Non-Invasive Genetic Sampling for Forest Carnivore Population Status at an Ecosystem Scale [TWS]

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We censused populations of grizzly bears and black bears during 1998-2000 on a 8,100-sq. km. study area in northwestern Montana by collecting hair from hair snares and scats from trap grids and survey routes and identifying individuals through DNA analysis. Of the 212 different individual grizzly bears identified during 1998; 121 were detected at systematically placed baited hair traps, 56 from unbaited rub trees, and 35 were detected via both types of samples. Species and gender ratios differed significantly between the three sampling methods. Surveys conducted the first half of the field season yielded larger numbers of samples than later surveys and detected most individuals identified during the entire May – October season. Population point estimates made using a variety of models and combinations of data sets ranged from 343–400 grizzly bears. The 95 percent confidence interval ranged from 263–575 or 33–71 bears per 1000 sq. km. We describe a new noninvasive approach for monitoring bear population trend based on systematic surveys for animal hair and feces. Field collection and population estimation methods, as well as potential sources of genotyping errors and recommendations for minimizing them are described.