# Population Structure of Rocky Mountain Bighorn Sheep from Microsatellites and Mitochondrial DNA Genotyping

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***Abstract:*** We collected bighorn sheep (*Ovis canadensis*) fecal samples non-invasively from Glacier National Park and hunter-kill tissue samples from across southern Alberta. We genotyped samples at 22 to 24 hypervariable microsatellite DNA loci and sequenced 800 base pairs of mitochondrial (mt) DNA. Microsatellite genotyping error rates, among the lowest recorded for non-invasive studies (0.13% – 1.6% per locus), varied significantly between sampling locations and times ($P < 0.001$). This illustrates the importance of quantifying genotyping error rates for each study population separately (and for each sampling period), before initiating a non-invasive study. Preliminary analyses suggest substantial substructure and limited gene flow on a relatively fine geographic scale. For example, 2 sampling locations in Glacier Park were separated by ~30 miles but differed substantially for microsatellite markers ($F_{ST} > 0.10$) and for maternally-inherited mtDNA markers ($F_{ST} > 0.50$). Although preliminary, this suggests male-biased gene flow exists and approximately 1 to 10 reproductively-successful genetic migrants per generation. It also suggests these markers and data sets would be useful to detect poaching and track the source population of illegal trophies and body parts.

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