TOWARDS AN UNDERSTANDING OF THE GENETIC BASIS OF DIFFERENCES IN HORN SIZE IN BIGHORN SHEEP

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Abstract: Large horns are a defining feature of bighorn sheep (*Ovis canadensis*). Horn size affects many aspects of bighorn sheep ecology and life-history, and is the basis for many regulatory and management decisions. Yet, we know little about the genetic mechanism underlying this trait. Using a suite of 241 genetic markers genotyped in 310 pedigreed animals from the population on Ram Mountain (Alberta, Canada), we identified a specific region of DNA associated with differences in horn dimensions. Based on this result, and similar findings in feral Soay sheep (*Ovis aries*), we are now employing a candidate gene association approach to develop additional markers and fine-map the association to specific genes. Once found, the prevalence of genetic variants associated with large horns can be assessed in the current Ram Mountain population, and changes in allele frequency tracked through time. This suite of markers could also easily be applied to other populations of bighorn sheep to rapidly assess the genetic potential of the sheep in that population to grow large horns, a statistic known as genetic merit. In many populations it is impractical to directly measure horn size of every sheep. Instead, the genetic merit of horn size can b eassessed and monitored based on population level genetic diversity. Cross population comparisons would further shed light on the genetic basis of horn morphology, and help define an evolutionary stable management strategy.

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