

Evolutionary History of North American Wild Sheep: Morphometric and mtDNA Analyses

JOHN D. WEHAUSEN, University of California, White Mountain Research Station, 3000 E. Line Street, Bishop, CA 93514

CLINTON W. EPPS, Dept. of Fisheries and Wildlife, Oregon State University, Corvallis, OR 97331-4501

ROB R. RAMEY II, Conservation Science Foundation, P.O. Box 386, Nederland, CO 80466

Abstract: Since this research was discussed at the meeting 4 years ago, the first author has added a significant number of samples to the DNA sequence data bases of two mtDNA genes (control region and ND5), and increased the amount of ND5 sequence by 50%. Additional samples were chosen to fill in geographic gaps in the data for the desert and Rocky Mountain region. Samples also were chosen to allow comparison of phylogenetic analyses based on sequence and RFLP data. The latter were developed in the 1980s by Rob Ramey and Gordon Luikart, and we were able to develop sequence data from a wide sampling of the same DNA samples they used. Cranial morphometric analyses have found 5 defensible groups of sheep in North America: 2 thinhorn subspecies and 3 bighorn subspecies. However, phylogenetic analyses of mtDNA sequences indicate a complex evolutionary history that results in trees that do not coincide entirely with the morphometric data. For instance, morphometrically there is one well-defined group of Rocky Mountain bighorn, but there are two mtDNA clades of Rocky Mountain bighorn sheep. To complicate this further, 2 of 3 distinct mtDNA lineages of thinhorn sheep are on the bighorn sheep clade, including a group from the Brooks Range. This complex pattern reflects a phenomenon known as cytonuclear dissociation or mtDNA capture, which results from directional hybridization events associated with habitat and climate change. Yet further complicating this is strong evidence of 2 colonizations of North America by Siberian Snow Sheep. I will discuss how well RFLP data elucidated these complex patterns and the limitations of mtDNA analyses in general relative to taxonomic divisions, given the potential problem of cytonuclear dissociation.

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Email: wehausen@qnet.com