A Genome Wide Set of SNPs Detects Population Substructure and Long Range Linkage Disequilibrium in Wild Sheep

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Abstract: Single nucleotide polymorphisms (SNPs) provide several advantages over other genetic markers including: abundance in the genome, distribution in both expressed and intronic sequences, and ease of genotyping through automation. Therefore, SNPs are fast becoming the genetic marker of choice for addressing a wide variety of evolutionary and population genetic questions. However, the development of large scale SNP resources for wild species is still in its infancy. Cross-species utilization of technologies developed for their domestic counterparts has the potential to unlock the genomes of organisms that currently lack genomic resources. Here we apply the OvineSNP50 BeadChip, developed for domestic sheep, to two related wild ungulate species: the bighorn sheep (*Ovis canadensis)* and the thinhorn sheep (*Ovis dalli*). Over 95% of the domestic sheep markers were successfully genotyped in bighorn sheep while over 90% were genotyped in thinhorn sheep. Pooling both species we found 868 SNPs distributed on all autosomes and the X-chromosome. This panel of SNPs was able to discriminate between the two species, assign individuals to their population of origin, and detect substructure within a population corresponding to known family groups. Further application of these markers to multiple populations holds the prospect of dramatically informing and enhancing existing management strategies that currently rely on demographics and population structure estimates inferred from a few neutral markers.

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