on the skeletal remains of 23 individuals excavated from two separate cemeteries, one group from Eel Point Locus C (SCLI-43C) and the other from the Nursery Site (SCLI-1215), both on San Clemente Island. The focus of this research was to determine haplogroup distributions in the two populations. Initial typing was conducted using primers to amplify and sequence the markers within the coding region specific for each of the five Native American founding haplogroups. Haplogroup-associated polymorphisms within the HVSI region were identified secondarily through sequencing. Therefore, highly localized or specific loci within HVSI were targeted, rather than the entire D-loop. To increase the likelihood of successfully amplifying and sequencing the DNA, primers were utilized which produce a short amplicon ~150 base pairs (Table 2). This strategy was adopted because of the highly degraded nature and low concentrations of the DNA. If an individual could not be typed on the basis of coding region markers, haplogroup-defining HVSI markers were utilized.

Either a section of rib cortical bone or a phalanx from each individual was ground to a fine powder after physical cleaning of the bone surface with 0.25% sodium hypochlorite solution (5% Clorox® Bleach), UV irradiation, and removal of the outer 0.50 mm. of the bone surface with a Dremel® aluminum oxide grinding stone head.[1] The hood, the Dremel®, all cutting/polishing/drilling heads, and the grinder were thoroughly cleaned with 0.25% sodium hypochlorite solution (5% Clorox®

Table 2

PRIMERS USED TO AMPLIFY DIAGNOSTIC SITES

Primer Name	Nucleotide Position rCRS	Sequence
DL3U[1]	np 16,171 to 16,189	5'-ATCCACATCAAAACCCCCT-3'
DL3L[1]	np 16,341 to 16,360	5'-GAGAAGGGATTTGACTGTAA-3'
1,6151U	np 16,132 to 16,151	5'-ACCATAAAT ACTTGACCAC-3'
1,6285L	np 16,268 to 16,285	5'-GGTTGTTGGTATCCTAGTG-3'
Hae III	np 663U 550 to 566	5'-AACCAAACCCCAAAGACA-3'
Hae III	np 663L 710 to 728	5'-GAGGGTGAACTCACTGGAA-3'
DdeI 1,715U[3]	np 1,651 to 1,670	5'-ACTTAACTTGACCGCTCTGA-3'
DdeI 1,715L[3]	np 1,775 to 1,793	5'-CCCTTGCGGTACTATATC-3'
Alu 5,176U[1]	np 5,109 to 5,128	5'-ACCGCATTCCTACTACTCAA-3'
Alu 5,176L[1]	np 5,193 to 5,210	5'-GGTGGATGGAATTAAGGG-3'
Deletion 8,215U[2]	np 8,195 to 8,215	5'-ACAGTTTCATGCCCATCGTC-3'
Deletion 8,215L[2]	np 8,297 to 8,316	5'-ATGCTAAGTTAGCTTTACAG-3
HincIIU13,259[1]	np 13,146to13,166	5'-CCCACTAATCCAAACTCTAAC-3'
HincIIL13,259[1]	np 13,291 to 13,309	5'-TAGGTGTGGTTGGTTGATG-3'

DL (D-loop) primers amplify segments in HV I.
[1]Primers designed by A. Potter, [2]Stone and Stoneking (1998), [3]Malhi and Smith (1999).

Bleach) and UV-irradiated between the processing of each sample. Between 0.50 and 0.80 grams of bone powder was placed in STET buffer (Potter 2004) and placed in a 42º C water bath to digest for a minimum of five days. Digest supernatant was recovered and cleaned with a standard phenol:chloroform:isoamyl alcohol (P:C:I) wash as described by Potter (2004). The DNA pellet was re-suspended in 75 uls. sterile water.

To detect potential contamination in the extraction reagents, blank extractions were performed. Blanks were tested using polymerase chain reaction (PCR), gel electrophoresis, and sequencing. No DNA sequences were obtained from reagent blanks.

All PCR reactions were set up under sterile conditions in a Class II Biosafety Cabinet. To prevent contamination, the hood was thoroughly cleaned with a 0.50% sodium hypochlorite solution (10% Clorox® Bleach) and rinsed with sterile water. All pipettes were cleaned with 0.50% sodium hypochlorite solution (10% Clorox® Bleach), as were the vortex mixer and all tube racks. Disposable sterile tubes and aerosol-resistant plugged tips were used to make master mixes and for PCR setup. Decontaminated gloves were worn inside the hood at all times and a clean disposable lab coat with cuffs was worn. Decontamination procedures were performed before and after each reaction set up. A negative control was used for each primer set for every PCR. To limit the contamination potential of reagents, smaller aliquots of working stocks were prepared and disposed of after several uses. Aliquots were prepared in a decontaminated hood where post-PCR product was never present. To confirm the authenticity of results, multiple extractions, PCR amplifications, and sequencing reactions were performed. Additionally, two samples were re-extracted, amplified, and sequenced in separate laboratories (SCLI-43C-10 and SCLI-1215-2).

PCR amplification was performed as described by Potter (2004). PCR product was size separated on a 2% agarose gel stained with ethidium bromide to verify amplification. All positive PCR products were cleaned with Shrimp Alkaline Phosphate and Exonuclease I. Clean PCR product was directly sequenced using ABI Big Dye Terminators, following the protocol described by Potter (2004). Alcohol-precipitated sequencing product was electrophoresed on an ABI PRISM 377 or the ABI 3700 capillary machine.

Electropherograms were base called using the ABI Sequence Analysis software. ABI files were aligned and edited in Sequencer 4.2. The Revised Cambridge Reference Sequence (Andrews et al. 1999) was used as the reference sequence to determine Single Nucleotide Polymorphisms (SNPs) or base pair substitutions in the sample sequences. All variable sites are numbered relative to the revised Cambridge Reference Sequence (rCRS).

Multiple Oligo Ligation PCR (MOL-PCR, described in detail in International Publication Number WO 2004/099431 A2), is a highly sensitive method for determining the base pair at a specific nucleotide position. Because of the increased sensitivity of the method, it was tested on several of the San Clemente Island samples where initial DNA isolations were refractory to PCR, or were PCR amplified but failed to yield clean sequence data. Briefly, the method uses allele-specific ligation of modular oligonucleotides (moligos), followed by PCR amplification with a universal primer to type samples. Resultant PCR product is visualized on a 2% agarose gel. Product is only seen in the lanes containing the product of the ligation reaction that contained the primer with the complimentary base pair to the site being typed. The accuracy of MOL-PCR for typing DNA was tested on microbial isolates possessing known polymorphisms relative to a microbial reference sequence. The polymorphic loci in the assay were used to identify the organism and strain. MOL-PCR was found to be highly discriminating, with no false base calls. Failure of MOL-PCR resulted in no PCR product for any of the alleles, rather than false base calling.

Genetic distances were calculated between all pairs of populations in California, southwestern Arizona, the Pacific Northwest, the Great Basin, and the San Clemente Island prehistoric groups, with the five Native American haplogroups considered as five alleles at a single locus (Table 3). Phylogenetic trees were inferred from distance matrices created using the program Gendist of the phylogeny inference application PHYLIP 3.572 (Felsenstein 1998). Three measures were used to calculate the disances: Cavalli-Sforza and Edwards Chord Distances (Cavalli-Sforza and Edwards 1967), Reynolds et al. (1983), and Nei's D (Nei 1972). Both the Neighbor Joining method and UPGMA were used to construct the phylogenetic trees based on the calculated distance results of each of the three measures using the NEIGHBOR

Table 3

CULTURE AND LANGUAGE

Culture	Language Stock
Haida	Isolate
Bella Coola	Salish
Nuu-Chah-Nulth	Wakashan
Yuman	Hokan
Yok-Utian	Penutian
N Paiute	Uto-Aztecan (Numic)
Washo	Hokan
Pima	Uto-Aztecan (Piman)
Eel Point C	?
Takic	Uto-Aztecan
Yakama	Penutian
Nursery Site	?
Wishram	Penutian
Chumash	Isolate

program in the PHYLIP 3.572 software package. The CONSENSUS program in the PHYLIP 3.572 software package was used to construct a final consensus tree.

Fisher's exact test was used to calculate an exact probability value between Eel Point and the Nursery Site, and pairwise between each SCLI population and ethnoliguistic group in Table 3 in a two-by-five cross-table using SISA (Uitenbroek 1997).

RESULTS

The frequency distributions for Eel Point Locus C (SCLI-43C) and the Nursery Site (SCLI-1215) are presented in Table 4 and Table 5, respectively. Coding-region marker sequence results and associated HVSI sequence results for both SCLI sites are presented in Tables 6 and 7, respectively. Bone samples representing nine individuals excavated from Eel Point Locus C (SCLI-43C) were subjected to DNA extraction, and DNA was successfully isolated from eight of the samples. It was possible to confidently determine the haplogroup for seven of the eight samples; no DNA was obtained from sample 43C-8. One individual was found to belong to Haplogroup A, two belonged to Haplogroup B, four were typed as Haplogroup C, no burials were typed to Haplogroup D, and one sample did not possess any of the coding region markers (Table 6). However, more recent extractions and sequence analyses have revealed that the sample (SCLI-43C-2) possesses HVSI Single Nucleotide Polymorphisms

Table 4

HAPLOGROUP FREQUENCIES EEL POINT C (SCLI-43C)

Haplogroup	Frequency N=7	Number
Haplogroup A	0.143	1
Haplogroup B	0.286	2
Haplogroup C	0.571	4
Haplogroup D	0.000	0
Haplogroup X	0.000	0

Table 5

HAPLOGROUP FREQUENCIES NURSERY SITE (SCLI-1215)

Haplogroup	Frequency N=13	Number
Haplogroup A	0.076	1
Haplogroup B	0.461	6
Haplogroup C	0.154	2
Haplogroup D	0.308	4
Haplogroup X	0.000	0

Table 6

CODING REGION RESULTS HAPLOGROUP DEFINING MARKERS PRESENT (+) OR ABSENT (–)

Sample	Haplogroup	Site Gain HaeIII np 663	Site Loss AluI np 5176	Nine Base Pair Deletion	Site Gain AluI np 13262
43C-1b	C	–	–	–	+
43C-2*	?	–	–	–	nd
43C-3	B	–	–	+	–
43C-5a	C	–	–	–	+
43C-5b**	C	–	–	–	+
43C-7	B	–	–	+	–
43C-9	C	–	–	–	+
43C-10	A	+	–	–	–
1215-2	D	–	+	–	–
1215-3	B	nd	nd	nd	nd
1215-5	D	–	+	–	–
1215-6	C	–	–	–	+
1215-8	C	–	–	–	+
1215-10	A	nd	–	–	–
1215-11	B	–	–	+	–
1215-12	B	–	–	+	–
1215-13	B	–	–	+	–
1215-14**	D	–	+	–	–
1215-16	B	nd	–	+	–
1215-19	D	–	+	–	–
1215-22	B	–	–	+	–

* Not included in analysis; ** Initially typed using MOL-PCR and subsequently confirmed using PCR and sequencing

Table 7

HAPLOGROUP DEFINING SINGLE NUCLEOTIDE POLYMORPHISMS BETWEEN NUCLEOTIDE POSITIONS 16189 AND 16325

Nucleotide Position		16,189	16,217	16,223	16,278	16,290	16,298	16,304	16,311	16,319	16,325
	rCRS	T	T	C	C	C	T	T	T	G	T
	HAPLOGROUP										
43C-10	A	*	*	T	*	T	*	*	C	A	*
1215-10	A	*	*	T	*	T	*	*	*	A	*
43C-3	B	*	*	*	*	nd	nd	nd	nd	nd	nd
43C-7	B	C	C	*	*	nd	nd	nd	nd	nd	nd
1215-3	B	C	C	*	*	nd	nd	nd	nd	nd	nd
1215-11	B	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
1215-12	B	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
1215-13	B	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
1215-16	B	C	C	*	*	nd	nd	nd	nd	nd	nd
1215-22	B	C	C	*	*	nd	nd	nd	nd	nd	nd
43C-1b	C	*	*	T	nd	nd	nd	nd	nd	nd	nd
43C-2	?	*	*	T	*	*	C	*	*	A	C
43C-5a	C	*	*	T	*	*	C	*	*	*	?
43C-5b**	C	*	*	T	*	*	C	*	*	*	?
43C-9	C	*	*	T	*	*	C	*	*	*	?
1215-6	C	*	*	T	*	*	C	*	*	*	?
1215-8	C	*	*	T	*	*	C	*	*	*	?
1215-2	D	*	*	T	*	*	*	*	*	A	C
1215-5	D	*	*	nd	nd	nd	nd	nd	nd	nd	nd
1215-14**	D	nd	nd	nd	nd	nd	nd	nd	nd	nd	nd
1215-19	D	*	*	T	nd	nd	nd	nd	nd	nd	nd

* indicates no base change; nd = no sequence data; **initially typed using MOL-PCR; ? = data unclear

(SNPs) associated with both Haplogroup A and C (Table 7). A comparison with the lineages included in Johnson and Lorenz (2006) suggests that this individual may belong to Haplogroup C; nonetheless, the sample was not included in further analyses.

Twenty-one Nursery Site samples were processed for DNA extraction; DNA was successfully amplified and sequenced from fifteen. The mtDNA haplogroup could confidently be determined for thirteen individuals (Table 6 and 7). Two of the fifteen samples were found to lack any of the Native American-specific markers. Although unlikely, contamination cannot be ruled out. Therefore, these samples were not included in further analyses. DNA was not recovered from four individuals.

This study was designed to determine individual haplogroup affiliations based on coding region markers. However, HVSI SNPs were used to assign haplogroup affiliations to those samples for which we were not able to confidently use coding region data. When possible, haplogroup-defining single nucleotide polymorphisms (SNPs) within the Hypervariable Segment 1 (HVSI) between nucleotide positions 16,189 and 16,340 were sequenced to confirm coding-region marker haplogroup results. The overall degraded nature and low concentrations of the DNA extracted from the SCLI burials limited our ability to amplify larger HVSI fragments or to obtain complete sequence data, resulting in missing information.

Samples that were determined to belong to Haplogroup B, based on the coding region sequencing, failed to amplify using the DL3 set of primers. Therefore, these samples, as well as several samples not confidently identified using coding region, were amplified using the 16,151/16,285 set of primers. These primers were able to extend through the poly-C tract created with the T to C transition at 16,189. Unfortunately, the use of this primer set limited data for samples sequenced using the 16,151/16,285 primer set to base pairs 16,132 to 16,285.

Table 8

HAPLOGROUP FREQUENCIES WITHIN ETHNOLINGUISTIC GROUPS

	A	B	C	D	X	N
Chumash	0.524	0.000	0.143	0.333	0.000	21
Bella Coola	0.655	0.107	0.095	0.143	0.000	84
NCNulth	0.451	0.069	0.157	0.255	0.069	102
Haida	0.854	0.024	0.073	0.049	0.000	41
Yok-Utian	0.118	0.294	0.118	0.471	0.000	42
N Paiute	0.000	0.426	0.096	0.479	0.000	94
Washo	0.000	0.536	0.357	0.107	0.000	28
Yakama	0.048	0.667	0.071	0.167	0.048	42
Wishram	0.212	0.515	0.000	0.273	0.000	33
Takic	0.000	0.200	0.533	0.267	0.000	15
Yuman	0.030	0.590	0.380	0.000	0.000	100
Pima *	0.050	0.570	0.380	0.000	0.000	42
Eel Point C	0.143	0.286	0.571	0.000	0.000	7
Nursery Site	0.076	0.461	0.154	0.308	0.000	13

Comparative frequencies from Eshleman et al. 2004; * from Malhi et al. 2003

Two samples were preliminarily typed using MOL-PCR. Additional PCR reactions and re-extraction allowed us to confirm the initial interrogation of the coding region using MOL-PCR. Those samples were SCLI-43C-5b and SCLI-1215-14.

Tables 4 and 5 present the haplogroup frequency distributions for Eel Point and the Nursery Site. Haplogroup frequency distributions for all cultures and populations included in this study are presented in Table 8. Eel Point and the Nursery Site differ in their distributions, with Eel Point having a high frequency of Haplogroups B (0.286) and C (0.571), and no occurrence of Haplogroup D, while the Nursery Site has a high frequency of Haplogroups B (0.461) and D (0.301). However, both SCLI (43C and 1215) populations have a low frequency of Haplogroup A (0.143 and 0.076, respectively). Overall, the Eel Point (SCLI-43C) haplogroup frequency distribution is most similar to the distributions for extant Yumans and Pimans. Additionally, there is some correspondence with the Takic group. Eel Point has a low frequency of Haplogroup A (0.143), high frequencies of Haplogroup B (0.286) and Haplogroup C (0.571), and no occurrence of Haplogroup D. The Yuman haplogroup distribution is 0.030 (Haplogroup A), 0.590 (Haplogroup B), 0.380 (Haplogroup C), and 0.000 (Haplogroup D), and the Piman 0.050 (Haplogroup A), 0.570 (Haplogroup B), 0.380 (Haplogroup C), and 0.000 (Haplogroup D). The Takic distribution is 0.000 (Haplogroup A), 0.200 (Haplogroup B), 0.530 (Haplogroup C), and 0.270 (Haplogroup D). The Eel Point distribution is dissimilar to that of the Chumash (Haplogroup A = 0.524, Haplogroup B = 0.000, Haplogroup C=0.143, Haplogroup D=0.333).

The Nursery Site distribution most closely resembles that of the Northern Paiute, with a low frequency of Haplogroup A (0.076), high frequency of Haplogroup B (0.461), low to moderate frequency of Haplogroup C (0.154), and high frequency of Haplogroup D (0.308). The distribution for the Northern Paiute is characterized by an absence of Haplogroup A (0.000), high frequency of Haplogroup B (0.426), low to moderate frequency of Haplogroup C (0.096), and high frequency of Haplogroup D (0.479). The Nursery Site and Chumash distributions are different (Haplogroup A=0.524, Haplogroup B= 0.000, Haplogroup C=0.143, Haplogroup D=0.333).

Genetic distances are presented in Tables 9, 10, and 11. The genetic distance analyses and the reconstructed consensus tree placed the southern California groups and the Pima in a clade with the Washo as a sister taxon (Fig. 3). The southern California clade includes

Table 9

NEI'S D (1972) RESULTS

Chumash	0.000	0.077	0.020	0.143	0.450	0.869	1.568	1.583	0.671	0.886	1.854	1.693	0.988	0.693
Bella Coola	0.077	0.000	0.063	0.022	0.752	1.283	1.435	1.272	0.601	1.364	1.399	1.288	0.939	0.673
NCNulth	0.020	0.063	0.000	0.140	0.408	0.761	1.094	1.120	0.530	0.737	1.222	1.134	0.737	0.518
Haida	0.143	0.022	0.140	0.000	1.272	2.616	2.541	2.137	0.946	2.252	2.190	1.948	1.211	1.086
Yok-Utian	0.450	0.752	0.408	1.272	0.000	0.037	0.414	0.332	0.165	0.387	0.607	0.601	0.826	0.146
N Paiute	0.869	1.283	0.761	2.616	0.037	0.000	0.299	0.194	0.138	0.433	0.459	0.466	0.893	0.120
Washo	1.568	1.435	1.094	2.541	0.414	0.299	0.000	0.124	0.283	0.230	0.015	0.016	0.186	0.106
Yakama	1.583	1.272	1.120	2.137	0.332	0.194	0.124	0.000	0.076	0.705	0.145	0.153	0.668	0.065
Wishram	0.671	0.601	0.530	0.946	0.165	0.138	0.283	0.076	0.000	0.796	0.340	0.337	0.855	0.045
Takic	0.886	1.364	0.737	2.252	0.387	0.433	0.230	0.705	0.796	0.000	0.321	0.311	0.127	0.387
Yuman	1.854	1.399	1.222	2.190	0.607	0.459	0.015	0.145	0.340	0.321	0.000	0.001	0.172	0.154
Pima	1.693	1.288	1.134	1.948	0.601	0.466	0.016	0.153	0.337	0.311	0.001	0.000	0.157	0.150
Eel PointC	0.988	0.939	0.737	1.211	0.826	0.893	0.186	0.668	0.855	0.127	0.172	0.157	0.000	0.418
Nusery Site	0.693	0.673	0.518	1.086	0.146	0.120	0.106	0.065	0.045	0.387	0.154	0.150	0.418	0.000

Table 10

REYNOLD'S ET AL. (1983) DISTANCE RESULTS

Chumash	0.000	0.056	0.016	0.185	0.177	0.290	0.361	0.389	0.242	0.282	0.408	0.390	0.313	0.246
BellaCoola	0.056	0.000	0.050	0.066	0.265	0.367	0.382	0.395	0.253	0.362	0.412	0.392	0.335	0.291
NCNulth	0.016	0.050	0.000	0.185	0.136	0.234	0.277	0.306	0.179	0.220	0.321	0.302	0.236	0.181
Haida	0.185	0.066	0.185	0.000	0.462	0.561	0.563	0.580	0.447	0.540	0.588	0.568	0.502	0.484
Yok-Utian	0.177	0.265	0.136	0.462	0.000	0.025	0.175	0.169	0.080	0.157	0.248	0.237	0.262	0.041
N Paiute	0.290	0.367	0.234	0.561	0.025	0.000	0.159	0.128	0.080	0.195	0.237	0.231	0.306	0.031
Washo	0.361	0.382	0.277	0.563	0.175	0.159	0.000	0.089	0.144	0.126	0.014	0.014	0.114	0.070
Yakama	0.389	0.395	0.306	0.580	0.169	0.128	0.089	0.000	0.057	0.284	0.114	0.114	0.292	0.060
Wishram	0.242	0.253	0.179	0.447	0.080	0.080	0.144	0.057	0.000	0.260	0.187	0.178	0.285	0.036
Takic	0.282	0.362	0.220	0.540	0.157	0.195	0.126	0.284	0.260	0.000	0.182	0.171	0.078	0.145
Yuman	0.408	0.412	0.321	0.588	0.248	0.237	0.014	0.114	0.187	0.182	0.000	0.001	0.121	0.123
Pima	0.390	0.392	0.302	0.568	0.237	0.231	0.014	0.114	0.178	0.171	0.001	0.000	0.108	0.117
EelPointC	0.313	0.335	0.236	0.502	0.262	0.306	0.114	0.292	0.285	0.078	0.121	0.108	0.000	0.201
NurserySite	0.246	0.291	0.181	0.484	0.041	0.031	0.070	0.060	0.036	0.145	0.123	0.117	0.201	0.000

Table 11

CAVALLI-SFORZA CHORD DISTANCES (1967) RESULTS

Chumash	0.000	0.079	0.073	0.101	0.225	0.483	0.585	0.505	0.365	0.426	0.642	0.605	0.441	0.323
BellaCoola	0.079	0.000	0.057	0.034	0.179	0.429	0.453	0.319	0.195	0.433	0.419	0.382	0.289	0.215
NCNulth	0.073	0.057	0.000	0.120	0.144	0.356	0.406	0.270	0.238	0.332	0.438	0.407	0.308	0.192
Haida	0.101	0.034	0.120	0.000	0.354	0.662	0.653	0.509	0.348	0.619	0.554	0.510	0.366	0.402
Yok-Utian	0.225	0.179	0.144	0.354	0.000	0.064	0.173	0.110	0.094	0.152	0.312	0.302	0.323	0.012
N Paiute	0.483	0.429	0.356	0.662	0.064	0.000	0.111	0.102	0.170	0.124	0.308	0.316	0.419	0.045
Washo	0.585	0.453	0.406	0.653	0.173	0.111	0.000	0.109	0.304	0.067	0.069	0.079	0.158	0.082
Yakama	0.505	0.319	0.270	0.509	0.110	0.102	0.109	0.000	0.100	0.229	0.170	0.170	0.283	0.050
Wishram	0.365	0.195	0.238	0.348	0.094	0.170	0.304	0.100	0.000	0.409	0.369	0.355	0.448	0.092
Takic	0.426	0.433	0.332	0.619	0.152	0.124	0.067	0.229	0.409	0.000	0.206	0.212	0.207	0.117
Yuman	0.642	0.419	0.438	0.554	0.312	0.308	0.069	0.170	0.369	0.206	0.000	0.001	0.059	0.183
Pima	0.605	0.382	0.407	0.510	0.302	0.316	0.079	0.170	0.355	0.212	0.001	0.000	0.047	0.178
EelPointC	0.441	0.289	0.308	0.366	0.323	0.419	0.158	0.283	0.448	0.207	0.059	0.047	0.000	0.231
NurserySite	0.323	0.215	0.192	0.402	0.012	0.045	0.082	0.050	0.092	0.117	0.183	0.178	0.231	0.000

Yuman and Uto-Aztecan speakers. Within the southern California clade, the Takic and Eel Point C populations are sister taxa, and the Pima and Yumans are sister taxa. The Takic and Pima people speak languages within the Uto-Aztecan language stock. However, the Yuman populations speak dialects hypothesized to be within the Hokan language stock. The Takic, Yuman, and Piman people occupy contiguous regions within southern California and southwestern Arizona. The Nursery Site is placed closest to the Northern Paiute and the Penutian speaking groups, including the Yok-Utian, Wishram, and Yakama (Fig. 3).

Results of Fisher's exact test are both confirmatory and conflicting with the dendrogram reconstructed based on measures of genetic distance. The results indicate that Eel Point and the Nursery Site are statistically different (Table 12). Additionally, p-values of all pairwise comparisons are significant, with the exception of Eel Point and Pima, meaning that we can reject the null hypothesis of compared groups being drawn from the same larger population. Contrary to the phylogenetics analysis, the Fisher's exact p-value comparing Eel Point with Takic distribution is significant, indicating these two populations can be differentiated. However, sample sizes are small, and the results may be skewed due to sampling effects. Neither the Eel Point or the Nursery Site population is closely related to the Chumash. Genetic

Table 12

FISHER'S EXACT TEST

	Fisher's Exact P values	
	Nursery Site	Eel Point
Chumash	0.00004	0.00035
Bella Coola	0.00005	0.00019
NCN	0.00001	0.00027
Takic	0.00707	0.02902
Northern Paiute	0.00603	0.00004
Haida	0.00000	0.00005
Yok-Utian	0.03437	0.00273
Washo	0.00711	0.02024
Wishram	0.00567	0.00007
Yuman	0.00001	0.03142
Piman	0.00017	*0.06271*
Nursery Site		0.01084
Eel Point	0.01084	

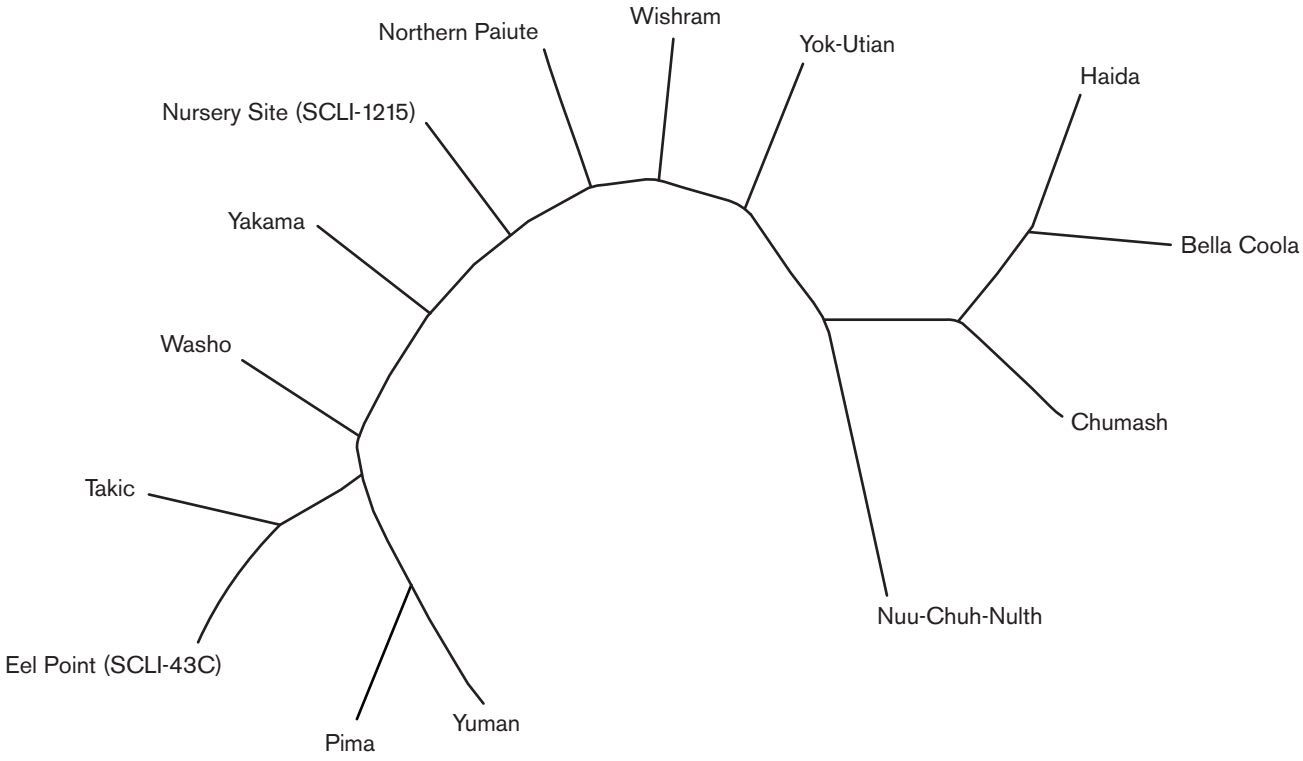

Figure 3. Consensus tree of southern California, Great Basin, and Pacific Northwest Native American populations based on genetic distances.

distances between Eel Point and the Chumash, and the Nursery Site and the Chumash, are large. Confirming Eshleman et al.'s (2004) results, phylogenetic analysis places the Chumash in a clade with the Bella Coola and the Haida, with the Nuu-chuh-nulth as a sister taxon. Fisher's exact p-values are significant for pairwise comparison of the SCLI sites with the Chumash, Bella Coola, Haida, and Nuu-chuh-nulth, further supporting the conclusion that neither the Eel Point nor the Nursery Site population was similar to the Chumash or these Pacific Coast populations.

DISCUSSION

The purpose of this study was to address the genetic affinities of the prehistoric people of San Clemente Island. Therefore, results will be discussed in the context of the Eel Point and Nursery Site populations' relationships to the comparative groups; for a complete discussion of comparative population affinities see Eshleman et al. (2004). The SCLI data must be interpreted cautiously. Haplogroup frequency distributions within skeletal populations are not the same as those among living populations of known genealogy. The observed frequency distributions within the SCLI cemetery samples, and the seemingly limited sequence diversity within the D-loop between coordinates 16,189 and 16,340, may in fact be reflective of close maternal familial relationships between individuals. The remains may well be those of family members interred in close proximity to one another. Additionally, the sample sizes for both Eel Point and the Nursery Site are small and subject to stochastic or sampling effects. Such small sample sizes can not capture the full range of genetic diversity or cover subtle temporal shifts. Finally, the HVSI sequence data are incomplete, as only key haplogroup-defining sites within the HVSI region were examined and the poor quality of the DNA limited success. Despite these limitations, the data may contribute to discussions of population contact and migration in prehistoric southern California, and thereby increase our understanding of population dynamics within the region.

Although Hill (2001) has argued that the ancestral homeland of the northern branch of Uto-Aztecan was central Mexico, followed by a northward expansion in conjunction with the spread of maize agriculture, Nichols (1981) has used linguistic data to argue for an early presence of Uto-Aztecan speakers in California before a southward expansion of Uto-Aztecans. Therefore, as Eshleman et al. (2004) discussed, the proto-Takic, proto-Yuman, and proto-Piman peoples may have been neighbors for several thousand years and experienced significant mtDNA gene flow. The mtDNA data suggest gene flow occurred across linguistic boundaries, at least on the maternal side. The phylogenetic tree reconstructed here—reconstructed using genetic distances (Tables 9, 10, 11)—suggests that the prehistoric Eel Point C population may have had the closest maternal genetic affinities with modern Takic speakers living in the Los Angeles basin. However, results from Fisher's exact test indicate that the Eel Point C and Takic haplogroup frequencies are statistically different, while Eel Point and Pima distributions can not be differentiated. These data suggest a situation involving complex and fluid prehistoric population contacts, genetic exchanges, and migration or expansion within the Los Angeles basin for at least the last 3,000 years. The genetic distance estimates and phylogenetic analysis seem to be consistent with Uto-Aztecan people being present within the southern California bight by at least 3,000 years ago. However, Sutton's (2009) hypothesis that the Takic language was adopted by neighboring Yuman people complicates the picture of ancient San Clemente Island population genetic affinities. Sutton suggests that a significant portion of the Takic individuals included in recent mtDNA analyses of living California ethnolinguistic groups are biologically Yuman (Sutton 2009). This may explain the small genetic distances observed between the earlier Eel Point people and extant Takic speakers. Sutton (2009) proposes that by 3,500 B.P., Penutian expansion into the San Joaquin Valley pressed Takic people (proto-Gabrielino/proto-Cupan) to move south into coastal southern California, displacing Hokan and Yuman people within the region. Between 1,500 and 1,000 B.P., the neighboring Yuman people adopted the Gabrielino language, which then began differentiating to eventually become the Cupan languages (Sutton 2009). Therefore, extant Cupan speakers are actually biologically Yuman. The Eel Point data were compared with haplogroup frequencies of extant Takic populations, which thus may include a significant number of individuals who are biologically Yuman. Therefore, the Eel Point people were Yuman. This would also explain the apparent differences between the Eel Point and Nursery Site haplogroup distributions.

The Nursery Site shares a high frequency of Haplogroup B and D with Great Basin Numic speakers, as well as with several Penutian groups. Eshleman et al. (2004) found that the mtDNA of the Numic-speaking Northern Paiute more closely resembled that of non-Uto-Aztecan-speaking Penutian groups such as the Yakama, Wishram, and Yok-Utian. The consensus tree generated from pairwise genetic distances confirms their results, and places the prehistoric San Clemente Island Nursery Site population as having the closest mtDNA affinities with the Northern Paiute and Penutian-speaking groups. The Nursery Site population mtDNA haplogroup distribution does not resemble that of the extant Takic or the prehistoric Eel Point populations, although Takic and Numic are within the northern Uto-Aztecan language stock. Genetic distances between Eel Point and the Nursery site are moderate, and Fisher's exact P-values are statistically significant at the 0.05 level. Therefore, the mtDNA data do not indicate that the Eel Point and Nursery Site populations are very closely related. Genetic distances and phylogenetic analysis suggest that the populations with which the Nursery Site people had the closest mtDNA affinities inhabited northern and central California, the western edges of the Great Basin (Yakama, Yok-Utian, Wishram) and the internal Great Basin (N. Paiute).

The expansion of the Numic branch of northern Uto-Aztecan into the Great Basin is hypothesized to have occurred between 1,000 and 500 years ago (Bettinger and Baumhoff 1982; Kaestle and Smith 2001; Lamb 1958; Sutton 1994; True 1966; Wallace 1962; Young and Bettinger 1992). Lamb (1958) proposed a proto-Numic homeland in the southwestern Great Basin, i.e., Death Valley. However, others have found evidence for a proto-Numic homeland to the southwest of the Great Basin in the Owens Valley (Fowler 1982; Kaestle and Smith 2001; Miller et al 1971; Nichols 1981). Some archaeologists and linguists have found evidence for great time depth to the Numic presence in the Great Basin and have suggested

an *in situ* development and adaptation of Numic peoples. Nonetheless, there is mtDNA genetic evidence supporting gene flow between Numic Great Basin populations and the Penutian and Hokan people inhabiting the western edges of the Great Basin and southern California (Eshleman et al. 2004, Eshleman and Smith 2007; Kaestle and Smith 2001). It is possible, therefore, that the prehistoric Nursery Site people represent an early wave of Numic coastal expansion.

The presence of Haplogroup A in individuals from both Eel Point and the Nursery site is supportive of recent suggestions that Haplogroup A is an ancient remnant from initial coastal colonizing people that has survived at a low level in Uto-Aztecan and Hokan populations, and that it may indicate admixture between the Chumash and the San Clemente Island inhabitants (Eshleman et al. 2004). With a coastal location and geographic proximity to their northern Chumash neighbors, it is not surprising that haplogroup A occurs at a low frequency in both the Eel Point and Nursery Site populations.

Archaeological data suggest the existence of a "sphere of cultural interaction" with roots extending into the Middle Holocene. Bead distribution data and language distributions (Hokan, Penutian, Uto-Aztecan, Chumash) demarcate a zone of Uto-Aztecan interaction in the Los Angeles Basin, San Diego/Baja Alto, and Great Basin regions (Byrd and Raab 2007; Howard and Raab 1993; Raab 1997).

Possibly the most prominent archaeological evidence comes from *Olivella* Grooved Rectangle (OGR) beads. OGR beads are a distinctive bead type made from the *Olivella biplicata* shell. These beads were manufactured on the southern Channel Islands and the adjacent coast of Los Angeles and Orange counties, and then traded throughout southern California and the Great Basin. Except for a single site bordering Santa Barbara and Ventura counties (CA-SBA-119), these beads have only been recovered from areas historically inhabited by Uto-Aztecan people (Vellanoweth 2001). OGR beads have not been recovered from Chumash or Hokan sites—sites occupied by Chumash or Yuman-speaking people. The beads have been found in sites ranging in age from approximately 4,300 to 5,200 B.P. (Jenkins and Erlandson 1996; King 1990; Raab 1992; Raab et al. 1994; Vellanoweth 2001, 1995). The bead distribution data are consistent with a model in which a separate Uto-Aztecan cultural interaction sphere was well established in the Middle Holocene that encompassed populations on the southern Channel Islands, in the adjacent Los Angeles Basin, coastal Orange County, the Mojave Desert, and in the Great Basin as far north as DJ Ranch, Fort Rock, Oregon (Byrd and Raab 2007; Howard and Raab 1993; Jenkins and Erlandson 1996; Raab 1997; Vellanoweth 1995, 2001).

Other types of commodities appear to have been traded between Los Angeles Basin and Great Basin populations as well. Sutton (1988, 2009) has noted that trade between southern California and the Great Basin appears to have been important during the Late Holocene/Late Prehistoric within the western Mojave region. A heavy trade in obsidian and shell is indicated, while trade in ceramics and fish occurred to a lesser degree. The location of the western Mojave—along a natural corridor between the Owens Valley/Coso area and much of southern California—led Robinson to suggest that prehistoric residents of the western Mojave may have acted as middlemen in the exchange of Coso obsidian and southern California coastal shell (Sutton 1988, 2009). In addition to the numerous types of shell beads present at western Mojave sites, inlaid steatite ornaments, similar to those recovered from coastal southern California (Kelly 1997; Koerper 1979; Sutton 1988, 2009), are also present. Data from other sites throughout the Great Basin have suggested trade with southern California coastal populations as well; Kramer Cave and Hidden Cave, Nevada, have both yielded coastal California shell beads, as have Muddy River sites (Kelly 1997).

The existence of a culturally and linguistically defined network of interaction only in lands historically documented as having been inhabited by Uto-Aztecan peoples suggests that as early as 4,800 years ago, Uto-Aztecan people were on San Clemente Island. However, it remains unclear—in light of Sutton's (2009) recent hypothesis—whether the mtDNA data for Eel Point and the Nursery Site support a model of late Middle Holocene occupation of the island by Uto-Aztecan people. Although the haplogroup frequency data presented here are not sufficient to determine ancestry, there is some support for a presence of Uto-Aztecan peoples on San Clemente Island by 1,400 B.P., as represented by the Nursery Site sample. What remains

in question is the conclusion that Eel Point individuals appear to more closely match the mDNA distributions of California Uto-Aztecans (Takic speakers), while the Nursery Site burials more closely match extant Great Basin Uto-Aztecans (Numic speakers) in their mtDNA frequencies. However, a past migration in small waves is possible, and the effects of well-established trade patterns and contact with Great Basin Uto-Aztecan populations not necessarily belonging to the Takic language family may have had an impact on mtDNA haplogroup distributions through intermarriage, particularly when one considers that mtDNA reflects maternal migrations and lineages. Populations within the boundaries of the interaction sphere included Yuman, Piman, Takic, Eel Point C, Nursery Site, Washo, Yakama, Wishram, N. Paiute, and Yok-Utian. Not unexpectedly, the consensus tree parallels the cultural interaction sphere. Although shared culture does not necessarily imply common ancestry, prolonged contact and established trade networks may have facilitated genetic exchanges through marriage that strengthened social alliances.

Tribal-specific private polymorphisms are most robust for elucidating ancestor/descendant relationships. Although the HVSI sequence data included in this study are incomplete, several individual sequences were interesting and should be mentioned. Recent work by Johnson and Lorenz (2006) has resulted in the availability of a comparative data set of extant southern California mtDNA variations within the HVSI. Sequence data were analyzed and described for 126 contemporary California Indian descendants with maternal lineages of known and verified ethnolinguistic affiliation at the time of historic contact (Johnson and Lorenz 2006). The results of a comparison of three individual SCLI mtDNA HVSI sequences with Johnson and Lorenz's (2006) data set were unexpected. Nonetheless, because the SCLI HVSI sequence data are incomplete and only cover a portion of HVSI (16,151 to 16, 341, potentially), it is impossible to confirm shared haplotypes between extant and ancient individuals. However, the sequences are provocative. Burial SCLI-1215-2 has HVSI base pair substitutions (16,223 C:T, 16,319 G:A, 16,325 T:C) between the nucleotide positions examined in this study that are similar to those within the same segment of a contemporary individual belonging to the Cahuilla (Takic Branch) ethnolinguistic group with a documented origin in the *Wavaaikitum* Desert Cahuilla (Johnson and Lorenz 2006). Burial SCLI-43C-10 has an HVSI sequence (16,223 C:T, 16,290 C:T, 16,311 T:C, 16,319 G:A) between np 16,174 and 16,341 that is similar to that (haplotype A02) observed in two contemporary individuals belonging to the Chumash ethnolinguistic group with documented origins at *Snajalayegua* and *Nomgio* (Johnson and Lorenz 2006). Interestingly, burial SCLI-43C-2 shares a HVSI sequence (16,223 C:T, 16,298 T:C, 16,319 G:A, 16,325 T:C, 16,327 C:T) within the coordinates examined in this study with two contemporary individuals belonging to the Luiseño ethnolinguistic group with documented origins at *Cuqui* and the Pechanga Reservation, an Ipai individual (Batiquitos origin), and a contemporary Cahuilla (Soboba Reservation). Although this motif is observed only in members of Haplogroup C in the Johnson and Lorenz (2006) study, SCLI-43C-2 was not included in haplogroup frequency-based distance analysis because initial sequencing failed to reveal any of the coding region haplogroup markers and we are unable to confirm Haplogroup A or Haplogroup C.

CONCLUSIONS

The mtDNA raw haplogroup frequency distributions of the Eel Point people resemble those of the extant Yuman and Piman peoples. However, phylogenetic analysis reconstructed the Eel Point people as being most closely related to extant Takic people of the Los Angeles Basin and coastal bight. The presence of Haplogroup A in both the Eel Point and Nursery Site samples supports recent suggestions that Haplogroup A is an ancient remnant haplogroup in California coastal populations (Eshleman et al. 2004). The similarity between the HSVI Haplogroup A sequence of SCLI-43C-10 and two contemporary Chumash individuals may support a model of limited admixture between the Eel Point people and their proto-Chumash neighbors to the north. The mtDNA genetic affinities support a model of a Uto-Aztecan presence within the region for at least 1,400 years. However, haplogroup frequency analysis indicates that the Nursery Site people did not have the closest mtDNA genetic affinities with the Eel Point people or with living Takic peoples. Instead, phylogenetic analysis indicates that the Nursery Site population may have had the closest maternal affinities with living Numic (N. Paiute) peoples

occupying the Great Basin. The mtDNA data suggest a complex picture of movement and contacts which may have included genetic exchanges through marriage. The Nursery Site population may represent an early, small wave of expansion of proto-Numic people onto the Island. Interestingly, there appears to have been gene flow between the unrelated language groups occupying northern California, the rim of the Great Basin, and the Great Basin for at least 1,400 years. Archaeological data, such as bead distributions, support a model of extensive trade throughout the Great Basin, Death Valley, the Owens Valley, and the Los Angeles Basin region.

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NOTES

[1]Kemp and Smith (2005) recently demonstrated that exogenous contaminating DNA is successfully removed without damaging endogenous DNA by an immersion of the bone or tooth sample in sodium hypochlorite solution ranging in concentration from 3.0% to 6.0% for 15 minutes.

REFERENCES

Andrews, R. M., A. T. Bankier, B. G. Barrell, M. H. de Bruijn, A. R. Coulson, J. Drouin, I. C. Eperon, D. P. Nierlich, B. A. Roe, F. Sanger, P. H. Schreier, A. J. Smith, R. Staden, and I. G. Young
1999 Reanalysis and revision of the Cambridge reference sequence for human mitochondrial DNA. *Nature Genetics* 23(2):147.

Arnold, J. E.
1992 Complex Hunter-Gatherer-Fishers of Prehistoric California: Chiefs, Specialists, and Maritime Adaptations of the Channel Islands. *American Antiquity* 57:60–84.

Bailliet, G., F. Rothhammer, F. R. Carnese, C. M. Bravi, and N. O. Bianchi
1994 Founder Mitochondrial Heliotypes in Amerindian Populations. *American Journal of Human Genetics* 55:27–33.

Bettinger, R. L., and M. A. Baumhoff
1982 The Numic Spread: Great Basin Cultures in Competition. *American Antiquity* 47:485–503.

Bonatto, S. L., and F. M. Salzano
1997 A Single and Early Migration for the Peopling of the Americas Supported by Mitochondrial DNA Sequence Data. *Proceedings National Academy of Science, USA* 94:1866–1871.

Byrd, B. F., and L. M. Raab
2007 Prehistory of the Southern Bight: Models for a New Millennium. *California Prehistory*, T. L. Jones and K. A. Klar, eds., pp. 215–227. Lanham, Md.: Altimira Press.

Carlyle, S. W., R. L. Parr, G. M. Hayes, and D. H. O'Rourke
2000 Context of Maternal Lineages in the Greater Southwest. *American Journal of Physical Anthropology* 113:85–101.

Cavalli-Sforza, L. L., and A. W. F. Edwards
1967 Phylogenetic analysis models and estimation procedures. *American Journal of Human Genetics* 19:223–257.

Drover, C. E., and J. N. Spain
1972 An Early Articulated Inhumation From 4-ORA-64: A Discussion. *Pacific Coast Archaeological Society Quarterly* 8(4):35–44.

Erlandson, J. M.
1994 *Early Hunter-gatherers of the California Coast*. New York: Plenum Press.
1997 The Middle Holocene Along the California Coast. In *Archaeology of the California Coast During the Middle Holocene*, J. M. Erlandson and M. A. Glassow, eds., pp. 1–10. Los Angeles, CA: University of California.

Eshleman, J.
2003 Molecular Analysis for the Burial Population at CA-LAN-2233. In *Prehistory in the Transverse Ranges of California: An Archaeological Investigation in the Santa Clara River Valley*, G. Waugh, ed., pp. 77–80. Sacramento, Ca.: California State University Press.

Eshleman, J .A., R. S. Malhi, J. R. Johnson, F. A. Kaestle, J. Lorenz, and D. G. Smith
2004 Mitochondrial DNA and Prehistoric Settlements: Native Migrations on the Western Edge of North America. *Human Biology* 76:55–75.

Esh leman, J. A., and D. G. Smith
2007 Prehistoric Mitochondrial DNA and Population Movement. *California Prehistory*, T. L. Jones and K. A. Klar, eds., pp. 215–227. Lanham, Md.: Altimira Press.

Felsenstein, J.
1998 PHYLIP (phylogeny inference package) version 3.572. Seattle: Department of Genetics, University of Washington.

Forster, P., R. Harding, A. Torroni, and H. J. Bandelt
1996 Origin and Evolution of Native American mtDNA Variation: A Reappraisal. *American Journal of Human Genetics* 59:935–945.

Fowler, C.
1982 Settlement Patterns and Subsistence Systems in the Great Basin: The Ethnographic Record. In *Man and Environment in the Great Basin*. D. B. Madsen and J. F. O'Connell, eds., pp. 121–138. Washington D.C.: Society of American Archaeology.

Hill, J. H.
2001 Proto-Uto-Aztecan: A Community of Cultivators in Central Mexico? *American Anthropologist* 103(4): 913–934.

Howard, W. J., L. M. Raab
1993 *Olivella* Grooved Rectangle Beads as Evidence of an Early Period Southern Channel Islands Interaction Sphere. *Pacific Coast Archaeological Society Quarterly* 29(3): 1–11.

Jenkins, D. L, and J. M. Erlandson
1996 *Olivella* Grooved Rectangle Beads from a Middle Holocene Site in the Fort Rock Valley, Northern Great Basin.*Journal of California and Great Basin Anthropology* 18(2):296–302.

Johnson, J. R., and J. G. Lorenz
2006 Genetics, Linguistics, and Prehistoric Migrations: An Analysis of California Indian Mitochondrial DNA Lineages. *Journal of California and Great Basin Anthropology* 26(1):33–64.

Kaestle, F. A.
1998 *Molecular Evidence for Prehistoric Native American Population Movement: The Numic Expansion*. Ph.D. dissertation, University of California at Davis.

Kaestle, F. A., and D .G. Smith
2001 Ancient Mitochondrial DNA Evidence for Prehistoric Population Movement: The Numic Expansion. *American Journal of Physical Anthropology* 115:1–12.

Kelly, R. L.
1997 Late Holocene Great Basin Prehistory. *Journal of World Prehistory* 11(1):1–49.

Kemp, B. M., and D. G. Smith
2005 Use of Bleach to Eliminate Contaminating DNA from the Surface of Bones and Teeth. *Forensic Science International* 154:53–61.

Kerr, S.
2005 *The People of the Southern Channel Islands: A Bioarchaeological Study of Adaptation and Population Change in Southern Calofornia*. Ph.D. dissertation, University of California, Santa Barbara.

King, C. D.
1990 *Evolution of Chumash Society*. New York: Garland Publishing.

Koerper, H. C.
1979 On the Question of the Chronological Placement of Shoshonean Presence in Orange County, California. *Pacific Coast Archaeological Society Quarterly* 15(3): 69–83.

Kroeber, A. L.
1925 *Handbook of the Indians of California*. Bureau of American Ethnology Bulletin 78. Washington, DC: Smithsonian Institution.

Lamb, S. M.
1958 Linguistic Prehistory in the Great Basin. *International Journal of American Linguistics* 24(2):95–100.

Lorenz J. G., and D. G. Smith
1994 Distribution of the 9-bp Mitochondrial DNA Region V Deletion Among North American Indians. *Human Biology* 66(5):777–788.
1996 Distribution of Four Founding mtDNA Haplogroups Among Native North Americans. American Journal of Physical Anthropology 101:307–323.
1997 Distribution of Sequence Variation in the mtDNA Control Region of Native North Americans. *Human Biology* 69:749–776.

Malhi R. S., and D. G. Smith
2002 Brief Communication: Haplogroup X Confirmed in Prehistoric North America. *American Journal of Physical Anthropology* 119:84–86.

Malhi, R. S., H. M. Mortensen, J. A. Eshleman, B. M. Kemp, J. G. Lorenz, F. A. Kaestle, J. R. Johnson, C. Gorodezky, and D. G. Smith
2003 Native American mtDNA Prehistory in the American Southwest. *American Journal of Physical Anthropology* 120:108–124.

Masters, P. M., and D. R. Gallegos
1997 Environmental Change and Adaptations in San Diego County During the Middle Holocene. In *Archaeology of the California Coast During the Middle Holocene*, J. M. Erlandson and M. A. Glassow, eds., pp. 11–22. Los Angeles: University of California.

Miller, B. W.
1991 *The Gabrielino*. Los Osos, Calif.: Sand River Press.

Miller, W. R., J. Tanner, and L. Foley
1971 A Lexicostatistical Study of Shoshoni Dialects. *Anthropological Linguistics* 13:142–164.

Mithun, M.
1999 *The Languages of Native North America*. New York: Cambridge University Press.

Moratto, M. J.
1984 *California Archaeology*. Orlando: Academic Press.

Nei, M.
1972 Genetic Distance Between Populations. *American Naturalist* 106:283–292.

Nichols, M. J. P.
1981 Old California Uto-Aztecan. In *Reports from the Survey of California and Other Indian Languages*, Report I, A. Schlichter, W. L. Chafe, and L. Hinton, eds., pp. 5–41. Berkeley.

Parr, R. L., S. W. Carlyle, and D. H. O'Rourke
1996 Ancient DNA Analysis of Fremont Amerindians of the Great Salt Lake Wetlands. *American Journal of Physical Anthropology* 99:507–518.

Porcasi, J.
1995 *Identification and Analysis of Mammalian and Avian Remains Recovered from 1994 Excavation at Eel Point, San Clemente Island, California*. Master's thesis, California State University, Northridge.

Potter, A. B.
1998 *Paleopathology: Incidence and Trends Among Skeletal Remains from San Clemente Island, California*. Master's thesis, California State University Northridge.
2004 *The Genetic Affinities of the Prehistoric People of San Clemente Island, California: An analysis of Ancient DNA*. Ph.D. dissertation, University of Oregon.

Raab, L. M.
1992 An Optimal Foraging Analysis of Prehistoric Shellfish Collecting on San Clemente Island, California. *Journal of Ethnobiology* 12:63–80.
1997 The Southern Channel Islands During the Middle Holocene. In *Archaeology of the California Coast during the Middle Holocene*, J. M. Erlandson and M. A. Glassow, eds., pp. 23–34. Los Angeles: Institute of Archaeology, University of California, Los Angeles.

Raab, L. M., K. Bradford, and A. Yatsko
1994 Advances in Southern Channel Islands Archaeology: 1938 to 1993. *Journal of California and Great Basin Anthropology* 16(2):243–270.

Raab, L. M., and D. O. Larson
1997 Medieval Climatic Anomaly and Punctuated Cultural Evolution in Coastal Southern California. *American Antiquity* 62(2):319–336.

Raab, L. M., and A. Yatsko
1992 Ancient Maritime Adaptations of the California Bight: A Perspective from San Clemente Island. In *Essays on Prehistory of Maritime California*, T. L. Jones, ed., pp. 173–194. Davis: Center for Archaeological Research at Davis.

Reynolds, J. B., B. S. Weir, and C. C. Cockerham
1983 Estimation of the Coancestry Coefficient: Basis for a Short-Term Genetic Distance. *Genetics* 105:767–779.

Rigby, J.
1985 *A Preliminary Report on the Excavations at the Nursery Site* (SCLI-1215). MS on file at Natural Resources Office, Naval Air Station North Island, San Diego.

Salls, R. A.
1988 *Prehistoric Fisheries of the California Bight*. Ph.D. dissertation, University of California, Los Angeles.
1992 Ten-Thousand Years of Fishing; The Evidence for Alternate Stable States in Nearshore Ecosystems as the Results of Overexploitation of the California Sheephead by Prehistoric Fishermen on San Clemente Island, California. Paper presented at the IX International Symposium on Marine Biology, Universidad Autonoma de Baja California Sur, La Pas, Mexico.

Schurr, T. G., S. W. Ballinger, Y. Y. Gan, J. A. Hodge, D. A. Merriweather, D. N. Lawrence, W. C. Knowler, K. M. Weiss, and D. C. Wallace
1990 Amerindian Mitochondrial DNAs have Rare Asian Mutations at High Frequencies, Suggesting they Derived from Four Primary Maternal Lineages. *American Journal of Human Genetics* 46:613–623.

Smith, D. G., R. S. Malhi, J. Eshleman, J. G. Lorenz, and F. A Kaestle
1999 Distribution of mtDNA Haplogroup X Among Native North Americans. *American Journal of Physical Anthropology* 110:271–284.

Stone, A. C., and M. Stoneking
1993 Ancient DNA from a Pre-Columbian Amerindian population. *American Journal of Physical Anthropology* 92:436–471.
1998 MtDNA Analysis of a Prehistoric Oneota Population: Implications for the Peopling of the New World. *American Journal of Human Genetics* 62:1153–1170.

Sutton, M. Q.
1988 On the Late Prehistory of the Western Mojave Desert. *Pacific Coast Archaeological Society Quarterly* 24(1):22–29.
1994 The Numic Expansion as Seen from the Mojave Desert. In *Across the West: Human Population Movement and the Expansion of the Numa*, David B. Madsen and David Rhode, eds., pp. 133–140. Salt Lake City: University of Utah Press.
2009 People and Language: Defining the Takic Expansion into Southern California. *Pacific Coast Archaeological Society Quarterly* 41(2–3):31–93.

Swadesh, M.
1964 Linguistic Overview. In *Prehistoric Man in the New World*, J. D. Jennings and E. Norbeck, eds., pp. 527–556. Chicago: University of Chicago Press.

Titus, M. D.
1987 *Evidence for Prehistoric Occupation of Sites on San Clemente Island by Hokan and Uto-Aztecan Indians*. Master's thesis, University of California, Los Angeles.

Titus, M. D, and P. L. Walker
2000 Skeletal Remains from San Clemente Island. *Pacific Coast Archaeological Society Quarterly* 36(2): 79–93.

Torroni, A., T. G. Schurr, C. Yang, E. J. E. Szathmary, R. C. Williams, M. S. Schanfield, G. A. Troup, W. C. Knowler, and D. N. Lawrence
1992 Native American Mitochondrial DNA Analysis Indicates that the Amerind and Na-Dene Populations were Founded by Two Independent Migrations. *Genetics* 130:153–162.

Torroni, A., T. G. Schurr, M. F. Campbell, M. D. Brown, J. V. Neel, M. Larsen, D. G. Smith, C. M. Vullo, and D. C. Wallace
1993 Asian Affinities and Continental Radiation of the Four Founding Native American DNAs. *American Journal of Human Genetics* 53:563–590.

True, D. L.
1966 *Archaeological Differentiation of Shoshonean and Yuman Speaking Groups in Southern California*. Ph.D. dissertation, University of California, Los Angeles.

Uitenbroek, D. G.
1997 SISA-Binomial. Electonic document, http://www.quantitativeskills.com/sisa/distributions/binomial.htm, accessed November 2009.

Vellanoweth, R. L.
1995 New Evidence from San Nicolas Island Concerning the Distribution and Manufacture of *Olivella* Grooved Rectangle Beads. *Pacific Coast Archaeological Society Quarterly* 31(4):13–22.
2001 AMS Radiocarbon Dating and Shell Bead Chronologies: Middle Holocene Trade and Interaction in Western North America. *Journal of Archaeological Science* 28 (9):941–950.

Walker, P. L.
1986 Porotic Hyperostosis in a Marine-Dependent California Indian Population. *American Journal of Physical Anthropology* 69:345–354.

Wallace, D. C., K. Garrison, and W. C. Knowler
1985 Dramatic Founder Effects in Amerindian Mitochondrial DNAs. *American Journal of Physical Anthropology* 68:149–155.

Wallace, W. J.
1962 Prehistoric Cultural Development in the Southern California Deserts. *American Antiquity* 28(2):172–180.

Ward, R. H., B. L. Frazier, K. Dew-Jager, and S. Paabo
1991 Extensive Mitochondrial Diversity Within a Single Amerindian Tribe. *Proceedings of the National Academy of Science USA* 88:8720–8724.

Warren, C. N.
1968 Cultural Tradition and Ecological Adaptation on the Southern California Coast. *Eastern New Mexico University Contributions in Anthropology* 1(3):1–15.

Young, D. A., and R. L. Bettinger
1992 The Numic Spread: A Computer Simulation. *American Antiquity* 57:85–99.