DEMOGRAPHY AND GENETIC STRUCTURE OF A RECOVERING GRIZZLY BEAR POPULATION

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The threatened grizzly bear (*Ursus arctos*) population in northwestern Montana has been managed for recovery since 1975, yet no rigorous data were available to monitor program success. We assessed population status using data from one of the world's largest noninvasive genetic sampling efforts and 33–years of physical captures. Our population estimate, $N = 765$ (CV = 3.8%) was double the working estimate. Based on our results, the recent human–caused mortality rate approached a sustainable 4 percent although the high proportion of female mortalities raises concern. Genetic interchange has recently increased in areas exhibiting generations of low gene flow. This study illustrates the power of molecular techniques to rapidly assess populations at landscape scales and provide detailed demographic and genetic data needed to guide and evaluate recovery efforts.