

Mitochondrial DNA variation of Yuman speaking populations

C.R. Monroe¹, B.M. Kemp², D.G. Smith².

¹Department of Anthropology, University of California Santa Barbara, ² Department of Anthropology, University of California Davis

Mitochondrial DNA (mtDNA) has been instrumental in aiding reconstruction of North American prehistory and determining population relationships. However, in the Southwestern United States, limited sampling of Yuman speaking populations has restricted the ability to draw conclusions about genetic relationships between these populations, as well as with other, non-Yuman speaking populations. We, therefore, conducted a more extensive study of mtDNA variation to address these issues. Approximately 200 samples from the Yavapai, Quechan, and Havasupai were categorized as belonging to one of the five New World mtDNA haplogroups: A, B, C, D, or X. Haplogroup frequencies as well as hypervariable region sequence data were used to assess the relationship of these populations with previously studied populations from the Southwest, Baja California, Mexico, and Southern California. One of our preliminary findings is that the Yavapai experienced high levels of gene flow with Athabaskan speaking populations, which resulted in a breakdown of genetic differentiation between these two groups, despite their respective preservation of linguistic continuity. Additionally, this data suggests that Yuman speaking populations are not homogeneous and display genetic differentiation despite their linguistic affinity.

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