

Genetic and Linguistic Prehistory of California Indian Populations

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Anthropology 131CA

THE STRUCTURE OF DNA

Basic Genetics

Strands of DNA are composed of four nucleotides called "bases":

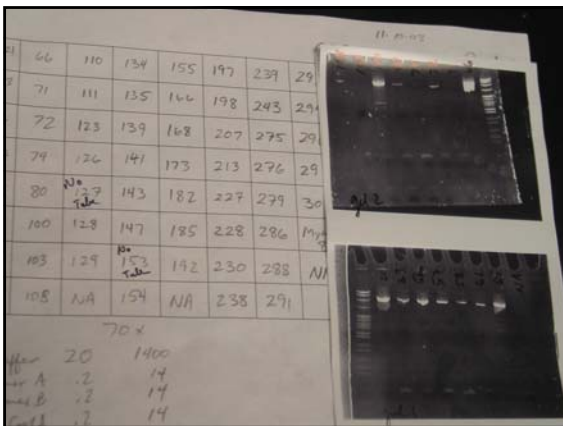
- Adenine
- Guanine
- Cytosine
- Thymine

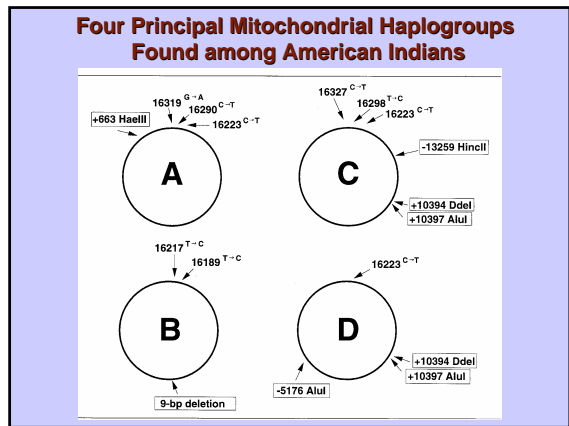
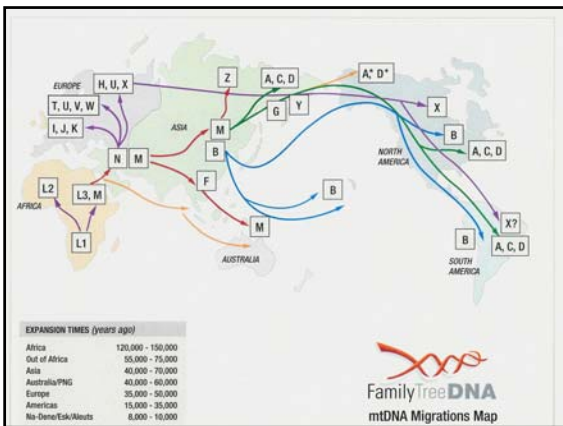
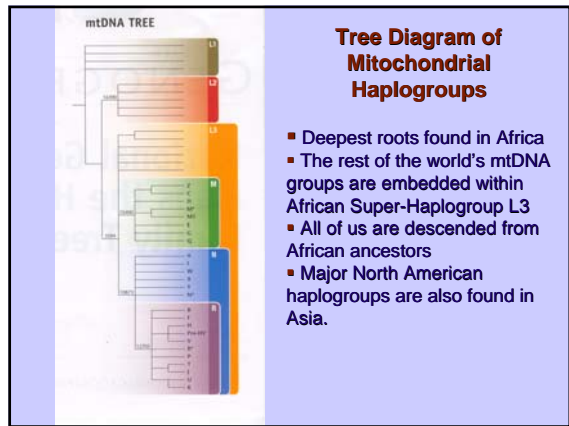
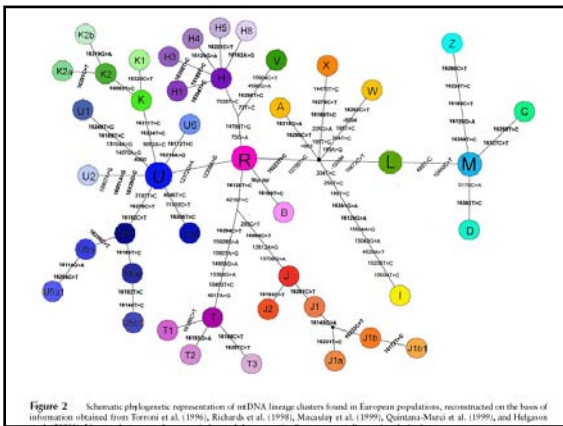
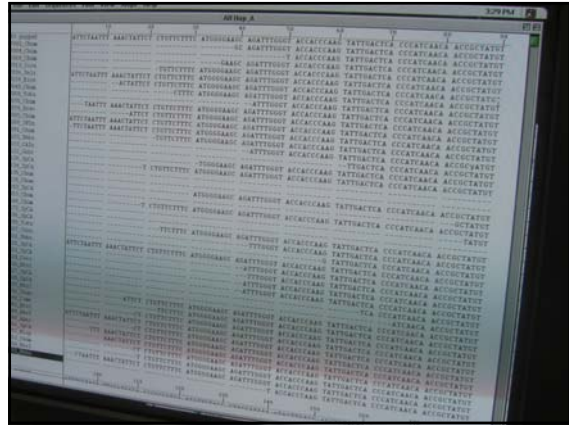
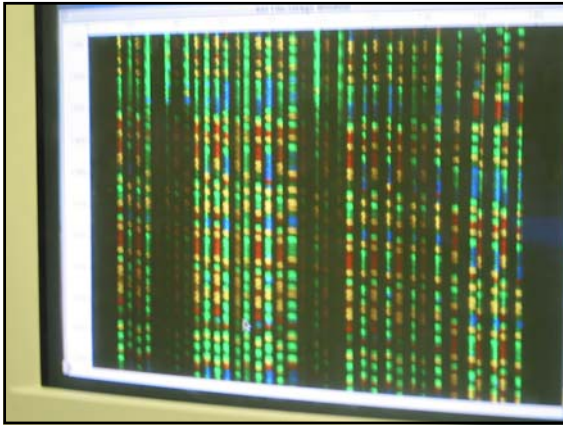
The sequences of these bases provide a genetic bar code that distinguishes us one from another.

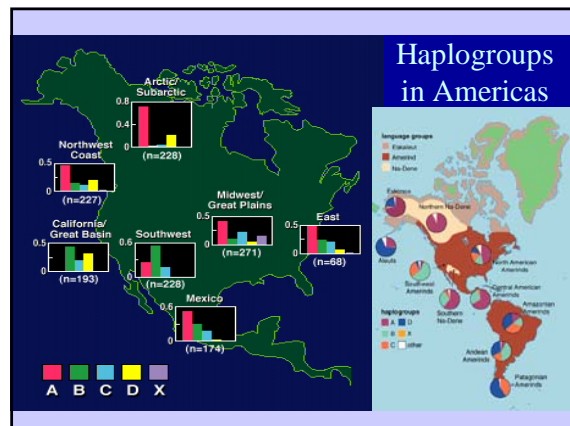
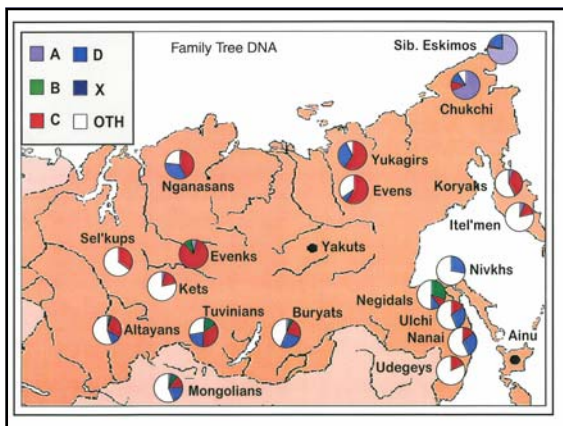
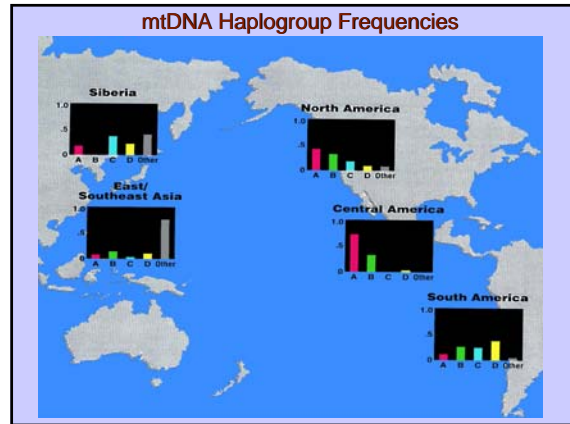
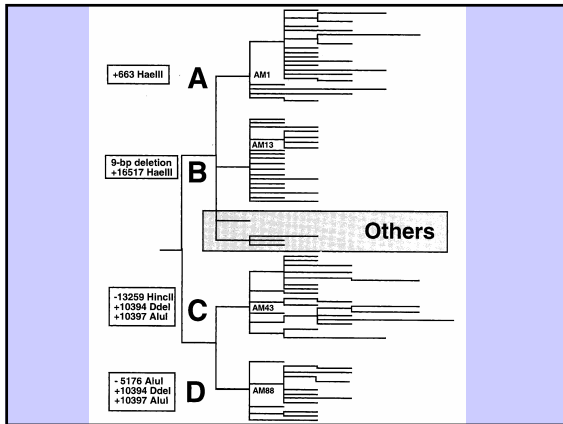
Mitochondrial DNA

Nucleus

- 100s of mitochondria exist in each cell outside the nucleus.
- Each human mitochondrion contains 5 to 10 identical circular molecules of DNA.
- Each mtDNA molecule contains 16,569 base pairs carrying information for 37 genes.

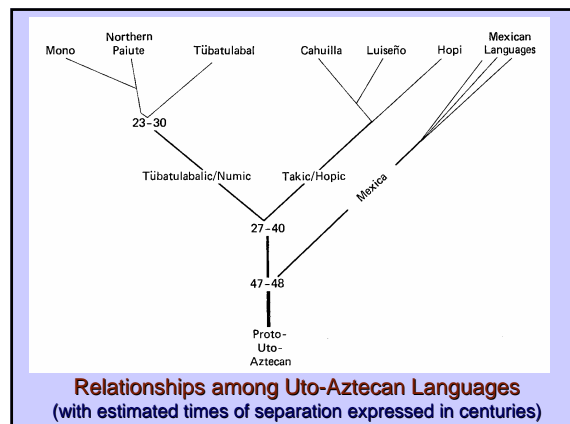


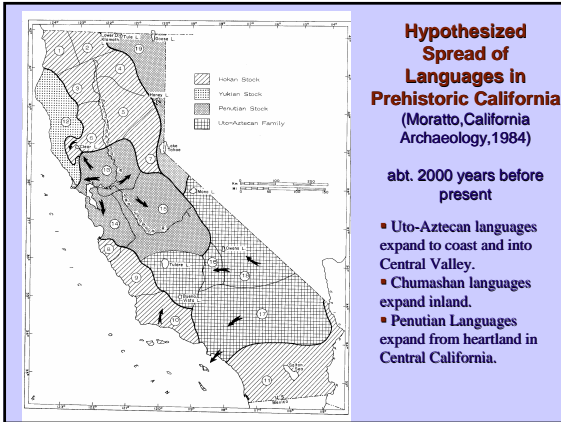




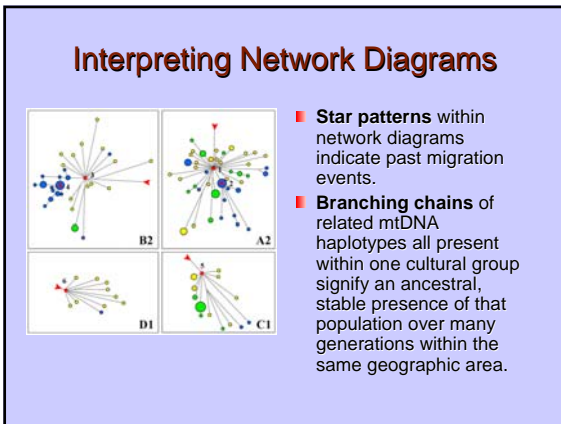
Why is the California Culture Area Interesting?

- High degree of linguistic diversity
- Residual zone because of high ecological diversity
- Evidence of past migrations resulting in spread language families
- Major North American language families present in the region as well as linguistic isolates, like Chumashan





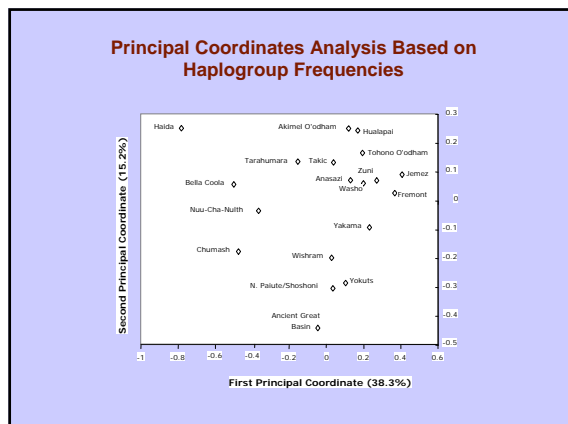
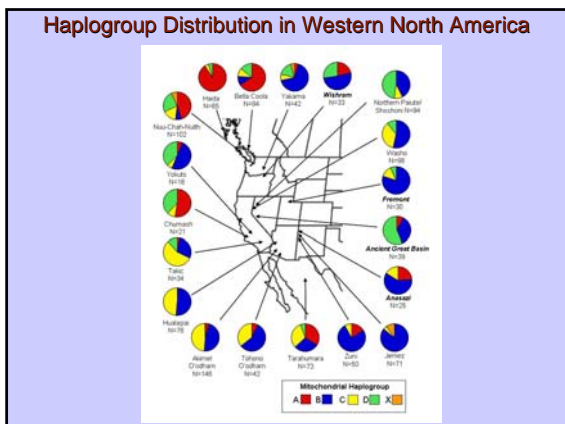
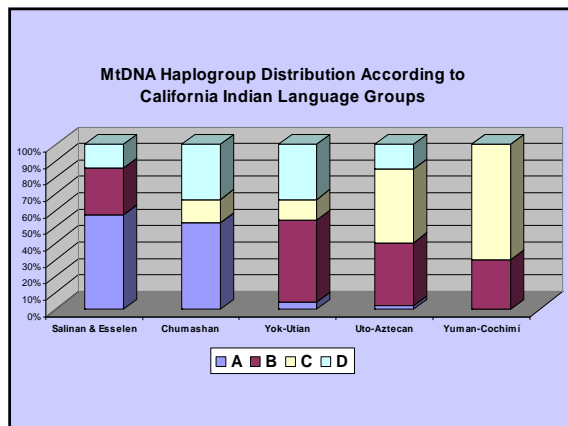
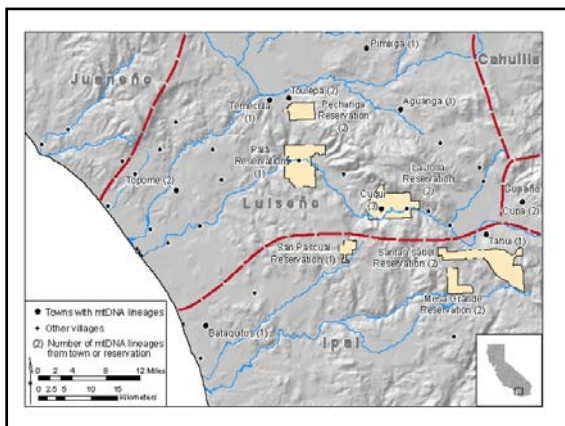
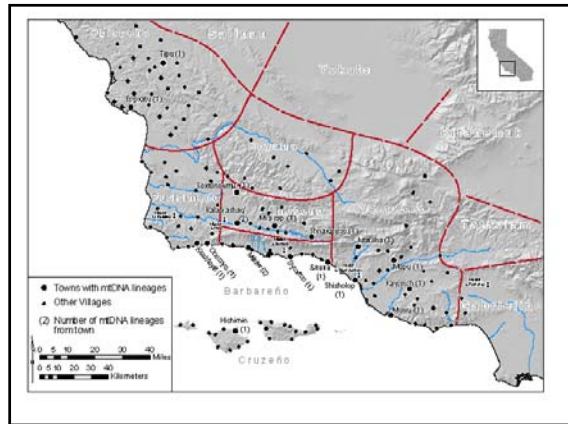
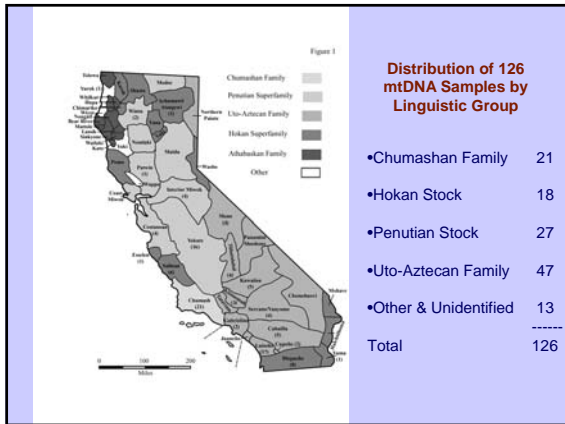
- ### Some Scenarios for Language Change in Prehistoric California
- Initial colonization by Paleoindians followed by gradual changes through time through isolation and differentiation
 - Population replacement
 - Elite dominance
 - Intermarriage of adjacent peoples leading to mixed linguistic communities and eventual change to a different language

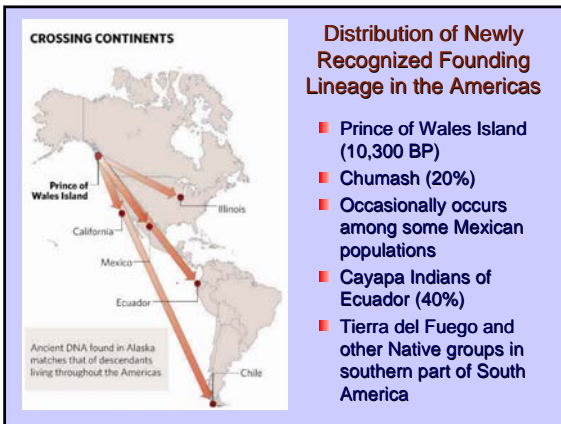
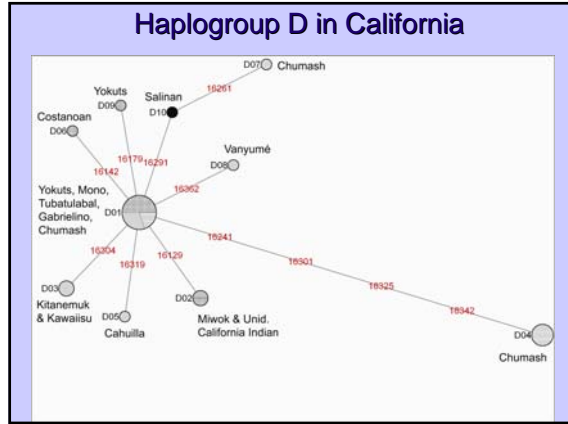
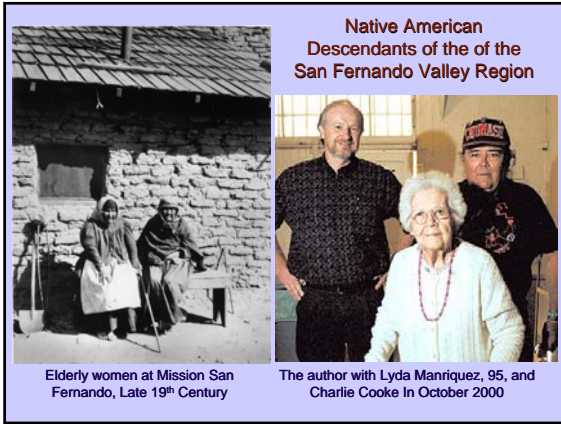


- ### Genetic Results of Language Changes in Prehistoric California
- For ancient populations: Group specific markers and branching chain-like patterns of mtDNA variation in network diagrams
 - For population replacement through migration: Differences with earlier peoples and star-like patterns of mtDNA variation in network diagrams
 - Elite dominance: no genetic difference between past and present, but language substratal influences
 - Intermarriage results in shared genetic lineages between populations speaking unrelated languages

- ### Predictions for California
- Chumash populations will be genetically distinctive because of ancient presence and practice of matrilineal residence
 - Hokan and Penutian superfamilies will harbor ancestral lineages although widely separated geographically
 - Yokutsan and Uto-Aztecan families, being more recent arrivals, will share lineages with regions of origin and less common lineages form groups absorbed during expansion
 - Adjacent groups with significant intermarriage will share mitochondrial lineages and exhibit phonological convergence



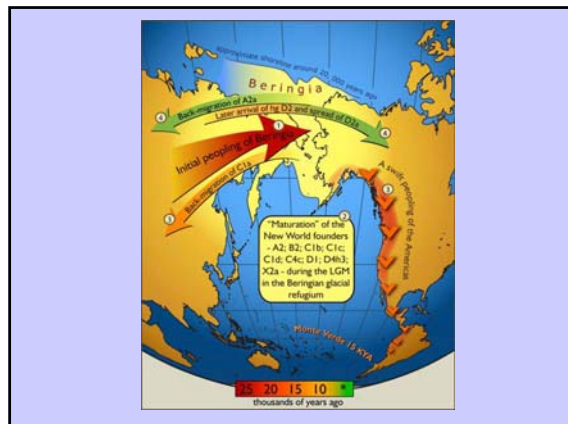
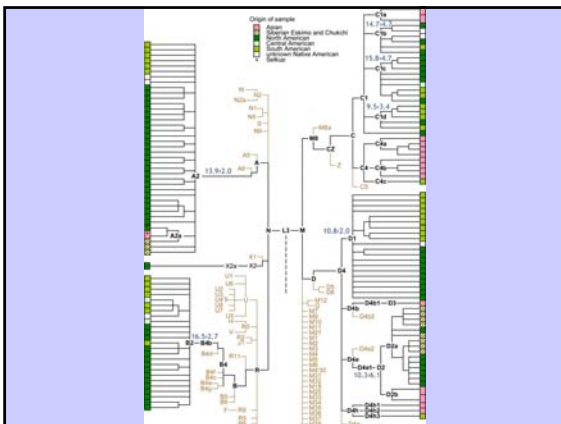




Complete Genome Sequencing of Native American Indian mtDNAs

Table 1. Defining mutations for Native American mtDNA haplogroups

Hg	HVS I	HVS II	Coding region
A1	16223-16296-16319	73-225-263	1651-1705, 4126, 4638, 8794
A2	16111-16223-16296-16319-16362	64-73-146-158-225-263	4027, 5267
A2a	16111-16223-16296-16319-16362	64-73-146-158-225-263	3330
B	16189	73-263	426-439, 626
B1	16189-16217	73-263	822-1035
B1a	16189-16217	73-263	495, 492G, 1330G
B2	16189-16217	73-263	354T, 407T, 647G, 995G, 1117T
C	16223-16296-16327	73-249A-263	332A, 90A, 117A, 123A, 1451G
C1	16223-16296-16426-16327	73-249A-263-290-291A	-
C1b	16223-16296-16325-16327	73-249A-263-290-291A	493
C1c	16223-16296-16325-16327	73-249A-263-290-291A	189A, 1939A
C1d	16223-16296-16325-16327	73-249A-263-290-291A	786T
C4	16223-16296-16327	73-249A-263	222A, 620A, 1196A, 1524A
C4a	16223-16296-16299-16327	73-263	1546G, 1336A, 1443G, 1614G
D	16223-16362	73-263	408G, 511A
D1	16223-16362	73-263	301G, 341A, 1468G
D1a	16223-16362-16362	73-263	289G
D2	16129-16223-16271-16362	73-263	331A, 346A, 879G, 933A, 1121A
D2a	16129-16223-16271-16362	73-263	139G
D2b	16129-16223-16271-16362	73-263	919T
D4b3	16223-16261-16261-16462-16462	73-263	333G, 339A, 346A, 354A, 426A, 626A, 846A, 941A, 1119A
D5	16223-16469-16362	73-263	89G, 402G, 1012G, 1446G, 1597T
F	16189-16223-16276	73-153-263	822T, 1071T, 1396A, 1462G
K2a	16189-16271-16273-16276	73-153-199-260-263	171G, 891G, 1239T, 1462G



To what extent did Coastal Paleoasiatic populations contribute to the peopling of the Americas?



Ainu man



Chumash man

Summary

- California's linguistic prehistory can be better understood by examining population dynamics through mtDNA research.
- Particular genetic lineages are correlated with linguistic groupings, but the reverse is not true, i.e., speakers of a given language are not composed of only one genetic lineage.
- Yokuts expansion from the Great Basin or Plateau regions is supported by mtDNA data and is marked by a distinctive genetic clade.
- Uto-Aztecan (and Yuman?) expansion into southern California is derived from the growth of agriculturally based populations in the American Southwest and subsequent spread into California after 2100 years ago.
- The Chumash Indians are a group that established themselves early in the settlement of the Americas. Geographic distribution of a distinctive founding lineage that occurs among the Chumash suggests a Late Pleistocene coastal migration.