

nated. We encourage experimentation with and adaptation of the methods described in this chapter to create new hair sampling approaches. We also recommend using domestic and captive animals in initial trials of hair snagging devices and structures, as well as testing the efficacy of novel techniques with pilot studies before launching larger projects. The notes sections of journals, and methods-oriented periodicals in general, should be fully utilized to make sure that the details of newly emerging hair collection methods are made available to other scientists and managers.

CASE STUDY 6.1: DNA SURVEY FOR FISHERS
IN NORTHERN IDAHO

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Location: Northern Selkirk Mountains in northern Idaho.

Target species: Fisher.

Size of survey area: ~1,500 km².

Purpose of survey: Unique haplotypes indicating the presence of a residual native population of fisher were found in central Idaho (Vinkey et al. 2006). Fishers had been detected previously using camera sets in the Selkirk Mountains just south of the Canadian border, but their population status and genetic composition were unknown. The purpose of the study was to provide a comprehensive survey of the northern Selkirk Mountains and to determine the genetic makeup (and therefore population source) of detected fishers.

Survey units: Creek drainages ≥ 30 km² in area.

Survey method: This study used cubbies constructed from folded plastic sheeting. In 2003–4, the cubby design followed Zielinski et al. (2006). The cubbies used in 2005–6 were triangular by cross section, with sides 41 cm in length, and each contained three 7.62 mm gun brushes in addition to the Z of barbed wire described in Zielinski et al. (2006). Both years, the cubbies were baited with a carpet pad soaked in beaver castoreum and approximately 125 cm² cube of deer meat. These items were attached to hardware cloth (i.e., wire mesh) on the inside of the

cubby. A sponge splashed with skunk essence was hung above the cubbies as a lure.

Survey design and protocol: The Selkirk Mountains are a granite batholith cut by deep canyons. As fisher habitat was located in the densely timbered valleys, surveys were concentrated in the valley bottoms, while the higher elevation areas were not surveyed. Surveys were conducted during the winters of 2003–4 and 2004–5. Cubbies were placed at approximately 1 km intervals along roads and trails in major creek drainages (figure 6.18), and were checked and rebaited once after a period of sixteen to thirty-six days. Total sampling periods varied from thirty to seventy-three days. Snowmobiles were used to set and check hair snare cubbies, with the exception of a single roadless area that was surveyed using snowshoes. Efforts were made to survey all drainages larger than 30 km², although there were some holes in the survey due to lack of access.

Analysis and statistical methods: Hair samples from mustelids were analyzed to the species level using restriction enzymes for all samples (Riddle et al. 2003). A small group of nonmustelid samples were sequenced and compared to published sequences in GenBank (www.ncbi.nlm.nih.gov/BLAST/).

Results and conclusions:

During both years combined, 344 cubbies (186 in year one, 158 in year two) were placed along roads and trails in twenty major creek drainages (figure 6.18).

2003–4 Field Season

- Of 300 hair samples, most were collected from the floor of the cubby versus from barbs.
- Only 55% of samples produced DNA of sufficient quality for analysis.
- Eighteen samples collected from eight cubbies were identified as fisher; twenty-two samples collected from fourteen cubbies were identified as marten.
- Of the eighteen fisher samples, one had a haplotype associated with native fishers. The other

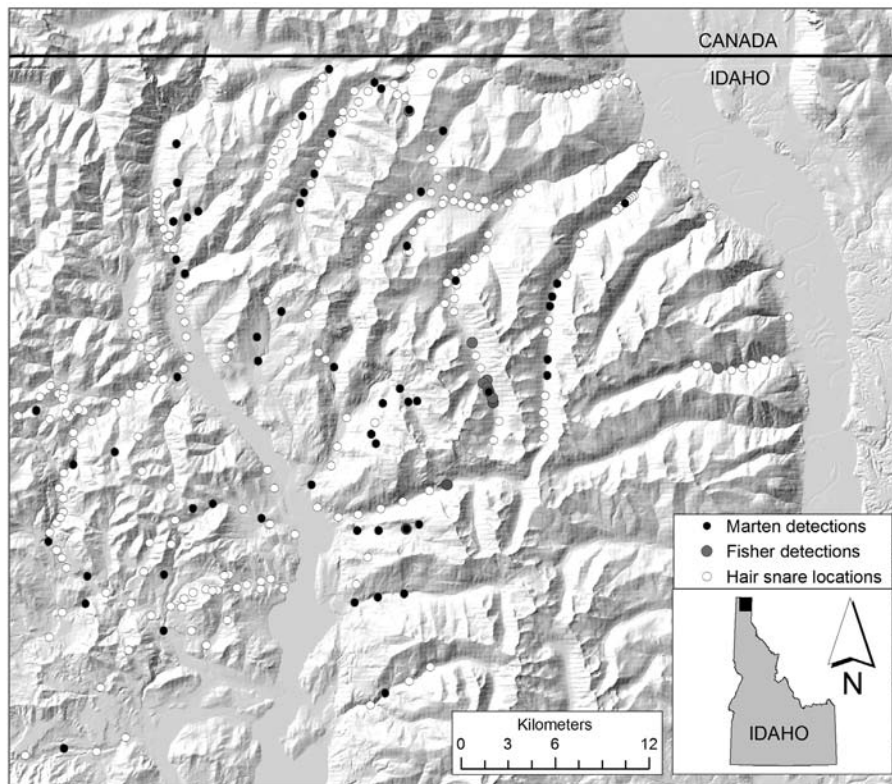


Figure 6.18. Hair sampling locations for fishers in the Selkirk Mountains of northern Idaho.

haplotypes were associated with fishers from Wisconsin and Minnesota (Vinkey et al 2006; Drew et al 2003).

2004–5 Field Season

- In all, 337 samples were collected; 6 of the samples were taken from barbed wire, 183 from gun brushes, and 148 from the bottom or sides of the cubbies.
- Of the 260 samples tested, 83% yielded sufficient DNA for species identification. The 77 untested samples were deer hair from the bait.
- Eight fishers were detected at three cubbies; all fisher haplotypes indicated Midwestern origin.
- Eighty-three marten samples and one wolverine sample were also collected.
- Other species detected included red squirrel (*Tamiasciurus hudsonicus*), striped skunk,

short-tailed weasel, coyote, wolf or dog, and bobcat.

Synthesis

- At the time of the survey, a relatively small population of fishers occurred in the northern Selkirk Mountains.
- Most of the samples collected were likely associated with an introduction of Midwestern fishers into the Cabinet Mountains in 1989–91 (Vinkey et al. 2006), but at least one fisher was maternally descended from native fishers.

CASE STUDY 6.2: BEAR RUB TREE SURVEY

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Location: Glacier National Park, Montana.

Target species: Black bear, grizzly bear.

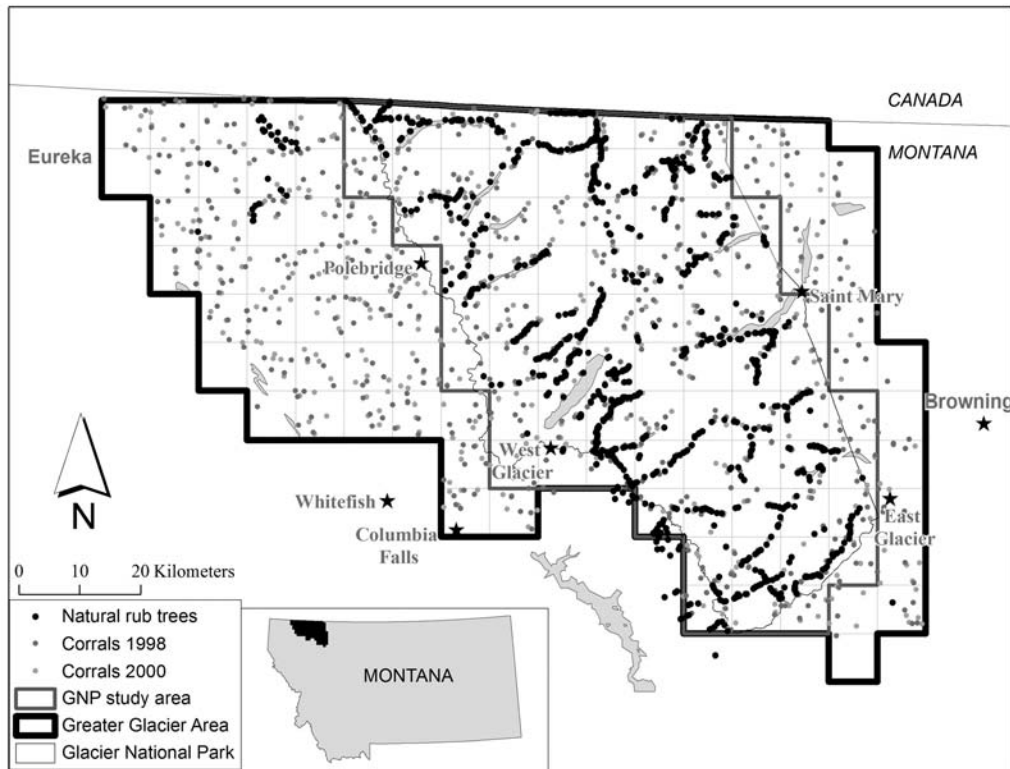


Figure 6.19. Locations of natural rub trees and baited hair corrals used to sample grizzly bear and black bear hair in and around Glacier National Park.

Size of survey area: 4,100 km².

Purpose of survey: To test rub tree survey methodology, compare detection bias between bear rub tree and barbed wire corral grid sampling methods, and compare the bias and precision of capture-recapture population estimates made using joint rub tree/hair corral data with hair corral-only detections.

Survey units: Hair was collected from rub trees identified on maintained trails in the Glacier National Park area. Hair corrals were distributed systematically on an 8 x 8 km grid with one corral per cell.

Survey method: Hair snagging devices comprising three to four short (~30 cm) pieces of barbed wire, totaling nine to twelve barbs, were stapled to each selected tree in a zigzag pattern on the rub surface.

Survey design and protocol: As part of a study to estimate density and distribution of grizzly bear and black bear populations in the greater Glacier area, 1,185 km of maintained trails were surveyed to identify bear rub trees. Based on the level of bear use and geographic distribution, 884 trees were selected for monitoring (figure 6.19). Rub trees were surveyed concurrently with hair corral surveys, which consisted of five, two-week sampling occasions on a grid of 126 baited hair corrals. Rub tree surveys were conducted on foot at approximately four-week intervals in 1998 and two-week intervals in 1999 and 2000. All hair from each barb was placed in its own sample envelope and sent for genetic analysis.

Analysis and statistical methods: Genetic analysis was initially attempted on all hair samples with at least five follicles. For those sites where no grizzly

bears were identified during the initial analysis, all hair corral samples with at least one follicle, and the two largest hair samples per rub tree survey, were analyzed. The bear species associated with a given sample was determined via analysis of mitochondrial DNA and confirmed with microsatellite analysis. The individual identity of grizzly bears was established using six highly variable microsatellite loci, and gender was determined using the Amelogenin system (see chapter 9). Population estimates using hair corral data alone and joint rub tree/hair corral data were compared using Huggins closed mixture models and the Lincoln-Petersen estimator in program MARK (Boulanger et al. 2008).

Results and conclusions:

- The mean number of surveys per tree ranged from 2.46 in 1998 to 6.10 in 2000.
- Two hundred thirty-eight grizzly bears were identified through rub tree sampling during three summers.
- Rub trees were more heavily used by grizzly bears than black bears; the grizzly to black bear ratio was 57:43 at rub trees and 30:70 at hair corrals.
- Male grizzly bears used rub trees more than females during the mid-May through September survey period, however, detection of females increased from virtually no samples in May to

50% or more of the samples from September and October. The male to female ratio of unique grizzly bears sampled was 70:30 at rub trees and 41:59 at hair corrals.

- Of the 231 individual grizzly bears identified in 1998 and 2000, when both hair corrals and rub trees were sampled, 28% were found only at rub trees and another 29% were found at both corrals and rub trees. Thus, including rub trees in the survey significantly increased the number of detected bears.
- The joint rub tree/hair corral data set produced population estimates of similar magnitude but greater precision than hair corral grid data alone (Boulanger et al. 2008).

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