ASSESSING GENETIC DIVERSITY BETWEEN BIGHORN SHEEP POPULATIONS IN WESTERN MONTANA

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This study investigates two remote bighorn sheep populations in the southern Bitterroot Valley affected by a pneumonia outbreak in 2010. Limited information is available regarding the genetic relatedness among bighorn sheep populations and how pneumonia related die offs could impact genetic diversity and herd resilience to future outbreaks. To contribute to local research efforts we developed scat collection and DNA extraction protocol for advanced high school students in a community science program. This study gathers baseline information about the genetic relatedness between two relatively close but isolated populations, and will estimate the heterozygosity and the number of distinct alleles at several microsatellite loci. DNA from bighorn sheep scat was collected, extracted, and genotyped from samples in June of 2011 ($n = 19$) and 2012 ($n = 25$). The small sample size will reduce our ability to make broad conclusions; the number of samples represents about 20 percent of the estimated herd size in 2011 and 2012. Although our ability to make conclusions may be limited, this data could contribute to bighorn sheep management strategies for the Bitterroot and long term genetic monitoring for a sustainable population. Additional samples will be collected and analyzed yearly to look for changes in heterozygosity over time and in response to any future translocations.