

Phylogenetic Analyses Reveal Evidence for Multiple Glacial Refugium for Thinhorn Sheep

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ABSTRACT Past glaciation events have played a major role in shaping the genetic diversity and distribution of wild sheep in North America. The advancement of glaciers can isolate populations in ice-free refugia, where they can survive until the recession of ice sheets. Thinhorn sheep (*Ovis dalli*) populations were previously thought to have survived glacial periods in the major Beringia refugium. While isolation in the major refugium can account for much of the genetic and morphological diversity seen in extant thinhorn sheep populations, mounting evidence suggests the persistence of populations in smaller minor refugia. We investigated the refugial origins of thinhorn sheep via a cross species application of the domestic sheep ovine high density single nucleotide polymorphism array to genotype 52 thinhorn sheep and 5 bighorn sheep (*Ovis canadensis*) samples. Maximum parsimony and Bayesian phylogenetic analyses reveal evidence for 2 distinct clades of thinhorn sheep, which is consistent with the survival of thinhorn sheep in 2 glacial refugia. Bayesian admixture analysis also indicates the southeast Yukon to be a zone of contact as thinhorn sheep population recolonized North America subsequent to the recession of the ice sheets. The results of this study highlight the intricate role glaciation events can have on the evolutionary history of thinhorn sheep and the need to look beyond established refugia.

Biennial Symposium of the Northern Wild Sheep and Goat Council 19:4; 2014

KEY WORDS admixture, glacial refugia, *Ovis dalli*, phylogeography, single nucleotide polymorphism, thinhorn sheep.

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