

Spatial genetic structure of Rocky Mountain Bighorn Sheep (*Ovis canadensis canadensis*) at the northern limit of their native range

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ABSTRACT: The Canadian Rocky Mountains are one of the few places on Earth where the spatial genetic structure of wide-ranging species have been relatively unaffected by anthropogenic disturbance. We characterised the spatial genetic structure of Rocky Mountain bighorn sheep (*Ovis canadensis canadensis* (Shaw, 1804)) in the northern portion of their range. Using microsatellites from 1495 individuals and mitochondrial DNA sequences from 188 individuals, we examined both broad and fine scale spatial genetic structure, assessed sex-biased gene flow within the northern portion of the species range, and identified geographic patterns of genetic diversity. We found that broad-scale spatial genetic structure was consistent with barriers to movement created by major river valleys. The fine-scale spatial genetic structure was characterized by a strong pattern of isolation-by-distance, and analysis of neighborhood size using spatial autocorrelation indicated gene flow frequently occurred over distances of up to 100 km. However, analysis of sex specific spatial autocorrelation and analysis of mitochondrial haplotype distributions failed to detect any evidence of sex-biased gene flow. Finally, our analyses reveal decreasing genetic diversity with increasing latitude, consistent with patterns of post-glacial recolonization of the Rocky Mountains.

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