From:	Greg Watson
To:	John Guinotte
Subject:	FW: Requesting Wolverine Mortality Data
Date:	Wednesday, March 8, 2017 11:09:15 AM
Attachments:	Central Purcell Final Report FWCP.pdf CSEKIRKSGULOFINAL.pdf FINAL REPORT2012_112312akdh.pdf FINAL REPORT2013_final.pdf FWCP report W-F15-11_akdhFINAL.pdf

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Greg Watson
Chief, Office of Landscape Conservation
US Fish and Wildlife Service R6
Office 303-236-8155
Cell 303-929-8069
"Mundi est latrina meum"

From: Mowat, Garth FLNR:EX [mailto:Garth.Mowat@gov.bc.ca]
Sent: Wednesday, March 08, 2017 10:43 AM
To: 'Greg Watson'
Cc: dorishaus@shaw.ca; andrea kortello; Hamilton, Tony ENV:EX; Weir, Rich ENV:EX; Nietvelt, Cliff FLNR:EX
Subject: RE: Requesting Wolverine Mortality Data

Hello Greg,

There are a number of us who have been collecting wolverine inventory data in southern BC over the last few years and we are all at the write-up stage. We will be happy to share things with you as they are ready. For now, here are some progress reports for work done in the West Kootenay. We have been working with Michael Lucid in Idaho as well.

Sincerely,

Garth Mowat, PhD
Head-Natural Resource Science Section
Resource Stewardship Division - Kootenay-Boundary Region
Ministry of Forests, Lands and Natural Resource Operations
Suite 401, 333 Victoria St., Nelson
British Columbia, V1L 4K3, Canada
Ph. (250) 354 6142   FAX (250) 354-6332
Email: garth.mowat@gov.bc.ca

From: Greg Watson [mailto:greg_watson@fws.gov]
Sent: Tuesday, March 7, 2017 12:00 PM
To: Mowat, Garth FLNR:EX
Subject: Requesting Wolverine Mortality Data

Garth,
Good talking to you today. As we discussed on the phone, we (US Fish and Wildlife Service) would

like to acquire known wolverine mortality data in BC over the last 10 years (by year) within 200 km of the Canada/US border. We would like to be able to use these data as contributory to our forthcoming status assessment for listing status under the Endangered Species Act. You indicated that these data are likely available in a recently completed assessment/report. If you could forward my contact info to the appropriate personnel that would be able to provide these data, It would be greatly appreciated.

Additionally, you indicated that other analyses regarding demographics and distribution of the BC population may be available in the near future. Once these data/reports are available for release and distribution, we would also appreciate receipt of said information.

Thanks Much,

Greg Watson
Chief, Office of Landscape Conservation
US Fish and Wildlife Service R6
Office 303-236-8155
Cell 303-929-8069
greg_watson@fws.gov

Abundance and Distribution of Wolverine in the Kootenay Region

2016 Field Season Report: Central Purcell Mountains

Prepared For:

Fish and Wildlife Compensation Program- Columbia, Ministry of Forests Lands and Natural Resource Operations and Columbia Basin Trust

Prepared By:

Doris Hausleitner, M.Sc., R.P. Bio.

and

Andrea Kortello, M.Sc., R.P. Bio.

Seepanee Ecological Consulting

Prepared with financial support of the Fish and Wildlife Compensation Program on behalf of its program partners BC Hydro, the Province of BC, Fisheries and Oceans Canada, First Nations and public stakeholders.

December 2016

Executive Summary

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally and is harvested regionally, yet no inventory has been conducted to estimate population abundance and connectivity in the southern portion of the Kootenays. Thus, a non-invasive genetic study and collection of trapper carcasses was initiated in the southern Columbia Mountains in 2012 with the objectives of estimating abundance and assessing meta-population connectivity to inform harvest management and contribute to international conservation efforts. Inventory was conducted in the south Selkirk (2012), south Purcell (2013), central Selkirk (2014), Valhalla and south Monashee (2015) and central Purcell Mountains (2016). This report summarizes results from the central Purcell Mountains from 2016. Eight wolverine were identified in 2016: seven new individuals as one had been previously captured in adjacent cells in 2013. An additional 13 donated trapper carcasses were genotyped from other ranges in the Kootenays. We estimated a population size of 9 (7-12) individuals, less than half of the expected population size of 24(17-36). Estimates of occupancy (64%) were higher than the south Purcell (38%) and south Selkirk (55%) and lower than the Valhalla (70%) and central Selkirk Mountains (71%). Estimates of detectability were within the range of previous years and other studies. These data corroborate evidence from previous sampling seasons and appear to indicate low wolverine abundance and limited genetic connectivity between mountain ranges. These factors necessitate careful attention to harvest pressures on a range by range basis and indicate a need to monitor population trends and to identify and maintain existing movement corridors.

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Introduction

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally (BC CDC 2016, COSEWIC 2003) and is classified as Identified Wildlife under the Forest and Range Practices Act (MWLAP 2004). Population estimates for British Columbia have been derived from habitat modeling based on mark-recapture in the Omenica and Northern Columbia Mountains (Lofroth and Krebs 2007) but lack verification for much of the province, including the southern portion of the Kootenays. Considering that adjacent U.S. populations are known to be at critically low levels (USFWS 2016), with wolverine absent from much of the potentially viable habitat, reliable abundance estimates are crucial for species conservation in the region.

In the Kootenays, wolverine populations are characterized by small and declining fur yields (~8 pelts/year) and harvest rates in parts of the region may be unsustainable (Lofroth and Ott 2007). Populations with high connectivity are resilient to local overharvest or high mortality from other sources because of source/sink dynamics (Pulliam 1988). Although genetic evidence indicates increasing population fragmentation in a north to south gradient in B.C. (Cegelski et al. 2006), the extent of gene flow between neighboring ranges in the southern Kootenay region is unknown. Hence, assessing connectivity is important to local population resilience and evaluating harvest sustainability.

Barriers to dispersal include transportation routes, hydroelectric and residential development and land use changes (Gardner et al. 2010, Krebs et al. 2007, Slough 2007, Austin 1998). Similarly, wolverine habitat use and density are associated negatively with winter recreation, forest harvest, and positively with roadless areas (Fisher et al. 2013, Krebs et al. 2007). Mapping occupied habitat in the Kootenays and identifying factors contributing to the persistence of wolverine in these areas is an essential step to identifying where conservation efforts to improve habitat and connectivity should be focused. Additionally, the Kootenay region is one of only a few areas identified as a potential corridor for trans-boundary movement of wolverine into the US (McKelvey et al. 2011, Schwartz et al. 2009, Singleton et al. 2002). Such movement is critical for the persistence of US populations, and this project will provide vital information for wolverine conservation in the trans-boundary region.

Project objectives were to: (1) assess occupancy/abundance of wolverine in the central Purcell Mountains; (2) assess genetic connectivity amongst Monashee, Selkirk and Purcell populations; (3) evaluate current harvest levels; (4) evaluate broad-scale habitat factors that are associated with wolverine presence and; (5) cooperate inter-jurisdictionally for wolverine research.

Methods

Study Area

The study area was in the central Purcell mountain ranges within the Central Columbia Mountains, Northern Kootenay Mountains and Eastern Purcell Mountains Ecosections in the southern Interior Mountains Ecoprovince. The Purcells are dominated by sedimentary and metamorphic rock; largest peaks occur in the north and the range is divided by steep east-west valleys which drain into Kootenay Lake and Duncan River Valley to the east and The Kootenay and Columbia Rivers to the west (MacKillop and Ehman 2016). Our sampling area was bounded to the east by Highway 95, to the northeast by Horsethief Creek and East Creek to the northwest, Duncan Reservoir and Kootenay Lake to the west and by Fry Creek to the south (Figure 1). Major land use in this area was historically mining and forestry. Winter recreation, with snowmobiling, including groomed trails and huts, backcountry skiing and resort skiing (Panorama ski resort) all occur within these boundaries. The Purcell Wilderness Conservancy (198,115 ha) is a non-mechanized area and does not permit snowmobiles, vehicles or helicopters within its boundaries. Additionally, the Purcell Wilderness Conservancy Corridor Protected area (1990 ha) exists within the study area.

On the eastern side of the mountain ranges, in the dry climate subregion, starting in the valley bottom and progressing to the mountain peaks, biogeoclimatic ecosystem classification (BEC) units present are: Interior Douglas-fir, dry mild Kootenay variant (IDFdm2), Montane Spruce dry, cool Elk variant (MSdk1), Engelmann Spruce-Subalpine Fir dry, cool (ESSF dk1, ESSFdk2), Engelmann Spruce-Subalpine Fir dry cool woodland (ESSFdkw), Engelmann Spruce-Subalpine Fir dry cool parkland (ESSFdkp), and Interior Mountain-heather Alpine undifferentiated (IMAun; IMAP BC 2016). At lower elevations the forest is composed of Douglas fir (*Pseudotsuga menziesii*), Ponderosa pine (*Pinus ponderosa*), trembling aspen (*Populus tremuloides*) and lodgepole pine (*Pinus contorta*). Understory shrubs include snowberry (*Symphoricarpus albus*), Saskatoon (*Amelanchier alnifolia*), soopalallie (*Sheperdia canadensis*) and falsebox (*Paxistima myrsinites*). Pinegrass (*Calamagrostis rebescens*) and twinflower (*Linnaea borealis*) are common herbs in the understory. At higher elevations Englemann spruce (*Picea engelmannii*) and subalpine fir (*Abies lasiocarpa*) are the main tree species. Main shrubs include black huckleberry (*Vaccinium membranaceum*) and false azalea (*Menziesia ferruginea*).

On the western side of the mountain ranges, in the moist climate subregion, starting in the valley bottom and progressing to the mountain peaks, BEC units present are: Interior Cedar-Hemlock dry warm West Kootenay variant (ICHdw1), Interior Cedar-Hemlock moist warm Slocan variant (ICH mw2), Engelmann Spruce-Subalpine Fir wet, hot St. Mary (ESSF wh2), Engelmann Spruce-Subalpine Fir wet, mild Purcell (ESSF wm2), Engelmann Spruce-Subalpine Fir wet, mild woodland (ESSF wmw), Engelmann Spruce-Subalpine Fir wet, mild parkland (ESSF wmp), and

Interior Mountain-heather Alpine undifferentiated (MacKillop and Ehman 2016). At lower elevations the forest is composed of western redcedar (*Thuja plicata*) and western hemlock (*Tsuga heterophylla*) interspersed with Douglas fir, lodgepole pine, trembling aspen and western larch (*Larix occidentalis)*. The shrub layer consists of Douglas maple (*Acer glabrum*), false box, thimbleberry (*Rubus parviflorus*) and beaked hazelnut (*Crotylus cornuta*). False solomon seal (*Maianthemum racemosum*), horsetail (*Equisetum* spp.) and sedges (*Carex* spp.) made up the herbaceous layer in the mid-elevation forests. At higher elevations Englemann spruce and subalpine fir are the main tree species. Main shrubs include black huckleberry, false azalea, white rhododendrum (*Rhododendrum albiflorum*) and heather (*Cassiope* spp.).

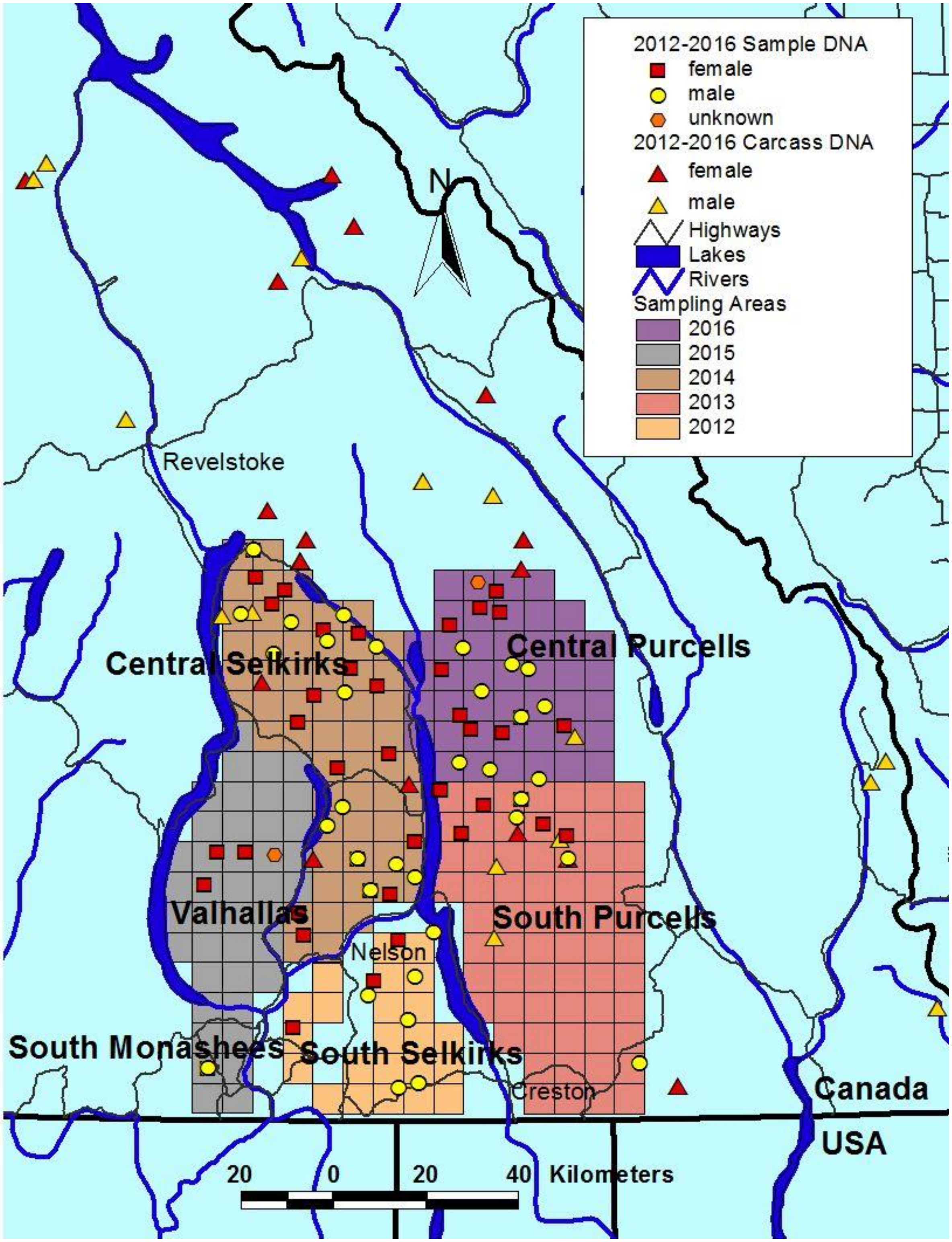

Figure 1. Wolverine non-invasive hair trapping results showing site locations where wolverines were detected (red squares, yellow circles, orange hexagon) in the south Selkirk (2012), south Purcell (2013), central Selkirk (2014), southern Monashee (2015) and central Purcell mountains (2016). Females are in red, males in yellow, unknown in orange. Individuals may be found at multiple locations. Trapper carcass collection is represented by triangles. All coloured quadrats were sampled with at least one site.

Survey methods

The study area was partitioned into 10 by 10 km cells that approximate the minimum size of a female home range. These 43 quadrats were sampled twice in approximately 30 day sampling intervals, from 8 February 2016 to 18 April, 2016 (Figure 1). Because of the rugged nature of the terrain, sites within cells were selected for ease of access by helicopter, snow machine or skis, using local knowledge of wildlife movements when available. Hair trap sites were created by affixing a bait item (deer head or elk head) to a tree approximately two meters from the ground or snow surface to entice the animal to climb (Fisher 2004). The bait item was nailed to the tree and the tree wrapped several times in barb wire to capture hair. During each check, the barb wire was examined for hairs or hair tufts, and the bait replenished if necessary. Hair was collected with forceps and stored in paper envelopes in a dry environment. We used Rencoynx Rapidfire trail cameras (Reconyx Inc., Holmen, WI) at six sites during the sampling period.

Additionally, we collected genetic samples from wolverine carcasses obtained by trappers. From each carcass a tissue sample was taken and carcasses were necropsied by Ministry of Forests Lands and Natural Resource Operations.

Genetic Analysis

Three-hundred and forty-six hair, tissue and scat samples were submitted to Wildlife Genetics International (WGI) in Nelson B.C. for genetic identification analysis. Of the hair samples submitted, 75% (n = 246) were sub-selected for analysis. Samples that did not contain guard hairs or >5 underfur were screened out because of insufficient genetic material. From the remaining samples, DNA was extracted using QIAGEN DNeasy Tissue kits, following the manufacturer's instructions (Qiagen Inc., Toronto, ON).

Species identification was based on a sequence-based analysis of a segment of the mitochondrial 16S rRNA gene (Johnson and O'Brien 1997). For samples that yielded wolverine DNA, WGI utilized multilocus genotyping, consisting of a ZFX/ZFY sex marker, and 8 additional microsatellite markers for individual identification. Locations of sampling sites and genetic samples were mapped in ARCVIEW 3.1 (ESRI Inc. 1998, Jenness 2005).

Occupancy

We used the single-season model in program PRESENCE (MacKenzie et al. 2002) to estimate the proportion of sample stations occupied by wolverine. A non-detection at a surveyed site could have meant wolverine were not present at the site or that we failed to detect an individual when it was present. PRESENCE uses a joint likelihood model to estimate the probability of missing a species when it is present at the site (p = *detectability*) and the probability that a site is occupied (Ψ = *occupancy*). To estimate these parameters repeat observations need to be conducted over a period of time during which site occupancy is assumed to be constant. In this way, non-detection from a site with at least one detection can be treated as a false negative and the detection probability can be estimated.

We used both track detections (set up, and two checks) and genetic data (check 1, check 2) to estimate occupancy. We constructed models with group effects on occupancy and time dependence on detectability.

Estimates of occupancy can act as a surrogate for abundance for territorial species such as wolverine when the sites sampled approximate territory sizes (MacKenzie et al. 2006). We selected a grid resolution (10 x 10 km) that corresponded to a minimum home range size for female wolverine. We used the genotyped individuals from two encounter occasions (check 1, check 2) to estimate abundance using a simple Lincoln-Peterson mark-recapture method (N = Mn/R, where N is the estimated population size, M is the number of animals identified in the first sampling session, R is the number of animals identified in the first session which are recaptured in the second session and n is the total number of animals identified in the second sampling session; Seber 1982).

Population genetics

We calculated individual pairwise genetic distances following Smouse and Peakall (1999). To visualize genetic relationships amongst individuals and study areas we performed a multivariate ordination using principal component analysis (PCA) in GenAlEx 6.5 (Peakall and Smouse 2006, 2012). This process finds and plots the major axis of variation within a multidimensional data set (i.e. multiple samples and multiple distances) to identify patterns within the data.

To evaluate patterns within the data we used Bayesian analysis in program STRUCTURE (Pritchard et al. 2000) to group individuals by most probable subpopulations and examine gene flow across the study area. STUCTURE estimates the most likely number of subpopulations (K) given the data. We ran calculations with no prior information, correlated allele frequencies and admixture. We utilized five independent runs of K=1-8 with 200,000 Markov Chain Monte Carlo (MCMC) repetitions and a 200,000 repetition burn-in. The K with the highest estimated log-likelihood value for posterior probability was selected, then wolverine were assigned to subpopulations based on the highest percentage of membership (q) in each derived subpopulation. Results were plotted on GIS (ESRI Inc. 1998).

Results

During the course of the field season we monitored 43 sites in the central Purcell Mountains (Figure 1). Six field days were required for setup and an additional 11 days for site monitoring. Detections of wolverine occurred at 51% of sites by snow tracking and/or genetic analysis (Figure 2). Wolverine tracks were detected in 23% (*n* = 10) of quadrats and were the exclusive detection method in 3 quadrats (Figure 2). Wolverine DNA was collected at 44% (*n* = 19) of quadrats and were the exclusive detection method at 12 of those sites (Figure 2). At 16% percent of quadrats (7 of 43), both wolverine DNA and tracks were detected. Other carnivores detected, using snow tracking, included canid tracks (*Canis* spp.), red fox (*Vulpes vulpes*) and coyote (*Canis latrans*).

We collected images using trail cameras at three sites (Figure 2) with a total monitoring period of 88 days. White tailed-deer (*Odecoileus virginianus*), American marten (*Martes americanus*) and black bear (*Ursus americanus*) were detected on camera.

Genetic analysis

We obtained genetic results from 244 hair, tissue and scat samples. One-hundred and fifty one samples were identified by mitochondrial DNA analysis as species other than wolverine (and not mixed). These species included American marten (*n* = 138), bobcat (*Lynx rufus*, *n* = 7), lynx *(Lynx canadensis, n* =2), coyote (*n* = 2), flying squirrel (*Glaucomis sabrinis*, *n* = 1) and black bear (*n* = 1). Wolverine DNA was detected at 19 of 43 sites in the central Purcell Mountains in 2016. From hair samples, 8 individual were assigned; three males and five females (Figure 2). One of these females had been captured previously in adjacent sampling cells in 2013. A sample that had not been submitted in 2015 resulted in a third wolverine detection (female) in the Valhalla Mountains.

Fifteen wolverine carcasses were submitted by the trapping community in 2015 (Figure 1). Two of these had been previously analysed and may have either been resubmitted by the trapper or resampled accidentally by our team. Of the thirteen new wolverine carcasses submitted, five were male and eight were female. This is in addition to twenty-eight (eighteen males, ten females) carcasses submitted from 2012- 2015 for a total of 41 trapper donated carcasses (Figure 1).

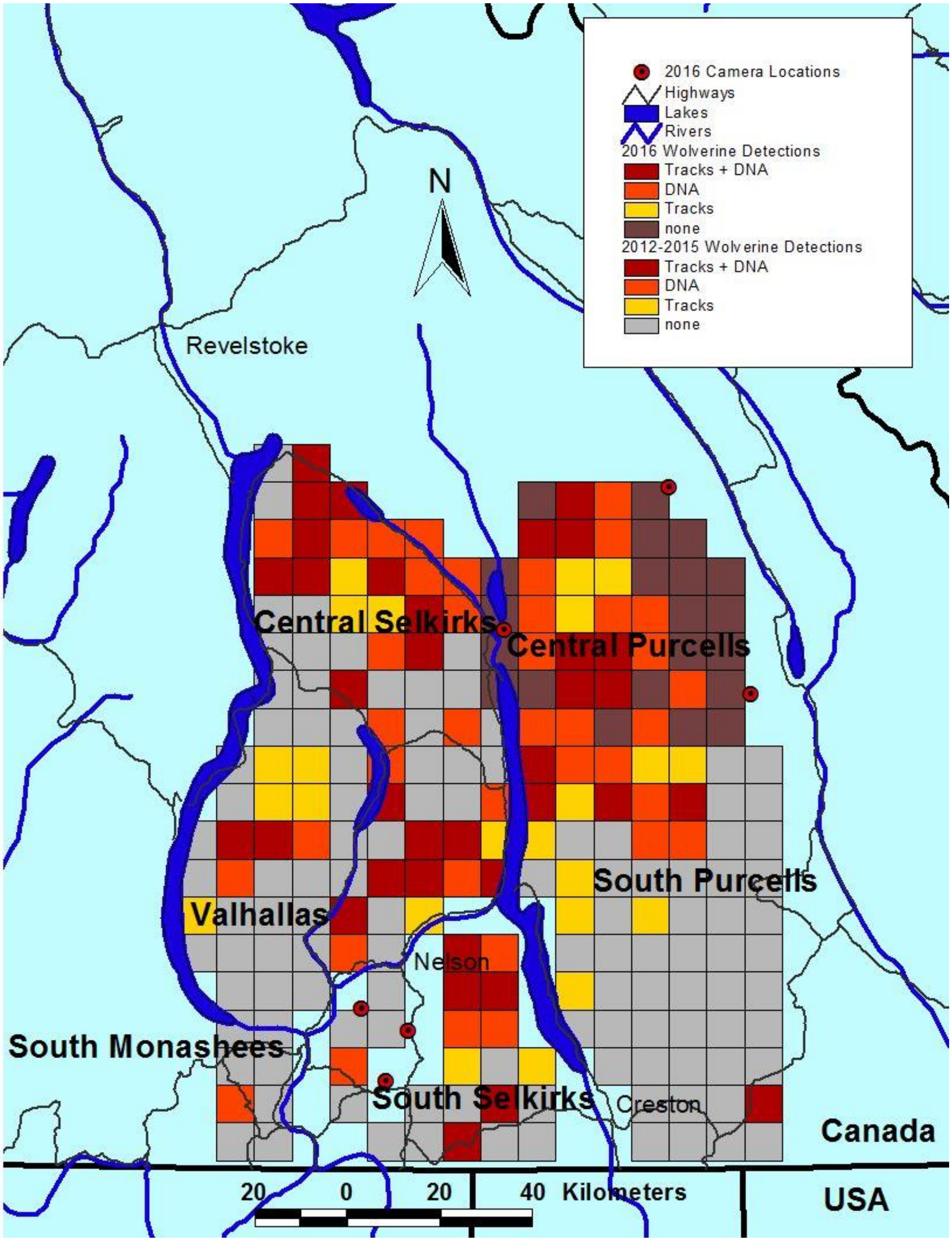

Figure 2. Wolverine non-invasive hair trapping results showing site locations and wolverines detected using DNA (orange) and snow tracking (yellow), or both (burgandy) in the south Selkirk (2012), south Purcell (2013), central Selkirk (2014) south Monashee (2015) and central Purcell Mountains (2016). An individual may be present at more than one site and some sites may have more than one individual.

Occupancy

The best model selected was one which predicted constant occupancy but a change in detection probabilities by sampling sessions (Δ AICc < 2; Table 1). As there was no competing model, we did not do model-averaged estimates of the parameters. Occupancy estimate for the highest ranking model in the central Purcells was 63.9% (*SE* = 12.6; Table 2). The probability of detection for each survey repetition was 3.6% (*SE* = 3.6) in repetition one, 40.0% (*SE* =11.3) in repetition two and 65.5% (*SE* = 13.9) in repetition three (Table 2). Occupancy rates amongst the mountain ranges varied from 35% in the south Purcell Mountains to 71% in the central Selkirk Mountains (Table 2). Detectability at set up was based on tracks only and ranged from 3.6%-23.6% for all years (Table 2). Detectability (by genetics and tracks) increased between first and second checks for all sampling areas (Table 2).

Table 1. Ranking for models of occupancy (ψ) and detectability (p) for track and genetic data of wolverine in the central Purcell Mountains 2016. Models were developed in Program PRESENCE and compared using AICc weights of evidence (Burnham and Anderson 1998). Δ AIC_c is the difference between a given model and the model with the lowest AIC_c[a] score, AIC_c weight (w_i) reflects the relative support for each model, K is the number of parameters estimated by the model.

Model	Δ AIC_c[a]	AIC_c weight (w_i)	K
ψ (.) p(survey specific)[b]	0.0	0.95	4
ψ (2 groups) p(survey specific)[c]	6.0	0.05	8
ψ (.) p(.)[d]	21.9	0.00	2
ψ (2 groups) p(.)[e]	25.9	0.00	4

[a] The lowest AICc score was 121.1

[b] constant ψ, survey specific p; the species has constant occupancy but different detection rates

[c] 2 groups, survey specific p = there are two groups of sites and different detection rates

[d] constant ψ , constant p= The species has constant occupancy and detection rates

[e] 2 groups, constant p= there are two groups of sites where the species has the same detection probabilities

Table 2. Model-averaged occupancy and detection probabilities for wolverine amongst the different study areas and mountain ranges 2012-2016.

		Detection Probabilities (SE)		
Population	Occupancy (SE)	Set up	Check 1	Check 2
South Selkirks	54.5 (14.4)	23.6 (12.5)	39.3 (15.1)	70.7 (17.2)
South Purcells	35.0 (23.7)	20.0 (0.09)	32.0 (11.0)	47.0 (14.0)
Central Selkirks	71.0 (10.0)	17.8 (5.9)	38.1 (8.2)	70.0 (6.4)
Valhallas/south Monashees	70.1 (57.8)	17.7 (16.4)	3.5 (4.6)	14.1 (13.5)
Central Purcells	63.9 (12.6)	3.6 (3.6)	40.0 (11.3)	65.5 (13.9)

A simple mark-recapture calculation yields an estimated 9 individuals (95% CI 7-12) in the central Purcell wolverine population. We reviewed published habitat-based population estimates (Lofroth and Ott 2007) for the sampled population units (Table 3). Mean annual number of wolverine trapped in the central Purcell Mountains (Wildlife Management Units (WMU) 4-19, 4-26, 4-27) was 0.25 for 2005-2014, 1.1 for 1995-2004 and 2.3 for 1985-1994. Data is missing for 2010 and 2011 in all management units and no animals have been reported harvested in these management units since 2012 (Figure 2). From 1985-2009, 94% (33/35) of wolverine harvested in the central Purcell Mountains came from WMU 4-26.

Table 3. Comparison of genetic-based and habitat-modeled population estimates (N) and annual harvest for wolverine populations in the south Selkirk, south Purcell, central Selkirk and Valhalla/south Monashee Mountains.

Population	Mark-recapture[a] N (95% CI)	Habitat-based[b] N (95% CI)	Mean annual harvest 2005-2014 (1995-2004) (1985-1994)[c]
South Selkirks	4 (n/a)	10 (7-14)	0 (0) (0)
South Purcells	18 (9-27)	27 (20-39)	1.7 (1.6) (1.5)
Central Selkirks	19 (14-23)	32 (22-49)	4.9 (2)(2.8)
Valhallas/south Monashees	2 (n/a)	17 (12-25)	1 (0.6) (0.9)
Central Purcells	9 (7-12)	24 (17-36)	0.25 (1.1)(2.3)

[a] Genetics study
[b] Lofroth and Ott, 2007
[c] data from 1985-2009 based on trapper survey, data missing for 2010, 2011 and 2012-2014 based on carcass collection

Population genetics

Principal Component Analysis of genetic distances between wolverines suggests broad genetic structure at a mountain range scale with individuals from the Purcell range (in blue shades) and Selkirk range (in red shades) forming overlapping clusters (Figure 3). The Monashee range (in green) does not form a discernable cluster. At a subrange scale, samples from the central Purcells also show large overlap with Selkirk samples. South Selkirk, Valhalla and south Monashee populations are included for the sake of completeness but have limited sample sizes.

Results from program STRUCTURE also indicate subpopulation structure. The highest probability for the data was at K=3 (Ln= -1343.1; Table 4). The Monashee mountains had the highest proportion of membership assigned to a subpopulation cluster (n=9, subpopulation 2, q=0.759), while individuals from the Selkirks (n=33, subpopulation 1, q=0.542) and Purcell ranges (3, q=0.476) show more admixture (Figure 4). Subpopulation 1 is clustered in the northern Monashees but with individuals widely dispersed throughout the entire study area (Figure 5). Subpopulation 2 is concentrated in the south Purcells and the core area for subpopulation 3 is in the central Selkirks. No individuals classed as subpopulation 2 were detected west of Kootenay or Duncan Lake.

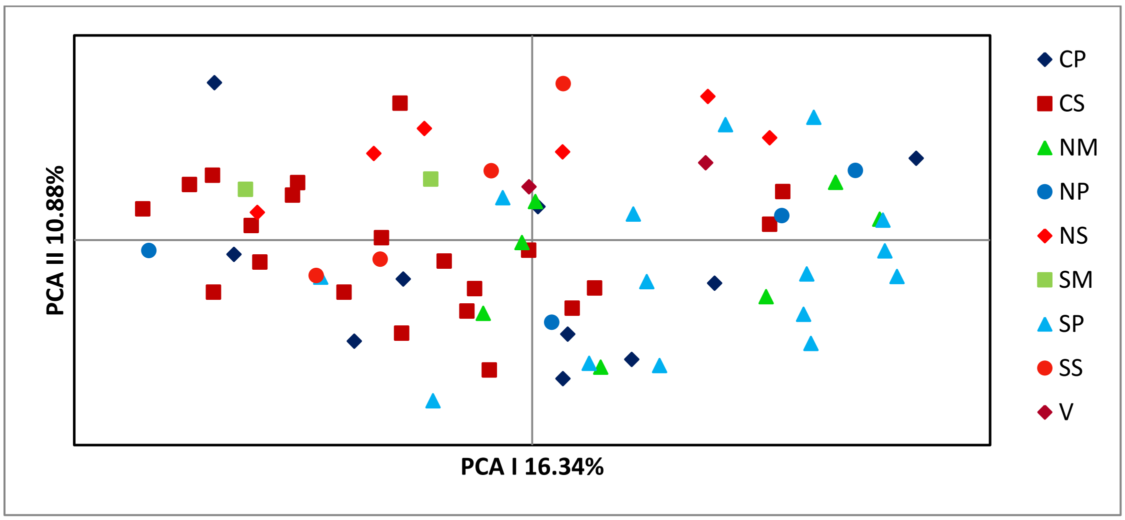

Figure 3. Principal Components Analysis (PCA) of 71 wolverine genetic samples from all subranges with hair or trapper samples in the Columbia Mountains of British Columbia; central Purcell (CP, n=10), central Selkirk (CS, n=21), north Monashee (NM, n=7), north Purcell (NP, n=4), north Selkirk (NS, n=6), south Monashee (SM, n=2) south Purcell (SP, n=15), south Selkirk (SS, n=4), and Valhalla (V, n=2).

Table 4. STRUCTURE results for Bayesian clustering of wolverine genotypes, where K is the inferred number of subpopulations in the data. The most probable value for K (highest estimated log likelihood value) is highlighted in bold.

K	Log P (k/x)	Variance Log P(k/x)
1	-1412	16.2
2	-1367.1	74.5
3	**-1343.1**	**131.7**
4	-1398.7	249.8
5	-1391.6	292.9
6	-1460.7	440.8
7	-1486.3	487.6
8	-1492.6	502.3

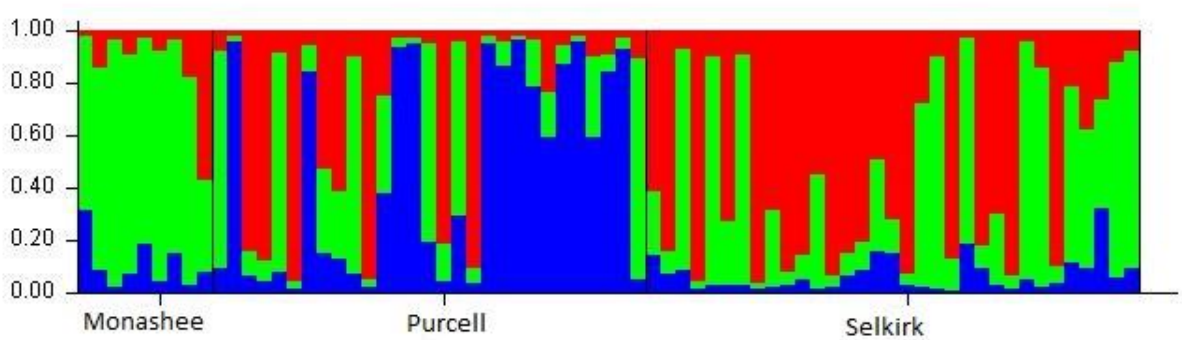

Figure 4. Bar plot of q values for sampled wolverine from three ranges in the Columbia Mountains 2012-2016. Green depicts subpopulation 1, blue depicts subpopulation 2, and red depicts subpopulation 3.

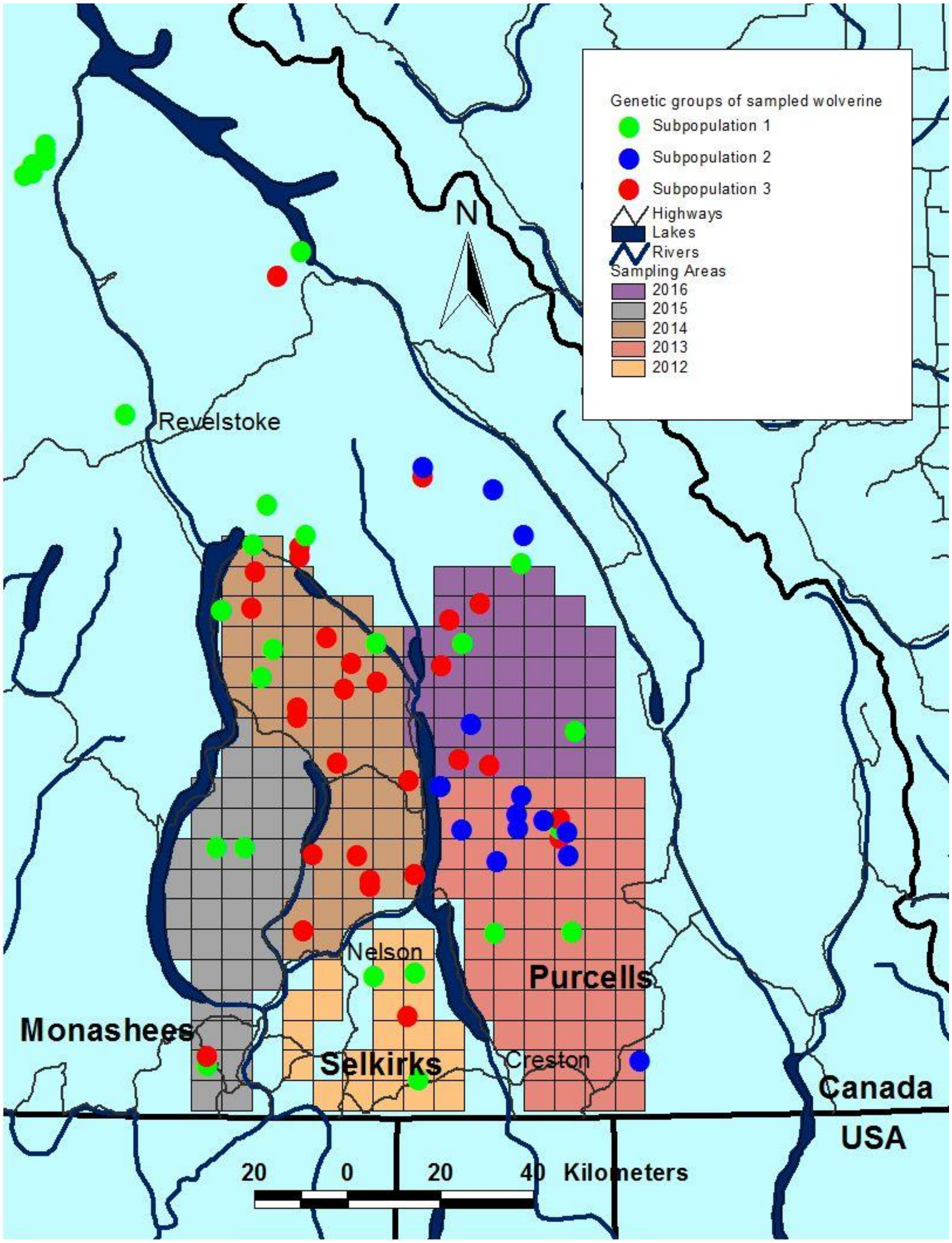

Figure 5. Locations and assigned subpopulations of wolverine in the Columbia Mountain ranges 2012-2016 as determined by STRUCTURE (Pritchard et al. 2000).

Discussion

This research represents the first on-the-ground attempt to inventory wolverine populations in the southern Kootenay region. The data is beginning to fill a critical knowledge gap for a species that is a conservation priority in the U.S. and Canada. In this fifth and final year of our project we obtained genotypes for 7 new individuals in the central Purcells and trappers donated an additional 13 carcasses for a total database of 78 wolverine in the Kootenay region.

Sampling in the central Purcells maintained the north to south gradient of wolverine observations in the Columbia mountain study area, with the higher concentrations occurring to the north. Wolverine were much more widely distributed in the central Purcells than south Purcells but the number of detections dropped off at the eastern edge of the range. The eastern edge of the Purcell mountains lies primarily within WMU 4-26, the management unit with the heaviest historic harvest pressure. Additionally, this area receives less snowfall than the west side of the mountains and has less rugged topography, making it more accessible to snowmobiles. Snowmobile access is assisted by groomed trails on Horsethief and Forester Creek FSR. Additionally this side of the valley is in close proximity to the population centers of Invermere, Golden, Kimberly and Cranbrook and even Calgary. These observations are consistent with other research linking wolverine presence to areas of high snowfall, rugged terrain and low human disturbance (Fisher et al. 2013, McKelvey et al. 2011, Krebs et al. 2007).

Similar to previous years, a disproportionate number of the wolverine identified in the central Purcells were located either in or immediately adjacent to protected areas (Purcell Wilderness Conservancy). Other areas that appeared to coincide with higher densities of wolverine included Darkwoods Nature Conservancy, Valhalla Provincial Park, Kokanee Glacier Provincial Park and Goat range Provincial Park. This suggests that protected areas may be important for wolverine populations and this relationship warrants further investigation in future analyses. Fisher et al. (2013) also found wolverine more abundant in rugged areas protected from anthropogenic development.

Occupancy estimates for the central Purcell Mountains (64%) was lower than the Valhallas/ south Monashees (70%) and the central Selkirk (71%) and higher than both the south Selkirk (54%) and south Purcell Mountains (35%). The central Purcells were rated as high quality wolverine habitat by Lofroth and Krebs (2007). Similarly, the central Selkirk, and Valhalla Mountains were also rated as high quality wolverine habitat (Lofroth and Krebs 2007). In contrast, the south Monashees contains both moderate and low quality habitat. The south Purcells, despite having the lowest occupancy rates were also rated as high but interspersed with moderate quality habitat. The south Selkirks were rated as only moderate habitat quality.

In most sampling years, detection probability increased as the season progressed. Similarly, this season we had the smallest detection probability (4%) in the first repetition (tracks only) and saw an increase in detection probability in the second (40 %) and third repetition (66%), respectively. These detection probabilities were comparable to other years (range 4-71%) and other studies (Fisher et al. 2013).

We deployed cameras at 6 sites but detected no wolverine through this method in 2016. We have had only 2 wolverines on cameras in 3 years. Cameras have been shown to improve detectability for wolverine occupancy studies in the Rocky Mountains (Fisher and Bradbury 2014). However, with so few cameras on the landscape, they have had little use in our study.
Our mark-recapture estimate of population size for the central Purcells; 9 (95% CI 7-12) is less than half of Lofroth and Ott's (2007) habitat-based population estimate of 24 (95% CI 17-36). Over the past five years, our on-the-ground sampling efforts have consistently yielded lower than expected from habitat-based population estimates. In the Valhallas we found a population that was only 11% of the expected, in the south Selkirks 40%, the south Purcells 66%, the central Selkirks 59% and central Purcells 37%. We recognize that mark-recapture methods may be biased low if a bait reward causes previously captured animals to be more susceptible to recapture, however, over the course of the study we intensively surveyed large areas of apparently good quality habitat with no sign of wolverine presence, either DNA or tracks (which would not be subject to the same bias). Consequently, we feel that these numbers are cause for concern.

The central Purcells were identified as a harvest management concern by Lofroth and Ott (2007); with an estimated population size of 24 (CI 17-36) and a median annual harvest of 2 wolverine (1985-2004), the population was thought to be overharvested by 139% annually. Though our population estimate is much lower than this, harvest rates have also declined considerably; a conservative harvest estimate of perhaps only 2 wolverine over the last decade (data missing for 2010, 2011). Historical harvest pressure has been particularly high in some geographic areas. Wildlife management unit 4-26 (94% of historical harvest) contains 16 individual traplines and includes Findlay, Dutch, Toby and Horsethief Creek drainages. Between 1985-2009, only 8 traplines within this management unit reported harvesting wolverine and 36 % (12 of 33) of wolverine were trapped within one trapline in Horsethief Creek drainage. Similarly, over the most recent 5 year period (2012-2016) for the entire Kootenay region, 56% (24/43) of trapper harvests came from only 8 traplines in the entire region and one trapline was responsible for 16% (7/43) of all reported harvests. Consequently, it seems that wolverine harvest hinges on the efforts of relatively few trappers.

Wolverine trapping techniques are non-selective with respect to gender; and 44% of the wolverine harvested during the sampling period were female. As wolverine occur in low densities, maintaining high annual survival of adult females is imperative for sustainable populations (Krebs et al. 2004, Dalerum et al. 2008). Sustained harvest of wolverine can be maintained by dispersal of individuals from untrapped neighbouring areas (Krebs et al. 2004), highlighting the importance of spatial harvest management and identifying and maintaining linkages amongst populations. Assuming this habitat is capable of sustaining many more wolverine than we found, maintaining low harvest mortality will be important for population recovery.

We were unable to document connectivity between the mountain ranges in our study area on the basis of individual movements. Although in 2016 we recaptured one individual in the central Purcells that was detected three years previous, 28 km away in the south Purcells, the split between central and south Purcell study units was based on WMU boundaries and does not correspond with any geographic division in the range; locations for both years were within the Purcell Wilderness Conservancy and north of the seasonal and only road bisecting the area. None of the four other recaptured individuals from our sampling efforts were located outside the range where they were previously identified. However, in previous years we have confirmed movement in the Selkirks across Highway 3 and into Idaho and between the south Purcells and the southern Rockies by detecting an additional two individuals identified in other research projects; highlighting the importance of co-operative effort in studies of wide-ranging species.

These observations of few individual movements between ranges were corroborated by genetic analysis. Gene flow requires not only dispersal but also successful ensuing reproduction. Clustering in Principal Component Analysis suggests some genetic differentiation between wolverine in the Purcell and Selkirk ranges but overlap of both subpopulations with individuals from the Monashee range.

The presence of three distinct subpopulations in the STRUCTURE analysis is a clearer indication of limited gene flow. These results are somewhat surprising in the context of the proximity of the Selkirk, Purcell and Monashee ranges, the dispersal capacity of wolverine and the relatively small human footprint for the region. In particular, the central Selkirk and south Purcell populations, separated by Kootenay Lake, demonstrate evidence of genetic structure. Conversely, the few wolverine detected in the southernmost portion of the study area, with higher highway densities and anthropogenic impacts, are mixed in terms of subpopulation assignment. Overall, these results support other research suggesting population fragmentation for wolverine in southeastern British Columbia (Cegelski et al. 2006). Genetically distinct populations imply a low probability of dispersal and reproduction amongst ranges and consequently, if populations are in decline, reduced potential for demographic rescue from adjacent ranges.

Nevertheless, our results also suggest that dispersal events are still occurring among ranges and subranges. The central Purcell geographic area is the only one where we detected all three inferred subpopulations. This may be an important area for connectivity among ranges. If roads and hydroelectric, residential and other valley bottom developments are putative barriers to animal movement, they are not complete barriers and viable linkages still exist. Consequently, there is an opportunity to identify and maintain these linkages before they are lost completely.

Recommendations

Results have been consistent over the past five years of sampling and this year's data corroborates previous work in which we identified lower populations than anticipated and low connectivity amongst mountain ranges. The central Purcell population appears to link the more genetically uniform south Purcell and central Selkirk Mountains.

Wolverine harvest data is currently being collected through this study and is at the discretion of individual trappers. Given the low populations we are seeing, high proportion of females harvested from 2012-2016, and low gene flow, we urge managers to implement strategies to obtain accurate harvest data in order to assess sustainability. Additionally, to sustain fur harvests, it may be necessary to ensure spatial refuges of untrapped populations with high connectivity to exploited populations.

The direction of future research should be in identifying regional and local movement corridors using habitat mapping and radio-marked individuals, and in particular conserving or enhancing linkages to the central Selkirk and Purcell Mountains. These linkages may be critical to meta-population health. Small, genetically differentiated populations may also be an indication that land management practices and/or recreational access may be impacting wolverine distribution. This can also be investigated further through examination of wolverine movements and behaviour in home ranges with different land-use practices (Heinemeyer and Squires 2012).

Since wolverine are a threatened species and our wolverine population estimates for the study area were only 11-67% of expected, we see a need for a repeat survey of wolverine occupancy in the core population areas; central Selkirks, south and central Purcells, after 5 years to assess population trends, and the potential impact of management actions.

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Abundance and Distribution of Wolverine in the Kootenay Region

2014 Field Season Report: Central Selkirk Mountains

Prepared For:

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Seepanee Ecological Consulting

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Executive Summary

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally and is harvested regionally, yet no inventory has been conducted to estimate population abundance and connectivity in the southern portion of the Kootenays. Thus, a non-invasive genetic study and collection of trapper carcasses was initiated in the southern Columbia Mountains in 2012 with the objectives of estimating abundance and assessing meta-population connectivity to inform harvest management and contribute to international conservation efforts. Inventory was conducted in the south Selkirk (2012), south Purcell (2013) and central Selkirk Mountains (2014). This report summarizes results in the central Selkirk Mountains from 2014. Estimates of occupancy (71%) were higher than in the south Selkirk (54%) and south Purcell mountains (38%). Our estimates of population size in the central Selkirk Mountains (19; CI 16-24) were lower than previously published habitat-based values. We also found evidence of poor genetic connectivity between sub-ranges within our study. Annual harvest appears to constitute a high proportion of our estimated population. Given this, the low abundance levels, and the evidence of genetic isolation, the sustainability of the population may be in question.

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Introduction

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally (BC CDC 2013, COSEWIC 2003) and is classified as Identified Wildlife under the Forest and Range Practices Act (MWLAP 2004). Population estimates for British Columbia have been derived from habitat modeling based on mark-recapture in the Omenica and Northern Columbia Mountains (Lofroth and Krebs 2007) but lack verification for much of the province, including the southern portion of the Kootenays. Considering that adjacent U.S. populations are known to be at critically low levels (USFWS 2013), with wolverine absent from much potentially viable habitat, reliable abundance estimates are crucial for species conservation in the region.

In the Kootenays, wolverine populations are characterized by small and declining fur yields (~8 pelts/year) and harvest rates in parts of the region may be unsustainable (Lofroth and Ott 2007). Populations with high connectivity are resilient to local overharvest or high mortality from other sources because of source/sink dynamics (Pulliam 1988). Although genetic evidence indicates increasing population fragmentation in a north to south gradient in B.C. (Cegelski et al. 2006), the extent of gene flow between neighboring ranges in the southern Kootenay region is unknown. Hence, assessing connectivity is important to local population resilience and evaluating harvest sustainability.

Barriers to dispersal include transportation routes, hydroelectric and residential development and land use changes (Gardner et al. 2010, Krebs et al. 2007, Slough 2007, Austin 1998). Similarly, wolverine habitat use and density are associated negatively with winter recreation, forest harvest, and positively with roadless areas (Fisher et al. 2013, Krebs et al. 2007). Mapping occupied habitat in the Kootenays and identifying factors contributing to the persistence of wolverine in these areas is an essential step to identifying where conservation efforts to improve habitat and connectivity should be focused. Additionally, the Kootenay region is one of only a few areas identified as a potential corridor for trans-boundary movement of wolverine into the US (McKelvey et al. 2011, Schwartz et al. 2009, Singleton et al. 2002). Such movement is critical for the persistence of US populations, and this project will provide vital information for wolverine conservation in the trans-boundary region.

Project objectives were to: (1) assess occupancy/abundance of wolverine in the central Selkirk Mountains; (2) assess genetic connectivity between the Selkirk and Purcell populations; (3) evaluate current harvest levels; (4) evaluate broad-scale habitat factors that are associated with wolverine presence and; (5) cooperate inter-jurisdictionally for wolverine research.

Methods

Study Area

The study area was within the central Selkirk mountain range within the Central Columbia Mountains Ecosection in the southern Interior Mountains Ecoprovince. It was bounded to the east by Kootenay lake and Highway 31, to the north by the Lardeau Valley and Trout lake, to the west by Upper Arrow Lake and Slocan Valley and the west arm of Kootenay lake and Highway 3A to the south (Figure 1). Major land use in this area was historically mining and forestry and currently there is an expanding recreation element. Several winter use tenures for ski-based operations exist within the study area. Two provincial parks Goat Range Provincial Park (78,947 ha) and Kokanee Glacier Provincial Park (32,035 ha) are within this area. Starting in the valley bottom and progressing to the mountain peaks, biogeoclimatic ecosystem classification (BEC) units present are: Interior Cedar-Hemlock dry warm variant (ICHdw1), Interior Cedar Hemlock moist warm variant (ICHmw2), Engelmann Spruce Subalpine Fir wet, cold variant (ESSFwc1, ESSFwc4), Engelmann Spruce Subalpine Fir wet cold woodland (ESSFwcw), and Engelmann Spruce Subalpine Fir wet cold parkland (ESSFwcp).

At lower elevations the forest is composed of western redcedar (*Thuja plicata*) and western hemlock (*Tsuga heterophylla*) interspersed with Douglas fir (*Pseudotsuga menziesii),* lodgepole pine (*Pinus contorta*), trembling aspen (*Populus tremuloides*) and western larch (*Larix occidentalis)*. The shrub layer consists of Douglas maple (*Acer glabrum*), false box (*Paxistima myrsinites*), thimbleberry (*Rubus parviflorus*) and beaked hazelnut (*Crotylus cornuta*). False solomon seal (*Maianthemum racemosum*), horsetail (*Equisetum* spp.) and sedges (*Carex* spp.) made up the herbaceous layer in the mid-elevation forests). At higher elevations Englemann spruce (*Picea engelmannii*) and subalpine fir (*Abies lasiocarpa*) are the main tree species. Main shrubs include black huckleberry (*Vaccinium membranaceum*) false azalea (*Menziesia ferruginea*), white rhododendrum (*Rhododendrum albiflorum*) and heather (*Cassiope* spp.).

Survey methods

The central Selkirk Mountains study area was partitioned into 10 by 10 km cells that approximate the minimum size of a female home range. These 56 quadrats were sampled twice in approximately 21 day sampling intervals, from 10 February to 7 April, 2014 (Figure 1). Within 7 of these quadrats, we sampled two sites. Additionally, two sites from the south Monashee region were sampled in 2014 (24 November-31 January). Because of the rugged nature of the terrain, sites within cells were selected for ease of access by helicopter, snow machine or skis, using local knowledge of wildlife movements when available. Hair trap sites were created by affixing a bait item (beaver or deer quarter or deer head) to a tree approximately two meters from the ground or snow surface to entice the animal to climb (Fisher 2004). The bait item was nailed to the tree and the tree wrapped several times in barb wire to capture hair. During each check, the barb wire was examined for hairs or hair tufts, and the bait replenished if necessary. Hair was collected with forceps and stored in paper envelopes in a dry environment. We utilized three Rencoynx Rapidfire trail cameras (Reconyx Inc., Holmen, WI) and two Bushnell Trophy cameras (XLT Model No. 110456) during the sampling period. The Bushnell Trophy cameras were set to take 30-60s video.

Additionally, we collected genetic samples from wolverine carcasses obtained by trappers. From each carcass a tissue sample was taken and carcasses were necropsied by Ministry of Forests Lands and Natural Resource Operations.

Genetic Analysis

Six hundred and sixty two hair, tissue and scat samples were submitted to Wildlife Genetics International (WGI) in Nelson B.C. for genetic identification analysis. Of the hair samples submitted, 69% were sub-selected for analysis. Samples that did not contain guard hairs or >5 underfur were screened out because of insufficient genetic material. From the remaining samples, DNA was extracted using QIAGEN DNeasy Tissue kits, following the manufacturer's instructions (Qiagen Inc., Toronto, ON).

Species identification was based on a sequence-based analysis of a segment of the mitochondrial 16S rRNA gene (Johnson and O'Brien 1997). For samples that yielded wolverine DNA, WGI utilized multilocus genotyping, consisting of a ZFX/ZFY sex marker, and 8 additional microsatellite markers for individual identification.

Locations of sampling sites and genetic samples were mapped in ARCVIEW 3.1 (ESRI Inc. 1998, Jenness 2005).

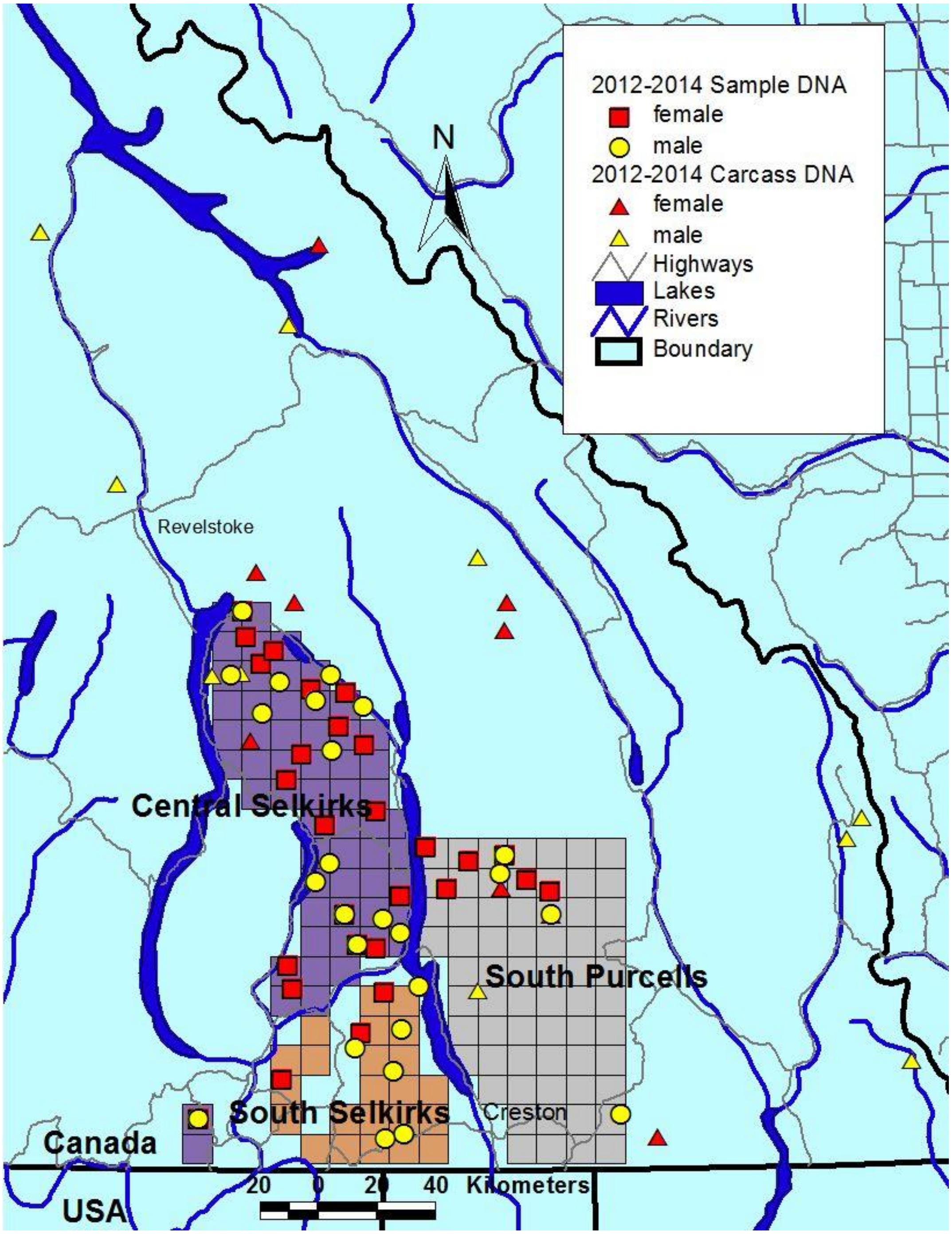

Figure 1. Wolverine non-invasive hair trapping results showing site locations where wolverines were detected (red squares, yellow circles) in the south Selkirk (2012), south Purcell (2013) and central Selkirk mountains (2014). An individual may be represented by more than one sample. Females are in red, males in yellow. Trapper carcass collection is represented by triangles. Two carcasses in 2013 lacked location information and were assigned to a management unit but not plotted on this map. All coloured quadrats were sampled with at least one site.

Occupancy and abundance

We used the single-season model in program PRESENCE (MacKenzie et al. 2002) to estimate the proportion of sample stations occupied by wolverine. A non-detection at a surveyed site could have meant wolverine were not present at the site or that we failed to detect an individual when it was present. PRESENCE uses a joint likelihood model to estimate the probability of missing a species when it is present at the site (p = *detectability*) and the probability that a site is occupied (Ψ = *occupancy*). To estimate these parameters repeat observations need to be conducted over a period of time during which site occupancy is assumed to be constant. In this way, a non-detection from a site with at least one detection can be treated as a false negative and the detection probability can be estimated.

We used both track detections (set up, and two checks) and genetic data (check 1, check 2) to estimate occupancy. For the 7 quadrats with more than one hair trap site, we randomly selected one site for occupancy analysis. We constructed models with group effects on occupancy and time dependence on detectability.

Estimates of occupancy can act as a surrogate for abundance for territorial species such as wolverine when the sites sampled approximate territory sizes (MacKenzie et al. 2006). We selected a grid resolution (10 x 10 km) that corresponded to a minimum home range size for female wolverine.

We used the genotyped individuals from two encounter occasions (check 1, check 2) to estimate abundance using a simple Lincoln-Peterson mark-recapture method ($N = Mn/R$, where N is the estimated population size, M is the number of animals identified in the first sampling session, R is the number of animals identified in the first session which are recaptured in the second session and n is the total number of animals identified in the second sampling session; Seber 1982).

Population genetics

To visualize genetic relationships amongst study areas we performed a multivariate ordination using principal component analysis (PCA) in GenAlEx 6.5 (Peakall and Smouse 2006, Peakall and Smouse 2012). This process finds and plots the major axis of variation within a multidimensional data set (i.e. multiple samples and multiple loci) to identify patterns within the data.

Results

During the course of the field season we monitored 56 sites in the central Selkirks and two in the southern Monashee ranges (Figure 1). Thirteen field days were required for setup and an additional 28 days for site monitoring. Detections of wolverine occurred at 59% of sites by snow tracking and/or genetic analysis (Figure 2). Wolverine tracks were detected in 39% (*n* = 22) of quadrats and were the exclusive detection method in 5 quadrats (Figure 2). Wolverine DNA was collected at 51% (*n* = 29) quadrats and were the exclusive detection method at 12 of those sites (Figure 2). At 30% percent of quadrats (17 of 56), both wolverine DNA and tracks were detected. Other carnivores detected, using snow tracking, included wolf (*Canis lupis*), cougar (*Puma concolor*), lynx (*Lynx canadensis*), and coyote (*Canis latrans;* Appendix 1).

We collected images using trail cameras at five sites (Figure 2) with a total monitoring period of 5,952 hours. Species detected included American marten (*Martes Americana*), stellars jay (*Cyanocitta stelleri*), wolverine, dog (*Canis familiarus*), raven (*Corvus corax*), and golden eagle (*Aquila chrysaetos*). We detected wolverine at 1 site, in the upper Lemon creek drainage (Figure 2). This site also provided hair samples for DNA analysis. A second camera, apparently working, in the Silverton creek drainage failed to detect wolverine, although wolverine DNA was obtained and evidence from the bait tree (deep scratches) suggested considerable activity.

Genetic analysis

We obtained genetic results from 304 hair, tissue and scat samples. One hundred and eighty-nine samples were identified by mitochondrial DNA analysis as species other than wolverine. These species included American marten (*n* = 176), bobcat (*n* = 6), cougar (*n* =2), northern flying squirrel (*n* = 2), short-tailed weasel (*n* = 2) and coyote (*n* = 1). Wolverine DNA was detected at 29 of 56 sites in the central Selkirks and at one of two sites in the southern Monashees. Eighty-four wolverine hair samples were assigned individual identification. From the 29 sites in the central Selkirks, we were able to identify 16 individual wolverines, 10 females and 6 males (Figure 2). At the site in the southern Monashees, we were able to identify a male and female wolverine.

Seven wolverine carcasses (six males, one female) were submitted by the trapping community in 2014 (Figure 1). This is in addition to four (two males, two females) and ten (six males and four females) carcasses submitted in 2012 and 2013, respectively (Figure 1).

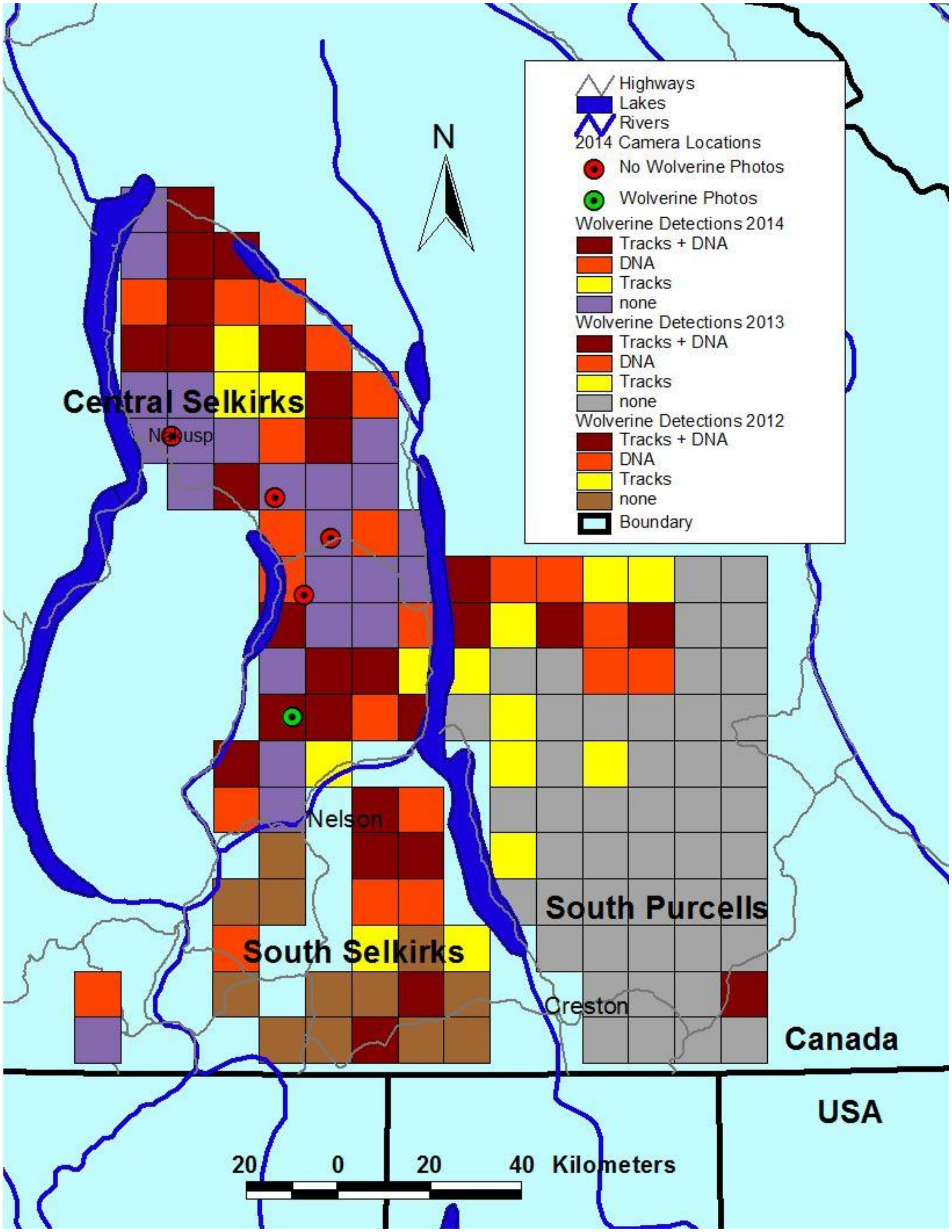

Figure 2. Wolverine non-invasive hair trapping results showing site locations and wolverines detected using DNA (orange) and snow tracking (yellow), or both (burgandy) in the south Selkirk (2012), south Purcell (2013) and central Selkirk (2014) mountains. An individual may be present at more than one site and some sites may have more than one individual.

Occupancy and abundance

Two models were considered as competing models in the analysis of occupancy using both tracks and genetics data (Δ AICc < 2; Table 1). The best model predicted constant occupancy with a change in detection probabilities with sampling sessions. The second competing model predicted two groups of sites with different detection probabilities in the sampling sessions. The model-averaged occupancy estimate was 71% (*SE* = 10.0). The probability of detection based on the weighted average of these two models was 17.8% (*SE* = 5.9) in repetition one, 38.1% (*SE* =8.2) in repetition two and 70.0% (*SE* = 6.4) in repetition three. Using tracks exclusively, the model-averaged occupancy estimate was 71.6 %, (*SE* = 27.0).

Table 1. Ranking for models of occupancy (ψ) and detectability (p) for track and genetic data of wolverine in the central Selkirk Mountains in 2014. Models were developed in Program PRESENCE and compared using AICc weights of evidence (Burnham and Anderson 1998). Δ AIC_c is the difference between a given model and the model with the lowest AIC_c[a] score, AIC_c weight (w_i) reflects the relative support for each model, K is the number of parameters estimated by the model.

Model	Δ AIC_c[a]	AIC_c weight (w_i)	K
ψ (.) p(survey specific)[b]	0.0	0.5948	4
ψ (2 groups) p(survey specific)[c]	0.77	0.4048	8
ψ (.) p(.)[d]	14.83	0.0004	2
ψ (2 groups) p(.)[e]	18.83	0.0000	4

[a] The lowest AICc score was 188.5

[b]constant ψ, survey specific p; the species has constant occupancy but different detection rates

[c]2 groups, survey specific p = there are two groups of sites and different detection rates

[d] constant ψ , constant p= The species has constant occupancy and detection rates

[e] 2 groups, constant p= there are two groups of sites where the species has the same detection probabilities

Using mark-recapture, the population was estimated at 19 (*SE* = 2.34, 95% *CI* = 16-24 individuals). We compared our population estimates and published habitat-based population estimates (Lofroth and Ott 2007) for the sampled population units (Table 2). Mean annual number of wolverine trapped in the central Selkirks was 4.9 for 2005-2014, 2 for 1995-2004 and 2.8 for 1985-1994. The same time intervals for the south Purcells yielded 1.7, 1.6 and 1.5 animals respectively, while the south Selkirks had no trapper harvest during these periods (data missing for 2010, 2011in all regions).

Table 2. Comparison of genetic-based and habitat-modeled population estimates (N) and annual harvest for wolverine populations in the south Selkirk, south Purcell and central Selkirk mountains.

Population	Mark-recapture[a] N (95% CI)	Habitat-based[b] N (95% CI)	Mean annual harvest 2005-2014 (1995-2004) (1985-1994)[c]
South Selkirks	4 (na)	10 (7-14)	0 (0) (0)
South Purcells	18 (9-27)	27 (20-39)	1.7 (1.6) (1.5)
Central Selkirks	19 (16-24)	32 (22-49)	4.9 (2)(2.8)

[a] This study
[b] Lofroth and Ott, 2007
[c] data from 1985-2009 based on trapper survey, data missing for 2010, 2011 and 2012-2014 based on carcass collection

Population genetics

Principal Component Analysis suggests genetic structure amongst populations with samples in the south Purcells (*n* =11), south Selkirks (*n* =4) and central Selkirks (*n* =19) clustering according to geographic region (Figure 3).

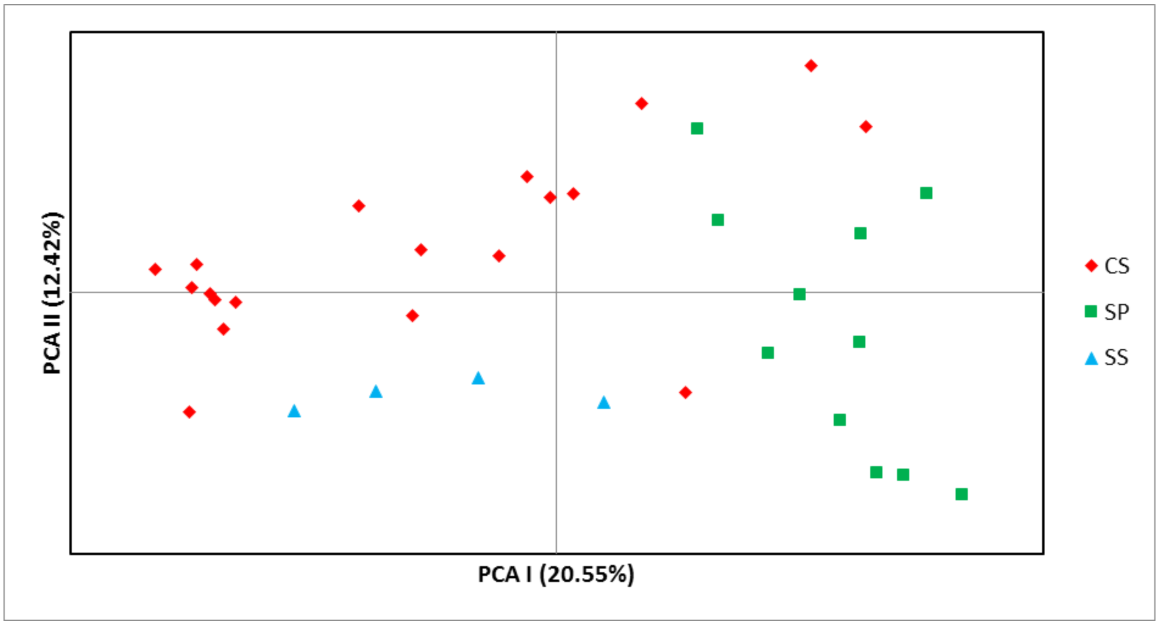

Figure 3. Principal Components Analysis (PCA) of 31 wolverine genetic samples from the 3 intensively sampled populations in southeastern British Columbia; central Selkirks (CS), south Purcells (SP), and south Selkirks (SS).

Discussion

This research represents the first on-the-ground attempt to inventory wolverine populations in the southern Kootenay region. The data is beginning to fill a critical knowledge gap for a species that is a conservation priority in the U.S. and Canada. In this third year of our project, we were able to almost double our number of genotyped individuals from 26 in 2013 to 51.

The central Selkirk mountains had higher occupancy estimates (71%) than both the south Selkirks (54%) and the south Purcells (35%). The central Selkirks were rated as high habitat quality for wolverine by Lofoth and Krebs (2007). The south Purcells, despite having the lowest occupancy rates were also rated as high but interspersed with moderate quality habitat. The south Selkirks were rated as moderate habitat quality.

In all sampling years, detection probability increased as the season progressed (Kortello and Hausleitner 2012, Kortello and Hausleitner 2014). While our initial detection probability (17.8%) is quite low, being track-based only, subsequent detection probabilities (38.1%, 70.0%) are comparable with other studies using similar methods for hair trapping wolverine (e.g. Fisher et al. 2013). Increases in detectability in later periods might be attributable to increased mobility due to snow conditions, increased mobility of denning females, and trap-happy individuals (Fisher et al. 2013).

We detected 2 wolverines using cameras in 2 years (2013 cameras located at 11 %, 7/65 sites in south Purcells and 2014 cameras at 9%, 5/56 of sites in central Selkirks). Although this information has been useful, cameras have not been an effective tool for calculating occupancy as we have so few on the landscape. Cameras have been shown to improve detectability for wolverine occupancy studies in the Rocky Mountains (Fisher et al. 2014).

Our population estimate based on mark-recapture of 19 (CI 16-24) individuals, is below the published habitat-based estimate of population size for the central Selkirks: 32 (CI 22-49), although confidence intervals overlap (Lofroth and Ott 2007). Over the past three seasons, our population estimates (Kortello and Hausleitner 2012, Kortello and Hausleitner 2014) have consistently been lower than the habitat-based estimates calculated by Lofroth and Ott (2007). However, we recognize that our non-invasive sampling may be underestimating occurrence (Fisher et al. 2014), and our mark-recapture estimates may be biased low because of a positive trap effect. Future analysis will model the spatial component of capture probability (Efford and Fewster 2013) for improved estimates.

Harvest rates in the central Selkirks are higher than both south Purcell and south Selkirks. The average annual harvest over the last 10 years, 4.9, represents a high proportion (26%) of our estimated population of 19 animals in the central Selkirks. Sustainable harvest of wolverine is thought to be 10% or less (Hatler and Beal 2003) of the fall population. Consequently, although the actual number of individuals harvested annually is quite variable (range 0-17), and our estimate of population is preliminary, these harvest levels may be risk-prone.

Fisher et al. (2013) found wolverine more abundant in rugged areas protected from anthropogenic development, similarly, although most of the terrain in our study area is quite rugged, the majority of wolverine detections (72%) have been within or immediately adjacent (within 10 km; conservatively one female home range width) to large protected areas; West Arm Provincial Park, Darkwoods Nature Conservancy, Purcell Wilderness Conservancy, St. Mary’s Alpine Provincial Park, Kokanee Glacier Provincial Park and Goat Range Provincial Park. These areas (including the 10 km buffer) encompass approximately 56% of our study area. This suggests that protected areas may be important for wolverine populations and this relationship warrants further investigation in future analyses.

None of the individuals detected in the central Selkirks in 2014 have been detected previously. To date we have been unable to document connectivity between south Selkirk, central Selkirk and south Purcell populations on the basis of individual movements. Additionally, our genetic analysis is limited by quite small sample sizes and the number of markers used. In spite of this, visual representations of genetic relatedness demonstrates evidence of genetic structure amongst the three subranges (south Selkirks, central Selkirks, and south Purcells; Figure 3). This data supports other research suggesting population fragmentation for wolverine in southeastern British Columbia (Cegelski et al. 2006). Genetically distinct populations imply a low probability of successful dispersal amongst ranges and consequently, if populations are in decline, reduced potential for demographic rescue from adjacent ranges.

Recommendations

Our data, suggests lower populations than expected and, surprisingly, low connectivity between this and other southern British Columbia populations, hence harvest should be carefully considered and managed with trapper input. The recent provincial effort to create a genetic database of a sample of harvested wolverine will augment the information gathered here, by using landscape genetics to identify functional population units, barriers and harvest sustainability at a larger scale (R. Weir 2014, pers. comm.).

Genetically structured populations point to a need for future efforts to restore connectivity and distinctly clustered wolverine detections also allude to the possible impact of land management practices and/or recreational access on wolverine distribution. This needs to be investigated further.

Data for wolverine harvest in 2012-2014 has come from carcass payments and is at the discretion of individual trappers. Ongoing, accurate harvest data is necessary to monitor population sustainability.

Considering tracks only, we would have detected almost 60% of the total occurrences in our occupancy modeling. Similarly, a concurrent caribou census (MLFNRO data) in the northern part of our study area under good tracking conditions obtained almost as many detections as our genetics work. Accordingly, when we based our occupancy estimates on tracks only, rather than tracks and genetics, we produced an almost identical occupancy rate but with higher variability, suggesting more repetitions would be necessary to increase precision. Track surveys present a potential time and cost saving avenue for future monitoring based on occupancy, if genetic information is not a priority and particularly if census is already underway for other species.

This research is being expanded into the Valhalla and southern Monashee region in 2015. With continued carcasses collected from trappers, and in collaboration with wolverine researchers in adjacent regions, we will increase the sample size of genotyped individuals, and continue to increase the strength of genetic analysis and spatial mark-recapture.

This information is crucial for identifying viable movement linkages and protecting habitat. These results will directly inform species harvest management. Further work should contribute to the management of crown land, acquisition of conservation properties, linkages and highway mitigation in the region. This study compliments similar research on grizzly bears to provide a multi-species perspective for regional conservation planning. Healthy, connected wolverine populations are an important ecosystem component of the Columbia River watershed, will sustain trapping opportunities for B.C. residents, and are critical for species persistence in the conterminous USA (Cegelski et al. 2006).

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Appendix 1. Carnivores detected by snow tracking during wolverine surveys in the central Selkirk and south Monashees November 2013-April 2014.

Location	UTM easting	UTM northing	Date (s)	Species
Beaver Lake	465242	5559810	March 26, April 20	coyote (1), lynx (1), wolf (3)
Beton Junction	450480	5616668	March 22	coyote
Gerrard	480379	5595102	April 18	coyote (1)
Kuskanux Creek	445068	5569617	March 23	coyote (1)
Ledrum Creek	503722	5514909	March 14, April 10	coyote (1)
Poplar Creek	491037	5584408	March 22	wolf (1)
Six mile Lakes	477195	477195	Feb 11	coyote (1)
Sproule Creek	467228	5489123	March 11	cougar (1)
Wilson Creek	473487	5552438	Feb 20, March 26	lynx (1)
Wilson Lake	451081	5565753	April 16	coyote (1)

Wolverine population and habitat assessment in the Kootenay Region.

2012 Field Season Report

Photo Credit: Mike Penno

Prepared For:

Columbia Basin Trust

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Seepanee Ecological Consulting

October 24, 2012

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INTRODUCTION

Wolverine are a species of conservation priority provincially and nationally (COSEWIC 2003, CDC 2011) and are classified as Identified Wildlife (IWMS) under the Forest and Range Practices Act (MWLAP 2004). However, current population status is inferred from small and declining fur yields, and wolverine mortality from trapper harvest may be unsustainable (Lofroth and Ott 2007).

Populations with high connectivity are resilient to overharvest because of source/sink dynamics but recent genetic evidence indicates population fragmentation in southern B.C. populations (Cegelski et al. 2006), and nearby US populations have already declined to critical levels (USFWS 2010). The landscape of the southern Kootenays is dissected by rivers, lakes, highways and corridors of dense human settlement which has led to isolation in grizzly bears and likely other wide ranging carnivores (Proctor et al. 2008).

Krebs et al. (2007) identified habitat barriers and winter recreation as factors limiting wolverine use of the landscape. These factors are more prevalent in the south Kootenay region than the Columbia Mountains where the study was conducted. In particular, the hydroelectric, transportation and residential development corridor, along the west arm of

Kootenay lake to Castlegar, represents a potential fracture line dividing populations in the Selkirks. This fracture, in addition to highway 3, has been identified as a barrier to gene flow for other carnivores such as grizzly bears (Proctor 2001, Proctor et al. 2008).

In 2011/2012, the South Selkirks portion of the Kootenays (Nelson and Bonnington Ranges) was selected for non-invasive wolverine sampling. This area was selected because it is the most fragmented and likely holds the smallest (and possibly most threatened) population of wolverine in the Kootenay region, based on the absence of trapper harvest in recent decades. This area has also been identified as a potential linkage route for wolverine dispersal into the U.S. (Singleton et al. 2002, Schwartz et al. 2009).

Genetic analysis using non-invasive DNA samples can provide a means to assess wolverine numbers and distribution in these ranges and contribute data essential for managing harvest, evaluating existing conservation areas and low-elevation linkages, and establishing protection measures if they are warranted. DNA-based species detections also enable habitat modeling to identify areas for land acquisition and those that may need to be managed for winter recreation.

METHODS

Field surveys

The South Selkirk study area was partitioned into 10 by 10 km cells that approximate the minimum size of a home range. Of the resulting cells, all 23 quadrats that encompassed preferred alpine and avalanche path habitat (Aubry et al. 2007, Krebs et al. 2007) were sampled twice in 20 to 30 day sampling intervals, from January to April, 2012 (Figure 1). Because of the rugged nature of the terrain, sites within cells were selected for ease of access by snow machine or skis, using local knowledge of wildlife movements when available. Hair trap sites were created by affixing a bait item (beaver or deer quarter) to a tree approximately two meters from the ground or snow surface to entice the animal to climb (Fisher 2004). The bait item was nailed to the tree and wrapped several times in wire. The tree was wrapped with barbed wire to capture hair. During each check, the barb wire was examined for hairs or hair tufts, and the bait was replenished if necessary. Hairs were collected with forceps and stored in paper envelopes in a dry environment.

Additionally, we submitted letters to all trappers in the provincial database in the Kootenay region. In this letter we introduced trappers to our research project and made a request for genetic samples from wolverines obtained by trappers.

Genetic Analysis

Hair samples were submitted to Wildlife Genetics International (WGI) in Nelson B.C. for DNA analysis. Samples that did not contain guard hairs or >5 underfurs were screened out because of insufficient genetic material. From the remaining samples, DNA was extracted using QIAGEN DNeasy Tissue kits, following the manufacturer's instructions (Qiagen Inc., Toronto, ON).

Species identification was based on a sequence-based analysis of a segment of the mitochondrial 16S rRNA gene (e.g. Johnson & O'Brien 1997). For samples that yielded wolverine DNA, WGI utilized multilocus genotyping, consisting of a *ZFX/ZFY* sex marker, and 12 additional microsatellite markers (13 markers total) for individual identification.

Occupancy and abundance

We used the single-season model in program PRESENCE (MacKenzie et al. 2002) to estimate the proportion of sample stations occupied by wolverine. A non-detection at a surveyed site could have meant wolverine were not present at the site or that we failed to detect an individual when it was present. PRESENCE uses a joint likelihood model to estimate the probability of missing a species when it is present at the site (p = detectability) and the probability that a site is occupied (Ψ). To estimate these parameters repeat observations need to be conducted over a period of time during which site occupancy is assumed to be constant. In this way, a non-detection from a site with at least one detection can be treated as a false negative and the detection probability can be estimated.

We used both track detections and genetic data to estimate occupancy. Locations of sampling sites and genetic samples were mapped in ARCVIEW 3.1 (ESRI Inc. 1998, Jenness 2005).

Population genetics

The program POPULATIONS (Langella 1999) was used to calculate shared allele distance (Chakraborty and Jin 1993), a simple measure of the degree of relatedness between individual genotypes in our samples. The proportion of shared alleles is estimated by $P_{SA} = \sum_u S / 2u$ where S is the number of shared alleles, summed over all loci u. Distance between individuals is estimated by $D_{SA} = 1 - P_{SA}$. To illustrate population substructure, these distances were used to plot a neighbour-joining tree (Saitou and Nei 1987) in DRAWTREE (part of the PHYLIP program package: Felsenstein 2005).

RESULTS

During the course of the field season we monitored 23 sites in the Nelson and Bonnington ranges that contained preferred wolverine habitat components (Figure 1). Nineteen field days were required for setup and an additional 40 days for site monitoring. From these we obtained 197 possible wolverine hair samples, two urine samples and a scat sample. Other carnivores detected, using snow tracking, included wolf (*Canis lupis*), cougar (*Puma concolor*), bobcat (*Lynx rufus*) and lynx (*Lynx canadensis;* Table 1).

Table 1. Other carnivores detected via snowtracking during surveys in the South Selkirks, 2012.

Date	**Location**	**Species**
5-Feb-2012	Maryland Creek	Wolf (1)
5-Feb-2012	Corn Creek	Bobcat (1)
9-Feb-2012	Give-out Creek	Cougar (1)
11-Feb-2012	Seeman Creek	Lynx (1)
17-Feb-2012	Lost Creek	Cougar (1), Wolf (1)
26-Feb-2012	Midgeley Creek	Cougar (1)
3-Mar-2012	Wildhorse Creek	Lynx (1)
11-Mar-2012	Seeman Creek	Lynx (1), Wolf (>4)
24-Mar-2012	Newington Creek	Lynx (1)
27-Mar-2012	Maryland Creek	Lynx (1)

Genetic analysis

Wolverine, pine marten, and flying squirrel were the species identified at sample stations by mitochondrial DNA (dioxy ribonucleic acid) analysis. Wolverine DNA was found at nine sites. From the nine sites, we were able to identify four individual wolverines, three males and one female. These came from six sites. An additional three sites had enough DNA for a species identification but not an individual identification (Figure 1). These could be animals already identified or new individuals. Three of the four wolverines demonstrated a parent-offspring genetic relationship; S1m and S2m, and S1m and S3f.

One animal, S4m, had been previously caught in the U.S. portion of the Selkiks in 2011, as part of a similar study conducted by Idaho Fish and Game. No wolverine harvest was reported for the South Selkirks but we collected three carcasses and one hair sample from trappers in the greater Kootenay region, including the Purcells, north Selkirks and Rocky mountain ranges. From each carcass a tissue sample was taken and carcasses were necropsied to determine body condition, age, sex and number of pregnancies. Necropsy data was submitted into a regional database and will contribute to long-term modeling of population structure. From trapper samples, we genotyped two males and two females. Locations of all genotyped individuals are shown in Figure 2.

Occupancy and abundance

Detections of wolverine occurred by snow tracking and/or genetic analysis (Table 2). Taken together, the naïve occupancy estimate, or number of cells occupied was 47.8% (Table 2, Figure 3). Taking detection rates into account (by calculating the probability of missed wolverine observations), the estimate of wolverine occupancy in the South Selkirk mountains becomes 55.4% (*SE* = 13.7). The best model predicted detection probability to be time specific (Table 3). The probability of detection was 23.6% (*SE* = 12.5) in repetition one, 39.3 % (*SE* =15.1) in repetition two and 70.7 % (*SE* = 17.2) in repetition three. However, the model with constant detectability and occupancy should be considered as a competing model (Table 3).

Table 2. Sample site and detection of wolverine (*Gulo gulo*) by identifiable tracks or genetic analysis (0= not detected, T = detected by tracks, DNA= detected by genetic analysis), in the Bonnington and Nelson ranges January-April 2012.

Grid	Site Name	Set up	Rep 1	Rep 2	Cumulative
N1	Mill Creek	T	0	T/DNA	T/DNA
N2	Wilson Creek	0	0	DNA	DNA
N3	Qua	T	0	T/DNA	T/DNA
N4	Seeman Creek	0	T/DNA	0	T/DNA
N5	Wildhorse Creek	0	0	DNA	DNA
N6	Cultus Creek	0	T	DNA	DNA
N7	Porcupine Creek	0	T	T	T
N8	Next Creek	0	0	0	0
N9	Wood Peak	0	T	0	T
N10	Aspen Creek	0	0	0	0
N11	Gamble Creek	0	0	0	0
N12	Bayonne Creek	T	0	DNA	T/DNA
N13	Newington Creek	0	0	0	0
N14	Lost Creek	0	0	0	0
N15	Wolf Peak	0	T	DNA	T/DNA
N16	Corn Creek	0	0	0	0
N19	Maryland Creek	0	0	0	0
B20	Give out Creek/Toad Mtn	0	0	0	0
B21	Siwash	0	0	0	0
B22	Hall Creek	0	0	0	0
B23	Grassy Mountain	0	0	DNA	DNA
B24	Mt. Kelly	0	0	0	0
B25	Archibald Creek	0	0	0	0
Number of Sites		**3**	**5**	**9**	**11**
Percent of Sites		**13.04**	**21.74**	**39.13**	**47.83**

Table 3. Ranking for models of occupancy (ψ) and detectability (p) for track and genetic data of Wolverine in the South Selkirk Mountains in 2012. Models were developed in Program PRESENCE and compared using AICc weights of evidence (Burnham and Anderson 1998).

Model	AICc	Delta AICc [a]	AICc Weights	Number of Parameters
ψ (.) p(survey specific)	76.1	0.0	0.69	4
ψ (.) p(.)	78.0	1.9	0.27	2
ψ (2 groups) p(.)[b]	82.0	5.9	0.04	4
ψ (3 groups) p(.)[c]	86.0	9.9	0.005	6

[a] A Δ AICc > 2 but < 4, provides weak evidence that the model is not the best fit for the data (Burnham and Anderson 1998).

[b] 2 groups, constant p= there are two groups of sites where the species has different detection probabilities

[c] 3 groups constant p= there are three groups of sites where the species has different detection probabilities

Population genetics

We calculated shared allele distances to illustrate genetic relationships between genotyped individuals (Figure 4). This analysis splits these animals into three groups, corresponding broadly to geographical areas (Figure 2). One group consists of animals found in the South Selkirks (S1, S2, S3), one of animals found north of the study area in the Northern Purcells, and adjacent Northern Selkirks and Rockies (P2, P3, P4). A third group consists of one animal from the Southern Selkirks and one from the Southern Purcells (P1 and S4; Figure 2).

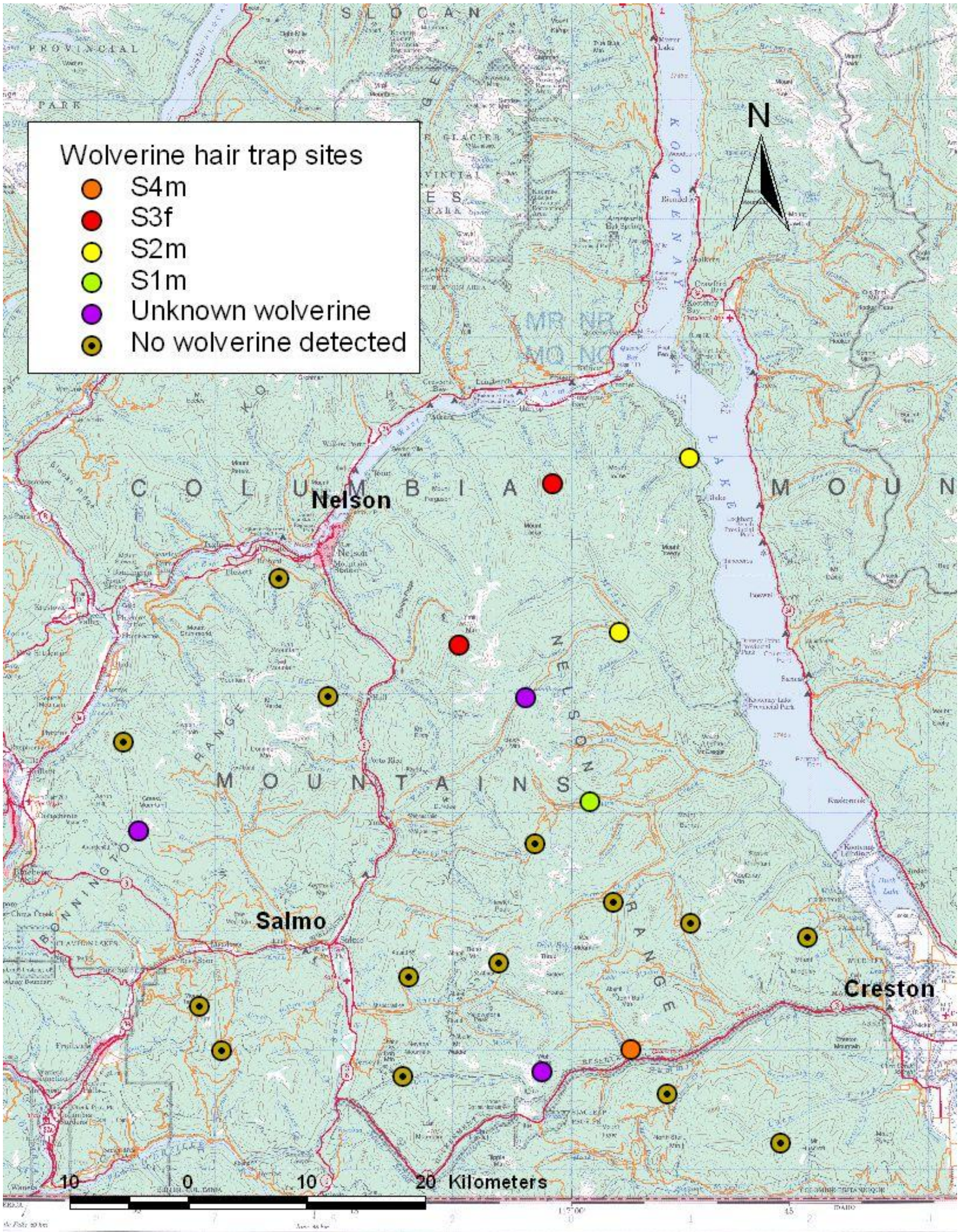

Figure 1. Wolverine non-invasive hair trapping results showing site locations and wolverines detected in the South Selkirk mountains, 2012. Suffix m and f denote male and female respectively.

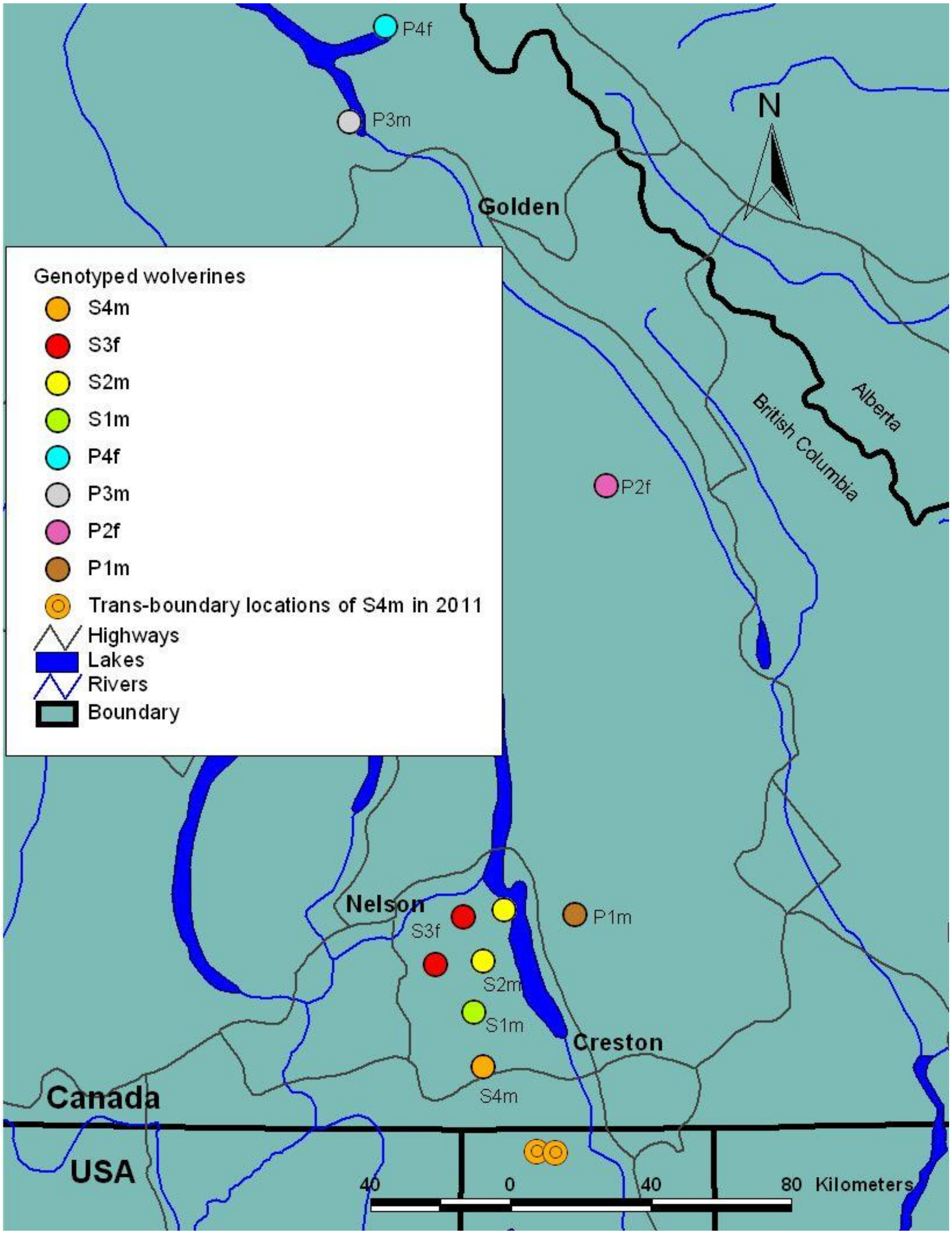

Figure 2. All genotyped samples obtained in 2012 using both hair traps in the South Selkirks (S1-S4) and carcass collection from trappers in southeastern B.C. (P1-P4). Transboundary locations of S4m were provided by M. Lucid of Idaho Fish and Game.

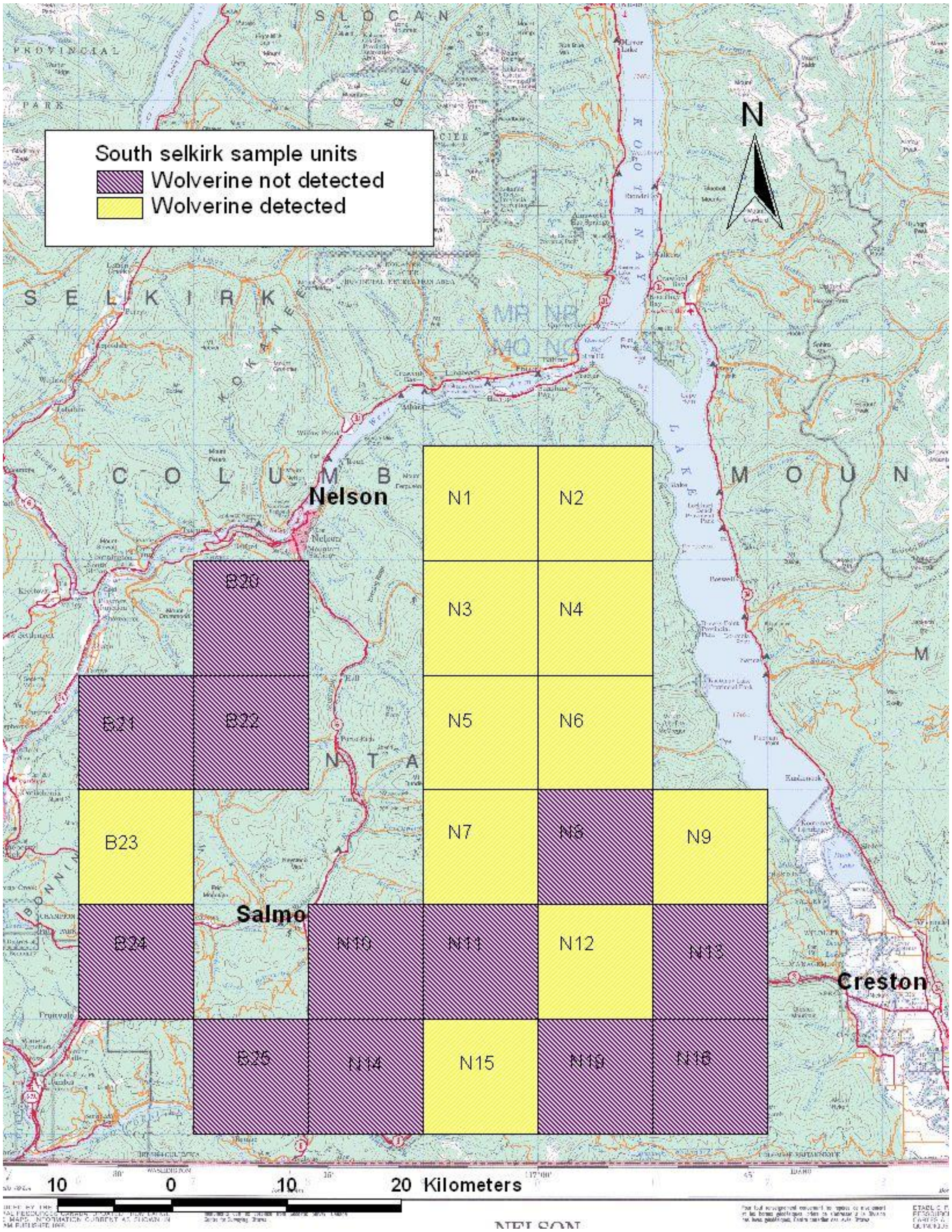

Figure 3. Sampling units with wolverines detected (naïve occupancy denoted by yellow), January- April, 2012.

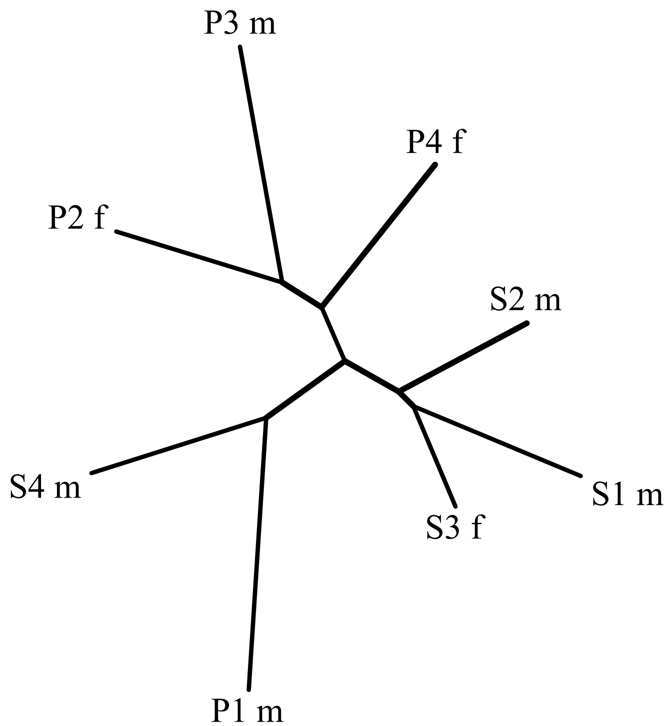

Figure 4. Neighbour-joining tree showing genetic distances between eight individuals in the South Selkirk (S) and other (P) populations, 2012.

DISCUSSION

This research is the first to examine wolverine distribution and connectivity in the South Selkirk Mountains of British Columbia. Our results provide the first recent evidence of a breeding population of wolverines in the South Selkirks. The last recorded trapper harvest of wolverine in this area was prior to 1985 (Lofroth & Ott, 2007), and recent observations of wolverine have been sporadic.

We documented a parent-offspring relationship between three of four wolverines genotyped. We also noted a pair of tracks traveling together in the Qua drainage in the Nelson range. For this solitary species, this typically indicates either a mating pair or a subadult and parent. Both observations show that these are not merely transient or dispersing individuals but a viable breeding population.

Our estimate of occupancy is 55% (±26.9, 95% C.I), approximately 13 of 23 quadrats or 1300 km^2. This provides a baseline for tracking changes over time and is useful as a measure of occupied habitat. Estimates of occupancy can act as a surrogate for abundance for territorial species such as wolverine when the sites sampled approximate territory sizes (MacKenzie et al. 2006). We selected a grid resolution (10 x 10 km) that corresponded to a minimum home range size for female wolverine. However, average home range size in the Columbia Mountains was 300 km^2 and 1000 km^2 for exclusive female and overlapping male wolverine, respectively (Krebs et al. 2007). With our estimate of occupied habitat in the South Selkirks between 1100 km^2 (defined by our naïve occupancy rate) and 1893 km^2 (defined by our upper confidence interval of occupancy), and assuming a 1:1 sex ratio (Magoun 1985, Banci 1987), this could be cautiously extrapolated to a population of 7-13 wolverines. However, underlying assumptions about animal distribution, population structure, habitat quality and edge effects may affect the accuracy of this estimate. Certainly we detected a minimum of four to seven wolverines from individual genotypes. Based on habitat attributes, Lofroth and Ott (2007) estimated a comparable wolverine population of 7-14 in the same area. Annual population recruitment (0.54 wolverines) and fur harvest sustainability was calculated using this habitat-based population estimate (Lofroth & Ott, 2007), but currently, with the absence of trapping pressure on this population, overharvest is not a consideration.

However, small populations are at risk of extirpation from other causes including demographic, environmental and genetic stochasticity (Shaffer 1981), consequently it is important to assess the connectivity of this population with adjacent populations in the Purcells and central Selkirks. Relatedness grouping between S4m from the South Selkirks and P1m in the South Purcells may indicate gene flow between the two areas. However, the current sample size is inadequate to draw conclusions. A low elevation linkage between these ranges has been identified for grizzly bears (*Ursus arctos;* Proctor et al. 2008) but its effectiveness for wolverine is unknown.

Our occupancy rate for wolverines of 55% contrasts sharply with the relative paucity of camera and DNA-based wolverine detections immediately south of the study area across the U.S. border (M. Lucid, Idaho Fish and Game, personal communication). This suggests a decline in habitat suitability, due to fragmentation, topography or some other factor, on the U.S. side. Certainly, highway 3 has been proposed as a barrier to wildlife movement (Proctor et al. 2002). We confirmed movement of one male wolverine across highway 3, indicating some permeability between U.S. and Canadian populations in the Selkirks. However research suggests a male-bias in dispersal abilities and willingness to cross barriers (Cegelski et al. 2006). More information is required to determine if this road is a barrier for female dispersal. If so, this may limit the effectiveness of this linkage zone for transboundary connectivity and population 'rescue' effects.

This project fills a critical knowledge gap for a species that is a conservation priority in the U.S. and Canada. This information is crucial for identifying and protecting critical habitat and viable movement linkages and justifying protection measures, such as the establishment of Wildlife Habitat Areas, which impacts timber harvest on crown land. These results will directly inform species management and potentially trapper harvest quotas. Further work will contribute to the acquisition of conservation properties, linkages and highway mitigation in the region.

This study compliments similar research on grizzly bears to provide a multi-species perspective for regional conservation planning. Healthy, connected wolverine populations are an important ecosystem component of the Columbia River watershed, will sustain trapping opportunities for B.C. residents and are critical for species persistence in the conterminous USA (Cegelski et al. 2006).

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Personal Communication

M. Lucid. Regional Wildlife Biologist, Wildlife Diversity Program. Idaho Department of Fish and Game.

Abundance and Distribution of Wolverine in the Kootenay Region

2013 Field Season Report: Purcell Mountains

Prepared For:

Ministry of Forests Lands and Natural Resource Operations and Columbia Basin Trust

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Seepanee Ecological Consulting

February 2014

Abstract

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally and is harvested regionally, yet no inventory has been conducted to estimate population abundance and connectivity in the southern portion of the Kootenays. Thus, a non-invasive genetic study was initiated in 2012 with the objectives of estimating abundance and assessing meta-population connectivity to inform harvest management and contribute to international conservation efforts. Our estimates of population size in the south Purcell Mountains were lower than previously published habitat-based values. We also found evidence of low genetic connectivity between the south Purcell population and other populations in southeastern British Columbia. At the same time, we detected at least one individual that had dispersed from the southern Rocky Mountains. Based on these revised population estimates, recruitment may not be sufficient to meet recent levels of harvest. We also detected wolverine south of Highway 3 in the Purcells in habitat contiguous with Montana and Idaho.

Introduction

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally (BC CDC 2013, COSEWIC 2003) and is classified as Identified Wildlife under the Forest and Range Practices Act (MWLAP 2004). Population estimates for British Columbia have been derived from habitat modeling based on mark-recapture in the Omenica and Northern Columbia Mountains (Lofroth and Krebs 2007) but lack verification for much of the province, including the southern portion of the Kootenays. Considering that adjacent U.S. populations are known to be at critically low levels (USFWS 2013), with wolverine absent from potentially viable habitat, reliable abundance estimates are crucial for species conservation in the region.

In the Kootenays, wolverine populations are characterized by small and declining fur yields (~8 pelts/year) and harvest rates in parts of the region may be unsustainable (Lofroth and Ott 2007). Populations with high connectivity are resilient to local overharvest or high mortality from other sources because of source/sink dynamics (Pulliam 1988). Although genetic evidence indicates increasing population fragmentation in a north to south gradient in B.C. (Cegelski et al. 2006), the extent of gene flow between neighboring ranges in the southern Kootenay region is unknown. Hence, assessing connectivity is important to local population resilience and evaluating harvest sustainability.

Barriers to dispersal include transportation routes, hydroelectric and residential development and land use changes (Gardner et al. 2010, Krebs et al. 2007, Slough 2007, Austin 1998). Similarly, wolverine habitat use and density are associated negatively with winter recreation, forest harvest, and positively with roadless areas (Fisher et al. 2013, Krebs et al. 2007). Mapping occupied habitat in the Kootenays and identifying factors contributing to the persistence of wolverine in these areas is an essential step to identifying where conservation efforts to improve habitat and connectivity should be focused. Additionally, the Kootenay region is one of only a few areas identified as a potential corridor for trans-boundary movement of wolverine into the US (McKelvey et al. 2011, Schwartz et al. 2009, Singleton et al. 2002). Such movement is critical for the persistence of US populations, and this project will provide vital information for wolverine conservation in the trans-boundary region.

Project objectives were to: (1) assess occupancy/abundance of wolverine in the Purcell Mountains; (2) assess genetic connectivity between the Selkirk and Purcell populations; (3) evaluate current harvest levels; (4) evaluate broad-scale habitat factors that are associated with wolverine presence and; (5) cooperate inter-jurisdictionally for wolverine research.

Methods

Field surveys

The southern Purcell Mountains study area was partitioned into 10 by 10 km cells that approximate the minimum size of a home range. These 65 quadrats were sampled twice in 21 day sampling intervals, from February to April, 2013 (Figure 1). Additionally, three sites from the South Selkirk region were resampled in 2013 (January-April). Because of the rugged nature of the terrain, sites within cells were selected for ease of access by helicopter, snow machine or skis, using local knowledge of wildlife movements when available. Hair trap sites were created by affixing a bait item (beaver or deer quarter or deer head) to a tree approximately two meters from the ground or snow surface to entice the animal to climb (Fisher 2004). The bait item was nailed to the tree and wrapped several times in wire. The tree was wrapped with barbed wire to capture hair. During each check, the barb wire was examined for hairs or hair tufts, and the bait replenished if necessary. Hairs were collected with forceps and stored in paper envelopes in a dry environment.

We utilized six Rencoynx Rapidfire trail cameras during the first session of sampling (approximate duration three weeks) and nine during the second (approximate duration four weeks; Figure 1). These cameras were deployed in sites in the Selkirk and Purcell ranges adjacent to Highway 3 to increase wolverine detectability in the event that they were visiting sites and not leaving samples and to assess linkage zones for wolverine across this putative barrier.

Additionally, we submitted a letter to all trappers in the provincial database in the Kootenay region soliciting genetic samples from wolverines obtained by trappers. From each carcass a tissue sample was taken and carcasses were necropsied to determine body condition, age, sex and number of pregnancies. Necropsy data was submitted into a regional database and will contribute to long-term modeling of population structure.

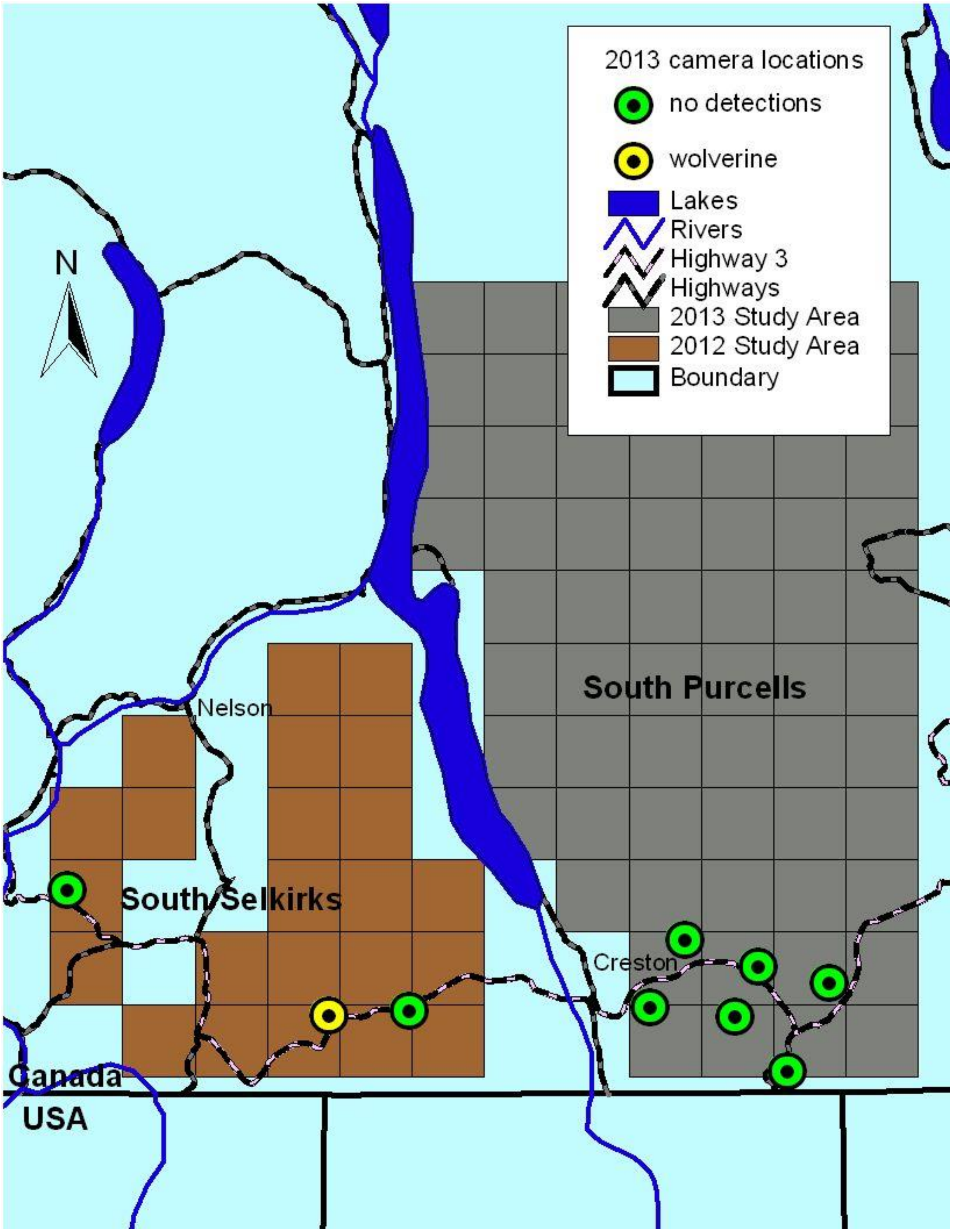

Figure 1. Trail camera locations along Highway 3 to detect wolverine at bait stations in the south Selkirk (2012) and south Purcell Mountain (2013) study areas.

Genetic Analysis

Hair samples were submitted to Wildlife Genetics International in Nelson B.C. for dioxy ribonucleic acid (DNA) analysis. Samples that did not contain guard hairs or >5 underfur were screened out because of insufficient genetic material. From the remaining samples, DNA was extracted using QIAGEN DNeasy Tissue kits, following the manufacturer's instructions (Qiagen Inc., Toronto, ON).

Species identification was based on a sequence-based analysis of a segment of the mitochondrial 16S rRNA gene (Johnson and O'Brien 1997). For samples that yielded wolverine DNA, WGI utilized multilocus genotyping, consisting of a *ZFX/ZFY* sex marker, and 12 additional microsatellite markers (13 markers total) for individual identification.

Occupancy and abundance

We used the single-season model in program PRESENCE (MacKenzie et al. 2002) to estimate the proportion of sample stations occupied by wolverine. A non-detection at a surveyed site could have meant wolverine were not present at the site or that we failed to detect an individual when it was present. PRESENCE uses a joint likelihood model to estimate the probability of missing a species when it is present at the site (p = detectability) and the probability that a site is occupied (Ψ). To estimate these parameters repeat observations need to be conducted over a period of time during which site occupancy is assumed to be constant. In this way, a non-detection from a site with at least one detection can be treated as a false negative and the detection probability can be estimated.

We used both track detections and genetic data to estimate occupancy. Locations of sampling sites and genetic samples were mapped in ARCVIEW 3.1 (ESRI Inc. 1998, Jenness 2005).

Estimates of occupancy can act as a surrogate for abundance for territorial species such as wolverine when the sites sampled approximate territory sizes (MacKenzie et al. 2006). We selected a grid resolution (10 x 10 km) that corresponded to a minimum home range size for female wolverine. However, average home range size in the Columbia Mountains was 300 km^2 and 1000 km^2 for exclusive female and overlapping male wolverine, respectively (Krebs et al. 2007). We applied the female density to our occupied habitat in the south Purcells and assumed a 1:1 sex ratio (Magoun 1985, Banci 1987) to derive a population estimate (female density times two), recognizing that animal distribution, population structure, habitat quality and edge effects may affect the accuracy of this estimate.

Additionally, a simple Lincoln-Peterson Method was used to estimate the population independent of occupancy; N = MN/R, where N is the estimated population size, M is the number of animals identified in the first sampling session, R is the number of animals identified in the first session which are recaptured in the second session and N is the total number of animals identified in the second sampling session (Seber 1982).

Population genetics

The program POPULATIONS (Langella 1999) was used to calculate shared allele distance (Chakraborty and Jin 1993), a simple measure of the degree of relatedness between individual genotypes in our samples. The proportion of shared alleles is estimated by $P_{SA} = \sum_u S / 2u$ where S is the number of shared alleles, summed over all loci u. Distance between individuals is estimated by $D_{SA} = 1- P_{SA.}$ To illustrate population substructure, these distances were used to plot a neighbour-joining tree (Saitou and Nei 1987) in DRAWTREE (part of the PHYLIP program package: Felsenstein 2013).

Results

During the course of the field season we monitored 65 sites in the Purcells and three in the Nelson and Bonnington ranges (Figure 1). Fourteen field days were required for setup and an additional 30 days for site monitoring. Other carnivores detected, using snow tracking, included wolf (*Canis lupis*), cougar (*Puma concolor*), lynx (*Lynx canadensis*), red fox (*Vulpes vulpes*) and coyote (*Canis latrans;* Appendix 1).

Using trail cameras, we collected 24,537 images over 9,476 hours of monitoring at bait sites. Species detected included flying squirrel (*Glaucomys sabrinus*), American marten (*Martes americana*, grey jay (*Perisoreus canadensis*), stellars jay (*Cyanocitta stelleri*), short-tailed weasel (*Mustela ermine*), red squirrel (*Sciurus vulgaris*), coyote, wolverine, bobcat (*Lynx rufus*), sharp-shinned hawk (*Accipiter striatus*), hairy woodpecker (*Picoides villosus*), human (*Homo sapien*) and mouse (*Peromyscus* spp.). We detected wolverine at one site, north of Highway 3 in the Nelson range, close to Kootenay Pass (Figure 1).

Genetic analysis

We obtained genetic results from 356 hair, tissue, scat and skull samples. The species identified by mitochondrial DNA analysis included American marten (*n* = 102), wolverine (*n* = 49), deer (*Odocileus* spp., *n* =11), cougar (*n* =7) northern flying squirrel (*n* = 6), elk (*Cervus canadensis*, *n* = 3), red squirrel (*n* = 2), coyote (*n* = 2), short-tailed weasel (*n* = 1), human (*n* = 1) and housecat (*Felis catus*, *n* = 1). Wolverine DNA was detected at ten sites. From those ten sites, we were able to identify eight individual wolverines, all females (Figure 2). At one of the three sites we re-sampled in 2013 in the south Selkirk we were able to confirm an individual identification where we had inadequate samples in 2012. Another individual in the south Selkirks was identified from hairs obtained opportunistically on a wolverine track. Both these individuals were previously detected at other sites in 2012.

Ten wolverine carcasses (six males, four females) were submitted by the trapping community in 2013 (Figure 2). This is in addition to four (two males, two females) submitted in 2012.

One of the submitted carcasses was a female wolverine that had been previously captured in a radio-telemetry study in the Flathead River in 2012. She was trapped just outside the south Purcell study area near Yahk in 2013 after travelling a distance of approximately 100 km across the East Kootenay Trench, likely crossing Highway 93 and the Koocanusa Reservoir (Figure 2).

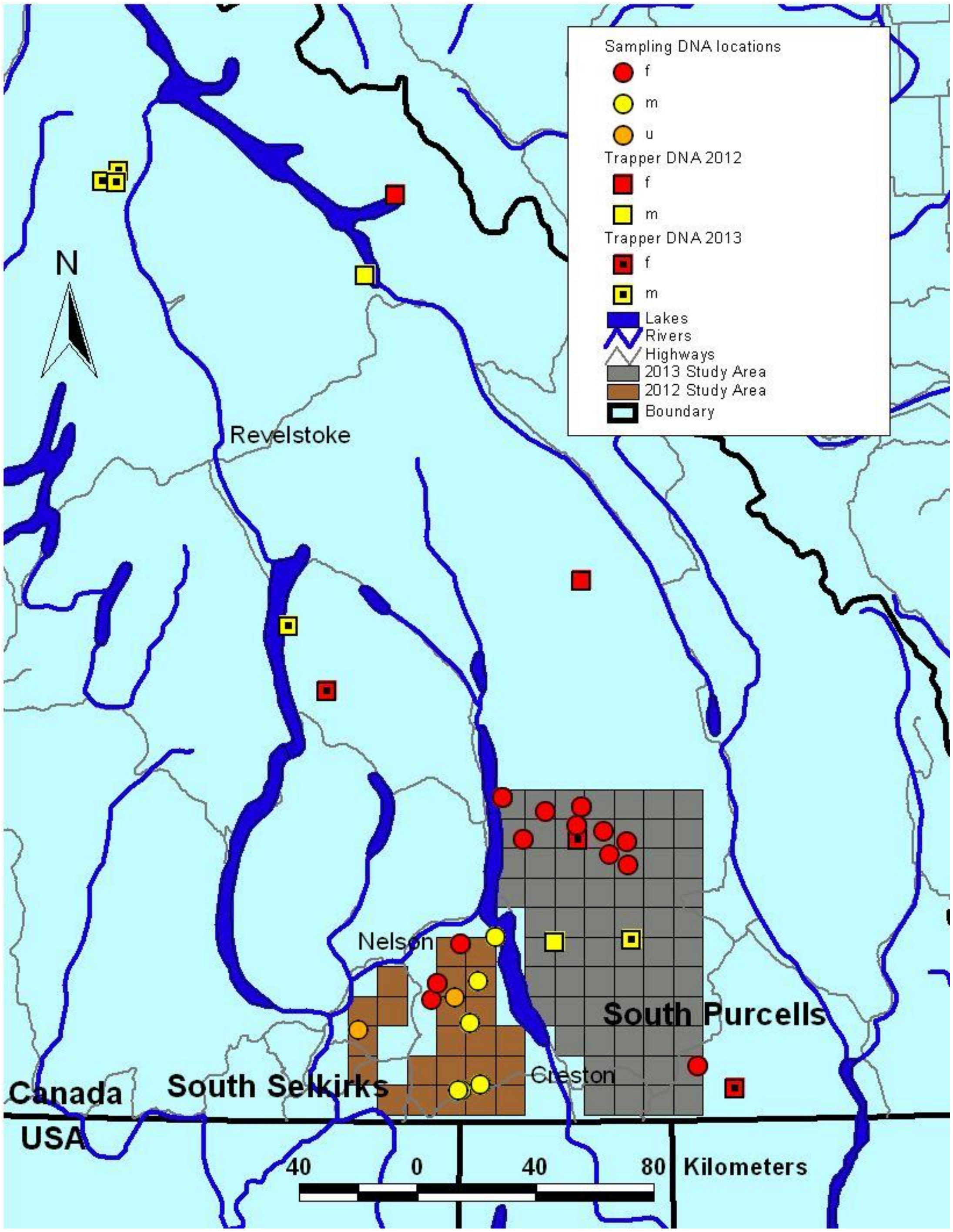

Figure 2. Wolverine non-invasive hair trapping results showing site locations and wolverines detected (orange circles) in the south Selkirk (2012) and south Purcell Mountains (2013). An individual may be represented by more than one sample. M is male, F is female and U is unknown sex. Trapper carcass collection is represented by squares (2012) and squares with dots (2013). Two carcasses in 2013 lacked location information and were assigned to a management unit but not plotted on this map.

Occupancy and abundance

Detections of wolverine occurred by snow tracking and/or genetic analysis (Figure 3). The naïve occupancy estimate, or number of cells occupied in the south Purcell Mountains was 27.3%. Taking detection rates into account (by calculating the probability of missed wolverine observations), the estimate of wolverine occupancy in the south Purcell mountains was 38.3% (*SE* = 10.2). Two models need to be considered as competing models (Δ AICc < 2; Table 1). The best model was one in which detection probabilities changed with sampling session. The probability of detection was 19.8% (*SE* = 9.0) in repetition one, 31.6 % (*SE* =11.5) in repetition two and 47.4 % (*SE* = 14.2) in repetition three. The competing model is one in which detection and occupancy is constant through sampling sessions.

Our occupancy-based population estimate was 17 wolverine for the south Purcell population. Using mark-recapture, the population was estimated at 18 (*SE* = 4.83, 95% *CI* = 9-27 individuals).

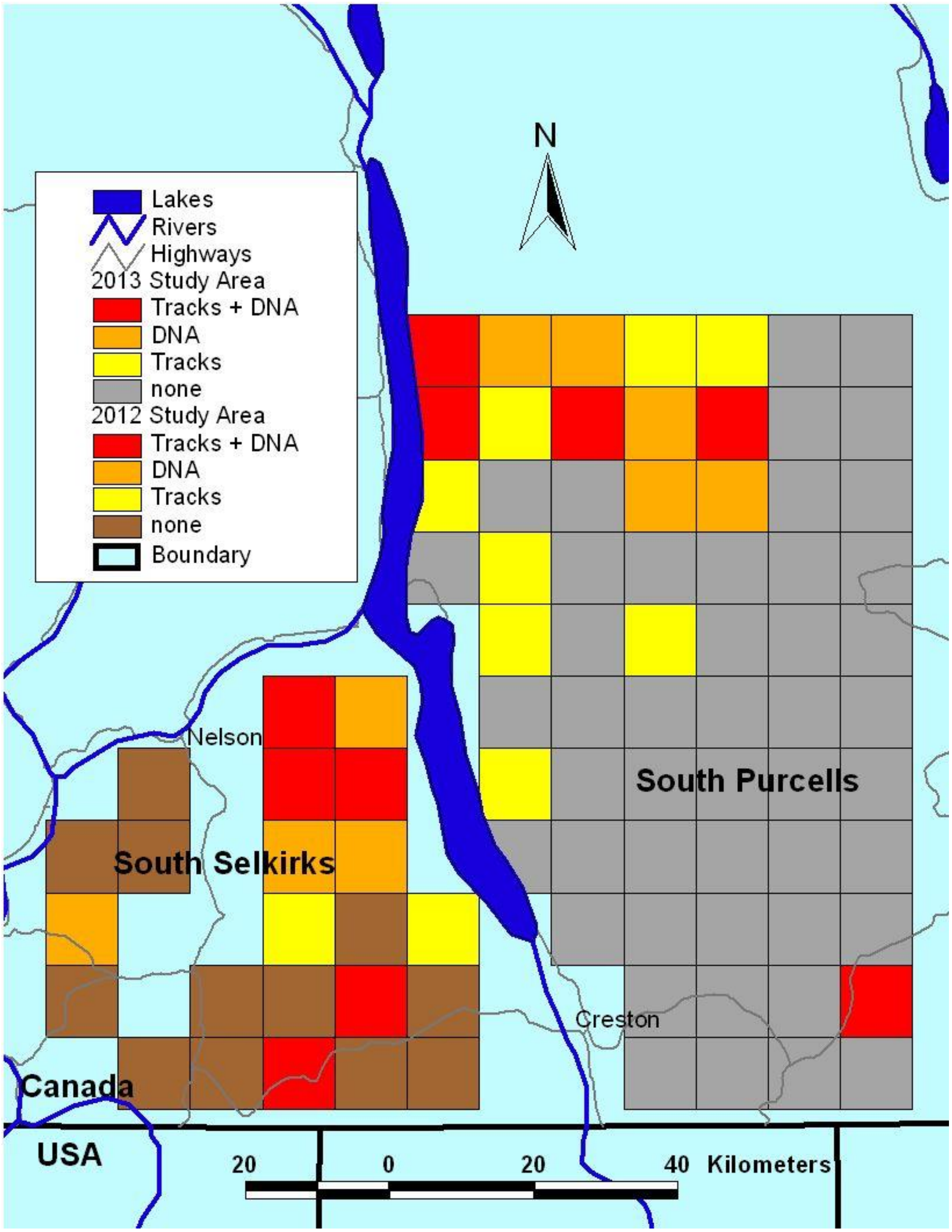

Figure 3. Wolverine detections by tracks and DNA in the south Selkirk and Purcell Mountains, 2012 and 2013.

Table 1. Ranking for models of occupancy (ψ) and detectability (p) for track and genetic data of Wolverine in the south Purcell Mountains in 2013. Models were developed in Program PRESENCE and compared using AICc weights of evidence (Burnham and Anderson 1998).

Model	AICc	Delta AICc [a]	AICc Weights	Number of Parameters
ψ (.) p(survey specific) [b]	146.7	0.0	0.50	4
ψ (.) p(.)[c]	147.1	0.4	0.40	2
ψ (2 groups) p(.)[d]	151.6	4.3	0.06	4
ψ (2 groups) p(survey specific)	155.1	8.4	0.04	8

[a] A Δ AICc > 2 but < 4, provides weak evidence that the model is not the best fit for the data (Burnham and Anderson 1998).

[b]constant ψ, survey specific p= The species has constant occupancy but different detection rates

[c] constant ψ , constant p= The species has constant occupancy and detection rates

[d] 2 groups, constant p= there are two groups of sites where the species has the same detection probabilities

Population genetics

Visual inspection of the neighbour-joining tree shows 10 of 11 wolverines from the south Purcells clustered on the same branch, and all three wolverines from the central Selkirk Mountains clustered together as well (Figure 4). Three of four south Selkirk wolverines share the same branch (Figure 4), although this cluster also includes individuals from the south Rockies and north Monashees. Individuals from the north Purcells (1), central Purcells (1), north Monashees (3), south Rockies (1) and central Rockies (2) populations do not appear to be clustered geographically (Figure 4).

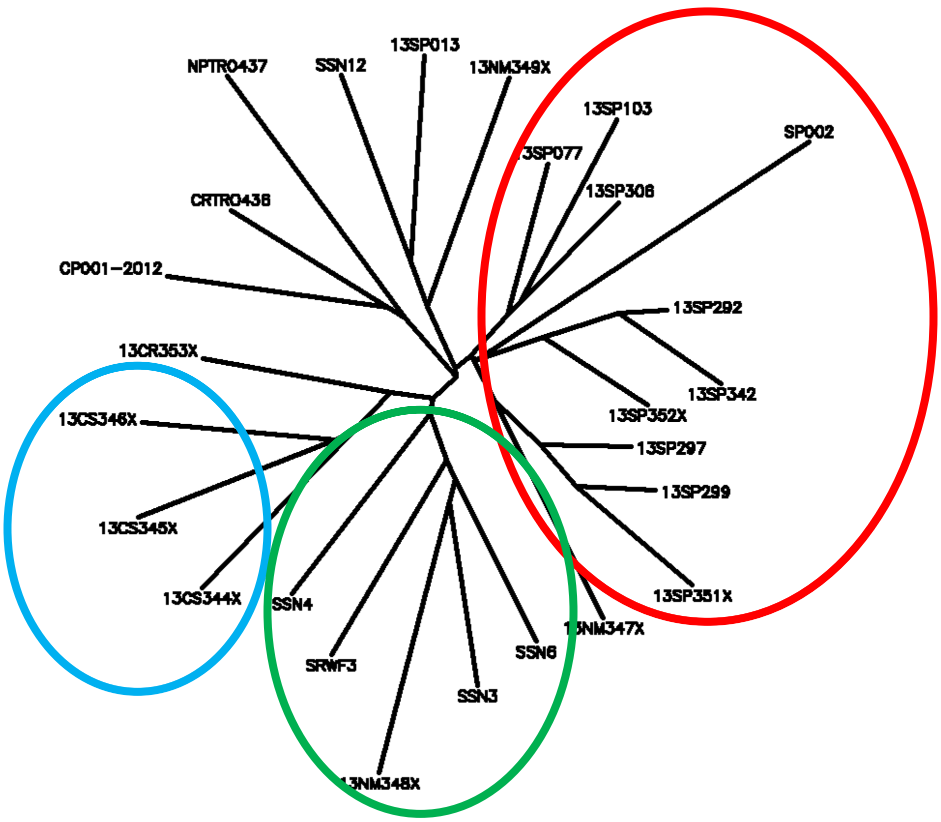

Figure 4. Neighbour-joining tree showing genetic distances between 26 wolverine in the south Selkirk (SS), central Selkirk (CS), south Purcells (SP),central Purcells (CP), north Purcells (NP), south Rockies (SR), central Rockies (CR), and north Monashees (NM) populations, 2012-2013. The three main clusters are the southern Purcells (red circle), southern Selkirks (green circle), and central Selkirks (blue circle).

Discussion

This research represents the first on-the-ground attempt to inventory wolverine populations in the southern Kootenay region. The south Purcell wolverine population was of particular interest because it had been identified as a management concern with respect to potential overharvest (Lofroth and Ott 2007).

Compared to 2012 results in the south Selkirks, the south Purcells had lower naïve (27.3% vs 47.8) and estimated occupancy (38.3% vs 55.4%) rates. Additionally, the south Purcells had lower detection probabilities (19.8% vs 23.6%; 31.6% vs 39.3%; 47.4% vs 70.7%) in all repetitions (Kortello and Hausleitner 2012).

Lofroth and Krebs (2007) analysis of wolverine habitat in British Columbia rated most of the southern Purcells as high quality habitat, and the southern Selkirks as moderate. Given the habitat ratings, and a larger contiguous area in the southern Purcells, we expected higher wolverine occupancy rates in the southern Purcells than in the southern Selkirks, but we found the opposite. Contributing factors may be related to harvest, forest management, prey abundance and habitat fragmentation, and likely a combination of factors. The south Selkirks has a higher proportion of land in protected areas with difficult access. Additionally, there is a difference in harvest rates between the two regions; there has been no reported trapping in the south Selkirk region since before 1985 (Lofroth and Ott 2007). In contrast, average annual harvest rate in the south Purcell management units sampled (4-5, 4-6, 4-19 and 4-20; 1985-2013; data for 2011 is unavailable) has been 1.4 wolverine. However, annual harvest is variable with an increase in the past five years (ten year average (2003-2013) = 1.2, five year average (2008-2013) = 2.0).

Our estimate of occupancy translates to 17 wolverine based on average home range sizes (Krebs et al. 2007). This estimate, in addition to the population estimate based on mark-recapture of 18 (CI 9-27) individuals, is below the published habitat-based estimate of population size for the south Purcells: 27 (CI 20-39), although confidence intervals overlap (Lofroth and Ott 2007). Additionally, we sampled a slightly larger area than the South Purcell population unit boundaries of Lofroth and Ott (2007). For our estimated population of 18 wolverine, annual recruitment is expected to be around one (Lofroth and Ott 2007). It appears that, in this population, harvest may be exceeding recruitment in some years.

Female productivity is strongly linked to body condition and hence food availability, particularly large ungulate carcasses (Lofroth et al. 2007, Persson 2005). Consequently net recruitment might be greater in unusually productive environments. However, a consistently high (relative to recruitment) harvest rate in the south Purcells might also explain the large number of females in our genetics sample and apparent lack of connectivity with other populations. Males have larger home ranges (Krebs et al. 2007) and are found at lower elevations (Lofroth 2001) than females, making them more susceptible to harvest. Dispersing wolverine would also be more vulnerable to harvest for similar reasons. Three of four wolverine harvested in the Purcells in the past two years fit these criteria (male or disperser).

There was a notable decline in wolverine detections in a north to south gradient in both the south Selkirk and Purcell Mountains. Fisher et al. (2013) found wolverine more abundant in rugged areas protected from anthropogenic development, similarly, although most of the terrain in our study area is quite rugged, the majority of wolverine detections have been within cells in or immediately adjacent to large protected areas; West Arm Provincial Park, Darkwoods Nature Conservancy, Purcell Wilderness Conservancy, and St. Mary's Alpine Provincial Park. The location of these areas may account for the north to south gradient in distribution in both ranges.

Despite very small sample sizes for populations, geographic clustering of genotypes supports other research suggesting some degree of population fragmentation for wolverine in southeastern British Columbia (Cegelski et al. 2006). The genetic similarity of the southern Purcell population is somewhat surprising, given the extent of the range northward and its close proximity to populations in the northern Selkirks. Additionally, the female wolverine from the Rockies that was later trapped in the southern Purcells indicates a viable travel corridor across the East Kootenay trench. Unfortunately, from the timing of when she was last detected in the Rockies, it is unlikely that this individual contributed reproductively to the south Purcell population prior to harvest. If this is the case for other dispersers, there is less probability of gene flow or demographic 'rescue' by immigrants.

Our camera array did not provide any insights into connectivity in the Purcells across Highway 3, but a repeat detection of a transboundary wolverine (detected in Idaho in 2011) at Kootenay Pass in the Selkirks highlights the importance of the Kootenay Pass area for movements between Canadian and US populations. Since DNA was collected at this site as well, the use of the camera did not improve our ability to detect wolverine but provided ancillary information on the timing of visits. We obtained DNA from two wolverine south of Highway 3 near Yahk. This area provides contiguous mountain habitat into the US without a major road crossing and might be a zone for wolverine movements into Montana and Idaho.

Our data, somewhat surprisingly suggest lower populations than expected and lower connectivity between this and other southern British Columbia populations, hence harvest should be carefully considered and managed with trapper input. Distinctly clustered wolverine detections also allude to the possible impact of land management practices and/or recreational access on wolverine distribution. This research is being expanded into the central Selkirk region in 2014. This, with continued carcasses donated from trappers, will increase the sample size of genotyped individuals, and continue to increase the strength of genetic analysis.

This project is beginning to fill a critical knowledge gap for a species that is a conservation priority in the U.S. and Canada. This information is crucial for identifying viable movement linkages and protecting habitat. These results will directly inform species harvest management. Further work will contribute to the management of crown land, acquisition of conservation properties, linkages and highway mitigation in the region. This study compliments similar research on grizzly bears to provide a multi-species perspective for regional conservation planning. Healthy, connected wolverine populations are an important ecosystem component of the Columbia River watershed, will sustain trapping opportunities for B.C. residents, and are critical for species persistence in the conterminous USA (Cegelski et al. 2006).

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We would like to thank Rick Allen and Columbia Basin Trust for financial support for this project. Additional funding was received from Ministry of Forests Lands and Natural Resource Operations and the Wolverine Foundation.

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Appendix 1. Carnivores detected by snow tracking during wolverine surveys in the south Purcells and south Selkirks January-April 2013.

Location	**UTM easting**	**UTM northing**	**Date (s)**	**Species**
Clearwater Creek	488451	5468811	19 Jan	Coyote (1)
Bombi Summit	462420	5455674	22 Jan, 19 Feb	Cougar (1), Lynx (1), Coyote (1)
Wolf Peak	498559	5438243	3 Feb, 1 April	Coyote (1)
Baribeau/Redding Confluence	533238	5498381	10 Feb	Coyote (1)
Redman Point	521371	5466658	11 Feb, 4 March	Coyote (1), Wolf (1)
Mount Thompson	542908	5439398	11 Feb	Coyote (1)
Hazel Creek	557901	5445092	11 Feb, 7 March	Coyote (1)
Kid Creek	562293	5456220	13 Feb	Cougar (1)
Englishman Creek	567682	5442896	14 Feb, 6 March	Red fox (1), Coyote (1)
Houghton Creek	516079	5505834	15 Feb, 10 March	Coyote (1)
Lamb Creek Headwaters	572409	5457717	19 Feb	Wolf (1)
Rabbitfoot Creek	576255	5463107	19 Feb	Lynx (1)
St Mary/Dewer Junction	544627	5507441	20 Feb	Wolves (>1)
Buhl/Skookumchuck Confluence	569600	5534736	21 Feb	Coyote (>1)
Kianuko Creek	540833	5476179	4 March	Red fox (1)
Leadville	549498	5453477	5 March	Coyote (1)
Kianuko/Goat Confluence	544464	5465158	5 March	Coyote (1)
Kitchener	547812	5448713	5 March	Coyote (1), Red fox (1)
Little Moyie	554758	5438204	5 March, 4 April	Coyote (1)
Mt Sommerfeld	556468	5450470	6 March	Coyote (1)
St. Mary's	551216	5497089	15 March	Wolf (1), Cougar (1)
Maryland Creek	509671	5438961	1 April	Wolf (1)
Birchdale	512369	5537026	11 April	Coyote (1)
Mather/Cherry Creek	574678	5517433	11April	Lynx (1)

Abundance and Distribution of Wolverine in the Kootenay Region

2015 Field Season Report: Valhalla and South Monashee Mountains

Prepared For:

Fish and Wildlife Compensation Program- Columbia, Ministry of Forests Lands and Natural Resource Operations and Columbia Basin Trust

Prepared By:

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Seepanee Ecological Consulting

December 2015

Executive Summary

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally and is harvested regionally, yet no inventory has been conducted to estimate population abundance and connectivity in the southern portion of the Kootenays. Thus, a non-invasive genetic study and collection of trapper carcasses was initiated in the southern Columbia Mountains in 2012 with the objectives of estimating abundance and assessing meta-population connectivity to inform harvest management and contribute to international conservation efforts. Inventory was conducted in the south Selkirk (2012), south Purcell (2013), central Selkirk (2014) and Valhalla and south Monashee Mountains (2015). This report summarizes results in the Valhalla and south Monashee Mountains from 2015. We identified only two wolverines in the Valhallas and none in the south Monashees, although two individuals from the south Monashees had been identified the previous year. An additional 7 donated trapper carcasses were genotyped from other ranges in the Kootenays. Although we were unable to estimate population size for the Valhallas, we believe this is indicative of a very low population in an area expected to be high quality habitat. Estimates of occupancy (46%) were lower than in the central Selkirk and south Selkirk (54%) but higher than the south Purcell Mountains (38%). Our estimate of detectability (12%) was low compared to previous years (range 18-71%); unusual weather may have been a factor. Though limited, these data corroborate evidence from previous sampling seasons and appear to indicate low wolverine abundance and low genetic connectivity between mountain ranges. These factors necessitate careful attention to harvest pressures on a range by range basis.

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Introduction

Wolverine (*Gulo gulo*) is a species of conservation priority provincially and nationally (BC CDC 2013, COSEWIC 2003) and is classified as Identified Wildlife under the Forest and Range Practices Act (MWLAP 2004). Population estimates for British Columbia have been derived from habitat modeling based on mark-recapture in the Omenica and Northern Columbia Mountains (Lofroth and Krebs 2007) but lack verification for much of the province, including the southern portion of the Kootenays. Considering that adjacent U.S. populations are known to be at critically low levels (USFWS 2013), with wolverine absent from much of the potentially viable habitat, reliable abundance estimates are crucial for species conservation in the region.

In the Kootenays, wolverine populations are characterized by small and declining fur yields (~8 pelts/year) and harvest rates in parts of the region may be unsustainable (Lofroth and Ott 2007). Populations with high connectivity are resilient to local overharvest or high mortality from other sources because of source/sink dynamics (Pulliam 1988). Although genetic evidence indicates increasing population fragmentation in a north to south gradient in B.C. (Cegelski et al. 2006), the extent of gene flow between neighboring ranges in the southern Kootenay region is unknown. Hence, assessing connectivity is important to local population resilience and evaluating harvest sustainability.

Barriers to dispersal include transportation routes, hydroelectric and residential development and land use changes (Gardner et al. 2010, Krebs et al. 2007, Slough 2007, Austin 1998). Similarly, wolverine habitat use and density are associated negatively with winter recreation, forest harvest, and positively with roadless areas (Fisher et al. 2013, Krebs et al. 2007). Mapping occupied habitat in the Kootenays and identifying factors contributing to the persistence of wolverine in these areas is an essential step to identifying where conservation efforts to improve habitat and connectivity should be focused. Additionally, the Kootenay region is one of only a few areas identified as a potential corridor for trans-boundary movement of wolverine into the US (McKelvey et al. 2011, Schwartz et al. 2009, Singleton et al. 2002). Such movement is critical for the persistence of US populations, and this project will provide vital information for wolverine conservation in the trans-boundary region.

Project objectives were to: (1) assess occupancy/abundance of wolverine in the Valhalla and south Monashee Mountains; (2) assess genetic connectivity amongst Valhalla, Selkirk and Purcell populations; (3) evaluate current harvest levels; (4) evaluate broad-scale habitat factors that are associated with wolverine presence and; (5) cooperate inter-jurisdictionally for wolverine research.

Methods

Study Area

The study area was within the Valhalla and southern Monashee mountain ranges within the Central Columbia Mountains and Selkirk Foothill Ecosection in the southern Interior Mountains Ecoprovince. The Valhalla Mountains were bounded to the east by Slocan Lake and Highway 6, to the north by Highway 6 and Upper Arrow Lake, to the west and south by Upper and Lower Arrow Lake (Figure 1). The southern Monashee Mountains were bounded to the north by Lower Arrow Lake. To the east and west, the Columbia River and Big Sheep Creek, respectively and the US border to the south (Figure 1). Major land use in this area was historically mining and forestry and currently there is an expanding recreation element. Several winter use tenures for ski-based operations exist within the study area. Two provincial parks; Syringa Park (4,499 ha) and Valhalla Provincial Park (49,828 ha) are within this area. Starting in the valley bottom and progressing to the mountain peaks, biogeoclimatic ecosystem classification (BEC) units present are: Interior Cedar-Hemlock dry warm variant (ICHdw1), Interior Douglas fir-undifferentiated (IDFun), Interior Cedar-Hemlock moist warm variant (ICHmw2), Engelmann Spruce-Subalpine Fir wet, cold variant (ESSFwc1, ESSFwc4), Engelmann Spruce-Subalpine Fir wet cold woodland (ESSFwcw), Engelmann Spruce-Subalpine Fir wet cold parkland (ESSFwcp), Interior Mountain-heather Alpine undifferentiated (IMAun).

At lower elevations the forest is composed of western redcedar (*Thuja plicata*) and western hemlock (*Tsuga heterophylla*) interspersed with Douglas fir (*Pseudotsuga menziesii)*, lodgepole pine (*Pinus contorta*), trembling aspen (*Populus tremuloides*) and western larch (*Larix occidentalis)*. The shrub layer consists of Douglas maple (*Acer glabrum*), false box (*Paxistima myrsinites*), thimbleberry (*Rubus parviflorus*) and beaked hazelnut (*Crotylus cornuta*). False solomon seal (*Maianthemum racemosum*), horsetail (*Equisetum* spp.) and sedges (*Carex* spp.) made up the herbaceous layer in the mid-elevation forests. At higher elevations Englemann spruce (*Picea engelmannii*) and subalpine fir (*Abies lasiocarpa*) are the main tree species. Main shrubs include black huckleberry (*Vaccinium membranaceum*) false azalea (*Menziesia ferruginea*), white rhododendrum (*Rhododendrum albiflorum*) and heather (*Cassiope* spp.).

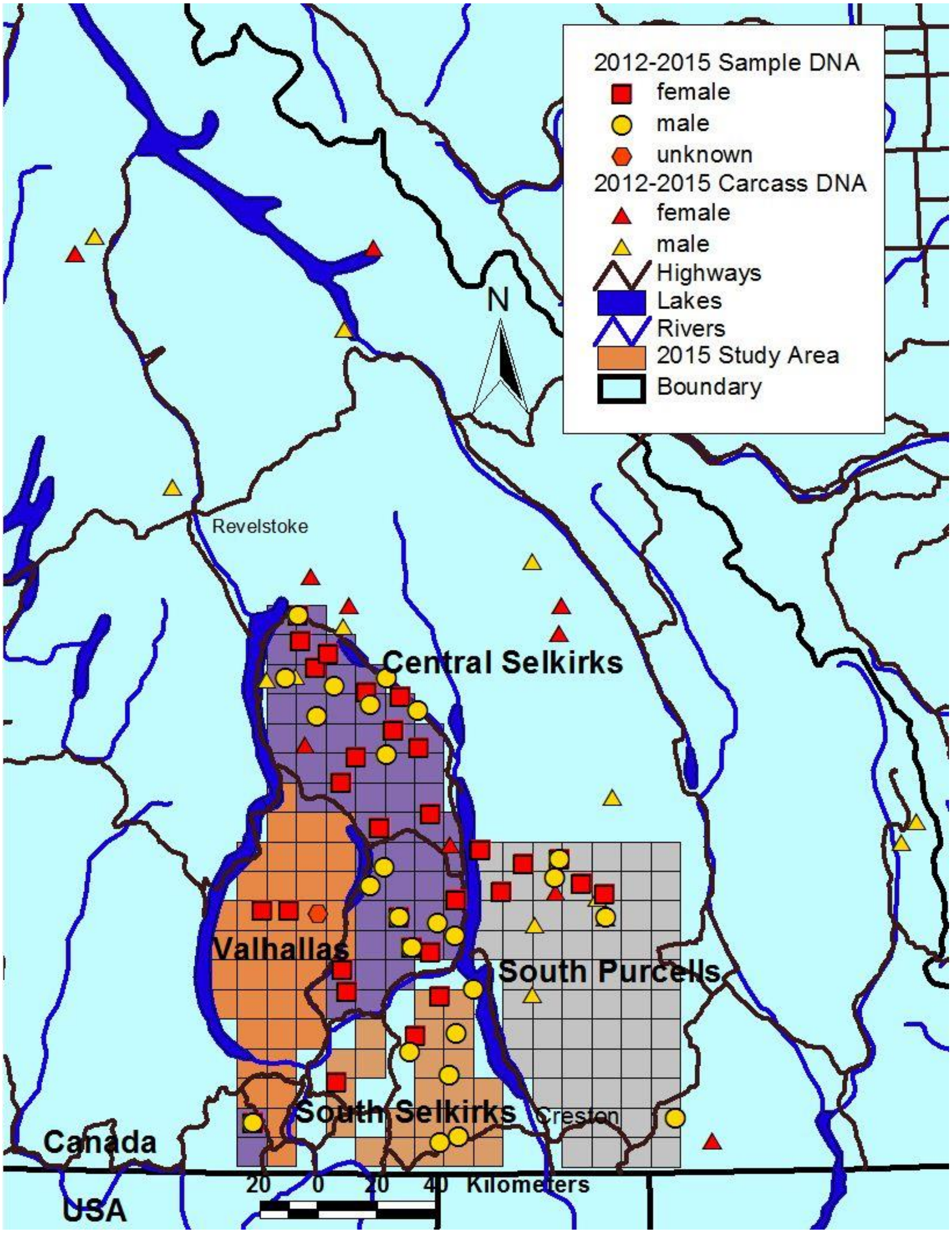

Figure 1. Wolverine non-invasive hair trapping results showing site locations where wolverines were detected (red squares, yellow circles, orange hexagon) in the south Selkirk (2012), south Purcell (2013), central Selkirk (2014) and Valhalla and southern Monashee mountains (2015). An individual may be represented by more than one sample. Females are in red, males in yellow, unknown in orange. Trapper carcass collection is represented by triangles. Two carcasses in 2013 lacked location information and were assigned to a management unit but not plotted on this map. All coloured quadrats were sampled with at least one site.

Survey methods

The study area was partitioned into 10 by 10 km cells that approximate the minimum size of a female home range. These 40 quadrats were sampled twice in approximately 21 day sampling intervals, from 6 December 2014 to 17 April, 2015 (Figure 1). Three sites in the southern Monashee Mountains had previously been sampled in 2013/2014 and were resampled in 2014/2015. Because of the rugged nature of the terrain, sites within cells were selected for ease of access by helicopter, snow machine or skis, using local knowledge of wildlife movements when available. Hair trap sites were created by affixing a bait item (beaver, sheep, deer quarter or deer head) to a tree approximately two meters from the ground or snow surface to entice the animal to climb (Fisher 2004). The bait item was nailed to the tree and the tree wrapped several times in barb wire to capture hair. During each check, the barb wire was examined for hairs or hair tufts, and the bait replenished if necessary. Hair was collected with forceps and stored in paper envelopes in a dry environment. We utilized three Rencoynx Rapidfire trail cameras (Reconyx Inc., Holmen, WI) during the sampling period.

Additionally, we collected genetic samples from wolverine carcasses obtained by trappers. From each carcass a tissue sample was taken and carcasses were necropsied by Ministry of Forests Lands and Natural Resource Operations.

Genetic Analysis

Two-hundred and sixty four hair, tissue and scat samples were submitted to Wildlife Genetics International (WGI) in Nelson B.C. for genetic identification analysis. Of the hair samples submitted, 38% (n = 98) were sub-selected for analysis. Samples that did not contain guard hairs or >5 underfur were screened out because of insufficient genetic material. From the remaining samples, DNA was extracted using QIAGEN DNeasy Tissue kits, following the manufacturer's instructions (Qiagen Inc., Toronto, ON).

Species identification was based on a sequence-based analysis of a segment of the mitochondrial 16S rRNA gene (Johnson and O'Brien 1997). For samples that yielded wolverine DNA, WGI utilized multilocus genotyping, consisting of a ZFX/ZFY sex marker, and 8 additional microsatellite markers for individual identification.

Locations of sampling sites and genetic samples were mapped in ARCVIEW 3.1 (ESRI Inc. 1998, Jenness 2005).

Occupancy

We used the single-season model in program PRESENCE (MacKenzie et al. 2002) to estimate the proportion of sample stations occupied by wolverine. A non-detection at a surveyed site could have meant wolverine were not present at the site or that we failed to detect an individual when it was present. PRESENCE uses a joint likelihood model to estimate the probability of missing a species when it is present at the site (p = *detectability*) and the probability that a site is occupied (Ψ = *occupancy*). To estimate these parameters repeat observations need to be conducted over a period of time during which site occupancy is assumed to be constant. In this way, a non-detection from a site with at least one detection can be treated as a false negative and the detection probability can be estimated.

We used both track detections (set up, and two checks) and genetic data (check 1, check 2) to estimate occupancy. We constructed models with group effects on occupancy and time dependence on detectability.

Estimates of occupancy can act as a surrogate for abundance for territorial species such as wolverine when the sites sampled approximate territory sizes (MacKenzie et al. 2006). We selected a grid resolution (10 x 10 km) that corresponded to a minimum home range size for female wolverine. Abundance estimates were not conducted as there were too few samples for mark-recapture.

Population genetics

We calculated individual pairwise genetic distances following Smouse and Peakall (1999). To visualize genetic relationships amongst individuals and study areas we performed a multivariate ordination using principal component analysis (PCA) in GenAlEx 6.5 (Peakall and Smouse 2006, Peakall and Smouse 2012). This process finds and plots the major axis of variation within a multidimensional data set (i.e. multiple samples and multiple loci) to identify patterns within the data.

Results

During the course of the field season we monitored 33 sites in the Valhallas and 7 in the southern Monashee ranges (Figure 1). Eleven field days were required for setup and an additional 34 days for site monitoring. Detections of wolverine occurred at 20% of sites by snow tracking and/or genetic analysis (Figure 2). Wolverine tracks were detected in 18% (n = 7) of quadrats and were the exclusive detection method in 5 quadrats (Figure 2). Wolverine DNA was collected at 8% (n = 3) quadrats and were the exclusive detection method at one of those sites (Figure 2). At 5% percent of quadrats (2 of 40), both wolverine DNA and tracks were detected. Other carnivores detected, using snow tracking, included wolf (*Canis lupis*), cougar (*Puma concolor*), lynx (*Lynx canadensis*), bobcat (*Lynx rufus*), red fox (*Vulpes vulpes*) and coyote (*Canis latrans*).

We collected images using trail cameras at six sites (Figure 2) with a total monitoring period of 325 days. Species detected included cougar (*puma concolor*), black bear (*Ursus americanus*), American marten (*Martes americana*), and grey jay (*Perisoreus canadensis*).

Genetic analysis

We obtained genetic results from 105 hair, tissue and scat samples. Eight-seven samples were identified by mitochondrial DNA analysis as species other than wolverine. These species included American marten (*n* = 78), bobcat (*n* = 6), cougar (*n* =1), bighorn sheep (*n* = 1), and deer (*n* = 1). Wolverine DNA was detected at 3 of 33 sites in the Valhalla Mountains and at no sites in the southern Monashees in 2015. Four wolverine hair samples were assigned individual identification. From the 3 sites in the Valhalla Mountains, we were able to identify 2 individual wolverines, both female (Figure 2). Two wolverine, one male and one female, were identified in the south Monashee Mountains during the 2014 season and were included in this report.

Seven wolverine carcasses (four males, three females) were submitted by the trapping community in 2015 (Figure 1). This is in addition to four (two males, two females), ten (six males and four females) and seven (six males, one female) carcasses submitted in 2012, 2013, and 2014, respectively (Figure 1). Two of these carcasses (one male, one female) had been previously captured in non-invasive genetic sampling in the south Purcell Mountains.

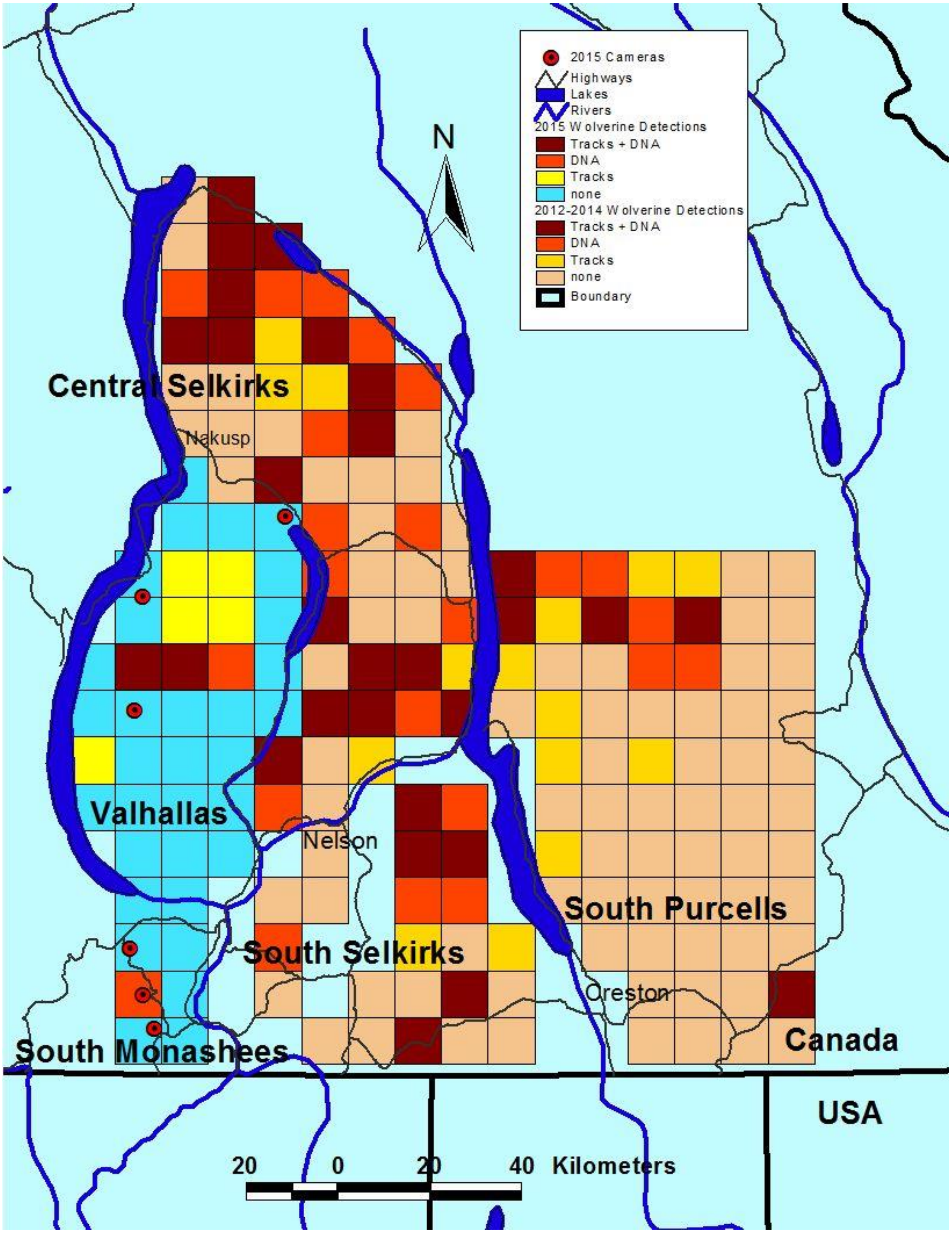

Figure 2. Wolverine non-invasive hair trapping results showing site locations and wolverines detected using DNA (orange) and snow tracking (yellow), or both (burgandy) in the south Selkirk (2012), south Purcell (2013), central Selkirk (2014) and Valhalla and south Monashee Mountains (2015). An individual may be present at more than one site and some sites may have more than one individual.

Occupancy

Two models were considered as competing models in the analysis of occupancy using both tracks and genetics data (Δ AICc < 2; Table 1). The best model predicted constant occupancy and constant detection probabilities for sampling sessions. The second competing model predicted constant occupancy with a change in detection probabilities with sampling sessions. The model-averaged occupancy estimate for the two competing models was 56% (*SE* = 46.0). Detection probability for the constant model was 11.6% (*SE* = 10.5). The probability of detection for the model showing differences in survey repetition was 22.4% (*SE* = 20.2) in repetition one, 4.5% (*SE* =5.7) in repetition two and 13.4% (*SE* = 13.1) in repetition three.

Table 1. Ranking for models of occupancy (ψ) and detectability (p) for track and genetic data of wolverine in the Valhalla and south Monashee Mountains 2015. Models were developed in Program PRESENCE and compared using AICc weights of evidence (Burnham and Anderson 1998). Δ AIC_c is the difference between a given model and the model with the lowest AIC_c[a] score, AIC_c weight (w_i) reflects the relative support for each model, K is the number of parameters estimated by the model.

Model	Δ AIC_c [a]	AIC_c weight (w_i)	K
ψ (.) p(.)[b]	0.0	0.54	2
ψ (.) p(survey specific)[c]	0.7	0.38	4
ψ (2 groups) p(.)[d]	4.0	0.07	4
ψ (2 groups) p(survey specific)[e]	7.7	0.01	8

[a] The lowest AICc score was 67.73

[b] constant ψ , constant p= The species has constant occupancy and detection rates

[c] constant ψ, survey specific p; the species has constant occupancy but different detection rates

[d] 2 groups, constant p= there are two groups of sites where the species has the same detection probabilities

[e] 2 groups, survey specific p = there are two groups of sites and different detection rates

We reviewed published habitat-based population estimates (Lofroth and Ott 2007) for the sampled population units (Table 2). Mean annual number of wolverine trapped in the Valhalla and southern Monashee (Management Units (MU) 4-9, 4-15 and 4-16) was 1 for 2005-2014, 0.6 for 1995-2004 and 0.9 for 1985-1994. Data is missing for 2010 and 2011 in all regions and no animals have been reported harvested in these management units since 2012 (Figure 2). Of these wolverine harvested, only one wolverine was harvested from the southern Monashes (MU 4-9) since 1985.

Table 2. Comparison of genetic-based and habitat-modeled population estimates (N) and annual harvest for wolverine populations in the south Selkirk, south Purcell, central Selkirk and Valhalla/south Monashee Mountains.

Population	Mark-recapture[a] N (95% CI)	Habitat-based[b] N (95% CI)	Mean annual harvest 2005-2014 (1995-2004) (1985-1994)[c]
South Selkirks	4 (na)	10 (7-14)	0 (0) (0)
South Purcells	18 (9-27)	27 (20-39)	1.7 (1.6) (1.5)
Central Selkirks	19 (16-24)	32 (22-49)	4.9 (2)(2.8)
Valhallas/south Monashees	2 (na)	17 (12-25)	1 (0.6) (0.9)

[a] Genetics study
[b] Lofroth and Ott, 2007
[c] data from 1985-2009 based on trapper survey, data missing for 2010, 2011 and 2012-2014 based on carcass collection

Population genetics

Principal Component Analysis suggests genetic structure amongst populations with samples clustering according to geographic region in the south Purcells and central Selkirks (Figure 3). South Selkirk, Valhalla and south Monashee populations are included primarily for the sake of completeness because of very limited sample sizes although genetic distances between individuals within each population are relatively small. Individuals in all three (south Selkirks, south Monashees, Valhallas) populations appear more closely related to the central Selkirk population than the south Purcell population.

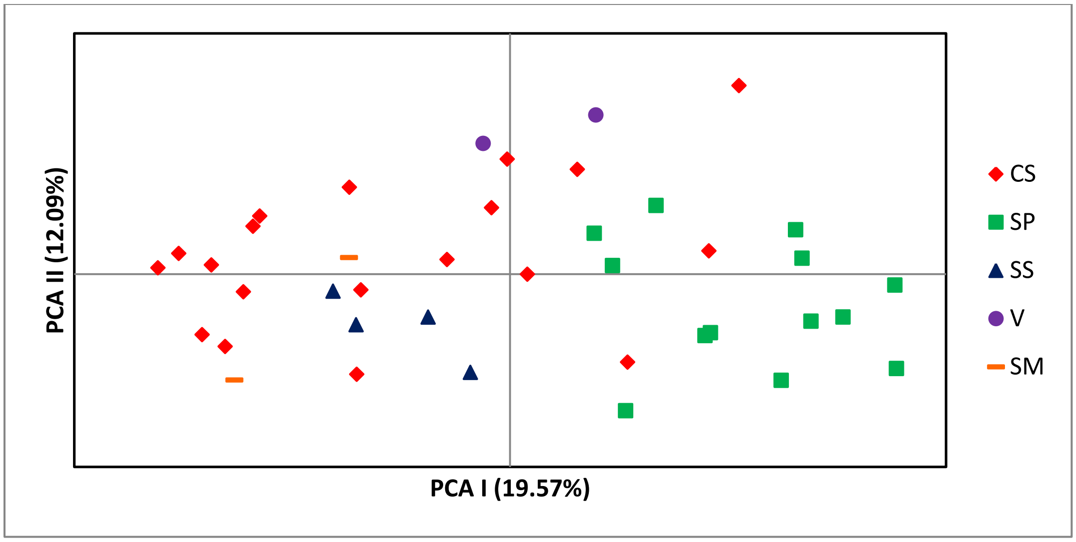

Figure 3. Principal Components Analysis (PCA) of 38 wolverine genetic samples from the 4 sampled populations in southeastern British Columbia; central Selkirks (CS, n=19), south Purcells (SP, n=13), south Selkirks (SS, n=4), Valhallas (V, n=2) and south Monashees (SM, n=2).

Discussion

This research represents the first on-the-ground attempt to inventory wolverine populations in the southern Kootenay region. The data is beginning to fill a critical knowledge gap for a species that is a conservation priority in the U.S. and Canada. We were disappointed to genotype only 2 animals from our 2015 sampling session in the Valhallas/south Monashees, in contrast to the 16 animals we were able to genotype in the central Selkirks the previous year. With additional carcasses donated by trappers, we increased our number of genotyped individuals in 2015 by 7 animals for a total of 58.

Occupancy estimates for the Valhallas/ south Monashees were lower (46%) than both the central Selkirk (71%) and south Selkirks (54%), but higher than the south Purcell Mountains (35%). Like the central Selkirks, the Valhallas were rated as high quality wolverine habitat by Lofroth and Krebs (2007), hence we were surprised by our low capture success. In contrast, the south Monashees contains both moderate and low quality habitat. The south Purcells, despite having the lowest occupancy rates were also rated as high but interspersed with moderate quality habitat. The south Selkirks were rated as only moderate habitat quality.

In all other sampling years, detection probability increased as the season progressed (Kortello and Hausleitner 2012, Kortello and Hausleitner 2014, Hausleitner and Kortello 2014). This season, however, we had the largest detection probability (22%) in the first repetition (tracks only) and saw a decline in detection probability in the second repetition (5%) with a moderate increase in the third (13%). These detection probabilities were low in comparison to other years (range 18-71%) and other studies (Fisher et al 2013). Winter conditions were abnormal in 2015 with most of the snow for the season falling in January (Weatherspark 2015). Lower elevation sites had no snow at them by the last repetition in April and at higher elevations the snowpack was so hard it made snow tracking difficult.

We were unable to calculate a mark-recapture estimate of population size for the Valhallas because, in addition to the low sample size, we had no recaptures. Our minimum number of individuals for the population, two, is drastically lower than the habitat-based population estimate of 17 (95% CI 12-25) reported in Lofroth and Ott (2007). While we recognize that our non-invasive sampling may be underestimating occurrence (Fisher et al. 2014), in previous years our sampling protocol provided genotypes for 44% (8 of 18, south Purcells) and 84% (16 of 19, central Selkirks) of our mark-recapture estimated populations. Additionally, 67% (4/6) of animals either trapped or captured subsequent to the year in which their home range was sampled were recaptures of previously identified individuals. Consequently we believe our sampling protocol is able to capture a high proportion of the individuals in the population and that the low capture success of this season is representative of very low population numbers in the Valhallas and south Monashees. However, we also recognize that sampling is going to miss individuals; we were unable to recapture 2 wolverine in the south Monashee Mountains, that were detected through genetic sampling in 2014 (Hausleitner and Kortello 2014). A wolverine was captured by camera in 2015 in the south Monashee Mountains in another study on lynx (D. Greaves, pers. comm. 2015).

We detected no wolverines using cameras in 2015 and have had only 2 wolverines on cameras in 3 years. Cameras have been shown to improve detectability for wolverine occupancy studies in the Rocky Mountains (Fisher et al. 2014). However, with so few cameras on the landscape, they have had little use in our study.

None of the individuals detected in the Valhallas/south Monashees in 2015 had been detected previously in other ranges. To date we have been unable to document connectivity between any of the mountain ranges sampled on the basis of individual movements. Our genetic analysis is limited by quite small sample sizes and the low number of markers used. Regardless, the central Selkirk and south Purcell populations demonstrate evidence of genetic structure and hence low gene flow between populations. The remaining populations (south Selkirks, south Monashees, Valhallas) may or may not be distinguishable from the central Selkirk population, but all appear distinct from the south Purcell population, suggesting lower connectivity across the Creston valley and Kootenay Lake. The data for the central Selkirks and south Purcells supports other research suggesting population fragmentation for wolverine in southeastern British Columbia (Cegelski et al. 2006). Genetically distinct populations imply a low probability of successful dispersal amongst ranges and consequently, if populations are in decline, reduced potential for demographic rescue from adjacent ranges.

The Valhallas were not identified as a harvest management concern by Lofroth and Ott (2007); with an estimated population size of 17 (CI 12-25) and a median annual harvest of 1 wolverine (1985-2004), estimated recruitment rates were sufficient to maintain the population. However, our very low sampling success would seem to indicate a very small population for the Valhallas, much smaller than estimated by Lofroth and Ott (2007), and hence vulnerable to overharvest, even at the most recent 10 year average of one wolverine per year (2005-2014; Table 2). To our knowledge there has been no harvest in the area for the past 4 years. Assuming this habitat is capable of sustaining many more wolverine than we found, maintaining low harvest mortality will be important for population recovery.

Similar to previous years, most of our wolverine detections for the Valhallas were clustered either in or immediately adjacent to protected areas (Valhalla Provincial Park). This suggests that protected areas may be important for wolverine populations and this relationship warrants further investigation in future analyses. Fisher et al. (2013) also found wolverine more abundant in rugged areas protected from anthropogenic development.

Recommendations

This year's data corroborates previous year's work in which we identified much lower populations than anticipated and low connectivity amongst mountain ranges. The central Selkirk population is emerging as regionally important: not only is it geographically central, but at the moment it appears to have the healthiest wolverine population. The direction of future research should be in identifying any movement corridors using habitat mapping and radio-marked individuals, and in particular conserving or enhancing linkages to the central Selkirk Mountains. These linkages may be critical to meta-population health.

Wolverine harvest data is currently being collected through this study and is at the discretion of individual trappers. Given the low populations we are seeing, we urge managers to implement strategies to obtain accurate harvest data in order to assess sustainability.
Genetically differentiated populations point to a need for future efforts to restore connectivity but may also be an indication that land management practices and/or recreational access may be impacting wolverine distribution. This can also be investigated further through examination of wolverine movements and behaviour in home ranges with different land-use practices (Heinemeyer and Squires 2012).

This research is being expanded into central Purcell region in 2016. With continued carcasses collected from trappers, and in collaboration with wolverine researchers in adjacent regions, we will increase the sample size of genotyped individuals, and continue to increase the strength of genetic analysis and spatial mark-recapture.

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