



Evaluating Sample Size to Estimate Genomic Relatedness in Bighorn Sheep Populations

ELIZABETH P. FLESCH, *Animal and Range Sciences Department, Montana State University, Bozeman, MT, USA 59717*

JAY J. ROTELLA, *Fish and Wildlife Ecology and Management Program, Ecology Department, Montana State University, Bozeman, MT, USA 59717*

JENNIFER M. THOMSON, *Animal and Range Sciences Department, Montana State University, Bozeman, Montana 59717*

TABITHA A. GRAVES, *Northern Rocky Mountain Science Center, USGS, West Glacier, MT, USA 59936*

ROBERT A. GARROTT, *Fish and Wildlife Ecology and Management Program, Ecology Department, Montana State University, Bozeman, MT, USA 59717*

ABSTRACT: Inbreeding and relationship metrics among and within populations are useful measures for genetic management of wild populations, but accuracy and precision of estimates can be influenced by the number of individual genotypes analyzed. Biologists are confronted with varied advice regarding the sample size necessary for reliable estimates when using genomic tools. We developed a simulation framework to identify the optimal sample size for three widely used metrics to enable quantification of expected variance and relative bias of estimates and a comparison of results among populations. We applied this approach to analyze empirical genomic data for 30 individuals from each of four different free-ranging Rocky Mountain bighorn sheep (*Ovis canadensis canadensis*) populations in Montana and Wyoming, USA, through cross-species application of an Ovine array and analysis of approximately 14,000 single nucleotide polymorphisms (SNPs) after filtering. We examined intra- and interpopulation relationships using kinship and identity by state metrics, as well as F_{ST} between populations. By evaluating our simulation results, we concluded that a sample size of 25 was adequate for assessing these metrics using the Ovine array to genotype Rocky Mountain bighorn sheep herds. However, we conclude that a universal sample size rule may not be able to sufficiently address the complexities that impact genomic kinship and inbreeding estimates. Thus, we recommend that a pilot study and sample size simulation using R code we developed that includes empirical genotypes from a subset of populations of interest would be an effective approach to ensure rigor in estimating genomic kinship and population differentiation.

Biennial Symposium of the Northern Wild Sheep and Goat Council 21:46; 2018

KEYWORDS Kinship; bighorn sheep; *Ovis canadensis*, sampling, single nucleotide polymorphism.