GRIZZLY BEAR POPULATION DENSITY AND DISTRIBUTION IN THE SOUTHERN COAST RANGES OF BRITISH COLUMBIA

Annual Progress & Data Summary Report

Year 2

2005/2006

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PROJECT OVERVIEW

There is little known of grizzly bear density, distribution, or population connectivity in British Columbia's southern Coast Ranges. This knowledge gap is of concern given the wide range of land resource demands, particularly in and around the Sea to Sky Planning Area where there is potential for excessive cumulative impacts resulting from the area's growing recreational popularity, associated development trends, and its accessibility from the nearby lower mainland. Currently, 4 of the 5 grizzly bear population units (GBPUs) in this region are considered "threatened". Addressing grizzly bear conservation issues such as mortality risk, population connectivity, and reserve allocation requires (1) an understanding of the density and spatial distribution of the regional population, (2) an understanding of the factors that influence this pattern, and (3) a means to integrate this knowledge within local and regional planning. Using established and proven noninvasive hair-snag techniques and DNA analyses, we are systematically sampling grizzly bear occurrence across a 40,000 km^2 area of the BC southern Coast Ranges over a period of 3 to 4 years. Population density will be estimated within defined areas using mark-recapture methods. Over a greater extrapolation area, grizzly bear population density, distribution and connectivity will be empirically modeled relative to landscape factors of habitat and human influence. Results will provide a basis for identifying population core and linkage landscapes, and for understanding the factors that determine them. Given an adequate sample size, we will also evaluate the influence of habitat conditions and human activity on grizzly bear gene flow and population connectivity at broad, landscape scales. This may provide a basis for more appropriate delineation of grizzly bear population units.

Products and information from this study will be provided in a form that can be easily and directly integrated into resource planning exercises, and that can provide decision-support for mitigating development impacts. This will benefit not only grizzly bears but many other species that may also be affected by cumulative human development and the fragmentation of habitat and populations. Without this study, managers and decision makers will be limited to purely subjective "best-guesses" in supporting resource planning decisions and mitigation options. Information from this study is also essential in evaluating the needs and options for grizzly bear recovery within defined GBPUs, and in assessing the likelihood that grizzly bear population harvest can eventually be reinstated in some landscapes. Finally, results will help to identify landscapes where more intensive research into grizzly bear movements and/or demographics is appropriate and feasible. 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 BC. This includes grizzly bear objectives specific to both the Lillooet and Sea to Sky LRMPs, as they progress toward government consultation with First Nations and into implementation.

INTRODUCTION

Issue

The British Columbia Grizzly Bear Conservation Strategy (MELP 1995) calls for the identification of core population areas, where human activities not compatible with grizzly bear conservation can be controlled, and for the provision of bear movement and genetic interchange among such areas. These considerations are especially important near the southern edge of grizzly bear range where populations are likely to exhibit a source-sink or metapopulation structure (Doak 1995, Craighead and Vyse 1996, Proctor et al. 2002). Most of this southern range lies in BC (McLellan 1998).

The distribution of grizzly bear core habitat and populations may be especially patchy in the southern Coast Ranges of BC given the high diversity of natural conditions and varying types and levels of human activity (Apps and Hamilton 2002). However, despite a wide range of land resource demands, there is little known of grizzly bear density, distribution, or population connectivity in this region. This knowledge gap has been of particular concern in and around the Sea to Sky Planning Area (Squamish Forest District) due to the potential for excessive cumulative impacts resulting from the area's growing recreational popularity, associated development trends (e.g., 2010 Winter Olympics), and its accessibility from the nearby lower mainland. Anecdotal reports suggest considerable variation in bear occurrence and habitat quality, and 4 of the 5 local grizzly bear population units are currently considered "threatened" (current population assumed to be 1-50% of potential; Hamilton et al. 2004). Understanding the spatial distribution of grizzly bears locally and the factors that influence this structure is necessary to address conservation issues such as mortality risk, population connectivity, and reserve allocation.

The maintenance and/or recovery of the local population requires that sound information on habitat quality and distribution as well as population connectivity be integrated with local and regional planning. As a first step in addressing this need, 2 subjective modeling efforts were completed (Apps 2001, Apps and Hamilton 2002). In both cases, spatial outputs have been associated with considerable uncertainty and have highlighted the importance of empirical data to develop refined and defensible predictions.

Objectives

1. Systematically sample grizzly bear occurrence over a defined study area using hair-snag techniques and DNA analysis for species and individual identification.
2. Apply mark-recapture methods to estimate grizzly bear population density within the survey areas.
3. Empirically model population density, distribution and connectivity relative to landscape factors of habitat and human influence. This will form the basis for (a) identifying population core and linkage landscapes, and (b) understanding the factors that determine them.
4. Given an adequate sample size, evaluate the influence of habitat conditions and human activity on grizzly bear gene flow at broad, landscape scales.

Localized Objectives Specific to Ashlu Creek

The involvement of Ledcor Power in Year 1 of this study was specifically to elucidate the status, abundance, and distribution of grizzly bears in the region of the company's proposed run-of-river hydroelectric development on Ashlu Creek, a tributary of the lower Squamish River. As described below (see Methods), this objective required ancillary sampling to establish the likelihood that grizzly bears are making movements through the Ashlu drainage and proposed development site to the Squamish River during the late-summer and fall to feed on spawning salmon. Results are expected to contribute to baseline knowledge of seasonal movements by grizzly bears that likely are though the development zone.

STUDY AREA

Multi-Year Focal Area

The multi-year focal area for this project encompasses approximately 40,000 km^2 of several major watersheds at the southwestern extent of current grizzly bear range. It is defined by the following grizzly bear population units (GBPUs) that are currently assigned a conservation status of "threatened" (current population = 1 – 50% of potential): Squamish-Lillooet, Garibaldi-Pitt, Stein-Nahatlatch, and the southern half of the South Chilcotin Ranges, as well as the Toba-Bute GBPU that is considered "viable" (Hamilton et al. 2004; Figure 1). These include the Southgate, Toba, Jervis, Squamish, Lillooet, Seton, Cayoosh, Bridge, Stein, Nahatlatch, and Pitt drainages. The overall focal area lies within both the Coast and Mountains Ecoprovince and the Southern Interior Ecoprovince (Demarchi 1996). The wetter, western portion falls within the Pacific Ranges Ecoregion, defining the southernmost ranges of BC's Coast Mountains; while in the northeastern portion of the study area, the Interior Transition Ranges Ecoregion is characterized by a drier coast-interior transition climate. There is currently no general open season or limited entry hunting for grizzly bears within the greater focal area.

Year 1 (2004) and Year 2 (2005) Sampling Areas

Our Year 1 (2004) and Year 2 (2005) sampling areas were subsections of the above-described multi-year focal area. They were each defined according to grizzly bear population unit boundaries and our expectations of increased demographic "closure" to current populations relative to geographic features. They were also constrained by budgetary and logistical considerations within the context of what we determined to be a minimum sampling intensity and duration (see Methods, below). We expected that these sampling areas extended well into landscapes currently assumed to be unoccupied by grizzly bears (Hamilton et al. 2004). We made this choice in light of our objective to better understand and model population distribution, and considering the highly generalized and anecdotal nature of the "occupied line". Thus, the Year 1 (2004) sampling area was 9,600 km^2 and encompassed all of the Squamish-Lillooet and part of the Toba-Bute GBPUs (Figure 1). The Year 2 (2005) sampling area comprised 8,200 km^2 and corresponded to the Stein-Nahatlatch GBPU.

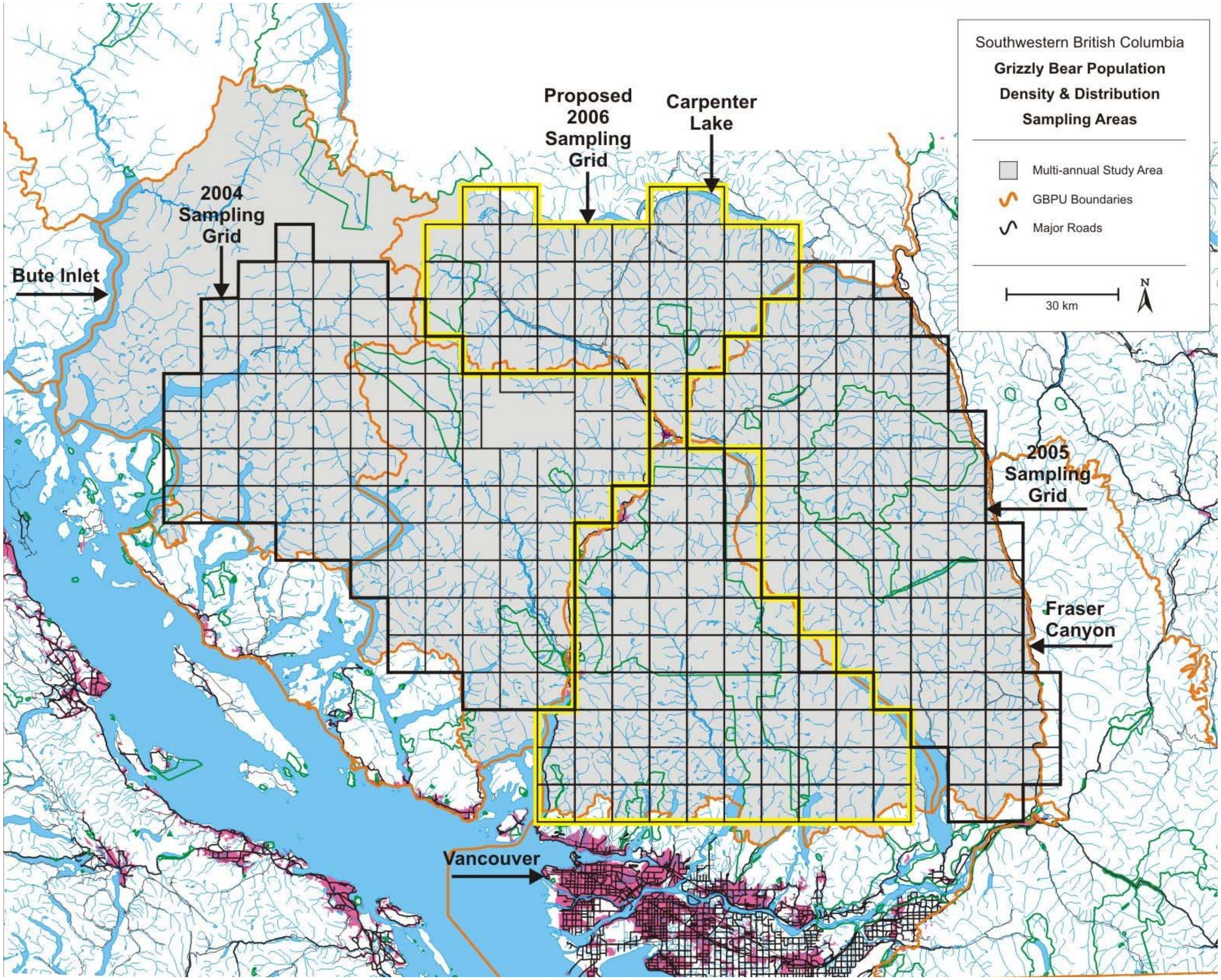

Figure 1. Multi-year focal area for sampling grizzly bear population density and distribution in the southern Coast Ranges of BC.

METHODS

Background

For bears, there have been recent advancements in noninvasive hair-capture, genetic tagging, and population density estimation (Woods et al. 1999, Mowat and Strobeck 2000, Boulanger and McLellan 2001, Boulanger et al. 2004). These developments have led to methods to develop spatially-explicit extrapolations of population density and to describe and test relationships between bear persistence and spatial factors of habitat and human influence (Apps et al. 2004). With adequate sample sizes, the degree of gene flow among broad landscapes can be evaluated and potential restricting factors can be identified (Proctor et al. 2002). Below, we describe progress towards addressing our study objectives using a combination of the above methods.

Year 1 (2004) and Year 2 (2005) Sampling

Field Methods – We have proposed that this survey be conducted over a 3 – 4 year period, with the multi-year study area split into at least 3 annual sampling areas of ~10,000 km^2. To sample grizzly bear occurrence, we are deploying noninvasive hair-snag stations (Woods et al. 1999). Stations are systematic-randomly distributed according to a grid with a 10 x 10 km cell size. We have sampled 90 cells during year 1 and 82 cells during year 2. Using consistent criteria based on office evaluation and aircraft reconnaissance, sites within each cell were selected 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 4-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 (3.8 litres rotted cow blood and 1.9 litres fish oil). Sites were installed by teams of 2 or 3.

Site Checks & Sample Collection – During both years, all sites were accessed by helicopter (Astar 350) for both installation and subsequent checks. Our year-1 effort consisted of 4 sampling sessions of approximately 10 days each between 10 June and 29 July. We used the same protocol during year 2 (4 June start); however, we conducted an additional (5th) sampling session (7 August end) because we expected that the unusually cold and wet weather during the first 4 sessions would result in relatively low bear detection rates. Between sessions, hair samples were collected, wire barbs were sterilized, and stations were re-lured but not moved. Samples (including probable black bears) were collected and stored, and a database of samples by site (cell) and session was built.

Fall Movements by Grizzly Bears from the Ashlu Drainage to the Squamish River

A localized sampling effort during the fall 2004 was funded entirely by Ledcor Power Inc. The objective was to apply the non-invasive DNA hair-snag sampling methods described above to identify any grizzly bears that are likely to be making movements during late summer and fall from or through landscapes of the upper Ashlu to the Squamish River to forage on spawning salmon. Such movements would be expected to occur through a topographic “pinchpoint” within which much of the proposed Ashlu hydro-electric development would be situated. As part of the regional survey effort described above, probable grizzly bear hair samples were collected at 2 hair-snag sampling stations in the upper Ashlu drainage during June and July, 2004. From September 28 to November 27, 9 sampling stations were established and monitored at locations along the Squamish River at the Ashlu/Squamish confluence and both upstream and downstream along the Squamish

River. The sampling objective was to maximize the likelihood of detecting and obtaining DNA samples from any salmon-feeding grizzly bears in the area. By matching the genetic signatures of these samples to those obtained from samples collected in surrounding drainages earlier in the year (when grizzly bears are more likely to be occupying the core of their home ranges), general movements may be inferred. Matches made to grizzly bears detected in the upper Ashlu will represent baseline knowledge of seasonal movements by grizzly bears that likely are though the development zone. It is against these baseline data that monitoring results during and after the development phase can be compared.

Genotyping of Samples

All hair-snag samples were sent to Wildlife Genetics International (WGI) of Nelson, BC, for DNA analysis under the supervision of Dr. David Paetkau.

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), many of our samples were of underfur and could not be visually screened in this way (D. Paetkau, WGI, *pers. comm.*). Considering the total number of samples collected (year 1 = 2,017; year 2 = 1,519), we applied subsampling rules to ensure that we would not exceed the available budget for DNA analysis. Specifically, samples collected on adjacent barbs were 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 were to be selected if the outer sample was of poor quality. Using these criteria, all eligible samples with guard-hairs were evaluated to species for a given site (cell) and session. Species determination involved visual inspection of guard-hair shafts to exclude obvious black bears, and a single-locus (G10J) test to 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 were recorded in the database. Species was to be initially determined for at least half (to a maximum of 4) of all eligible samples for each site and session. If necessary to meet this criterion, species was genetically determined from other eligible samples (underfur) with priority given to those with lighter-coloured hairs. If the above criteria resulted in a grizzly bear detection for a given site/session, then it was ensured that the species test was 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 was then conducted to 7 loci (Year 1) and 15 loci (Year 2) 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 analysis outset, WGI initially looked to the Owikeno and Kingcome studies (S. Himmer, *unpubl. data*) for guidance. In comparison to these datasets, WGI found lower genetic variability in the 59 of our Year-1 samples initially evaluated (see Results). This was especially apparent for one particular marker, which was excluded from consideration for individual genotyping. The genetic variability among our Year-2 samples was considerably lower still. Rather than the 5 or 6 markers typically required for other grizzly bear populations, WGI used 7 markers for individual genotyping of Year-1 samples. These same markers were used for Year-2 samples, but an additional 8 were also used (15 total) due to the very low genetic variability among individuals in this sampling area. After routine error-checking, it is highly improbable that the number of individuals identified has been overestimated due to inconsistent genotyping of different samples from the same individual (ibid.).

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 considered allele frequency data for other makers and performed a 6-locus assignment test against a sample of known black bears captured during a radiotelemetry study. Results provided an unambiguous confirmation that all samples successfully genotyped to individual were in fact from grizzly bears (ibid.).

Microsatellite Analysis and Error Checking for Individual Identification – Each grizzly bear sample was genotyped for individual identity. This involved a step-down process of exclusion and subsequent error-checking to ensure that the identification of unique genotypes was appropriately conservative but that individuals could be unequivocally distinguished from even their close relatives (Taberlet et al. 1996, Mills et al. 2000, Paetkau 2003). Samples that did not produce acceptable results for at least 4 of the 7 loci were excluded from further consideration. An enhanced second stage of analysis was conducted for samples that produced results at 4-6 loci resulting in a final set that produced results for all 7 loci. In the third (error-checking) stage, a computer search was conducted on all successfully genotyped samples to identify pairs with suspiciously similar genotypes (i.e., mismatch at only 1 or 2 loci), and these were re-analyzed to identify or rule-out genotyping errors. An automated search for identical genotypes was then conducted and multiple samples from the same individual were identified.

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

RESULTS & DISCUSSION – PRELIMINARY DATA – YEAR-1

Results

Samples Collected – During our Year 1 (2004) sampling effort, we collected 2,017 hair-snag samples over the 90 stations (cells), and 4 sessions, as well as from the 9 stations sampled during the fall. Of the 360 site/session combinations during the spring/summer, ≥ 1 sample was obtained from 306 (85%) site/sessions while 54 (15%) site/sessions yielded no samples. All samples were sent to the DNA lab (Wildlife Genetics International, Nelson, BC) where they were to be analyzed and/or stored in a controlled environment for at least 5 years.

Sample Classification – After processing by WGI, the 2,017 samples fell into the following classes (D. Paetkau, *unpubl. report*): 9% lacked suitable material for extraction; 46% were not extracted either because they had the visual appearance of black bear hair or because of subselection rules; 34% were genetically determined to be from black bears; 2% produced insufficient data to establish individual identify, either during the species test or during the multi-loci analysis; while 9% were grizzly bear samples that could be assigned to individuals.

Genetic Variability – In the evaluation of the initial 59 grizzly bear samples, WGI found heterozygosity (H_e) to be 61%, which is lower than samples collected for the Owikeno study further to the north (69%). The H_e from our samples is also lower than that reported for most other mainland populations studied (Paetkau et al. 1998), which are as high as 80% (Nahanni watershed, NWT; Weaver 2006). Results from our samples suggest low population connectivity with grizzly bears further north in the southern Coast Ranges. This will be explored further in a provincial-scale population connectivity evaluation for which our samples have been contributed and will be analyzed to 15 loci (M. Proctor and D. Paetkau, *pers. comm.*).

Individuals and Independent Detections – Using the subsampling criteria, genetic analyses indicated a minimum of 98 detections of 58 (33M, 25F) different grizzly bears. In total, 111 independent detections were recorded, including known grizzly bear detections for which individual identity could not be established (Table 1). During the fall (Ashlu/Squamish) sampling effort, at least 3 grizzly bears were detected 10 times (Table 2). One (M8) had been detected during 3 of the 4 spring/summer sampling sessions, while 2 others (M57, M58) had not been previously detected. Of the 360 site/session combinations during spring/summer sampling, at least 1 grizzly bear was detected at 91 (25%), at least 1 black bear was detected at 252 (70%), and both species were detected at 48 (13%) site/sessions. Variation in grizzly bear detection among sessions was relatively minor, though detection rate was slightly higher in the first session. The overall grizzly bear recapture rate among sessions was 0.19 (Table 3). This rate is surprisingly high given the low intensity of our sampling effort. For example, at least 4 other studies in British Columbia that used smaller cell sizes obtained lower capture probabilities, and one study that also achieved 0.19 used 7 x 7 km cells (Boulanger et al. 2002). Our high capture rate (relative to sampling intensity) may be a result of more extensive movements of grizzly bears (particularly males) in this population, perhaps due to the extremely rugged terrain and high amounts of inherently unsuitable habitat. We summarize known movements in Table 4.

Table 1. Visits of individual grizzly bears to hair-snag DNA stations by sampling cell and session in the Squamish-Lillooet and Toba-Bute grizzly bear population units of southwest British Columbia, June-July, 2004. Identifier codes refer to males "M" or females "F". "GB" refers to a grizzly bear detection without individual identification.

Cell	**Session I** Start: 10 June[a] End: 23 June	**Session II** Start: 23 June End: 3 July	**Session III** Start: 3 July End: 13 July	**Session IV** Start: 13 July End: 23 July	**Total (hits-indiv)**
1	M1				1 – 1
2	F2				1 – 1
3	M3		M39, F38	M39	4 – 3
4	F4		M40	M40	3 – 2
5				F47, F48	2 – 2
6	1 GB				1 – 1
7	M5	1 GB	1 GB	M5	4 – 1
8	M6	M26		M49	3 – 3
9		M27		M50	2 – 2
10		F28	M41		2 – 2
11		M30, F29	M30		3 – 2
12				M42	1 – 1
13			M42	M42	2 – 1
14		M10			1 – 1
15	M7, F31	M7, F31			4 – 2
16	M8		M7		2 – 2
17	M8, M9				2 – 2
18					
19					
20			M10		1 – 1
21	M10				1 – 1
22			M43	1 GB	2 – 1
23	F11	F11		M51	3 – 2
24	M8		M43		2 – 2
25					
26					
27	M14, F12, F13, F15	M14, F15	M32	M14	8 – 5
28		M32, M33	M32, M33	M33	5 – 2
29					
30					
31					
32					
33					
34	M16	F11			2 – 2
35			F44	1 GB	2 – 1
36			F21		1 – 1
37			M8		1 – 1
38					
39	F17		1 GB		2 – 1
40					
41					
42					
43					
44	F18	F34	1 GB	M52	4 – 3

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Table 1. Continued.

Cell	**Session I** Start: 10 June[a] End: 23 June	**Session II** Start: 23 June End: 3 July	**Session III** Start: 3 July End: 13 July	**Session IV** Start: 13 July End: 23 July	**Total (hits-indiv)**
45	F19			1 GB	2 – 1
46		M35		M35	2 – 1
47					
48					
49		1 GB			1 – 1
50				1 GB	1 – 1
51					
52					
53					
54					
55					
56					
57	M16				1 – 1
58					
59					
60	M20	M20	M20	1 GB	4 – 1
61	F21			M54, F53	3 – 3
62					
63	M23, F22	M23, F22, F36	M45, F36	F22	8 – 4
64					
65					
66			M16	1 GB	2 – 1
67					
68				F55	1 – 1
69		M8, M20	M20		3 – 2
70					
71				F36	1 – 1
72					
73					
74					
75	F24, F25			M20	3 – 3
76					
77					
78					
79					
80				F37	1 – 1
81					
82					
83		F24, F37	1 GB		3 – 2
84			M46		1 – 1
85			M46		1 – 1
86				M56	1 – 1
87					
88					
89					
90					
New Bears	25	12	9	10	111 - 98

[a] **Precise dates varied slightly among stations.**

Table 2. Sites, frequency, and results of hair-snag DNA sampling for grizzly bear detection along the lower Squamish River near the mouth of Ashlu Creek, October – November, 2004.

Site	Easting[a]	Northing	Check Date	Black Bear	Grizzly Bear	Grizzly Identified
Shovelnose #1	476102	5544637	Oct. 04		X	
			Oct. 12	X	X	
			Oct. 18			
			Oct.25	X		
			Nov. 2			
			Nov. 8	X	X	M8
			Nov. 17			
			Nov. 27		X	
Shovelnose #2	476149	5544619	Nov. 17			
			Nov. 27	X		
Ashlu #1	477482	5528006	Oct. 4		X	M57, M58
			Oct. 12	X	X	M57, M58
			Oct. 18	X		
			Oct. 25			
			Nov. 2	X		
			Nov.11			
			Nov. 17			
			Nov. 27		X	M57
Ashlu #2	478241	5527715	Oct. 20			
Ashlu #3	477224	5527943	Oct. 12	X		
			Oct. 18	X		
			Oct. 25			
			Nov.11			
Ashlu #4	477036	5528315	Nov. 17	X		
			Nov. 27			
Sigurd #1	478382	5527444	Oct. 25	X		
			Nov. 3	X		
			Nov. 8			
			Nov. 17	X		
			Nov. 27			
West Squamish #1	477802	5530223	Nov. 8			
			Nov. 17			
			Nov. 27		X	M57
Lovelywater Outlet #1	484476	5516733	Nov. 2			
			Nov. 12			

[a] UTM Zone 10, NAD27

Table 3. Capture summary by session for identified grizzly bears in the Squamish-Lillooet and Toba-Bute grizzly bear population units of southwest British Columbia, June-July, 2004.

ID#	Sex	Captures Per Session I	II	III	IV	Recapture Rate [a]	Fall Captures [b]
1	M	1				0	
2	F	1				0	
3	M	1				0	
4	F	1				0	
5	M	1			1	0.33	
6	M	1				0	
7	M	1	1	1		0.67	
8	M	3	1	1		0.67	1
9	M	1				0	
10	M	1	2	1		0.67	
11	F	1	2			0.33	
12	F	1				0	
13	F	1				0	
14	M	1	1		1	0.67	
15	F	1	1			0.33	
16	M	2		1		0.33	
17	F	1				0	
18	F	1				0	
19	F	1				0	
20	M	1	2	2	1	1	
21	F	1		1		0.33	
22	F	1	1		1	0.67	
23	M	1	1			0.33	
24	F	1	1			0.33	
25	F	1				0	
26	M		1			0	
27	M		1			0	
28	F		1			0	
29	F		1			0	
30	M		1	1		0.33	
31	F	1	1			0.33	
32	M		1	2		0.33	
33	M		1	1	1	0.67	
34	F		1			0	
35	M		1		1	0.33	
36	F		1	1	1	0.67	
37	F		1		1	0.33	
38	F			1		0	
39	M			1	1	0.33	
40	M			1	1	0.33	
41	M			1		0	
42	M			1	2	0.33	

Continues to next page…

Table 3. Continued.

ID#	Sex	Captures Per Session I	II	III	IV	Recapture Rate [a]	Fall Captures [b]
43	M			1		0	
44	F			1		0	
45	M			1		0	
46	M			2		0	
47	F				1	0	
48	F				1	0	
49	M				1	0	
50	M				1	0	
51	M				1	0	
52	M				1	0	
53	F				1	0	
54	M				1	0	
55	F				1	0	
56	M				1	0	
57	M						4
58	M						2
Summary		29	25	22	22	0.19	7

[a] Among sessions.

[b] Localized sampling during October/November along the Squamish River near the mouth of Ashlu Creek (see text for details).

Table 4. Maximum distance between multiple-detections of individual grizzly bears in the Squamish-Lillooet and Toba-Bute grizzly bear population units of southwest British Columbia, June-July, 2004. Bears with a maximum distance of 0 km between detections are those detected multiple times at a single station.

ID	Sex	Detections	Max Interval (Days)	Max Distance (Km)	Estimated Movement Area[a]
5	M	2	40	0	n/a
7	M	3	30	8	48
8	M	6	40	63	3,078
10	M	4	30	33	855
11	F	3	20	6	30
14	M	3	40	0	n/a
15	F	2	20	0	n/a
16	M	3	30	34	887
20	M	6	40	25	471
21	F	2	30	21	360
22	F	3	40	0	n/a
23	M	2	20	0	n/a
24	F	2	20	22	377
30	M	2	20	0	n/a
31	F	2	20	0	n/a
32	M	3	20	17	232
33	M	3	30	0	n/a
35	M	2	30	0	n/a
36	F	3	30	14	156
37	F	2	30	19	269
39	M	2	20	0	n/a
40	M	2	20	0	n/a
42	M	3	20	6	30
46	M	2	10	4	12

[a] Area (km^2) of a circle with diameter equal to the maximum distance between multiple detections.

Discussion

Spring/Summer Sampling – Generally, the distribution of grizzly bear detections matched landscapes that we expected to support resident animals, with some exceptions. Grizzly bears were detected in some landscapes where occupancy was uncertain (Figure 2). These included valleys leading to Salmon and Narrows Inlets (cells 80, 83, 84, 85, 86) and adjacent landscapes to the north that include the upper Ashlu drainage (cells 69, 75). Directly west of Jervis Inlet, grizzly bears were detected in the valleys of Brittania River and Slane Creek (cells 66, 57). Along the eastern edge of our sampling area, we detected grizzly bears between the Squamish River and Highway 99 in the upper Soo, Callaghan, and Brandywine drainages (cells 49, 50, 63, and 71). We also detected grizzly bears further north in the upper Pemberton (cell 39) and Ryan (cell 27, 28) drainages. It is also notable that we consistently did not detect grizzly bears directly east of Desolation Sound and in landscapes that drain to the upper reach of Powell Lake.

It should be noted that our sampling was conducted through late spring and early summer and that coastal grizzly bears are likely to have been well dispersed and gradually moving to higher elevations during our sampling period. We placed stations in relatively high elevation habitats where possible, but in several cases the only sites potentially available to us were valley-bottom and estuarine locations that are more likely to have been used earlier in the spring. Although it is important to acknowledge seasonal influences on site-specific detection rates, we felt that it was more important to sample the distribution of the population when bears were using landscapes most representative of annual home ranges, rather than at times when they may be more locally concentrated despite the higher detection rates that this may provide. Finally, it is important to note the potential influence of both weather and scent-lure on detection rates. Both temperature and precipitation will influence the attractiveness of hair-snag stations to bears, and stations were subject to a mix of weather conditions during the sampling period. Although detection rates will also be influenced by the lure being used, our lure and methods were standardized across sites and sessions.

Data Management – The interim database assembled from our sampling results includes records for all samples analyzed linked to cell, session, and station coordinates. Data have been consolidated and summarized according to species occurrence (Figure 2), the minimum number of different bears detected per site/session combination (Figure 3), and individual bears detected at stations and their frequency among sessions (Table 1; Figure 4).

Fall Sampling Near the Ashlu/Squamish Confluence – Of the 3 grizzly bears detected near the confluence of Ashlu Creek and the Squamish River during October and November, 2 had not been previously detected. However, 1 bear (M8) had been independently detected 5 times during the previous spring/summer sampling sessions (cells 16, 17, 24, 37, and 69). These detections were surprisingly widespread, and with the fall detection indicate a minimum home range of 792 km2 (actual home range is undoubtedly larger; see Table 4). Despite the fact that this bear was detected at site 69 in the upper Ashlu drainage, it is not obvious from the data that this bear moved directly between the upper Ashlu and the Squamish River as he may have come directly down the Squamish. However, given the extensive movements that M8 obviously does make and the number of other individual grizzly bears detected in the upper Ashlu and surrounding drainages (M20, M46, M56, F24, F25, F37, F55), it is likely that the lower Ashlu is at least periodically used as a movement route, particularly during the fall salmon run.

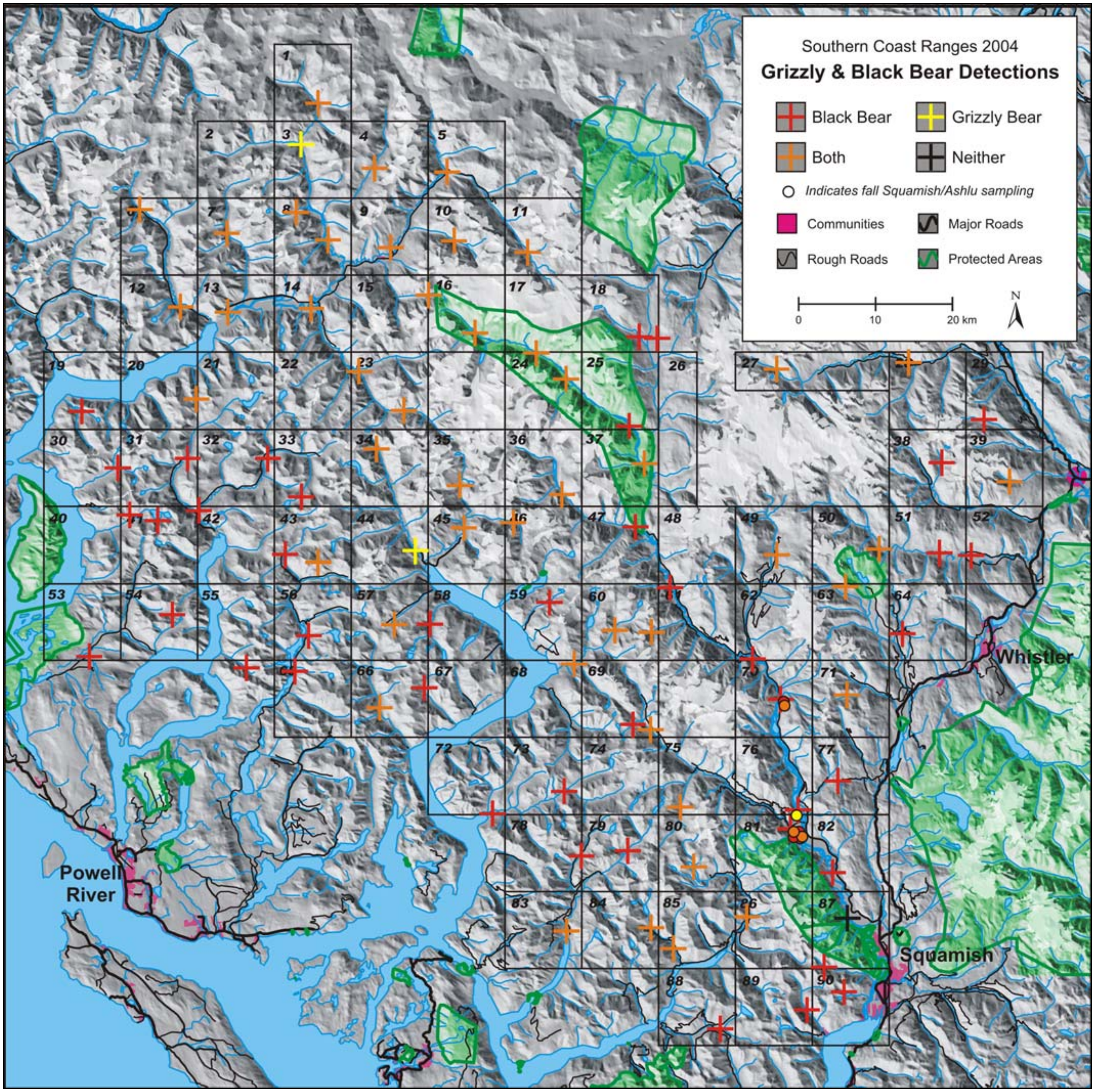

Figure 2. Detection of ≥ 1 black or grizzly bear at hair-snag DNA sampling stations across the Squamish-Lillooet and Toba-Bute (partial) grizzly bear population units of southwestern British Columbia. Data are from 4 sampling sessions during June and July of 2004. Additional detections from localized sampling during October and November, 2004, are also indicated (see legend).

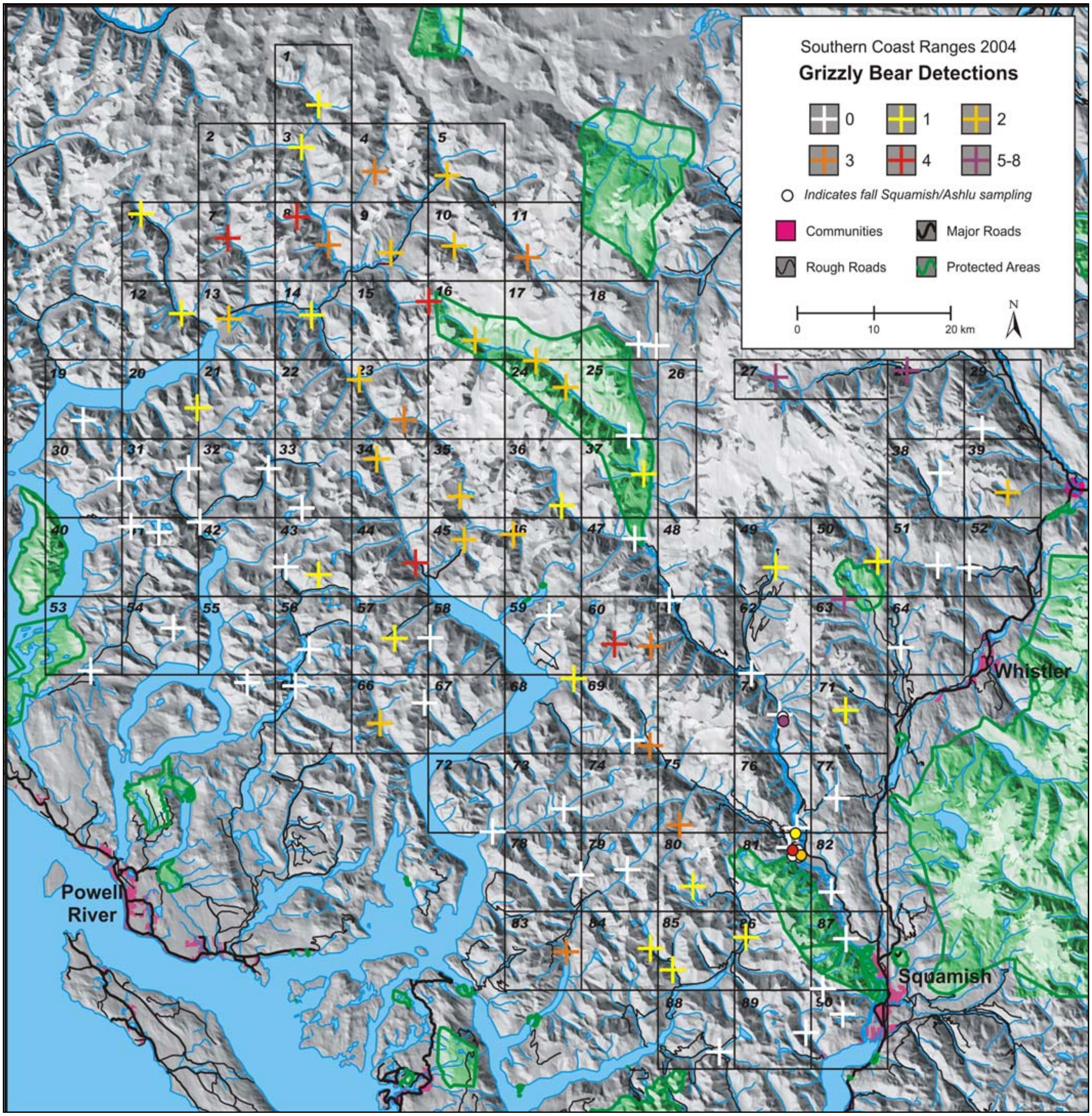

Figure 3. Independent detections by grizzly bears at hair-snag DNA sampling stations across the Squamish-Lillooet and Toba-Bute (partial) grizzly bear population units of southwestern British Columbia. Data are from 4 sampling sessions during June and July of 2004. Additional detections from localized sampling during October and November, 2004, are also indicated (see legend).

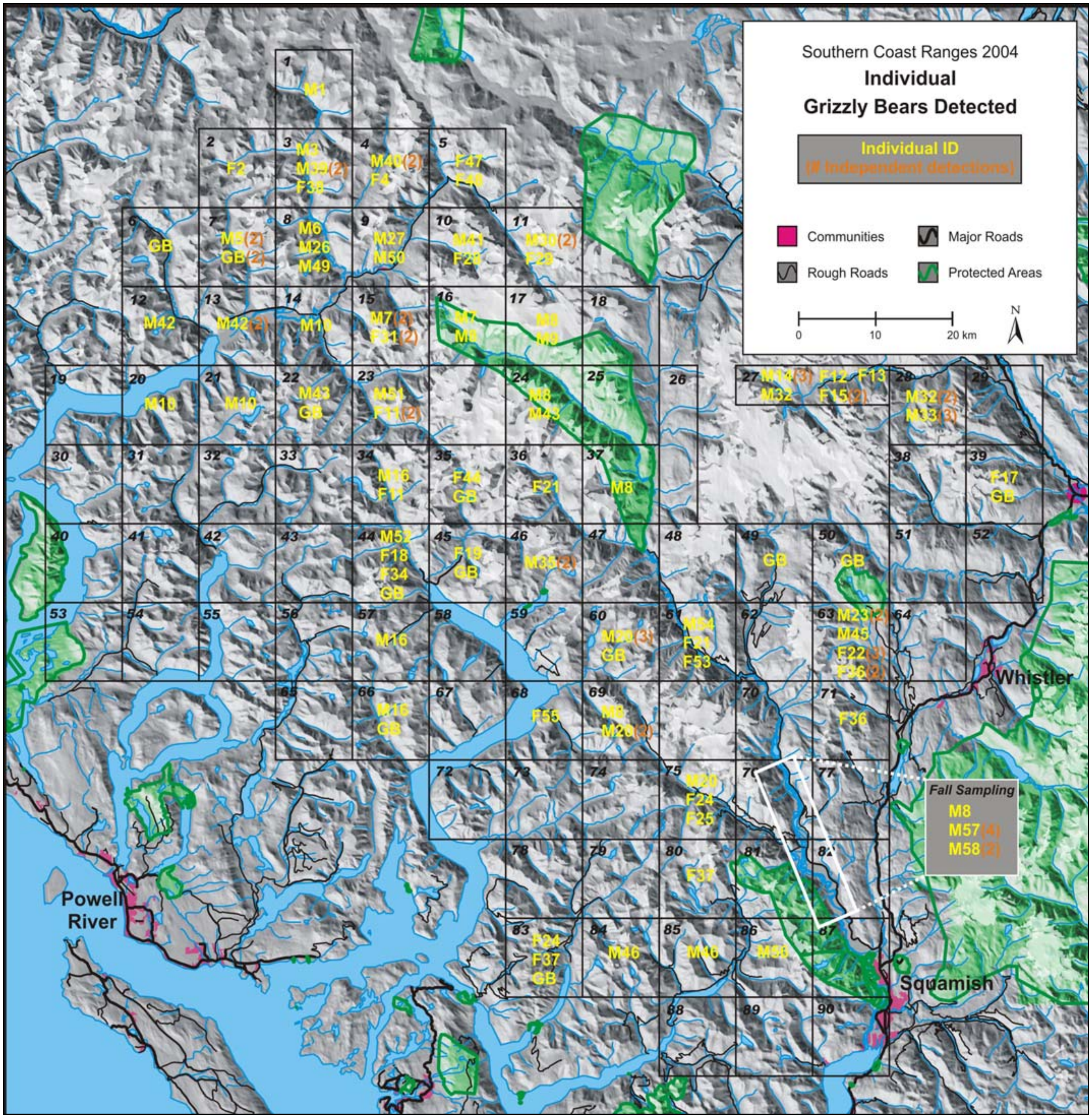

Figure 4. Known identities of grizzly bears detected at hair-snag DNA sampling stations across the Squamish-Lillooet and Toba-Bute (partial) grizzly bear population units of southwestern British Columbia. Data are from 4 sampling sessions during June and July of 2004. Additional detections from localized sampling during October and November, 2004, are also indicated (see legend).

RESULTS & DISCUSSION – PRELIMINARY DATA – YEAR-2

Results

Samples Collected – During our Year 2 (2005) sampling effort, we collected 1,519 hair-snag samples over the 82 stations (cells), and 5 sessions. Of these 410 site/session combinations, ≥ 1 sample was obtained from 308 (75%) while 112 (25%) site/sessions yielded 0 samples. All samples were sent to the DNA lab (Wildlife Genetics International, Nelson, BC) where they were to be analyzed and/or stored in a controlled environment for at least 5 years.

Sample Classification – After processing by WGI, the 2,017 samples fell into the following classes (D. Paetkau, *unpubl. report*): 2% lacked suitable material for extraction; 37% were not extracted either because they had the visual appearance of black bear hair or because of subselection rules; 51% were genetically determined to be from black bears; 3% produced insufficient data to establish individual identify, either during the species test or during the multi-loci analysis; <1% were mixed samples from >1 bear (>2 alleles per marker); while 8% were grizzly bear samples that could be assigned to individuals.

Genetic Variability – In the initial analysis of the 7 markers used for individual identification of the Year-1 samples, WGI found expected heterozygosity (H_e) to be 49%. This was markedly lower than the H_e of Year-1 samples (69%), which itself was lower than reported for other most other mainland populations studied (Paetkau et al. 1998). Because the frequency of similar genotypes was hundreds of times higher than that observed in most other studies, the 7-locus maker system lacked sufficient power for individual identification (i.e., a relatively high number of individuals differed at just one or 2 makers). Therefore, WGI selected and analyzed 3 additional markers, which reduced the number of individuals that differed at just 1 or 2 markers and resulted in the recognition of an additional individual.

Because of the low number of unique alleles per marker, it is difficult to identify "mixed" samples (different individuals leaving hair on the same barb during a sampling session), which could result in the erroneous recognition of a unique individual. Therefore, WGI extended the recognized individual genotypes to 5 additional loci, such that they now matched the 15 loci being used for provincial-level grizzly bear population genetics work. This did in fact confirm that one of the recognized individuals was in fact the result of a mixed sample.

Individuals and Independent Detections – Using the subsampling criteria, genetic analyses indicated 68 detections of 21 (9M, 12F)[1] different grizzly bears within the Stein-Nahatlatch GBPU. In total, 75 independent detections were recorded, including known grizzly bear detections for which individual identity could not be established (Table 5). Of the 410 site/session combinations, at least 1 grizzly bear was detected at 54 (13%), at least 1 black bear was detected at 273 (66%), and both species were detected at 29 (7%) site/sessions. Variation in grizzly bear detection among sessions was relatively minor, though detection rate was slightly higher in the fourth and fifth sessions. The overall grizzly bear recapture rate among sessions was 0.44 (Table 6). This recapture rate is very high, which is somewhat surprising given the low intensity of our sampling. To date, lower capture probabilities have been achieved by all other grizzly bear DNA hair-snag sampling projects of which we are aware (e.g., Boulanger et al. 2002), all of which used smaller cell sizes (more intensive sampling). As with Year-1, the high Year-2 recapture rate (especially given sampling intensity) may be a result of more extensive movements of grizzly bears in this

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[1] This number includes 1 bear (F67) that was detected only from a sample collected during field work for the Lillooet Grizzly Bear project. This sample corresponds to collared study animal GF2 "Heidi".

population, perhaps due to the rugged terrain and high amounts of inherently unsuitable habitat. Although males can be expected to move more extensively than females and thus should be detected more often, the recapture rate for males (0.44) was virtually the same as that of females (0.43). We summarize known movements of individual animals in Table 7.

Discussion

Distribution of the Population – The small grizzly bear population encompassed within the Stein-Nahatlatch GBPU is not evenly distributed. Grizzly bear detections were primarily associated with landscapes in and around Stein Provincial Park (Figure 5). Many of these stations were associated with multiple detections of several individuals (Figures 6 & 7). Notable watersheds where grizzly bears were detected south of the Stein River include Kwoiek Creek and the surrounding northern tributaries of the Nahatlatch and southern tributaries of the Stein. North of the Stein River, we detected grizzly bears in the Cottonwood, Scudamore, Texas, Gott, Blowdown, and Van Horlick drainages. Northwest of the Duffy Lake Road, we detected grizzly bears in the Melvin, Haylmore, and Lost Valley drainages. These visits were all by a single bear (M70)[2] who was also detected southeast of the road. Our results suggest that grizzly bears are conspicuously absent from the southern half of the sampling area, particularly south of the Nahatlatch River. Also, we had only one grizzly bear detection in cells associated with the western height of land in the west-central portion of the sampling area. In summary, it would appear that the small resident Stein-Nahatlatch grizzly bear population is associated with a rather localized and limited distribution.

Population Size – A specific population estimate for the Stein-Nahatlatch GBPU will be derived at a later stage of this study. However, given the very high recapture rate over 5 sampling sessions, the actual population during our sampling period cannot be markedly higher than the minimum count of 21 grizzly bears. Considering that that 4 of 5 radiocollared grizzly bears were detected through DNA hair-snag sampling, a crude adjustment factor of 1.2 could be applied to the count of 20 bears detected by hair-snagging to derive a population estimate of 24.

Genetic Variation – We expected that the genetic variability among grizzly bears within the Stein-Nahatlatch GBPU likely is lower than most other mainland populations. However, an observed heterozygosity value of 0.49 among 15 loci was in fact far lower than expected. The lack of variability within this population stands out on a continental scale. The significance of this result is apparent when compared against other populations. For example a specific subset of 8 markers from the Stein-Nahatlatch bears show variability of 0.44; this is notably lower than the 0.50 measured from the same 8 markers sampled from grizzly bears on Baranof Island off the Alaska Panhandle, a population that has been relatively small and isolated for thousands of years. The only grizzly bear population in North America currently known to have lower heterozygosity than Stein-Nahatlatch bears is that of Kodiak Island at 0.30, a population that is known to have been isolated for ~10,000 years (Paetkau et al. 1998). Populations with a more recent history of anthropogenic isolation, most famously the Yellowstone population, have considerably higher heterozygosity (e.g., 0.55 for Yellowstone) than the Stein-Nahatlatch population. Variation within the southern Selkirk population, also apparently isolated, is even higher at 0.66 (Proctor et al. 2002).

Loss of genetic variation within a population is often cited as an important conservation concern (reference). However, the main threat is not the absolute level to which variation

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[2] This particular bear is the collared study animal GM1 "Cod".

declines but the speed at which variation is lost. This is because slow drift in a larger population (like Kodiak Island at the end of the Pleistocene) allows deleterious genes to be purged without catastrophic loss of fitness. While, to some degree, geographic features and ecosystem variation around the Stein-Nahatlatch population likely have contributed to reduced population connectivity, anthropogenic factors must play a large role given our result in context with other island and isolated mainland populations. Hence, it can be assumed that this population has experienced a very rapid loss of genetic variation over the last few generations since it has become isolated – a major concern with respect to population viability.

Population Connectivity over Multi-Year Sampling Area – Our preliminary data and results from Year 2 have given us the first indication that grizzly bears across the southern Coast Ranges are likely distributed as small, discrete and potentially disjunct populations. This is well illustrated by comparing the Stein-Nahatlatch genotypes to those of our Year-1 Squamish-Lillooet and Toba-Bute sampling effort. A preliminary evaluation was conducted using the program Structure to unambiguously assign the 15-locus genotypes to a population of origin. This analysis found no intermediate genotypes, confirming a lack of population connectivity between the 2 sampling areas, despite the fact that the 2 sampling areas were as close as 10 km (though separation ranged from 10 to 80 km, and 40 km separated the closest grizzly bear detections between the 2 sampling areas). Genetic distances among defined subpopulations within the multi-year study area will be evaluated and reported in the final project completion document.

Value of the 5th Sampling Session – Our sampling efforts during Year-2 were hindered by unusually high amount of precipitation. Due to limitations to helicopter flying, this inclement weather challenged our ability to adhere to the designated schedule of checks and re-luring for some stations. While the session start and end dates varied somewhat among stations as a result, the same number of sampling sessions (approximately 10-days or greater) was applied to all stations. Our greater concern was the impact of the excessive rainfall and cool temperatures on the attractiveness of our stations (and possibly on the movements of bears). We added a 5th sampling session to address this concern. This last session was the driest and warmest of the 5 and resulted in the greatest number of detections (17 as compared with 10 – 16 in each of the previous 4 sessions). This session also resulted in the identification of 3 grizzly bears (15% of total detected) that had been previously undetected (Table 6).

Data Management – The interim database assembled from our sampling results includes records for all samples analyzed linked to cell, session, and station coordinates. Data have been consolidated and summarized according to species occurrence (Figure 5), the minimum number of different bears detected per site/session combination (Figure 6), and individual bears detected at stations and their frequency among sessions (Table 5; Figure 7).

Table 5. Visits of individual grizzly bears to hair-snag DNA stations by sampling cell and session in the Stein-Nahatlatch grizzly bear population unit of southwest British Columbia, June-July, 2005. Identifier codes refer to males "M" or females "F". "GB" refers to a grizzly bear detection without individual identification.

Cell	**Session I** Start: 5 June[a] End: 16 June	**Session II** Start: 16 June End: 27 June	**Session III** Start: 27 June End: 8 July	**Session IV** Start: 8 July End: 19 July	**Session V** Start: 19 July End: 30 July	**Total hits-indiv**
1						
2						
3		M70			M70	2 – 1
4						
5						
6						
7						
8		M70		M70		2 – 1
9			M70			1 – 1
10			F68, M72	F60, F68	F68	5 – 3
11					1GB	1 – 1
12						
13						
14						
15						
16	F64, M70	F64, M79		M69, M70	1GB	7 – 4
17	M72, 1GB	F59	M79	M72		5 – 3
18	M65				M63, F73	3 – 3
19						
20						
21						
22						
23		M72	F64	M72	M72	4 – 2
24	M62		M72		F61, F64	4 – 4
25						
26		F61		F61		2 – 1
27						
28						
29						
30						
31		F61				1 – 1
32	F76, M77		F78	F75, M77, F78	F74, F75	8 – 5
33						
34					F76, F78	2 – 2
35				M62	1GB	2 – 1
36						
37						
38						
39	F76, F78, M77	M66, M77, F76	M77, F76		M65	9 – 5
40	F75, F78, M77			F76, M77, F78	M66, M77, F78	9 – 5
41						
42						
43						
44						

Continues to next page…

Table 5. Continued.

Cell	**Session I** Start: 5 June[a] End: 16 June	**Session II** Start: 16 June End: 27 June	**Session III** Start: 27 June End: 8 July	**Session IV** Start: 8 July End: 19 July	**Session V** Start: 19 July End: 30 July	**Total hits-indiv**
45						
46					F71	1 – 1
47		F71, 2GB	F71	F71		5 – 1
48						
49		F71			F71	2 – 1
51						
52						
53						
54						
55						
58						
60						
61						
50						
57						
56						
59						
62						
63						
64						
65						
66						
67						
68						
69						
70						
71						
72						
73						
74						
75						
76						
77						
78						
79						
80						
81						
82						

[a] Precise dates varied slightly among stations.

Table 6. Capture summary by session for identified grizzly bears in the Stein-Nahatlatch grizzly bear population unit of southwest British Columbia, June-July, 2005.

ID#	Sex	Captures Per Session					Recapture Rate [a]
		I	II	III	IV	V	
59	F	0	1	0	0	0	0.00
60	F	0	0	0	1	0	0.00
61	F	0	1	0	1	1	0.50
62	M	1	0	0	1	0	0.25
63	M	0	0	0	0	1	0.00
64 [b]	F	1	1	1	0	1	0.75
65	M	1	0	0	0	1	0.25
66	M	0	1	0	0	1	0.25
67 [c]	F	0	0	0	0	0	
68 [d]	F	0	0	1	1	1	0.50
69	M	0	0	0	1	0	0.00
70 [e]	M	1	2	1	2	1	1.00
71	F	0	2	1	1	2	0.75
72 [f]	M	1	1	2	2	1	1.00
73	F	0	0	0	0	0	1.00
74	F	0	0	0	0	1	0.00
75	F	1	0	0	1	1	0.50
76	F	2	1	1	1	1	1.00
77	M	3	1	1	2	1	1.00
78	F	2	0	1	2	2	0.75
79	M	0	1	1	0	0	0.25
Total		13	12	10	16	17	0.44
New Individuals detected		9	5	1	2	3	

[a] Among sessions.

Corresponding collared study animal =

[b] GF1 “Vanessa”; [c] GF2 “Heidi”; [d] GF3 “Tex”; [e] GM1 “Cod”; [f] GM2 “Scud”

Table 7. Maximum distance between multiple-detections of individual grizzly bears in the Stein-Nahatlatch grizzly bear population unit of southwest British Columbia, June-July, 2005. Bears with a maximum distance of 0 km between detections are those detected multiple times at a single station.

ID	Sex	Detections	Max Interval (Days)	Max Distance (Km)	Estimated Movement Area[a]
59	F	1			
60	F	1			
61	F	3	9	18	1006
62	M	2	36	31	3069
63	M	1			
64	F	4	45	11	375
65	M	2	46	34	3622
66	M	2	35	6	120
67	F	0			
68	F	3		0	n/a
69	M	1			
70	M	7	45	11	373
71	F	6	10	15	718
72	M	7	45	12	459
73	F	1			
74	F	1			
75	F	3	34	6	131
76	F	6	46	8	225
77	M	8	23	6	115
78	F	7	45	8	225
79	M	2	13	11	363

[a] Area (km^2) of a circle with diameter equal to the maximum distance between multiple detections.

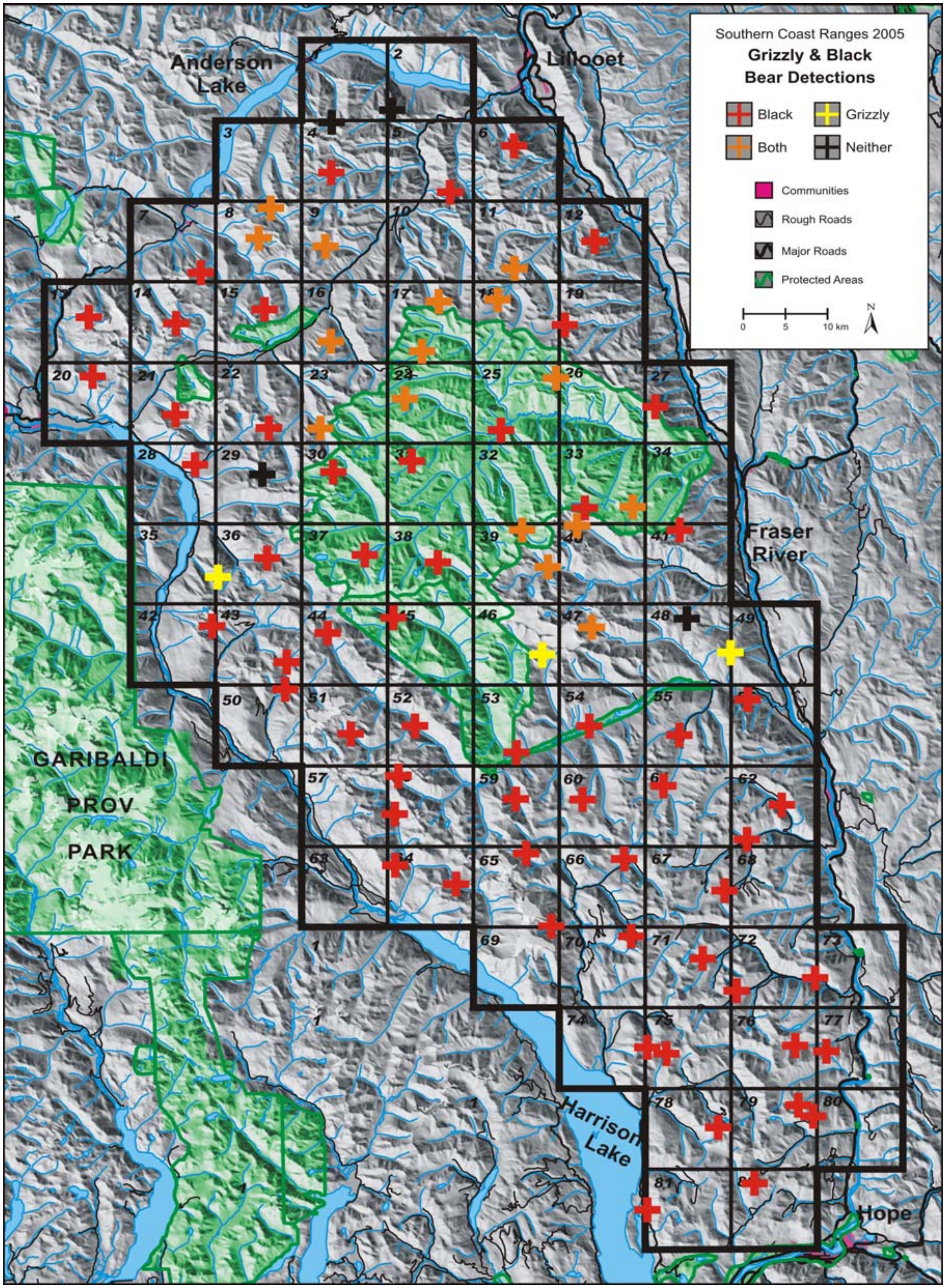

Figure 5. Detection of ≥ 1 black or grizzly bear at hair-snag DNA sampling stations across the Stein-Nahatlatch grizzly bear population unit of southwestern British Columbia. Data are from 5 sampling sessions during June and July, 2005.

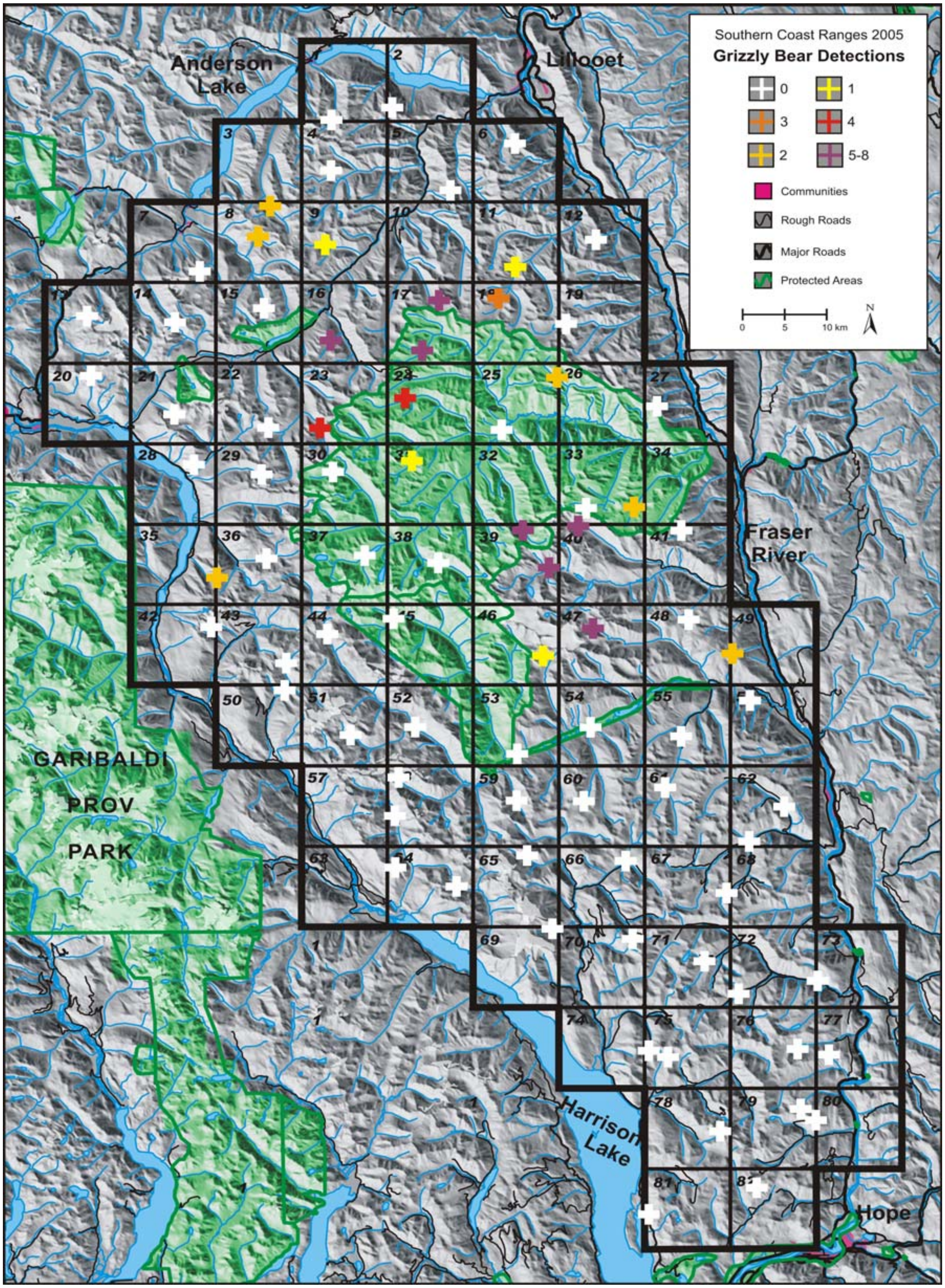

Figure 6. Independent detections by grizzly bears at hair-snag DNA sampling stations across the Stein-Nahatlatch grizzly bear population unit of southwestern British Columbia. Data are from 5 sampling sessions during June and July, 2005.

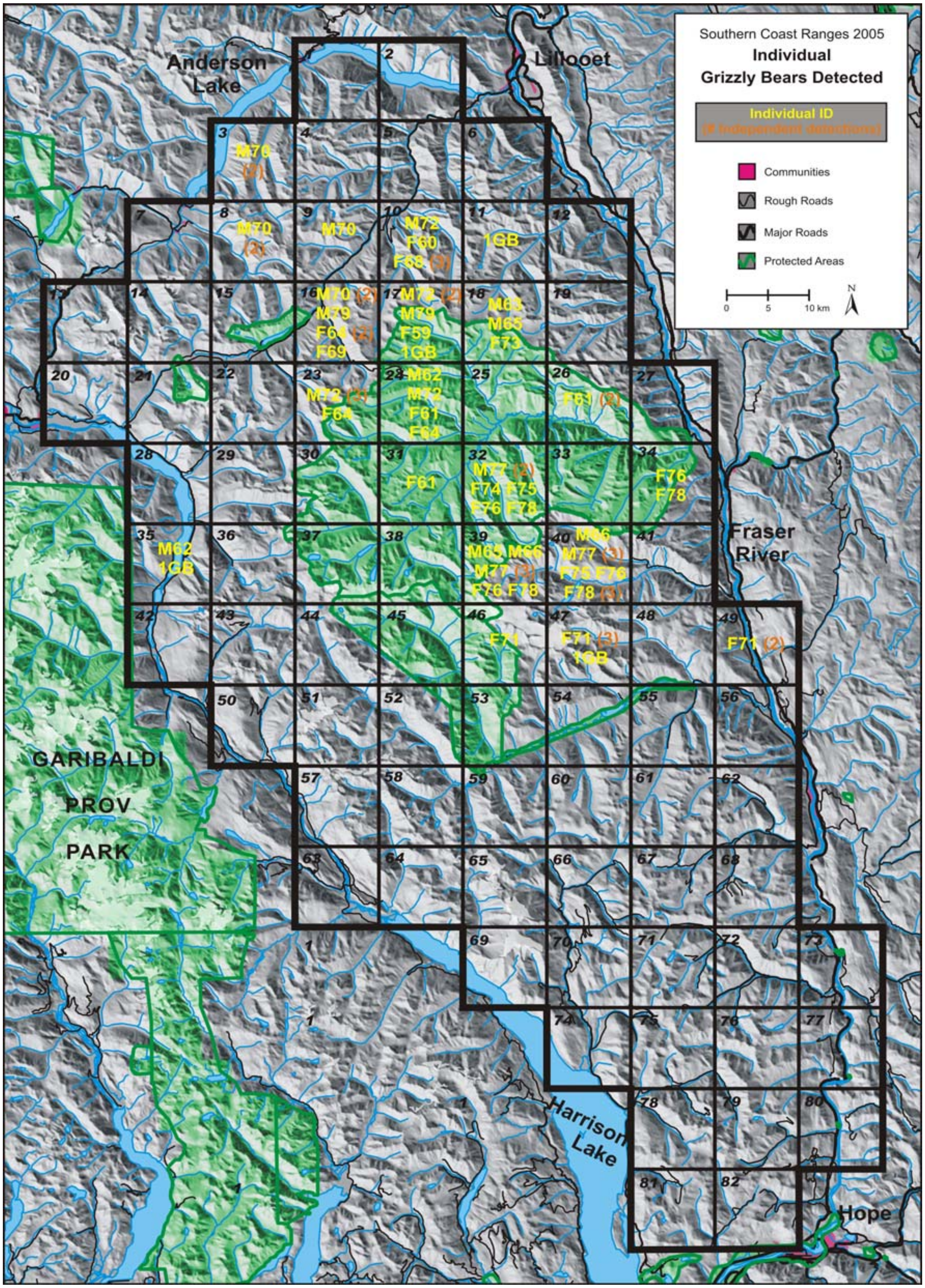

Figure 7. Known identities of grizzly bears detected at hair-snag DNA sampling stations across the Stein-Nahatlatch grizzly bear population unit of southwestern British Columbia. Data are from 5 sampling sessions during June and July, 2005.

RECOMMENDATIONS

Planned Spatial Analyses

During the analysis phase of this study, we will apply a multi-scale approach in analyzing how factors of habitat and human influence relate to spatial patterns of grizzly bear occurrence across the multi-year sampling area (*sensu* Apps et al. 2004). We also plan to analyze individual genotypes to 15 loci to address questions of population connectivity and individual relatedness (*sensu* Proctor et al. 2002) relative to landscape conditions and potential natural and human hindrance to movement. Many of the GIS databases necessary to derive relevant spatial variables have already been assembled (Apps and Hamilton 2002), and these will be updated given recent changes in habitat and/or human conditions. Variables considered will account for terrain conditions, forest overstory, land cover, vegetation productivity, point, linear, and polygon features relating to human activity types and levels, and climatic/physiographic associations. Source data will be mostly of 1:20,000 scale, with some of 1:250,000, and will also include Landsat TM satellite imagery at 30 m resolution. We will describe relationships between grizzly bear detection and each variable considered, and how these relationships may be influenced by spatial scales ranging from an expected daily foraging radius to an annual home range. Integrating results across scales, the spatial output from this analysis will be a map image of predicted grizzly bear occurrence probability within a defined greater extrapolation area across the southern Coast Ranges of BC. Using the density estimates for the intensive sampling areas, this output will be transformed to reflect spatial variability in estimated grizzly bear density (see below). This final output can be interpreted as an objective delineation of core habitat/population areas and landscape linkages among them.

The accuracy and robustness of predictions from our spatial models will reflect how representative our sampling has been of environmental variation within the southern Coast Ranges of BC (Hirzel and Guisan 2002). Therefore, prior to model extrapolation, we will conduct a secondary analysis to evaluate our sampling for representation of landscape habitat and human conditions in the greater region of BC's southern Coast Ranges (Elith et al. 2002). This will be used to objectively define a greater model extrapolation area and to provide a measure of confidence in spatial predictions of grizzly bear occurrence.

Population Density

Unique population density estimates will be derived for defined areas[3] using capture-recapture analyses and an open population estimator within program MARK (White and Burnham 1999). However, it is important to highlight that obtaining population estimates for defined sampling grids is not the ultimate goal of this study. Estimates of population density for defined areas are required only to transform spatially explicit predictions of occurrence probability (*sensu* Apps et al. 2004). The result will predict spatial variation in grizzly bear population density and distribution across the southern Coast Ranges of BC and can be used to infer population size or average density within any smaller area. Given the underlying goal of explaining patterns of population distribution in terms of landscape conditions (habitat and human influence), our sampling areas are extensive and encompass a wide range of conditions and expected grizzly bear densities. Sampling areas are also located to include landscapes of which grizzly bear occupancy is uncertain. Because we also wish to evaluate how natural and human factors may influence population connectivity, the sampling areas considered in each year (and most certainly over multiple years) are

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[3] will likely involve stratification within annual sampling areas

expected to straddle natural and human features that result in some degree of demographic discontinuity. These above criteria are in direct contrast to many previous DNA-based grizzly bear population "inventories" that have defined the location and configuration of sampling areas to maximize capture probabilities and demographic "closure", in turn maximizing statistical power for population estimation and placing discrete bounds on the *actual* area sampled (which of course can extend well beyond a sampling grid given the wide-ranging movements of grizzly bears). In order to sample large and extensive areas within a realistic budget, we have also chosen to sample less intensively (i.e., 10 x 10 km cell size). The implications of this dilution are that every bear in the sampled population may not have a >0 probability of capture (particularly females), and "open" population estimators are generally not robust to unequal capture probabilities (McDonald and Amstrup 2001). However, our capture probability in Year 1 (0.19) was better than at least 4 grizzly bear DNA-based population surveys that used 8 x 8 and 9 x 9 km cell sizes and was comparable to one study that used 7 x 7 km cells (Boulanger et al. 2002). Moreover, our Year-2 capture probability (0.44) was in fact higher than most if not all other studies to date. This suggests that grizzly bears in at least the 2 sampling areas considered to date ranged over relatively large areas and that our sampling intensity may be adequate for population estimation. Moreover, with respect to demographic closure, population estimates will not necessarily be derived for each exact annual sampling area. Rather, we will define one or more discrete units within each that are more likely to achieve demographic closure, and independent estimates will be derived for each. If deemed necessary, we will apply appropriate adjustments to population estimates to account for closure violation (Boulanger and McLellan 2001).

Coordination with other Studies

This research is being coordinated directly with a parallel effort to address grizzly bear population demographics and finer-scale movements and habitat associations in an area that straddles the boundary between the Stein-Nahatlatch and South Chilcotin Ranges GBPUs. This project is being conducted under the auspices of the Lillooet Grizzly Bear Working Group that has membership from the local community and First Nations. The 2 studies are complimentary and mutually beneficial, and involve most of the same principal researchers and collaborators. As previously noted, results from the DNA sampling will help to identify landscapes where more intensive research into grizzly bear movements and/or demographics is appropriate and feasible. Also, the opportunity to track the precise movements of individual grizzly bears can be helpful in evaluating certain assumptions of hair-snag DNA sampling. To date, study animals have been captured using helicopter darting. We recommend that this continue to be the only capture method employed, to ensure that captured bears are not subject to aversive conditioning to scent stations that may otherwise reduce (bias) their capture probabilities during DNA hair-snag sampling efforts.

MEASURES OF SUCCESS

In addition to the final data summary, measures of success upon project completion (final year) will include population estimates, spatial predictions of grizzly bear occurrence and distribution, and spatial variation in population density. Based on interpretation of analyses, population core areas and landscape linkages will be identified, conservation implications will be discussed, and management recommendations will be provided.

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APPENDIX: PROGRAM-SPECIFIC ITEMS

Measures of Results

During our Year 2 (2005) sampling effort, we collected 1,519 hair-samples over the 82 stations (cells), and 5 sessions. Of these 410 site/session combinations, at least one sample was obtained from 308 site/sessions while 112 site/sessions yielded no samples. All samples were sent to the DNA lab. Please see "Results & Discussion - Preliminary Data – Year 2" in the main report for details. In summary, like Year 1, the sheer volume of samples collected and the relatively high grizzly bear capture rate indicate that our first year was extremely successful. A summary and discussion of the data is provided in the main report.

Expected Benefits of the Study

Despite a wide range of land resource demands, there is little known of grizzly bear occurrence, density, distribution, or population connectivity in the southern Coast Ranges. Populations are currently expected to be <50% of carrying capacity (i.e., "threatened"), and extirpation has likely occurred in some landscapes. This study will provide empirically-grounded estimates of population density, distribution and connectivity. This information can be easily and directly integrated into resource planning exercises, such as access management, and can provide decision-support for mitigating development impacts. This will benefit not only grizzly bears but many other species that may also be impacted by cumulative human development and the fragmentation of habitat and populations. Such information is of particular importance in and around the Sea to Sky Planning Area (Squamish Forest District) given projected recreational demands and development trends. Without this study, managers and decision makers will be limited to purely subjective "best-guess" assessments in supporting resource management decisions and attempting to mitigate developmental impacts. Information from this study is also essential for evaluating the needs and options for grizzly bear recovery within defined GBPUs, and to assess the likelihood that a population harvest can eventually be reinstated in some landscapes. Finally, this study is essential for identifying landscapes where more intensive research into grizzly bear movements and/or demographics using VHF or GPS collars is appropriate and feasible. Ultimately, this study will help to ensure that the provisions of the provincial Grizzly Bear Conservation Strategy are met in the southern Coast Ranges.

Extension

Progress and preliminary results of this research are being communicated to managers in several ways. This annual report with map summaries of data to date (e.g., species, independent detections, and different grizzly bears detected per sampling station) is being provided to managers and project partners. Upon completion of the study, a final report will summarize all data and spatial products of grizzly bear population density, distribution, probable core areas, and linkages, and will be made available in digital and hard-copy formats. A powerpoint presentation and a poster will also be developed in the final year describing the issue, research, results, and management applications. This will be delivered to project partners, managers, and the public. There has been local media coverage to date of this research and its conservation utility within the communities of Lillooet and Squamish.

Because we have been sampling landscapes for which grizzly bear occupancy is uncertain, there has been particular interest in our preliminary data as they may suggest localized potential impacts to grizzly bears and mitigation options. In this regard, WLAP staff have communicated the objectives, activities, and some known results from this study at the ministerial level. Public presentations have also been given in Whistler and Lillooet.

Photographic Record

Digital photos and video of various aspects of field work and both landscapes and site-specific habitat conditions within both the Year-1 and Year-2 sampling areas. Select photos have been provided to one funder and are available others upon request.

APPENDIX

Grizzly Bear Population Density & Distribution in the Southern Coast Ranges
Financial Statement
April 1, 2005 - March 31, 2006

Funding	
Habitat Conservation Trust Fund	135,000
Bridge Coastal Restoration Program	98,354
Subtotal	233,354

Expenditures[1]	
Bio/Tech/GIS Labour[2]	47,572
Accommodation/Camp Costs	5,450
Vehicle Mileage	4,894
Helicopter Costs	134,686
DNA Analyses[2]	30,515
Field Supplies	4,189
Supplies Transport & Storage	1,583
Travel Costs	717
Office Expenses	748
Equipment Rental	800
Telephone/Communications	866
Shipping & Misc	1,334
Subtotal	233,354

[1] There were no capital expenditures during the fiscal year.

[2] Actual costs exceeded this amount.