

Application of the Ovine Infinium® HD SNP BeadChip to Rocky Mountain Bighorn Sheep

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IMPACT STATEMENT

This research is aimed at applying technology developed for livestock genetic improvement to inform the biology and management of wildlife management.

SUMMARY

The purpose of this study was evaluate the effectiveness of a domestic sheep genotyping chip, the Ovine Infinium® HD SNP BeadChip for utility in Rocky Mountain Bighorn Sheep. This pilot project aimed to extract Bighorn sheep DNA from archived blood cards and utilize the domestic sheep genotyping chip to evaluate the bighorn DNA. It also aimed to explore the biological insight that can be gained from the genotype analysis and to evaluate the technology for its potential to inform the biology and management of bighorn sheep.

INTRODUCTION

The principles of population genetics have been applied to domestic and wildlife populations for many years (Wright, 1931). The methods most commonly applied, first to domestic livestock and then to wildlife species have been microsatellite markers. This technology looks at heritable tandem repeated sequences in DNA that can serve as markers for segments of DNA that are causally related to health or productivity traits. The closer the marker is to the causal variant, the higher the likelihood it will be passed to resulting generations . Some examples of how this methodology has been applied to wild sheep are detection of signatures of selection on immune genes in thin horn sheep (Worley et al., 2006), evaluation of experimental genetic management in Oregon and California bighorn sheep (Olson,

et al., 2012), and evaluating genetic diversity, inbreeding, and gene flow in a metapopulation of bighorn in Rocky Mountain National Park (Driscoll et al., accessed 2014).

The gene sequencing era of the late 1990s and early 2000s has provided huge volumes of information and a host of new tools for genetic investigation and evaluation. The first draft of the domestic sheep genome was published in 2011 and a revised genome was published in 2013. An array of 50,000 single nucleotide polymorphisms (SNPs) was created and utilized in domestic sheep to start genetic marker assisted selection programs for wool and meat quality. A second array, the Ovine Infinium® HD SNP contains 700,000 SNPs was produced in early 2014 and has been successfully utilized in domestic sheep (Kiljas, 2014) and wild sheep (Miller, 2014) due to common ancestry, with approximately 24,000 of the SNPs informative for wild sheep. This represents a major advancement for Bighorn sheep as previous genetic analysis has involved < 200 genetic markers. This study had the objectives of: identifying potential associations between demographic performance of herd and their attributes; evaluate founder or bottleneck potentials for small herds; inventory and assess herd genetics; identify herds with low genetic diversity; determine if any herds are genetically unique.

PROCEDURES

Animals. DNA blood cards were obtained from the ongoing Greater GYE Mountain Ungulate Project. They represented 15 animals from four herds of bighorn sheep. An additional 14 samples were obtained for Glacier National Park with separate funding and under a separate project.

DNA. DNA was extracted from blood cards using a Promega Maxwell 16 semi-automated nucleic acid extraction instrument and an LEV Blood DNA kit also from Promega. DNA was quantified and normalized and then shipped on ice to GeneSeek (Lincoln, NE) where it was genotyped using the Ovine Infinium® HD SNP BeadChip. The genotypes were then provide electronically to Montana State University and analyzed using Golden Helix, a commercial genotype analysis package.

RESULTS AND DISCUSSION

The Ovine Infinium® HD SNP BeadChip was successfully used in Rocky Mountain Bighorn Sheep with 24, 687 markers being informative. Genetic distance as determined by Principal Component Analysis was able to distinguish the unique genetic signature of each herd sampled with overlap only occurring in herds which have been used to supplement one another or in herds in geographical proximity and in which it is reasonable to think animals would intermate (Figure 1.).

In addition to the unique signatures, we were able to assess inbreeding in the herds and determine that the Glacier and Eastern GYE herds had no detectable inbreeding, some was present in the Stillwater population, with higher inbreeding detected in the Tendoy and in the two animals tested for the Wild Horse Island population (Figure 2.).

These results demonstrate the effectiveness of this technology applied to wildlife species and that it has the potential to inform management decisions.

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Principle Component Analysis

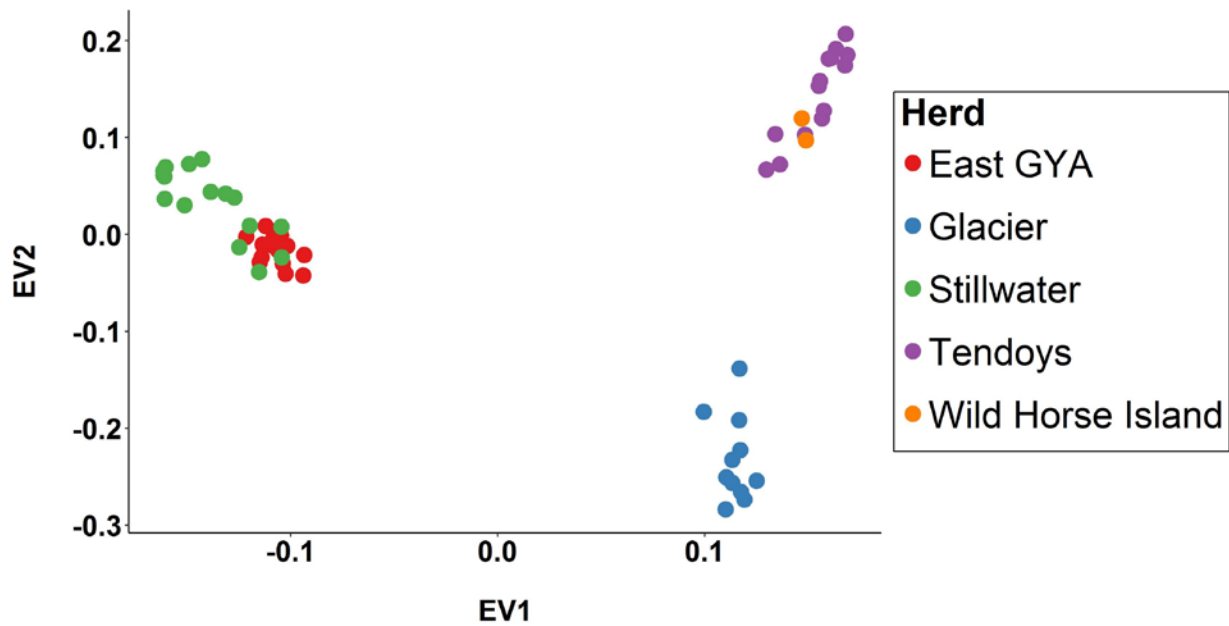


Figure 1. Principal component analysis of bighorn sheep herds in Montana and Wyoming demonstrating unique genetic signatures.

Inbreeding by Bighorn Sheep Herd

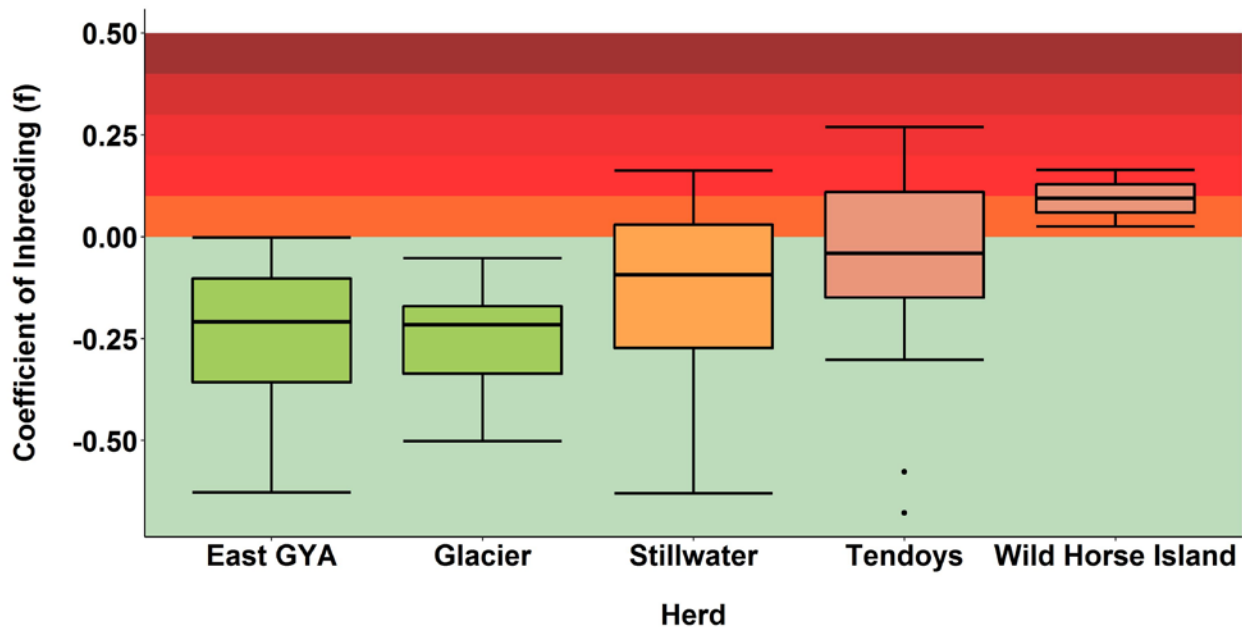


Figure 2. Genomically calculated inbreeding in Rocky Mountain Bighorn Sheep from Montana and Wyoming.