GRIZZLY BEAR
ABUNDANCE & DISTRIBUTION
WITHIN DRAINAGES OF TOBA & BUTE INLETS
OF BRITISH COLUMBIA'S SOUTHERN COAST

Interim Report

Year-1 (2008)

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For and in partnership with:

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INTRODUCTION

Little is known of grizzly bear population abundance, distribution or connectivity in BC's southern Coast Ranges. This knowledge gap is of concern given the wide range of land resource demands in the region and the potential for cumulative impacts. Addressing grizzly bear conservation issues such as mortality risk, population connectivity, and reserve allocation requires an understanding of (1) the density, spatial distribution, and connectivity of the regional population, (2) the factors that influence this pattern, and (3) a means to integrate this knowledge within local and regional planning.

A multi-year study conducted extensive sampling of grizzly bear occurrence and distribution across ~36,000 km2 of the Southern Coast Ranges using hair-snag/DNA survey methods. However, as part of this effort, it was possible to sample only a portion of the Toba/Bute grizzly bear population unit (GBPU), and sampling was of relatively low intensity (one station per 100 km^2). At present, the grizzly bear population within the Toba/Bute GBPU is assumed to be "Viable" with the north and central portion expected to support a higher population density than other sampled GBPUs. As such, its inclusion within the larger regional sampling effort is important in understanding factors that influence variation in relative grizzly bear abundance, distribution, and population connectivity across the region. Moreover, because of higher expected densities and inherent habitat productivity, this area may serve as a population "source" with emigrants helping to recover and sustain localized populations elsewhere in the southern Coast Ranges including GBPUs classed as "Threatened". Thus, it is appropriate that population trends be monitored across the Toba-Bute GBPU and especially where industrial development is increasing. This requires a baseline estimate of population density and distribution that can only be achieved through relatively intensive sampling.

This report describes progress for the first year of a proposed two-year effort to sample most of the Toba/Bute GBPU and the southern portion of the Homathko GBPU. Sampling is being conducted at a scale (controlled by a grid of 25 km^2 cell size) that is appropriate for deriving a population estimate with precision necessary for monitoring trend and assessing the potential impacts of various and cumulative human activities on grizzly bears. This more intensive sampling effort will also serve as a baseline for long-term population monitoring in response to current industrial activities and development in addition to any ongoing population harvest, as well as potential future development. Finally, the sampling will contribute to the objectives of the aforementioned southern Coast Ranges study, filling in the final gap of a ~50,000 km^2 regional study area and contributing essential information on the factors that contribute to the relative abundance of coastal grizzly bears in the Toba and Bute drainages and the relationship of this subpopulation with grizzly bears elsewhere in the region. Ultimately, this study will help to ensure that the provisions of the provincial Grizzly Bear Conservation Strategy are met in the southern Coast Ranges of British Columbia.

Objectives:

1. Apply hair-snag techniques and DNA analysis to systematically sample and resample (four sessions) grizzly bear occurrence at a relatively fine scale (per 25 km^2) across the Toba/Bute and southern portion of the Homathko GBPUs.
2. Apply mark-recapture methods to estimate grizzly bear population size within survey areas.
3. Empirically model population density, distribution and connectivity relative to landscape factors of habitat and human influence.

STUDY AREA

Our study area, proposed for survey over a two-year period, is defined by drainages of Toba and Bute Inlets within the Toba-Bute and Homathko GBPUs (Figure 1). The area occurs within the Northern Pacific Ranges ecosection and is composed of various subzones of the Coastal Western Hemlock and Mountain Hemlock biogeoclimatic ecosystem zones in addition to Alpine Tundra (Meidinger and Pojar 1991). Specifically, our year-1 sampling area is defined by the drainages of Toba Inlet and that of the Orford River which drains into Bute Inlet. This sampling area encompasses 3,675 km^2 including ice, rock and other inherently unsuitable grizzly bear habitat. Our proposed year-2 sampling area is defined primarily by drainages of the Southgate and Homathko Rivers, and encompasses ~6,000 km^2 although much of this is habitat known to be inherently unsuitable to grizzly bears and cannot be sampled. The main stem valleys in the study area and some of their tributaries have a history of industrial human activity that has primarily been logging, but development for hydro-electric generation is also currently prevalent in some parts of the study area. The study area is accessible to human vehicle traffic by boat/barge only.

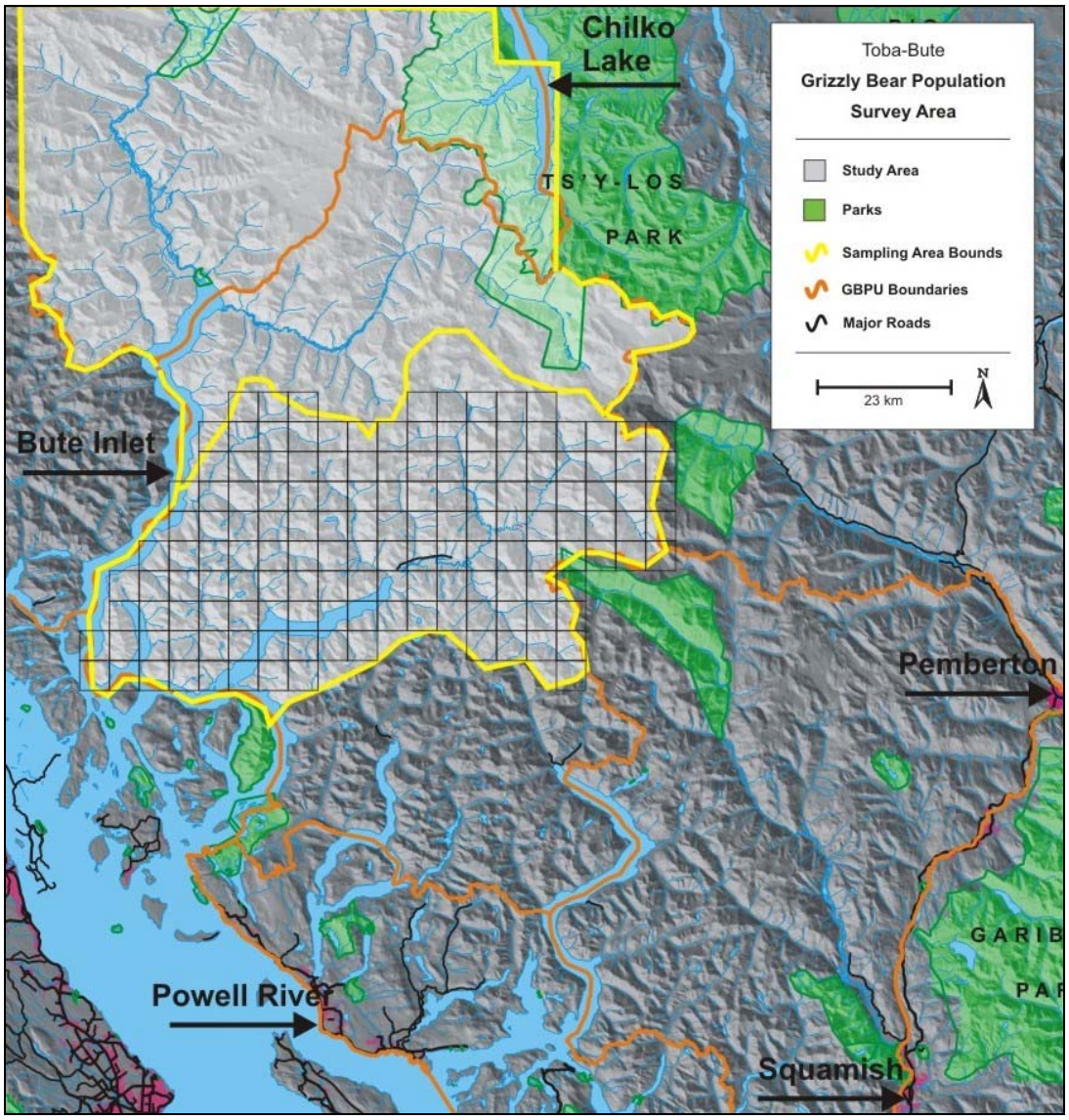

Figure 1. Toba-Bute grizzly bear population study area within the southern Coast Ranges of southwestern British Columbia. Field sampling within the southern (Toba Drainage) survey area was completed in 2008 (sampling grid shown). The northern (Southgate-Homathko) survey area is proposed for 2009.

METHODS

Field Sampling

We have split the study area into two annual sampling grids defined to maximize geographic closure of the resident grizzly bear population. In this first of two years, our sampling area totaled 3,675 km^2. To sample grizzly bear occurrence, we deployed stations to snag grizzly bear hair remotely and noninvasively, generally consistent with Woods et al. (1999). Stations were systematic-randomly distributed according to a grid with a 5 x 5 km cell size. We established a sampling site in each of 99 cells, and excluded 48 cells due to a lack of potential grizzly bear habitat and/or a suitable helicopter landing site. Using consistent criteria based on office evaluation and aircraft reconnaissance, we selected sites within each cell to maximize the likelihood of grizzly bear detection (in addition to helicopter landing-ability), with some also placed strategically within what are expected to be movement "pinch-points". At each site, a single strand (~25 m) of standard four-pronged barbed-wire was placed around a group of trees at a height of 40-50 cm to form a closed polygon, within which a small brush pile was built and baited with a liquid lure consisting of 3.8 litres rotted cow blood and 1.9 litres fish oil. We installed sites using two crews of three to maximize the synchronicity in session-dates among sites.

We accessed all sampling sites by helicopter (Astar™ 350) for both installation and subsequent checks. Consistent with our previous sampling during recent years in the southern Coast Ranges, our effort consisted of four sampling sessions of at least ten days each, from early June to early August. Between sessions, we collected hair samples, sterilized wire-barbs, and re-lured but did not move stations. Samples collected during each year (including probable black bears) were stored and we built an associated database by site (cell) and session.

Genotyping

All hair-snag samples were sent to Wildlife Genetics International (WGI) of Nelson, BC, for DNA analysis under the supervision of Dr. David Paetkau. Laboratory analyses have not been completed at the time of this report. Below, we present an overview of our intended methods.

Sample Subselection & Species Assignment – Although visual inspection in the laboratory can be used to exclude many if not most black bear samples with guard hairs (Woods et al. 1999), we expect that many of our samples will be underfur and cannot be visually screened in this way. We will apply subsampling rules to avoid costly redundancy in DNA extraction and analysis among samples. Specifically, samples collected on adjacent barbs are to be considered eligible for analysis if they were at either end of the contiguous sample string and were separated from the other "eligible" sample by at least one barb. Samples within an adjacency string are to be selected if the outer sample was of poor quality. Using these criteria, all eligible samples with guard-hairs are to be evaluated to species for a given site (cell) and session. Species determination will involve visual inspection of guard-hair shafts to exclude

obvious black bears, and a single-locus (G10J) test will confirm the species of remaining samples (associated alleles are odd-numbered in grizzly bears and even-numbered in black bears). These results and the colour of all other (underfur) samples not analyzed are to be recorded in the database. Species is to be initially determined for at least half (to a maximum of four) of all eligible samples for each site and session. If necessary to meet this criterion, species will be genetically determined from other eligible samples (underfur) with priority given to those with lighter-coloured hairs. If the above criteria results in a grizzly bear detection for a given site/session, then it will be ensured that the species test is conducted for half of all eligible samples, with no maximum, and according to an alternating selection of samples from their sequential order. Genotyping of grizzly bear DNA samples is then to be conducted to at least seven loci for identification of individual bears (see Selection and Variability of Genetic Markers, below).

Selection and Variability of Genetic Markers – The use of a minimum number of genetic markers is required to discriminate among individual grizzly bears with acceptably low error rates (Paetkau 2004). In selecting makers at the outset of analyses for any of our southern Coast Ranges samples, WGI initially looked to the Owikeno and Kingcome studies (S. Himmer, *unpubl. data*) for guidance. In comparison to these datasets, WGI found significantly lower genetic variability among grizzly bears across the southern Coast Ranges, including those from the Toba drainage (C. Apps et al., *unpubl. data*). Hence, WGI has selected a set of markers that is slightly different from those normally used, and for the Toba and Bute drainages, we expect that seven markers will be used rather than the five or six that are normally adequate for individual identity. Following the seven-locus analysis, all individuals are to be profiled to 15 loci for analysis of regional population genetics and associated spatial relationships. Any individuals we find to be genetically similar to those from the relatively homogenous Stein-Nahatlatch population will be re-analyzed to ten loci to avoid the potential error of identifying as one bear what is in fact multiple individuals. After routine error-checking, it is highly improbable that the number of individuals identified will be overestimated due to inconsistent genotyping of different samples from the same individual (Paetkau 2004). From our work to date in the larger region, we know there to be considerable genetic structuring among grizzly bears across the southern Coast Ranges, conforming to spatially defined groups (C. Apps et al., *unpubl. data*). Based on our 15-locus analysis, we will place individual grizzly bears sampled in the Toba and Bute drainages into a context of historical gene flow and population connectivity across the larger region.

Confirmation of Species Identity – WGI has found the standard species test (using the G10J marker) to be completely reliable for differentiating black from grizzly bears. However, for independent confirmation, they will consider allele frequency data for other makers and will perform a six-locus assignment test against a sample of known black bears captured during a radiotelemetry study. Results will provide an unambiguous confirmation that all samples successfully genotyped to individual are in fact from grizzly bears (Paetkau 2004).

Microsatellite Analysis and Error Checking for Individual Identification – Each grizzly bear sample will be genotyped for individual identity. This involves a step-down process of exclusion and subsequent error-checking to ensure that the identification of unique genotypes is appropriately conservative but that individuals can be unequivocally distinguished from even their close relatives (Taberlet et al. 1996, Mills et al. 2000, Paetkau 2003). Samples that do not produce acceptable results for at least four of the seven loci will be excluded from further consideration. An enhanced second stage of analysis will be conducted for samples that produce results at four to six loci resulting in a final set that produces results for all seven loci. In the third (error-checking) stage, a computer search will be conducted on all successfully genotyped samples to identify pairs with suspiciously similar genotypes (i.e., mismatch at only one or two loci), and these will be re-analyzed to identify or rule-out genotyping errors. An automated search for identical genotypes will then be conducted and multiple samples from the same individual will be identified.

Gender Analysis – For each individual grizzly bear identified, WGI will analyze for gender based on a size polymorphism in the amelogenin gene (Ennis and Gallagher 1994).

Estimating Population Abundance

This study is intended to address the primary objectives related to the estimation of current population abundance to assist in the assessment of cumulative human impacts and to provide a baseline for long-term population trend monitoring. Our field sampling approach was designed to optimally address this objective and that of modeling potential population distribution. In particular, our spatial sampling intensity was relatively high and we expect this will result in relatively high recapture rates, relatively low individual heterogeneity in detection probability (*sensu* Boulanger et al. 2004), and thus adequate power and minimal potential for bias in the estimation of population size.

Our approach to population estimation will involve the application of a K-sample capture-recapture design (Williams et al. 2002) with individuals identified through genetic profiling (described above). Annual sampling areas are defined to maximize geographic and demographic closure. We will evaluate our data for the selection of an appropriate estimator and will base model selection on quantitative assessment of our data coupled with knowledge of bear behaviour, as well as earlier simulations (Otis et al. 1978, Mowat and Strobeck 2000, Boulanger et al. 2007). We will adjust population estimates for potential bias caused by incomplete geographic closure using standard techniques (e.g., Boulanger and McLellan 2001).

Modeling Population Distribution and Habitat Cores

In addition to deriving a-spatial estimates of grizzly bear population abundance specific to annual sampling areas, an important goal of this study is to model the spatial distribution of that population and landscapes that are likely to represent population cores, peripheries and linkages among them. Such predictions are highly relevant to conservation planning and the assessment and mitigation of potential human impacts. To this end, we plan on conducting spatial analyses of our data relative to landscape factors of habitat and human influence in order to explain and predict (spatial) patterns of grizzly bear abundance and distribution (*sensu* Apps et al. 2004). Specifically, we will evaluate landscape composition relative to grizzly bear detection frequency sampled at the scale of population distribution across the two-year study area. We will then use generalized linear modeling as the basis for a probability-based spatial allocation of derived population estimates. Results and predictive output provide a foundation for local planning to minimize and mitigate population-level impacts to grizzly bears within the study area.

RESULTS

Samples

We deployed 99 hair-snag stations among 147 grid cells during our 2008 (year-1) work in the Toba drainage (Figure 2). We began deploying stations on 13 June and all stations were removed by 6 August. Session dates and duration varied slightly due to weather (Appendix 1), with session duration averaging 12.8 days and ranging from 11.2 to 14.9 days. Among stations and across four sampling sessions we collected 2,099 hair-snag samples (Figure 3). The laboratory analyses described above (see Genotyping) have yet to be completed at the time of this report.

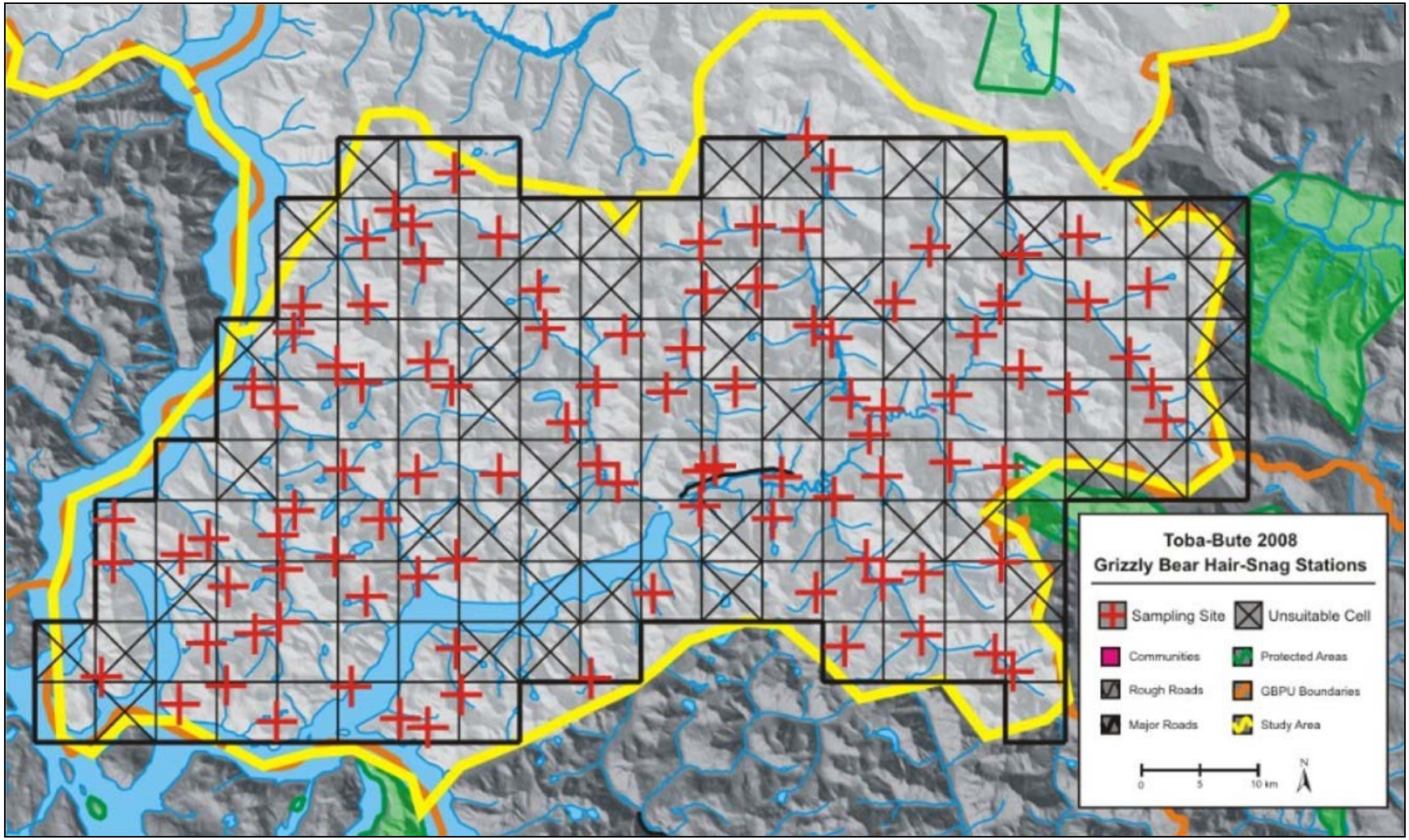

Figure 2. Grid and stations sampled during 2008 within the Toba-Bute grizzly bear population study area, southern Coast Ranges of southwestern BC.

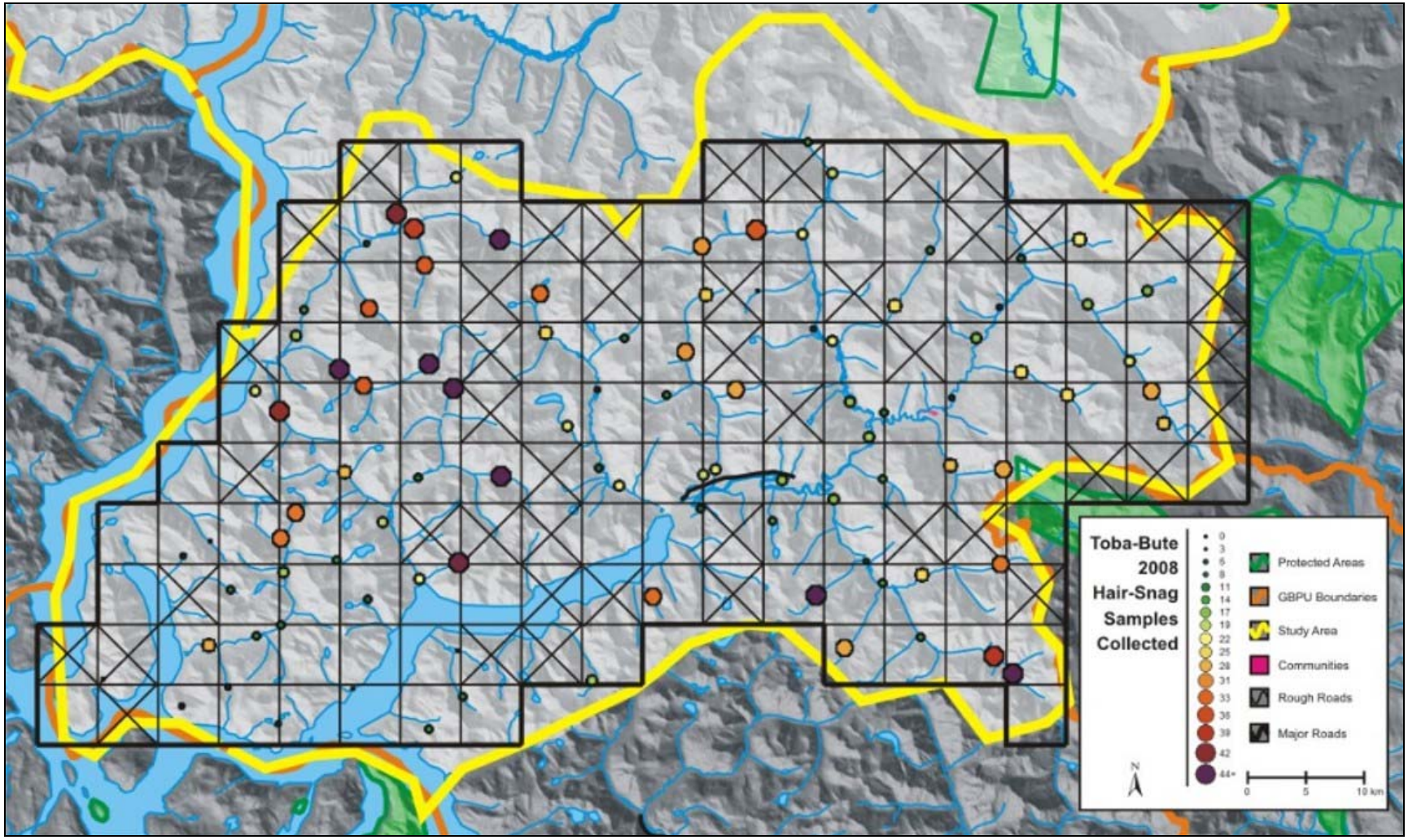

Figure 3. Hair-snag samples collected during 2008 within the Toba-Bute grizzly bear population study area, southern Coast Ranges of southwestern BC.

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Appendix 1. Start date (duration) of grizzly bear hair-snag/DNA sampling sessions in the Toba drainage of British Columbia's southern Coast Ranges during 2008.

	Start Date (Duration Days)			
Cell	Session I	Session II	Session III	Session IV
2	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
3	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
6	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
10	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
11	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
12	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
15	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
16	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
17	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
18	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
19	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
22	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
25	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
26	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
27	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
29	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
31	15/6 (12)	27/6 (15)	12/7 (12)	24/7 (12)
33	15/6 (12)	27/6 (14)	11/7 (10)	21/7 (14)
35	15/6 (12)	27/6 (14)	11/7 (10)	21/7 (14)
36	13/6 (14)	27/6 (14)	11/7 (10)	21/7 (14)
37	13/6 (14)	27/6 (14)	11/7 (10)	21/7 (14)
38	13/6 (14)	27/6 (14)	11/7 (10)	21/7 (14)
39	13/6 (14)	27/6 (14)	11/7 (10)	21/7 (14)
42	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
43	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
44	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
46	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
47	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
48	16/6 (10)	26/6 (16)	12/7 (12)	24/7 (12)
50	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
51	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
53	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
54	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
55	13/6 (14)	27/6 (14)	11/7 (10)	21/7 (14)
58	16/6 (11)	27/6 (16)	13/7 (12)	25/7 (12)
59	16/6 (11)	27/6 (16)	13/7 (12)	25/7 (12)
60	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
61	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (13)

Cell	Start Date (Duration Days)			
	Session I	Session II	Session III	Session IV
63	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
64	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
65	16/6 (10)	26/6 (16)	12/7 (12)	24/7 (12)
66	15/6 (11)	26/6 (16)	12/7 (12)	24/7 (12)
68	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
69	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
70	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
71	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
73	13/6 (14)	27/6 (14)	11/7 (10)	21/7 (14)
75	16/6 (12)	28/6 (15)	13/7 (12)	25/7 (12)
77	17/6 (11)	28/6 (15)	13/7 (12)	25/7 (12)
78	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
79	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
80	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
82	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
83	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
84	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
85	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
86	15/6 (11)	26/6 (15)	11/7 (10)	21/7 (14)
87	15/6 (12)	27/6 (14)	11/7 (7)	18/7 (17)
88	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
89	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
92	13/6 (14)	27/6 (14)	11/7 (10)	21/7 (14)
93	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
94	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
95	16/6 (12)	28/6 (15)	13/7 (12)	25/7 (12)
96	16/6 (12)	28/6 (15)	13/7 (12)	25/7 (12)
97	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
101	15/6 (12)	27/6 (15)	12/7 (12)	24/7 (12)
102	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
104	15/6 (12)	27/6 (15)	12/7 (12)	24/7 (12)
105	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
108	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
109	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
111	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
112	17/6 (11)	28/6 (15)	13/7 (12)	25/7 (12)
113	17/6 (11)	28/6 (15)	13/7 (12)	25/7 (12)
114	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (12)
115	16/6 (11)	27/6 (15)	12/7 (12)	24/7 (13)
118	13/6 (15)	28/6 (15)	13/7 (12)	25/7 (12)

Cell	Start Date (Duration Days)			
	Session I	Session II	Session III	Session IV
120	13/6 (13)	26/6 (16)	12/7 (12)	24/7 (12)
121	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
122	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
123	13/6 (13)	26/6 (15)	11/7 (10)	21/7 (14)
127	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
128	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
129	17/6 (11)	28/6 (15)	13/7 (12)	25/7 (12)
130	17/6 (11)	28/6 (15)	13/7 (12)	25/7 (12)
131	13/6 (15)	28/6 (15)	13/7 (12)	25/7 (12)
134	13/6 (15)	28/6 (15)	13/7 (12)	25/7 (12)
135	15/6 (13)	28/6 (14)	12/7 (12)	24/7 (12)
136	15/6 (12)	27/6 (14)	11/7 (10)	21/7 (15)
137	15/6 (12)	27/6 (14)	11/7 (10)	21/7 (15)
138	15/6 (12)	27/6 (14)	11/7 (10)	21/7 (15)
139	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
141	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
142	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
143	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
144	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
145	15/6 (13)	28/6 (15)	13/7 (12)	25/7 (12)
146	13/6 (15)	28/6 (15)	13/7 (12)	25/7 (12)
Average	14/6 (12.1)	26/6 (14.9)	11/7 (11.2)	23/7 (12.9)