

Population Genetics of the World's Thinhorn Sheep (*Ovis dalli*)

ZIJIAN SIM, *Department of Biological Sciences, University of Alberta, 116 St and 85 Ave, Edmonton, Alberta, Canada T6G 2R3, sim.zijian@gmail.com*

BILL JEX, *Ministry of Forests, Lands and Natural Resources Operations, Bag 5000 – 3726 Alfred Ave, Smithers, British Columbia, Canada*

TROY HEGEL, *Yukon Department of Environment, PO Box 2703, Whitehorse, Yukon, Canada, Y1A2C6*

COREY DAVIS, *Department of Biological Sciences, University of Alberta, 116 St and 85 Ave, Edmonton, Alberta, Canada T6G 2R3*

NICHOLAS C. LARTER, *Government of the Northwest Territories, Department of Environment & Natural Resources, PO Box 240, Fort Simpson, Northwest Territories, Canada X0E 0N0*

DAVID W. COLTMAN, *Department of Biological Sciences, University of Alberta, 116 St and 85 Ave, Edmonton, Alberta, Canada T6G 2R3*

ABSTRACT Thinhorn sheep (*Ovis dalli*) populations throughout northwestern North America are managed to maximize hunting, viewing, and sustenance opportunities. Central to effective conservation management is the identification of biologically relevant groupings, which can inform game management units. The identification of genetically discrete population units is essential for the delineation of true population boundaries, which can then form the basis for monitoring and the development of specific conservation action. We investigated the worldwide population genetics of thinhorn sheep by profiling ~2000 harvested thinhorn rams from across the species' range using 153 single-nucleotide polymorphism (SNP) markers. We used the genetic profiles to characterize the distribution of genetic variation and identify population boundaries across the entire geographic range of thinhorn sheep. We were also able to re-examine the current subspecies (Dall's and Stone's sheep) boundaries for thinhorn sheep and found that current boundaries likely do not reflect the evolutionary history of the species. Results from this study will be used to update the thinhorn management and harvest policies in British Columbia and Yukon, Canada.

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KEYWORDS Dall's sheep, *Ovis dalli*, phylogeography, population structure, Stone's sheep, thinhorn sheep

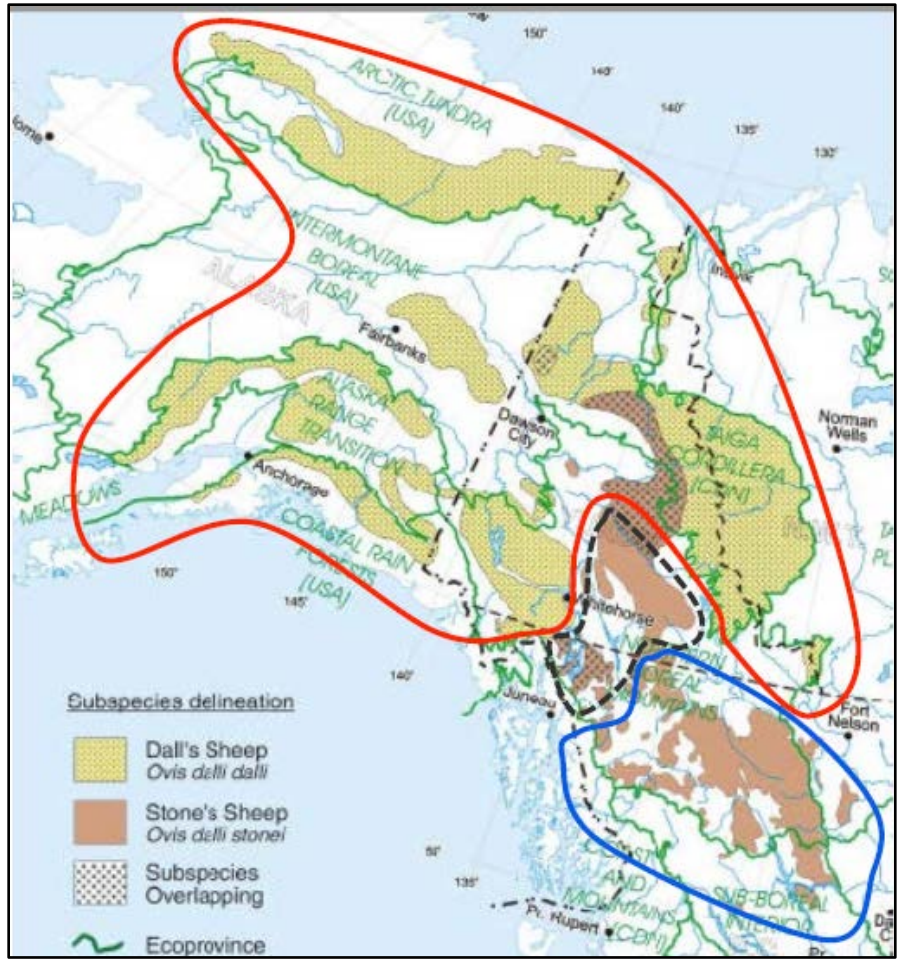


Figure 1: Map comparing subspecies genetic and current subspecies boundaries for thinhorn sheep. Red lines represent the approximate genetic boundaries for Dall's sheep (*Ovis dalli dalli*), blue for Stone's sheep (*O. d. stonei*). Dotted line represents admixed sheep.