An Evaluation of Genetic Diversity and Population Genetic Structure in Rocky Mountain Wolverines[TWS]

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The range of wolverines (*Gulo gulo*) has contracted substantially within North America and includes small, remnant populations within the conterminous United States in Colorado, California, Idaho, Oregon, Washington, Wyoming and Montana. The population size and trend of each of these populations and the connectivity to other populations in the conterminous United States is poorly known. I examined levels of genetic diversity and population genetic structure in three states (Idaho, Wyoming, and Montana) and two Canadian provinces (Alberta and British Columbia) using both mitochondrial (mtDNA) and nuclear microsatellite DNA. A Bayesian clustering analysis suggested that there were three distinct subpopulations in Montana: Rocky Mountain Front (RMF), Crazybelts (CB), and Gallatin (GA). Restricted levels of gene flow were measured among these subpopulations for both mitochondrial and nuclear DNA. However, the Rocky Mountain Front and Wyoming subpopulations displayed minimal nuclear genetic differentiation. Nuclear DNA diversity for these two subpopulations also was comparable to levels previously reported in North America. The other subpopulations exhibited significantly lower levels of nuclear diversity. The Idaho subpopulation had the lowest levels of mitochondrial and nuclear genetic diversity, and was more isolated than the other subpopulations. Based upon these data, I suggest the designation of three separate management units: Idaho, Crazybelts, and the Rocky Mountain Front/ Gallatin/ Wyoming units. The subpopulations in the conterminous United States have lower levels of gene flow and are much more fragmented than Northern populations in Alaska and Canada. Corridors for movement should be established among the fragmented subpopulations and may be incorporated into a large carnivore conservation strategy.