
GENETIC POPULATION STRUCTURE OF MULE DEER *ODOCOILEUS HEMIONUS* ACROSS MONTANA

John H. Powell*, Department of Ecology, Montana State University, Bozeman, Montana, 59717

Steven T. Kalinowski, Department of Ecology, Montana State University, Bozeman, Montana, 59717

Megan D. Higgs, Department of Mathematical Sciences, Montana State University, Bozeman, Montana, 59717

Paul C. Cross, Northern Rocky Mountain Science Center, U.S. Geological Survey, Bozeman, Montana, 59715

We conducted a genetic assessment of mule deer (*Odocoileus hemionus*) population structure across Montana in an effort to understand dispersal routes across the landscape. To assess genetic structure we genotyped 14 microsatellite loci in 359 individuals sampled primarily within Montana. Smaller samples were included from Wyoming, Colorado and Utah in order to provide a regional context for the levels of population structure observed within Montana. Additionally, we sequenced the control region of the mitochondrial genome of 76 individuals subsampled from our original samples across Montana. To avoid potential influences of a priori population designations, individual based analyses were used to test relatedness across the landscape. Weak isolation by distance characterized mule deer individuals across this region. In addition, we did not detect any evidence of spatial autocorrelation in discrete distance classes as small as 10 km. Female mule deer had higher average individual pairwise genetic distances than males, indicating the presence of a

contemporary male bias in dispersal rates. Mitochondrial DNA indicated the potential for either reduced overall or female-specific dispersal between a subset of the sampling regions within Montana. Finally, we were unable to detect a genetic signature of past translocations of mule deer across Montana. Taken together these results indicate that within this landscape mule deer populations are characterized by high levels of connectivity and experience few, if any, barriers to dispersal.