Estimates of Grizzly Bear Population Size and Density

for the 2014 Alberta Yellowhead Population Unit (BMA 3) and South Jasper National Park Inventory Project

Prepared for

Weyerhaeuser Ltd., West Fraser Mills Ltd, Alberta Environment and Parks, and Jasper National Park

fRI Research Grizzly Bear Program Report

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Abstract

The first provincial grizzly bear DNA population inventory assessment was conducted in Bear Management Area 3 (BMA 3) within the Yellowhead population unit in 2004. Ten years after this first inventory, funding and support were provided by provincial and federal government agencies along with two forest management tenure holders to repeat and expand the second grizzly bear population inventory in 2014.

The area studied in 2014 included BMA 3, along with an expansion into the White Goat Wilderness Area to the south. In addition, for the first time, the southern portion of JNP (JNP) was inventoried. The study design for this project incorporated our current knowledge of the study areas, applied spatially explicit capture recapture (SECR) methods, and used DNA hair samples collected using non-invasive approaches.

The goals of this study were to:

1. Apply a study design that would allow direct comparison of 2014 results with 2004 data in BMA 3,
2. Provide an estimate of the current population size within BMA 3,
3. Compare the spatial distribution of grizzly bears on the current landscape, and determine how this distribution relates to that found in 2004, and
4. Conduct a DNA inventory of south JNP (adjacent to provincial BMA 3) to gain information on grizzly bear occupancy and density for this area.

Overall, 108 unique bears were detected within the 2014 sampling area, including 63 bears in BMA 3, 16 bears in the White Goat Wilderness Area, and 29 bears in south JNP. The SECR population estimate indicates that the population estimate for BMA 3 is 74.2 grizzly bears (CI = 56.2 - 98.0) while the south JNP population estimate is 54.0 grizzly bears (CI = 39.8 – 73.2). An additional 10.4 (CI=7.6-14.2) bears are estimated in the White Goat and surrounding area. When viewed as a single ecosystem, the population estimate would be 138.6 grizzly bears, with a confidence interval of 114.6 to 167.7 animals.

These new population estimates indicate the population of bears in BMA 3 has increased since the previous population inventory work was completed in 2004. Estimates for the 2004 DNA sampling grid based on SECR analysis was 36 bears (CI 28.6- 45.3) in 2004 compared to 71.3 bears (CI 53.9-94.2) in 2014. Our findings represent an annual population rate of increase of approximately 7%, which is higher than commonly seen in most interior grizzly bear populations in North America. The reasons for this observed rate of population increase are unclear and require additional investigation and analysis to determine whether current and past management actions are contributing to this rate of increase.

In 2008, a DNA-based population estimate was completed in the northern half of JNP. Combining the north JNP population estimate with current data results in an estimated total of 113 grizzly bears residing within the boundaries of JNP. However, this estimate is based on the assumption that grizzly bear densities in north Jasper have remained constant since 2008.

Results from this inventory indicate that spatially explicit methods obtain robust estimates with less sampling effort through the use of sampling stratification. These techniques can be employed in future population inventory work in other provincial BMAs to reduce overall project costs.

Acknowledgements

Appreciation is extended to all who helped out during this project. Many thanks for the work of our field crews, who drove and hiked many kilometers in all weather, including: Leonie Brown, Amy Stenhouse, Cam McClelland, Brent Rutley, Audrey Lorincz, Natasha Mackintosh, Kelly Mulligan, Lisa Card, and Sean O'Donovan. Jasper DNA crews hiked hundreds of kilometers during the summer, TJ Gooliaff, Ed Healy, Sarah Fassina, and Theresa Westhaver. Terry Larsen, John Saunders, Terry Winkler and Bryan MacBeth assisted in grizzly bear capture and collaring efforts and collected biological samples that supported this inventory effort. We appreciate Paul Stenhouse for volunteering his time in the field. Many thanks to Mark Bradley and John Wilmshurst at Parks Canada and Jim Allen Alberta Environment and Sustainable Resource Development (AESRD) for having the foresight regarding the opportunity this project represents for grizzly bear conservation and recovery in Alberta, and for making this project happen. We also appreciated the fieldwork help from fRI Research staff members Karen Graham, Kevin Myles, Karine Pigeon, and Bill Tinge, along with Penny Bayfield, Heidi Fengler, Geoff Skinner, and Mike Wesbrook from Parks Canada. A number of brave volunteers also assisted in this project, including Emily Blythe, Hailey Deptuck, Marie-Helene Hamel, Julie Hewlett, Paula Klassen, Jason Lynds, Matt Reynolds, and Krista Russell. We greatly appreciate the cooperation of Parks Canada during this project, including the use of backcountry cabins and facilities, and logistical support.

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DNA laboratory analysis was performed by Wildlife Genetics International in Nelson, B.C., who continue to contribute to ongoing analysis to support our broader research program and grizzly bear conservation in Alberta.

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We also want to thank Sean Kinney, Fran Hanington, and Ben Williamson for handling pubic communication and notifications related to this project, and release and communication efforts for the final report for the program partners.

Lastly, it is important to note that this rather large undertaking represents an important shift in provincial grizzly bear recovery efforts, with a consortium of land and resource managers joining forces to work together to gather important data for the long term conservation of this species. A truly great team achievement.

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Introduction

Inventory of wildlife populations is often the first step needed to determine the appropriate conservation status of species and to develop or improve the management of those species (Martin et al. 2007). For threatened and endangered species, population monitoring is a critical step to developing effective recovery plans intended to stop or reverse the decline of a listed species (Martin et al. 2007). Recovery plans should be designed with the intent and ability to monitor the species throughout the recovery process as it serves to estimate trend in abundance and distribution and aids in understanding the ecological and human factors that influence those changes in time and space (Campbell et al. 2002). Thus, it also serves to track the response of the species to recovery efforts and to inform, in a timely manner, appropriate management responses (Gibbs et al. 1999, Campbell et al. 2002). However, often recovery plans face multifaceted ecological, political, economic, and social obstacles and are initiated without population estimates or other complete biological knowledge (Campbell et al. 2002).

These are the challenges faced by grizzly bear recovery and conservation efforts in Alberta, where the species is listed as Threatened (Festa-Bianchet 2010). Grizzly bears are a high profile and charismatic species often held with long-standing cultural value as a symbol of wilderness, ecological value as a top predator and umbrella species, and economic value for ecotourism (Kellert 1994, Kellert et al. 1996, Noss et al. 1996). Despite many values, the social tolerance of grizzly bears varies widely (Kellert et al. 1996) and grizzly bears have suffered dramatic range reductions and suspected population declines due to over-exploitation and habitat loss (Mattson and Merrill 2002, Ross 2002). These issues, and the continued threat of human-caused mortality rates (Festa-Bianchet 2010), have spurred conservation efforts in Alberta over the past decade. A province-wide hunting moratorium was instituted in 2006 and an extensive DNA-based capture-mark-recapture (CMR) study was conducted from 2004-2008. This CMR study provided the first population estimates for the majority (five out of seven) of the Bear Management Areas (BMAs) in the province. Baseline population estimates from these provincial DNA inventories were used, along with other information, to change the status of grizzly bears in Alberta to Threatened (Festa-Bianchet 2010).

DNA-based sampling techniques are a non-invasive adaptation of capture-mark-recapture (CMR) methods – the most frequently employed approach for estimating wildlife population size across a wide variety of wildlife species (Nichols 1992, Pradel 1996, Long 2008). A number of authors have concluded that noninvasive genetic sampling using hair is ideally suited for monitoring rare or hard-to-capture species like grizzly bears because the hair can be collected remotely without having to catch or disturb the animal (Taberlet et al. 1999, Mills et al. 2000). As a result, numerous projects outside of Alberta have also used this technique to estimate grizzly bear population size, including projects in British Columbia (Woods et al. 1999, Mowat and Strobeck 2000, Poole et al. 2001, (Boulanger et al. 2002), Apps et al. 2004, (Proctor et al. 2010)), the U.S.A. (Romain-Bondi et al. 2004, Kendall et al. 2008), and Europe (Gervasi et al. 2010, Schregel et al. 2012).

Due to the low densities and wide provincial distribution of grizzly bears, combined with habitats that are often difficult to access, it is likely that monitoring grizzly bears in Alberta will continue to require some form of genetic hair sampling methods, either alone or in combination with other sources of genetic materials and movement data from grizzly bears. The Alberta Grizzly Bear Recovery Plan (Alberta Grizzly Bear Recovery Team 2008) recommended that population inventories be repeated on a 5-year return interval to assist managers in understanding demographic trends and aid in evaluating ongoing land management and recovery efforts. Timely data and decision making is particularly important for grizzly bears given their low reproductive potential (Weaver et al. 1996), which makes them sensitive to anthropogenic impacts and vulnerable to further population decline and range contraction (Mattson and Merrill 2002). However, due to the high cost of population inventories and a desire to modify and improve inventory techniques, repeat inventories at the BMA scale have not occurred in any Alberta BMA, prior to 2014.

Fortunately, numerous research activities designed to improve our understanding of population monitoring techniques have been supported in Alberta and elsewhere. This includes research into new spatially explicit capture recapture (SECR) analysis methods (Efford 2011), new Resource Selection Function (RSF) models and habitat mapping (White et al. 2011), and improved design, methodology, and analysis of DNA inventory techniques (Boulanger 2015b, Boulanger et al. 2006, Rovang et al. 2015). The accumulation of new knowledge from this research has resulted in an improved ability to design more cost-effective population inventory methods, to analyse inventory data, and to interpret the results. In addition to the scientific progress since the first provincial DNA population inventory in 2004, current research and public opinion appears to suggest that there may be an increasing grizzly bear population in at least two provincial BMAs. A small scale

DNA inventory project using a fixed-site hair snag design suggested an increasing population trend between 2004 and 2011 in the north-west portion of BMA 3 (Rovang et al. 2015), while an on-going large scale DNA project in BMA 6 using un-baited hair snags, rub trees, and opportunistic samples also suggests an increasing grizzly bear population (Andrea Morehouse pers. comm.). Neither project, however, is able to determine population trend across an entire BMA. As a result, complete, precise, and defensible data upon which management decisions can be confidently based is still lacking for these two areas, and in fact all provincial grizzly bear management areas. Given that more than a decade has passed since the first DNA inventory in Alberta (BMA 3 in 2004), current and complete grizzly bear inventory data is needed to evaluate and adapt recovery and management efforts.

To address this need, we repeated the BMA 3 population inventory in 2014. Results from the 2004 inventory estimated 42 grizzly bears (CI=36 to 55) in the surveyed portion of BMA 3, and a density of only 5 bears per 1000 km2 (Boulanger et al. 2005). This low density was likely due to historic human-bear conflict, hunting, habitat loss, and high levels of industrial activity (AESRD 2010). The superpopulation of bears (including dependent offspring) for the 2004 grid and surrounding area was 53, with a confidence interval of 44 to 80 bears. It is important to recognize that the 2004 inventory in BMA 3 did not include any of the adjacent federal lands which are considered as part of the same ecosystem (i.e. JNP). Estimates of grizzly bear populations in south Jasper have previously been based on expert opinion and extrapolations from adjacent DNA surveys, applying RSF habitat selection models (Boulanger et al. 2011). However, a DNA-based population inventory has never been completed for JNP south of Highway 16, making south Jasper the only section of the national parks within Alberta where inventory data does not exist.

The goals of this study were to:

1. Apply a study design that would allow direct comparison of 2014 results with 2004 data for BMA 3,
2. Provide an estimate of the current population size within BMA 3,
3. Assess the spatial distribution of grizzly bears on the current landscape, and determine how this distribution relates to that found in 2004, and
4. Conduct a DNA inventory of south Jasper National Park (JNP) (adjacent to provincial BMA 3) to gain information on grizzly bear occupancy and density for this area.

As a result, this project will also provide the first DNA-based population estimate for south Jasper.

Study Area

This project had two study areas both within the Yellowhead grizzly bear population unit (BMA 3), and encompasses both provincial lands and the southern portion of JNP. We designated these two adjacent areas as separate study areas for the purposes of field planning, sampling and study design. However, we conducted an integrated data analysis that included each study area as a separate unit but acknowledging them as part of the same ecosystem, and allowing for movement by bears across the boundary between the two areas.

The DNA inventory of BMA 3 consisted of a 197-cell grid covering 9,650 km2 of the eastern foothills area of Alberta's Rocky Mountains (Figure 1). The study area included almost all habitat designated as core and secondary grizzly bear conservation zones and was bordered by Highway 16 in the north, Highway 11 in the south, and JNP to the west.

The south JNP study area consisted of 7,063 km2, including the region south of Highway 16 from the British Columbia border in the west to the JNP park boundary in the east, and south to Highway 11 at the Banff National Park boundary (Figure 1).

Elevation ranged from 880 m to 3,365 m, and included a diversity of habitats. Sub-alpine areas consisted primarily of Engelmann spruce (Picea engelmannii) and sub-alpine fir (Abies *lasiocarpa*) whereas upland forests consisted of aspen (*Populus tremuloides*), white spruce (*Picea glauca*), and open stands of lodgepole pine (*Pinus contorta*). Lowland forests were characterized by mixed forests of black spruce (*Picea mariana*), tamarack (*Larix laricina*), and lodgepole pine, while wetlands and riparian areas were dominated by willow (*Salix* spp.) and shrub-graminoid communities. Important bear foods occurring in the study area include buffaloberry (*Shepherdia canadensis*), alpine sweet vetch (*Hedysarum alpinum*), cow parsnip (*Heracleum lanatum*), and various blueberry species (*Vaccinum* spp.) (Munro et al. 2006). Other large predators found here are black bears (*Ursus americanus*), wolf (*Canis lupus*), and cougar (*Puma concolor*). Ungulate prey species within the study area include elk (*Cervus canadensis*), moose (*Alces alces*), white-tailed deer (*Odocoileus virginianus*), mule deer (*O. hemionus*), and bighorn sheep (*Ovis canadensis*).

Several different types of land-use activities occur within BMA 3, including forestry, open pit coal mining, oil and gas exploration and development, and outdoor recreation. Linear features such as roads, pipelines, seismic lines, and all terrain vehicle (ATV) trails are widespread on the landscape, making most of the study area accessible by vehicle and/or by foot, though some areas required helicopter support for access. JNP has a number of recreation activities that take place along the two major highway corridors (Highways 16 and 93), and the town site of Jasper occurs along Highway 16 in the Athabasca valley. The vast majority of the park is not accessible by either road or trail.

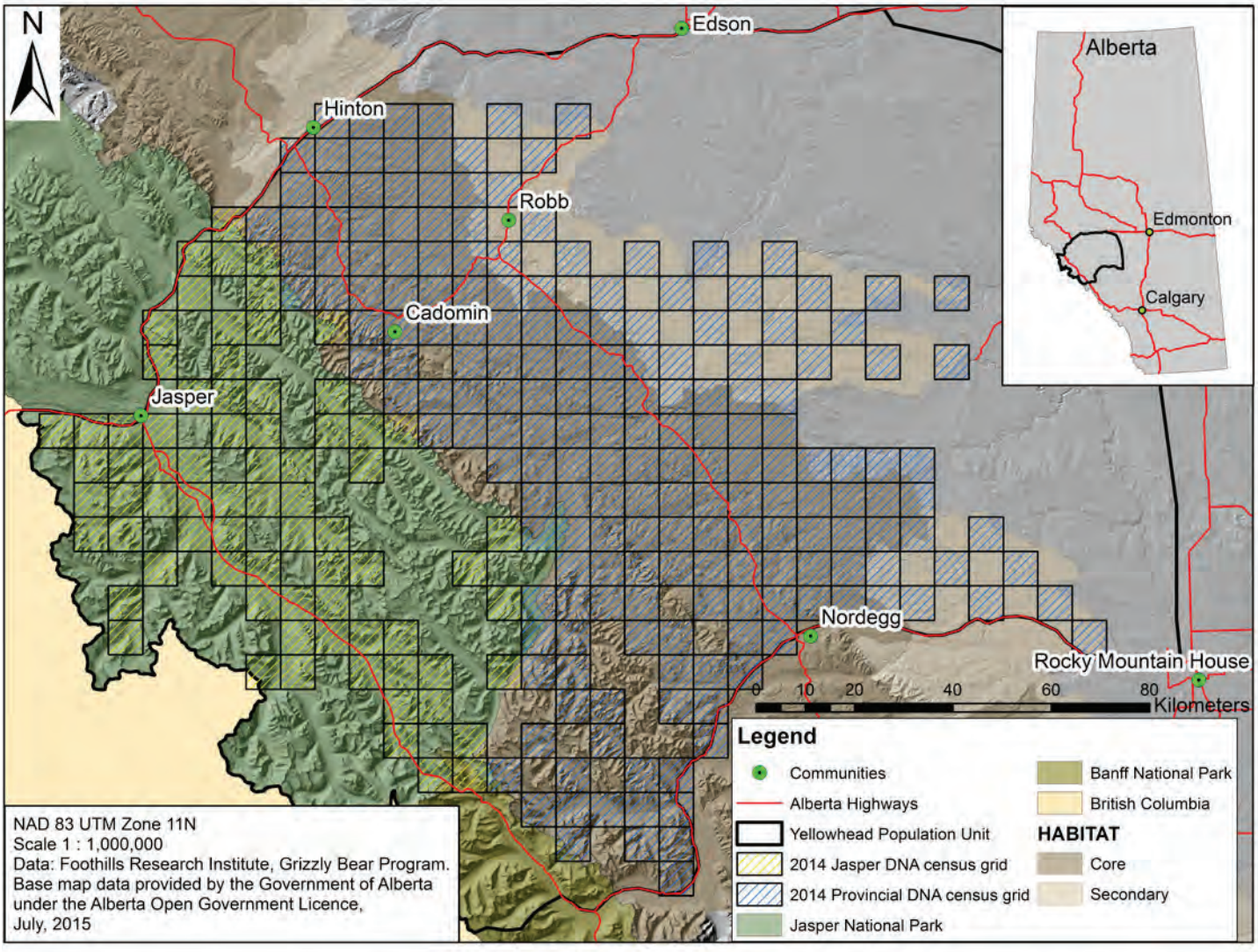


Figure 1. The Yellowhead population unit, including provincial lands and the southern portion of JNP.

Methods

Hair-snag sampling of grizzly bears in western Canada is usually based on a spatial sampling design that places one or more hair snag sites in each cell of an arbitrary square grid. This ensures good spatial coverage while allowing some latitude for the placement of hair snags within each cell. Overall sampling intensity is governed by the grid cell size, the number of sites per cell, and the duration of sampling.

BMA 3 Site Selection

In 2014, we selected site locations based on the 180-cell 7 km x 7 km grid system applied to BMA 3 during the 2004 grizzly bear DNA inventory. By maintaining close consistency between the 2004 and 2014 study design and sampling strategies, we facilitated direct comparisons between these two datasets. We modified the 2014 grid, however, to better reflect core and secondary grizzly bear conservation areas (Nielsen et al. 2009), which had not been established or mapped before the 2004 DNA inventory. Specifically, we placed additional cells within the Whitegoat Wilderness Area (Figure 2). One hair snag site was placed in each grid cell. Where possible, we placed sites at the same within-cell locations as in previous DNA surveys (2004, 2011, 2013) (Boulanger et al. 2005, Rovang et al. 2015). Where necessary, we generated new site locations in a geographic information system (GIS) prior to fieldwork using a grizzly bear RSF model (Nielsen et al. 2002), a model of buffaloberry abundance (Nielsen et al. 2010), aerial photographs, and expert opinion. Preference was given to areas of high RSF, high buffaloberry abundance, and reasonable access. In the field, we also targeted site locations near riparian areas, linear clearings, natural meadows, and cutblocks, based on research indicating site placement in these areas is important for maximizing detection at fixed hair snag sites (Rovang et al. 2015). Sites were also placed at least 100 m from roads, trails, and facilities.

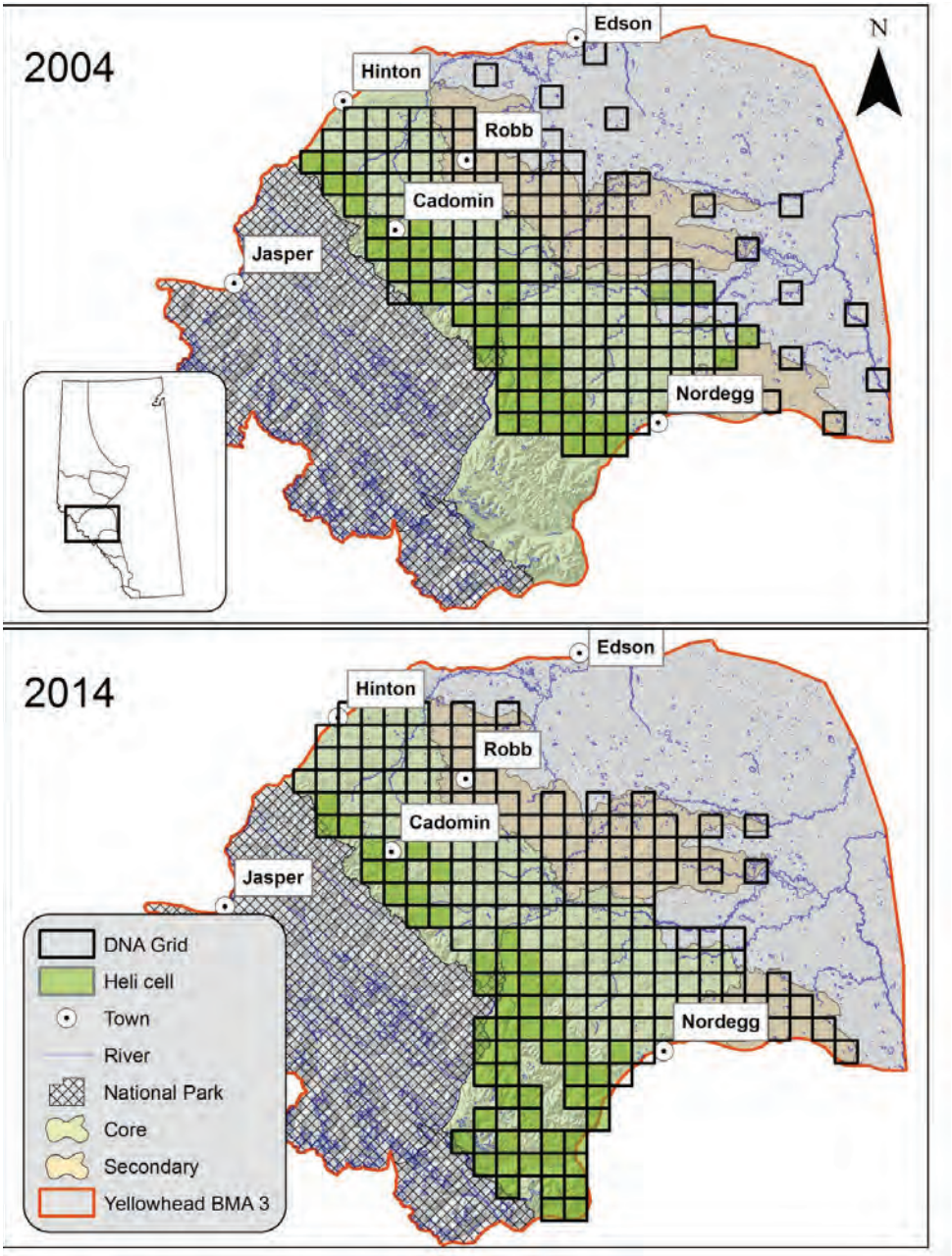


Figure 2. DNA grids used in the 2004 (180-cells) and 2014 (197-cells) inventories of the Yellowhead bear management area (BMA 3). Green highlighted cells depict cells that required helicopter access.

JNP Site Selection

For south JNP, we also applied the 7 km x 7 km grid system previously used for BMA 3 during the 2004 DNA survey, and extended this grid westward to cover the southern portion of the park. We used a spatially explicit capture recapture (SECR) approach to assist in the sampling design for the JNP inventory. SECR models the movement of grizzly bears on the sampling grid as well as the layout of sites within the sampling grid. Therefore, this approach is robust to heterogeneity of detection rates caused by trap layout relative to bear home ranges, and as a result, "holes" in trap coverage are allowed (Efford and Fewster 2013). In addition, edge effects and closure violation are not a biasing factor; therefore, radio-collar based corrections of estimates are not required [adapted from Boulanger and Efford AB 2014 JNP Design draft 4-28-2014 - see Appendix A].

SECR relies on estimating average density across a known region of interest; therefore, every part of the study area should have a known, non-zero chance of being sampled with a hair snag site. However, sampling "non-habitat" areas (barren areas of rock, snow or ice, above 2000 m) was not undertaken, based on the near-zero likelihood of detecting bears in these areas. In JNP, the majority of grid cells included both habitat and non-habitat areas; therefore, we chose to select a cell for sampling only if its centroid fell within 'habitat' areas. We note that this selection favours cells with higher quality habitat compared to cells with a larger area of rock and ice.

The exclusion of cells with centroids within non-habitat resulted in the dropping of 91 of 179 cells, leaving 88 cells selected for sampling in the original design. Eighteen of these cells were subsequently dropped due to lack of access, and 4 alternate cells were added, for a total of 74 cells sampled (Figure 3). Where substitutions were made, alternate cells were based on adjacency and similarity of habitat quality between the cells (as estimated by RSF values) in order to maintain a representative range of habitat quality.

Once the grid cells to be sampled were determined, potential hair snag sites for each cell were generated in a GIS. At the grid cell scale, site selection was focused on areas of high RSF values in order to maximize detection probability within the selected cells, and sites were placed as close to the center of the cell as possible, within the constraints of accessibility. To minimize the risk of bear-human encounters and to address public safety concerns, hair snags were at least 200 m from roads and trails, and 500 m from facilities such as campgrounds, picnic sites, or viewpoints. In the field, all hair snags were set up in locations that included a visual barrier between roads/trails/facilities and the site, such as trees or topographic features. To focus on areas of bear movement and foraging, site placement also targeted areas near riparian zones and natural meadows.

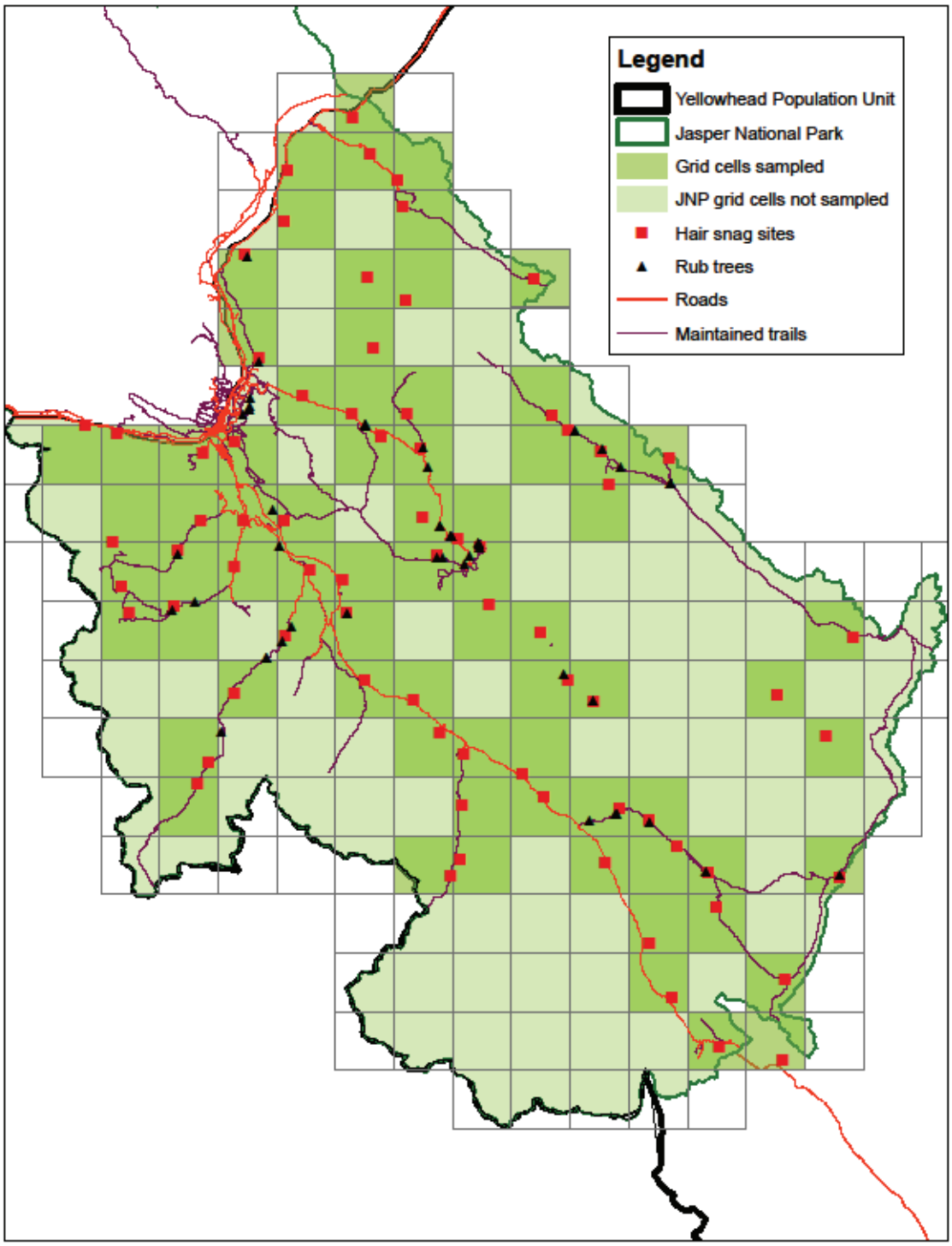


Figure 3. South JNP with 7 km x 7 km grid cells, hair snag sites, and rub trees. Cells that were not sampled either had centroids which fell in non-habitat or presented logistical constraints.

BMA 3 Field Methods and Sampling

We built hair snag sites using approximately 50 m of barbed wire strung around 3-6 trees at a height of 50 cm following protocols adapted from previous studies (Woods et al. 1999, Boulanger et al. 2005, 2006). We constructed a lure pile in the center of the corral using branches, rotten wood, and other forest debris, topped with a thick layer of moss or other absorbent material. Corrals were large enough so that the scent lure pile could be reached only when a bear crossed the barbed wire, and uneven ground (e.g. low or high spots) was filled or obstructed. During site setup and every two weeks thereafter, we baited the site with 2 L of scent lure (aged cattle blood) mixed with 500 mL of canola oil, and topped with conifer branches to protect the lure from rain. Use of a scent lure (instead of bait) attracts bears to the site without providing a food reward. Sites were not moved throughout the field season, since spatially explicit methods are theoretically more robust to heterogeneity caused by site placement relative to home range centers. Due to late snowmelt, we set up sites (n=56) in alpine habitat requiring helicopter access two weeks later than sites (n=141) accessed by motor vehicle. We sampled most sites (n=172) for 4 sessions, while sites (n=25) in White Goat Wilderness Area were sampled for 3 sessions as a result of late spring snow conditions.

We checked sites for hair every two weeks. Hair samples were collected into paper envelopes using tweezers or gloves. We also collected data regarding sample location, adjacency to other samples, and sample quality to facilitate the final sub-selection of hair samples for DNA analysis. Following collection of samples, we removed (burned) any remaining hair from the wire to ensure that hair found during subsequent visits was from the correct session. Throughout the field season, hair samples were stored with silica desiccant packs both in the field and in the office.

As part of ongoing research there were also some (n=7) active culvert trapping sites where grizzly bear capture and radio collaring work was underway during the DNA inventory data collection period. Bears captured or recorded at these sites (barb wire and cameras) also provided hair samples that were incorporated into the appropriate sampling period, to provide additional data on unique individuals present.

Wildlife Cameras

In 2004, grizzly bear habitat towards the eastern boundary was sampled using 17 isolated (non-contiguous) cells to investigate grizzly bear occurrence in these areas. At that time, no bears were detected in these eastern boundary cells using DNA hair snags, no bears were detected by hair snags in the southeastern portion of the main grid, and very few bears were detected in the northeast. Nonetheless, grizzly bear sightings have been reported in these areas. This raised the concern that bears were present towards the eastern boundary, but were not being detected by hair snag sites.

In response to this concern, during the 2014 survey we set up a total of 54 wildlife cameras along the eastern-most portion of the BMA 3 DNA grid, overlapping secondary grizzly bear habitat (Figure 4). Our goal was to investigate if and/or how many grizzly bears approached a DNA hair snag site but were not detected via a hair sample(s). We set up 43 cameras in session 1 during the first sampling session of the hair snag sites; 4 additional cameras were set up in session 2 (n=47); and 7 additional cameras were set up in session 3 (n=54). However, four cameras were removed following sampling in session 3, leaving a total of 50 cameras operating in session 4. Each camera was placed at a location that captured the entire hair snag site to ensure any bears approaching the site were detected by the camera. We downloaded camera data on the same 14-day sampling schedule as the DNA hair snag sites and removed the cameras following the last DNA sampling session (session 4). No cameras were used within JNP as part of our study.

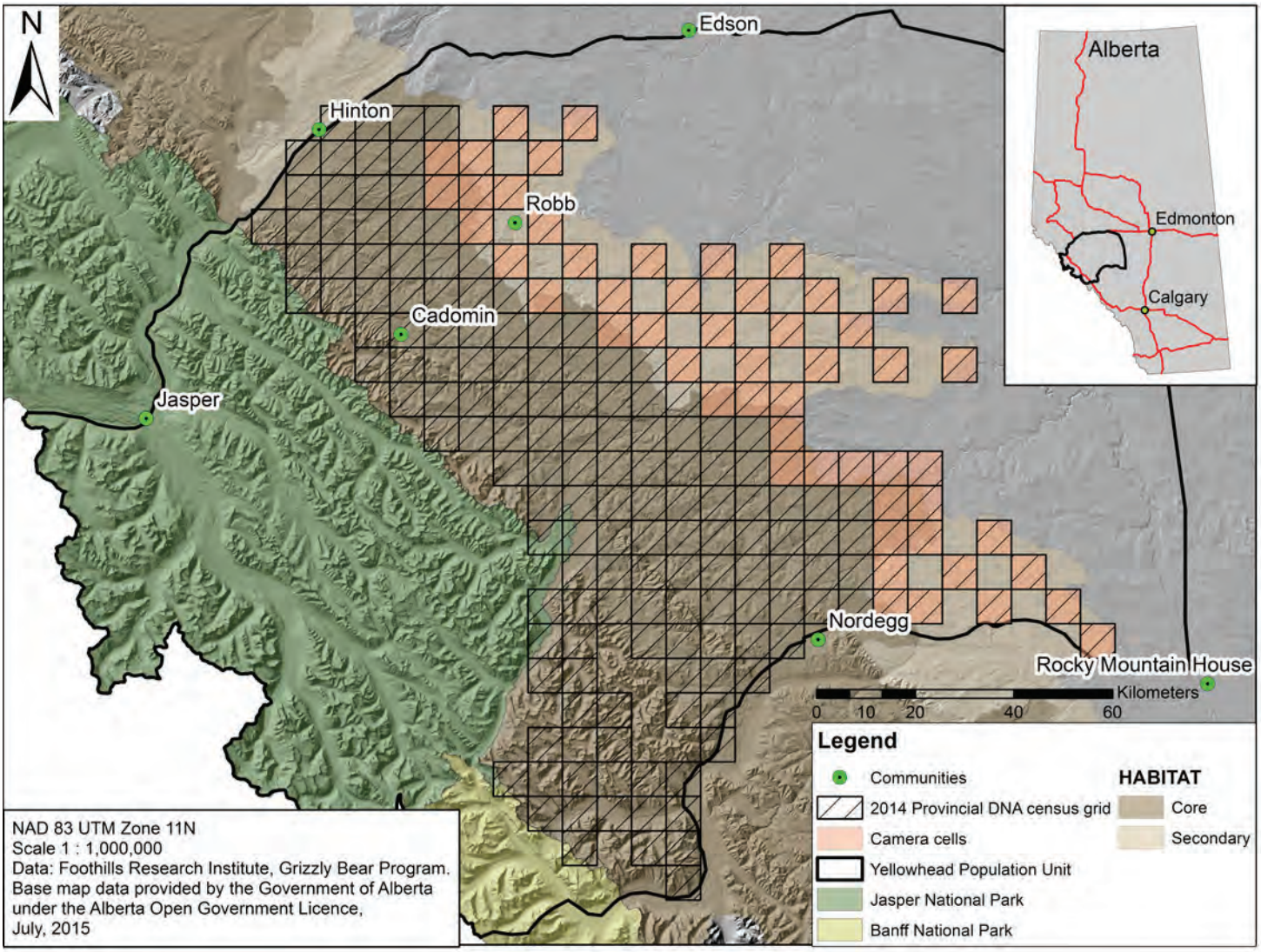


Figure 4. Grid cells that have a wildlife camera located at the DNA hair snag site.

JNP Field Methods and Sampling

The presence of naturally occurring bear rub trees along hiking trails in the national parks provides an opportunity for a non-invasive method of obtaining grizzly bear hair samples with relatively easy access. In south JNP, we sampled hair from 50 naturally occurring bear rub trees found along trails. Rub tree locations were either previously mapped by Parks Canada staff (n=25) or found during the 2014 field season by fRI Research staff (n=25). Rub trees were set up with a zig-zag "Z" formation of barb wire on the rubbed surface using 4 strands of barb wire with 3 barbs each, positioning the first three wires to cover as much of the rubbing surface as possible. The fourth strand was placed below the zig-zag at a height of approximately 25 cm as a "cub rub". Rub trees were not baited with scent lure. To exclude samples that may have been left from the previous year, we removed (burned) all hair present during setup.

While rub trees provide a relatively low-cost method of obtaining hair samples for DNA analysis, research suggests that using rub trees alone may result in an under-representation of females and family groups in the population inventory, as these groups may not use rub trees as often as male bears (Kendall et al. 2008). This appears to hold true in our study area; individuals identified from rub trees in JNP in 2013

included 14 males, but only 4 females (Mark Bradley, pers. comm.). Therefore, in addition to sampling rub trees, barb wire corrals were set up at 74 sites in south JNP including: 31 road accessible sites, 6 day hiking sites, 24 sites accessed by multi-day backcountry travel, 8 helicopter sites, and 5 sites accessed by boat (Figure 5). Corrals and lure piles were built using the same methods as in BMA 3. During site setup and every two weeks thereafter with 2 L of scent lure (aged cattle blood) mixed with 500 mL of canola oil. Due to late snowmelt, backcountry and high elevation sites were set up two weeks later than sites accessed by motor vehicle. Most sites (n = 62) were sampled for 4 sessions, while 13 sites were sampled for 3 sessions.

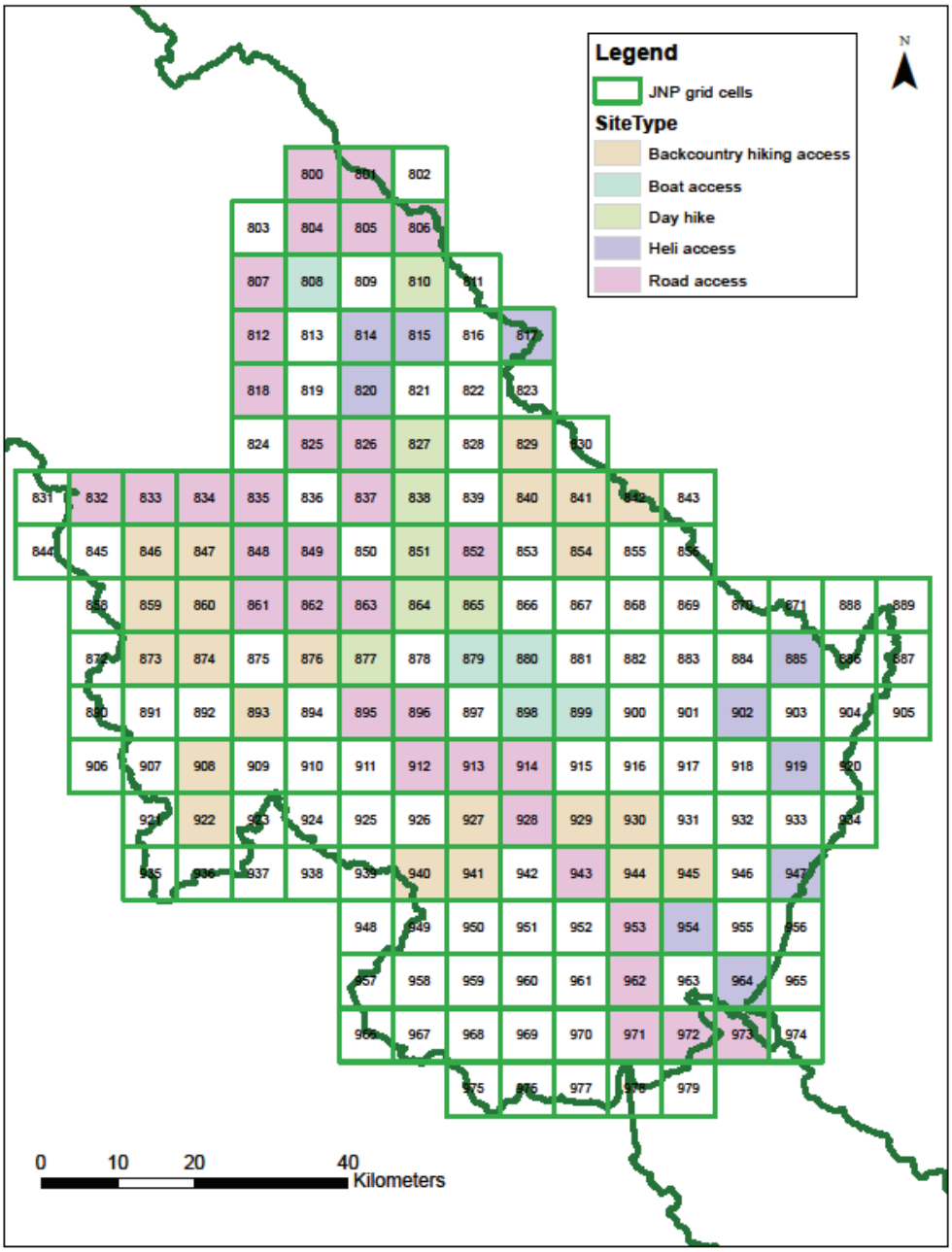


Figure 5. Grid cells sampled by access type: backcountry, boat, day hike, heli, or road.

Hair snags and rub tree sites were checked every two weeks for hair. Occasionally, samples were also collected opportunistically from bear scrapings on trees located near established hair snag and rub tree sites. Hair samples were collected into paper envelopes using tweezers or gloves. Data were collected regarding sample location, adjacency to other samples, and sample quality to facilitate the final sub-selection of hair samples for DNA analysis. Following collection of samples, any remaining hair was removed (burned) from hair snag and rub tree sites, to ensure that hair found during subsequent visits was from the correct session. Throughout the field season, hair samples were stored with silica desiccant packs both in the field and in the office.

Sub-Selection of Samples for DNA Analysis

As is the case in most large scale grizzly bear inventory projects, recognizing budget constraints, it was not possible to genotype all hair samples collected during 2014. To select a subsample of hair for DNA analysis, we followed a series of sub-selection criteria based on those previously used for DNA surveys in both Alberta and British Columbia. These sub-sampling criteria have been shown to result in a minimal reduction in the number of individual bears identified (Proctor et al 2012). Initial screening of hair samples excluded those identified as non-bear species, and those with a high confidence of species identified as black bear. In some cases, it was possible to confirm bear species using wildlife camera data from the hair snag site. Previous research (David Paetkau, pers. comm.) indicates that for successful genotyping, bear hair samples must include either 1) at least one guard hair, or 2) five or more underfur hairs. Samples that did not meet these minimum criteria were excluded based on the likelihood that they did not contain sufficient genetic material.

For hair snag sites, we reviewed each site and session separately, and applied further criteria to all samples not excluded in the initial screening. At a minimum, we selected the best sample for each site/session, as indicated by field data, hair sample size, and probability of grizzly bear species. In addition, we selected 1 in every 3 from adjacent samples, starting with the best sample in each barb group. If there were more than 3 samples in a barb group, for the remaining samples, greater preference was given to samples with a greater number of guard hairs and samples with greater confidence in grizzly bear species identification. Less preference was given to samples with unknown species, samples with black bear and grizzly bear hair on the same barb, and directly adjacent samples.

For rub tree sites, each rub tree and session was reviewed separately, and further criteria were applied to all samples not excluded in the initial screening. At a minimum, we selected the best sample for each rub tree/session. Barbs 1-3, 4-6, 7-9, and 10-12 (see site setup) were considered as groupings, based on their adjacency and height on the tree. Samples from the bark or from the ground were considered as separate groupings, unless samples on the bark were known to be immediately adjacent to each other. Samples on the wire (but not on a barb) were also considered as a separate grouping, unless known to be immediately adjacent to a barb. Based on these designated groupings, we selected the best sample in each grouping. Greater preference was given to samples with a greater number of guard hairs and samples with greater confidence in grizzly bear species identification. Less preference was given to samples with unknown species, samples with black bear and grizzly bear hair on the same barb, and directly adjacent samples.

DNA Analysis

Hair samples were sent to Wildlife Genetics International in Nelson, British Columbia, Canada for genotyping analysis. DNA was extracted using QiaGEN DNeasy Tissue kits following standard protocols (Paetkau 2003). Samples were examined under a dissecting microscope, and those with the visual appearance characteristics of black bears hair(jet black from root to tip) were removed. Samples that passed the visual examination underwent a prescreen using a species-specific marker (G10J) to distinguish grizzly bear from black bear samples (Paetkau 2003). Individual grizzly bears were genotyped to 7 loci (markers G10J, G1A, G10B, G1D, G10H, G10M, G10P) and sex was assigned using a ZFX/ZFY gender marker (Paetkau et al. 2003). To determine parent-offspring relationships within BMA 3, samples were genotyped to 21 loci (markers G1D, G10H, G10M, G10P, G10C, G10L, G10U, G10X, CXX20, CXX110, MU50, MU59, REN145P07, CPH9, Msut2, Mu51, Mu23). Error checking protocols included selective reanalysis of similar genotypes (those matching at 1, 2, or 3 loci) to confirm the genotype or resolve errors, thus eliminating genotypes created through genotyping error (Paetkau 2003, Waits and Paetkau 2005, Kendall et al. 2009).

Population Analysis

John Boulanger and Murray Efford.

1. Introduction

This section of the report provides an outline of spatially explicit mark-recapture estimation of grizzly bear DNA mark-recapture projects that occurred in BMA 3 and southern JNP in 2014. In addition, where possible these analysis approaches and results are compared to previous population inventory results from 2004. Recent advances in spatially explicit mark-recapture methods (SECR) potentially produce a more robust population estimate of these areas (Efford and Fewster 2013) and also allow inference about variation in density within the study areas through stratified sampling and density surface modelling (Royle et al. 2013, Efford 2014a).

These studies were designed to take advantage of the benefits of spatially explicit modelling (Boulanger and Efford 2014). In particular, sampling intensity was varied by geographic area based on management objectives, habitat, and logistic challenges. In addition, areas of non-habitat (as defined by barren habitat at greater than 2000 m) were not sampled in order to optimize efforts to areas of most contiguous habitat.

This exercise had the following objectives:

1. Fit parsimonious models to describe detection probability variation and scale of movements of bears in the Yellowhead population unit.
2. Use a stratified model to estimate density and regional population size for each region of interest (BMA 3 and southern JNP).
3. Compare estimates to previous estimates from 2004 (Boulanger et al. 2005) including the re-analysis of the 2004 data set using spatially explicit methods.

Other analyses, such as density surface modelling of the distribution of bears on the sampling grid, will be detailed in future reports.

2. Methods

Spatially explicit capture-recapture (SECR) methods (Efford 2004, Efford et al. 2004, Borchers and Efford 2008, Efford et al. 2009, Efford 2011, Royle et al. 2014) estimate population density allowing for the spatial scale of movement, estimated from the detection sites of bears that are detected repeatedly. Unlike closed models that pool data from multiple hair snag sites within each session for each bear, the SECR method used multiple detections of bears at unique hair snag sites within a session to model bear movements and detection probabilities. Using this information, the detection probabilities of grizzly bears at their home range center (g_0), spatial scale of grizzly bear movements (σ) around the home range center, and bear density were estimated.

An assumption of this method is that grizzly bear home range can be approximated by a circular symmetrical distribution of use (Efford 2004), but the method is robust to deviations from circularity (M. G. Efford unpubl. results). The configuration of the sampling sites is used in the process of estimating the scale of movements and density, and lack of geographic closure (incursion of bears centered outside the grid) is modeled directly. There is therefore no need to adjust for study-area size and closure violation as with previous closed models.

SECR models detections of bears with home ranges centered either directly on the sampling grid or in adjoining habitat; the grid and adjoining habitat together comprise the habitat 'mask'. Considering too little adjoining habitat as the potential source of detected bears can cause positive bias in density estimates. An initial analysis was conducted with sexes combined to determine the size of the mask (relative to study area size) needed to control bias in density estimates. The esa.plot and suggest.buffer functions of the R package 'secr' were run for a g_0(sex) σ(sex) conditional likelihood model. These suggested a buffer width of 35 km would give unbiased estimates; estimation is also expected to be unbiased with a wider buffer, but computation is then slower for a given spatial resolution.

Subsequent analyses were run separately for male and female grizzly bears to test for variation in detection probability at the home range center and scale of movements. Models were run separately for males and females.

Spatially explicit capture re-capture model fitting had three phases:

1. Baseline tests for temporal, behavioural, and heterogeneity variation in g_0 and σ to establish a baseline model of detection.
2. Addition of site covariates to baseline model to describe heterogeneity induced by site placement
3. Using the most supported model from step 2, strata-specific models were fit under the assumption that relationships between site covariates and g_0/σ were similar across strata.

Site covariates such as a terrain ruggedness index and canopy closure were evaluated at two spatial scales as potential predictors of the detection probability parameters (g_0 and σ) (Table 1) (Boulanger et al. 2009). The two scales ('site' and 'home-range') corresponded respectively to the distance at which bears encountered (responded to) hair snags and the typical home-range radius. We used 1.96 km as the site scale, based on estimates by Boulanger et al. (2004), and 10 km as the home range scale, corresponding to bear home range areas (Nielsen et al. 2004b). Humans often plan and influence land use activities approximately on the scale of bear home ranges (i.e., the township). In most cases site scale was used as a covariate for detection probabilities (g_0) and home range scale was used as a covariate for the σ scale parameter. For this phase of the analysis it was assumed that density was constant across the extent of the survey area.

Table 1. Site habitat and sampling covariates used to describe scale of movement and detection of bears.

Habitat variable	Description
TRI	Terrain ruggedness index (Riley et al. 1999)
dstream	Negative exponential decay (500m parameter) distance to stream
CC	Percent canopy cover
Rub tree (RT)	A binary covariate to indicate that site was a rub tree
Hair snag (HS)	A binary covariate to indicate a site was a hair snag site

Models were evaluated in terms of relative support information theoretic model selection methods Sample size adjusted AICc scores were used to define the best model as determined by the lowest AICc score (Burnham and Anderson 1998).

2.1. Defining Strata

Strata were defined based on a-priori boundaries of management interest, as well as likely difference in density and sampling intensity (Table 2 and Figure 6). White Goat Wilderness Area (hereafter White Goat) and the immediate area to the east, as well as JNP were primarily unroaded and/or protected areas and were therefore grouped as a single stratum. The eastern boundary of the White Goat Area boundary was partially also based upon the extent of sampling that occurred during the 2004 DNA mark-recapture inventory. However, population estimates were derived for JNP and White Goat separately.

Table 2. Strata used in spatially explicit capture-recapture analysis. Habitat area is defined by the total area minus area of barren landcover of greater than 2000 meters elevation.

Strata	Defined by	Sampling design	Area (km2) Total	Habitat
BMA 3 Core	AB BMA 3 grizzly bear zone	One site per 7x7 km cell		
		4 sessions	6738.8	6353.2
BMA 3 Secondary	AB BMA 3 grizzly bear zone	One site per 10x10 km cell		
		4 sessions	3509.4	3509.4
Jasper/ White Goat	Mountainous/ protected areas	One site per 7x7 km cell	7898.5 (JNP)	4342.9 (JNP)
		2-4 sessions	1707.6 (WG)	770.2 (WG)

The SECR model uses actual hair snag locations, so no special action was needed to represent spatial differences in sampling intensity between strata beyond using strata as a covariate for density when producing population estimates (Table 2). Some sites were not sampled in all sessions (see also 'Adjustment of sessions' below), and the resulting temporal variation was represented with a binary 'usage' matrix – a series of 1's and 0's for each site indicating the sessions in which it was active (1) or non-active (0).

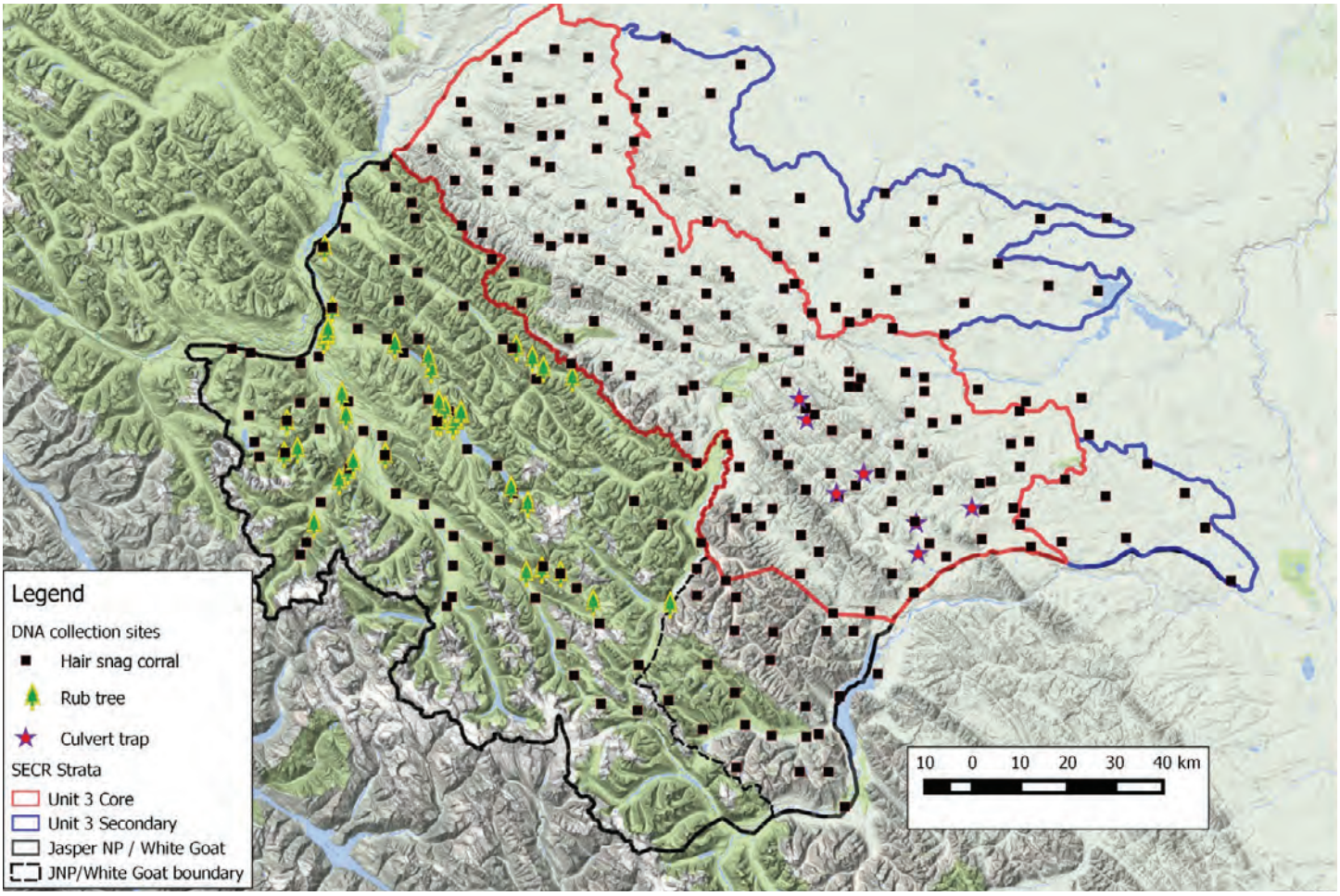


Figure 6. Spatially explicit (SECR) strata used in the analysis based upon management objectives and design of the study. Hair snag sites, rub trees, and culvert sites are also shown for reference. Areas shaded in green are protected areas (national or provincial parks).

The habitat mask for the SECR analysis used a discrete cell size (mask spacing) of 3 km for all analyses. A sensitivity analysis of mask spacing suggested 3 km was a good compromise between processing time and minimizing bias in estimates (no change in D with spacing of 3.5–2.5 km). Mask cells were categorized according the stratum of their centroid. Centroids outside the Yellowhead unit (where no sites were sampled) were assigned to the stratum of the nearest Yellowhead cell. Many of the sampling grids contained substantial areas of barren rock and ice which was not considered suitable habitat for grizzly bears (Figure 7). Cells received a single site if the centroid of the cell fell within grizzly habitat defined as non-barren landcover with an elevation less than 2000 meters. The main reduction of the number of sites sampled occurred in Jasper and White Goat that had higher proportions of non-habitat. Barren land cover above 2000 m was excluded from the habitat mask in the SECR analysis, as in previous habitat analyses using DNA mark-recapture data (Boulanger 2015) and in the design of the BMA 3 and JNP study (Boulanger and Efford 2014).

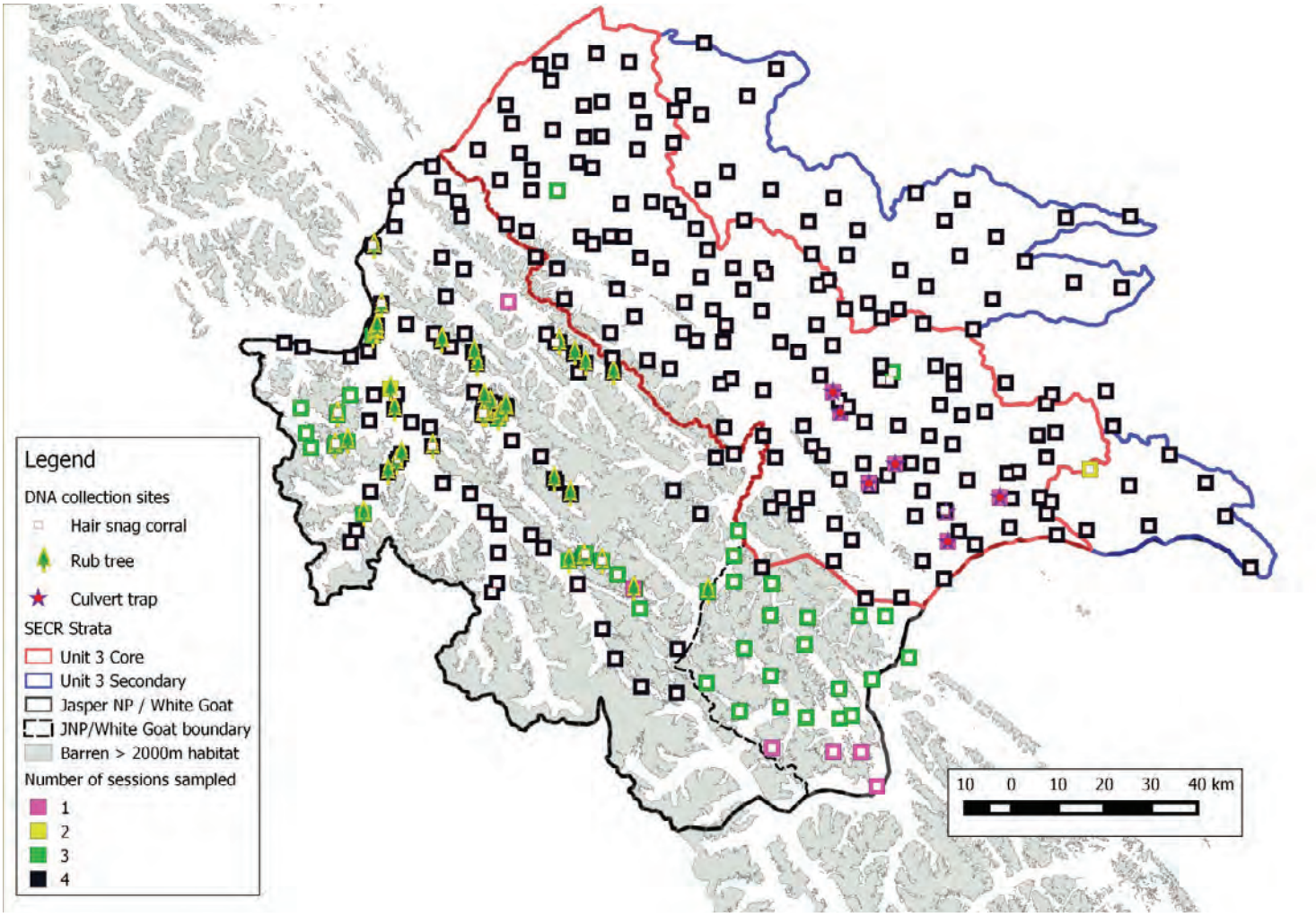


Figure 7. SECR strata with non-habitat defined as barren areas at elevations of 2000m or higher. Also indicated is the number of sessions each site was sampled.

2.2. Estimates of Abundance and Density

Expected population size and density estimates were derived from the most supported models for each sex and stratum combination. Estimates of grizzly bears on the entire sampling grid, and estimates for each stratum (Table 2) were produced. Expected population size is the expected number of bears that would be contained within the study area or regional area at one time (Efford and Fewster 2013). It is analogous to the average number of bears on the sampling grid given in previous survey reports. Density is then estimated as the expected number of grizzly bears divided by the entire area of the grid, or the habitat area within the grid. Log based confidence intervals on expected population size and density were generated using formulas from Efford and Fewster (2013). All spatially explicit analyses were done in package *SECR* (Efford 2014b) in R statistical software (R_Development_Core_Team 2009). In addition, data were screened using program DENSITY (Efford et al. 2004). Map figures were produced using program QGIS (QGIS_Foundation 2015).

2.3. Adjustment of Sessions

Due to a late spring, many higher elevation mountain sites were not sampled initially until late June or July. The sessions for each site were initially numbered sequentially, which led to a large degree of variation in session number among sites re-visited in the same week (Figures 7 and 8).

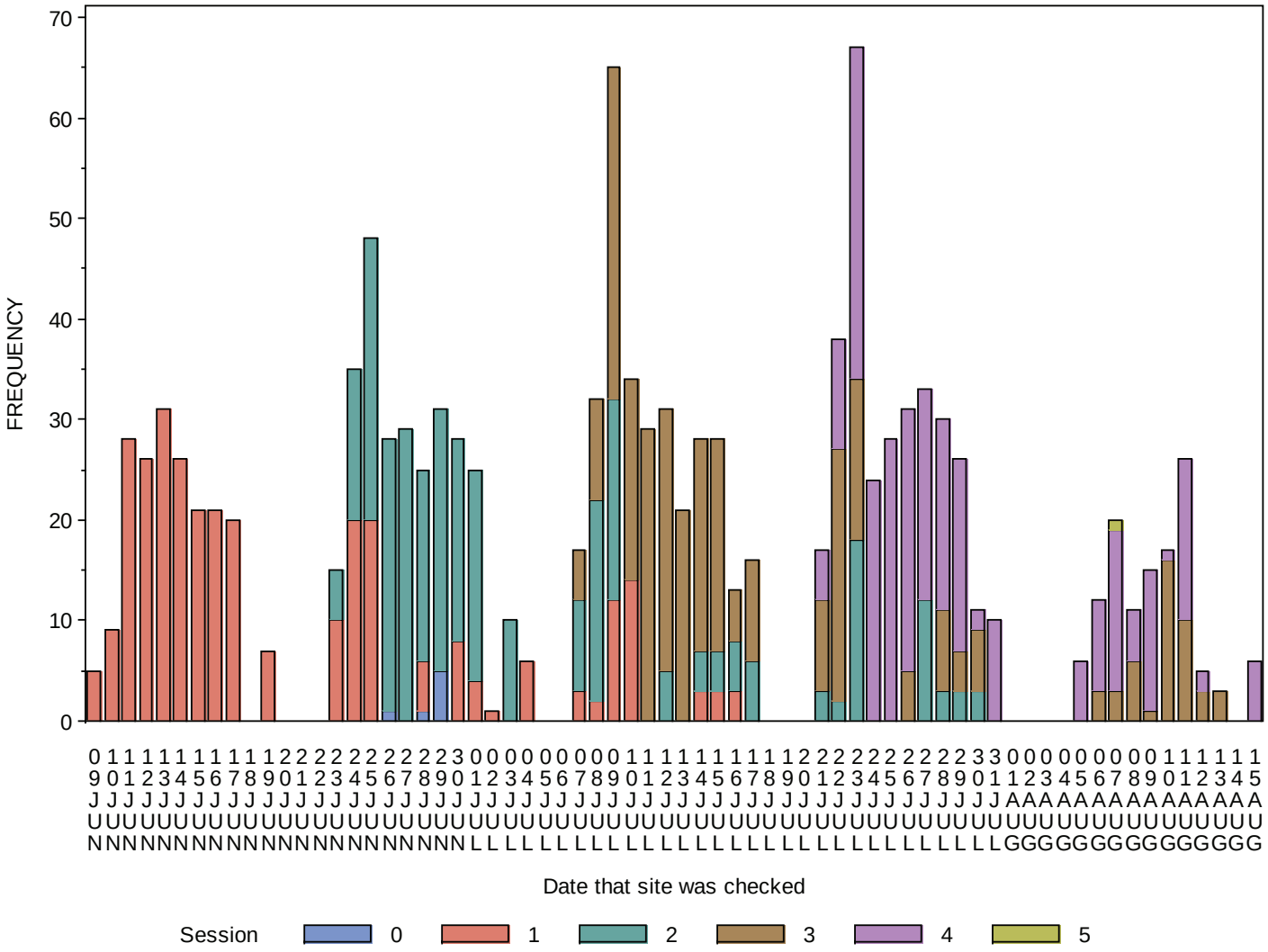


Figure 8. Dates in which sites were checked with session defined as the number of checks each individual site had received during the inventory.

This created a potential issue for modelling of temporal change in detection probabilities based on seasonality as well as behavioural responses. In addition, some sites were sampled into August which is usually considered as the berry season. It can be seen from Figure 8 that the sites were sampled in distinct temporal clusters. To resolve this, the sessions for each site were adjusted to be defined in each cluster (Table 3) which also meant a 5th session was added. This created synchronized sessions for each site (Figure 9). The trap usage matrix of the SECR trap file was used to inform the SECR model as to when each site was active.

Table 3. Dates of sessions and the number of sites active per session. Rub trees were only used in JNP and culvert traps were only used in BMA 3.

Session	Dates		Number of sites active		
	Start	End	Hair snag	Rub tree	Culvert
1	May 26, 2014	June 19, 2014	173	21	0
2	June 20, 2014	July 5, 2014	235	39	7
3	July 6, 2014	July 18, 2014	266	48	0
4	July 19, 2014	August 1, 2014	267	48	0
5	August 2, 2014	August 15, 2014	98	23	0

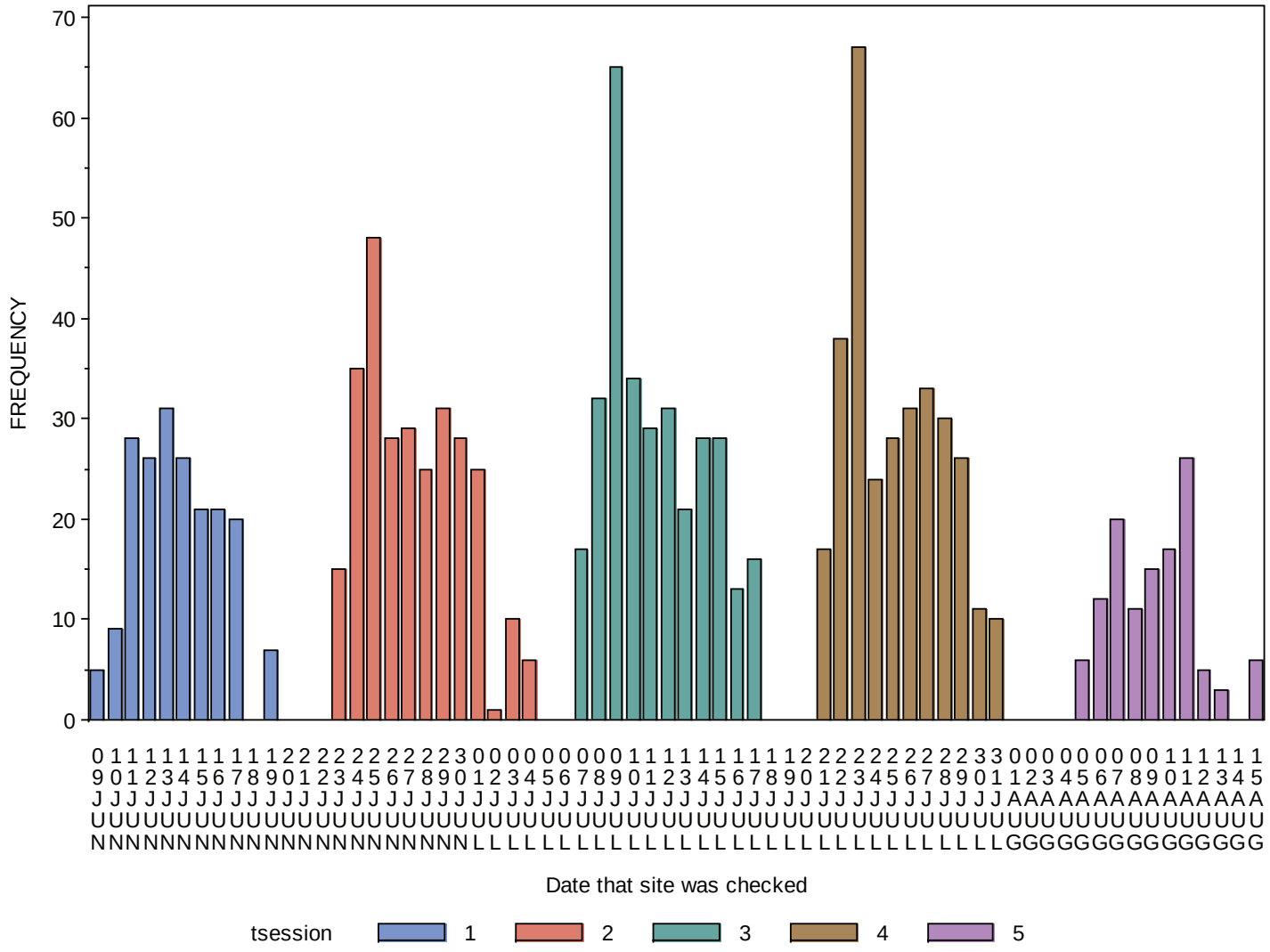


Figure 9. Dates in which sites were checked with session (tsession) by the clustering of checks for each date interval. This resulted in the addition of a 5th session in August.

3. Results

3.1. Summary

Overall, 108 unique bears were detected in the entire Yellowhead ecosystem DNA sampling area with 63 bears detected on provincial lands in BMA 3, 16 bears in the White Goat, and 29 bears in south JNP (Table 4). In many cases, bears were detected in more than one of these three strata; therefore, the number of bears detected based on detection location (116) was higher than that based on mean detection location (the mean of the x and y coordinates of DNA sites where a bear was detected across all sessions) (Table 4). Spatially explicit model estimates of population size and density account for detections across multiple strata by estimating density based upon home range centers, as well as likely movements of bears on the sampling grid.

Table 4. Numbers of individual bears detected in each stratum and stratum membership based upon mean detection locations.

Strata	Detections			Mean locations		
BMA 3	Males	Females	Total	Males	Females	Total
Core	34	27	61	33	26	59
Secondary	5	0	5	4	0	4
Jasper National Park/White Goat						
Jasper National Park	20	12	32	17	12	29
White Goat	9	9	18	9	7	16
Site outside of White Goat	1	0	1			
Total	69	48	117	63	45	108

Mean detection locations (Figure 10) illustrate that many bears in BMA 3 were detected along the border with JNP. We note that these detection locations are only based upon sampling conducted within the survey area, and therefore may not reflect the true home range centers of bears.

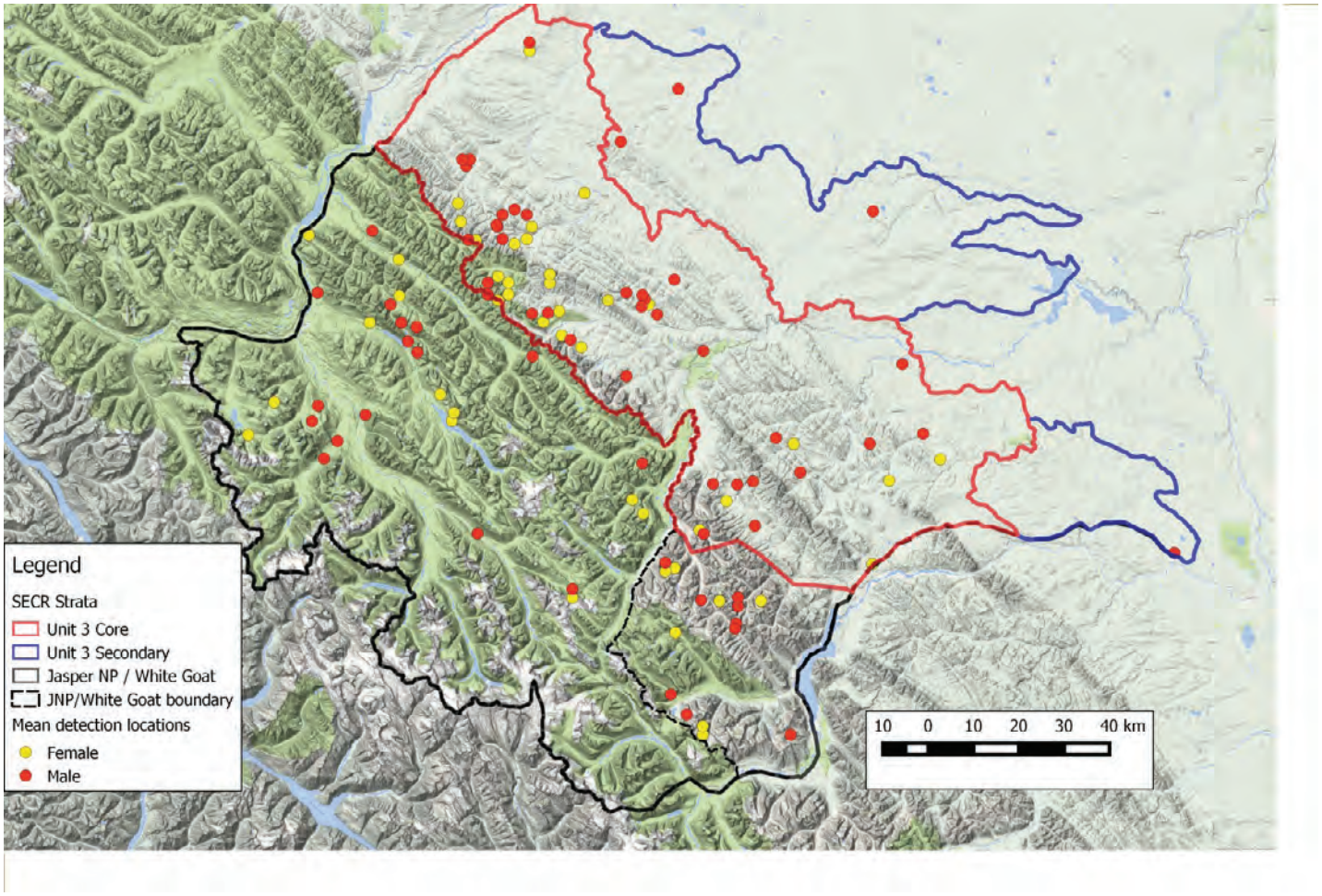


*Figure 10. Mean detection locations of male and female bears on the sampling grid based on cumulative detections at hair snag, rub tree, and culvert sites. Multiple mean detections at a single DNA site are delineated by a concentric ring of locations with a * denoting the central location.*

The majority of detections occurred with hair snag sampling which was presumably due to the fact the hair snags occurred throughout the study area whereas rub tree and culvert sampling were restricted to smaller areas and in the case of culverts for a limited and shorter time frame. (Table 3 and Figure 11).

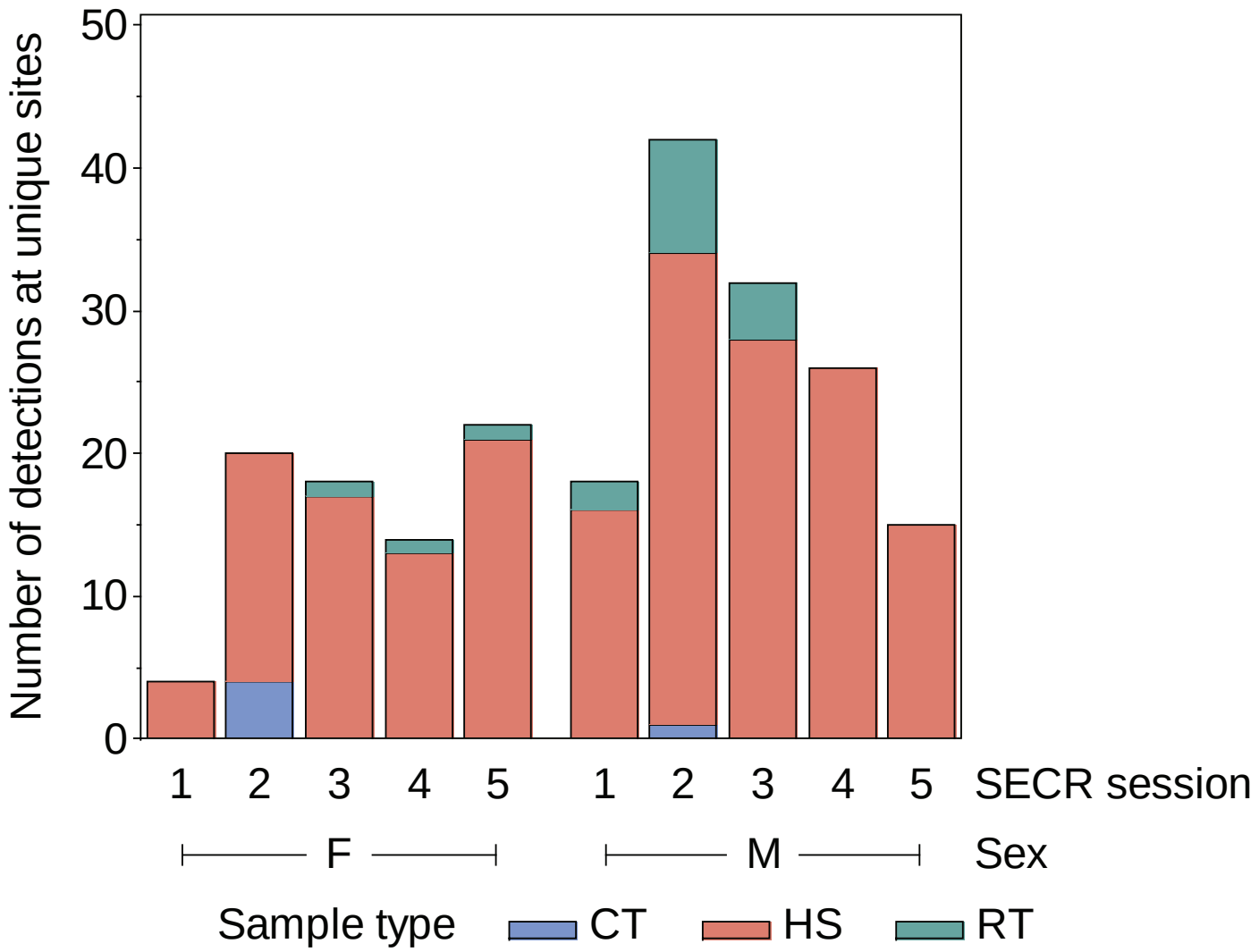


Figure 11. Number of detections as a function of hair snag (HS), rub tree (RT), and culvert traps (CT).

3.2. Spatially Explicit Analyses

Spatially explicit analyses were conducted separately for females and males, given the likelihood of sex-specific parameters as well as sex-specific distributions of bears on the sampling grid. This approach was simpler than attempting a pooled analysis with sex-specific terms for each parameter.

3.2.1. Females (2014)

Detections of females were lowest in the first session, then approximately constant until the last session, when detections increased (Table 5). The number of active sites (detectors) was lower in the first session, which may have contributed to the lower number of detections. However, the number of detectors was also lower in the fifth session, which had the highest number of detections. The number of unmarked bears detected decreased with each session, suggesting that sampling was relatively efficient. The number of new bears detected during session 5 in August was only 5 also suggesting that there was minimal immigration into the grid during the initial part of the August berry season.

Table 5. Summary statistics for detections of females in the Yellowhead Ecosystem 2014 sampling grid.

Statistic	Session(j)					
	1	2	3	4	5	Total
Detections (n_j)	4	16	16	12	21	68
Unmarked (u_j)	4	15	13	8	5	45
Cumulative marked (M_{t+1})	4	19	32	40	45	45
Frequencies ($f_{sessions}$)	24	18	3	0	0	45
Total site visits[A]	4	20	18	14	22	78
Detectors visited	4	18	16	12	19	69
Detectors available	194	281	314	315	121	1225

[A]Includes multiple visits to different sites within single sessions.

Detections and movements occurred mainly in mountainous areas with only a few detections in the eastern part of the core stratum and no detections in the secondary stratum (Figure 12). There were no detections of female bears in the Athabasca River Valley of JNP.

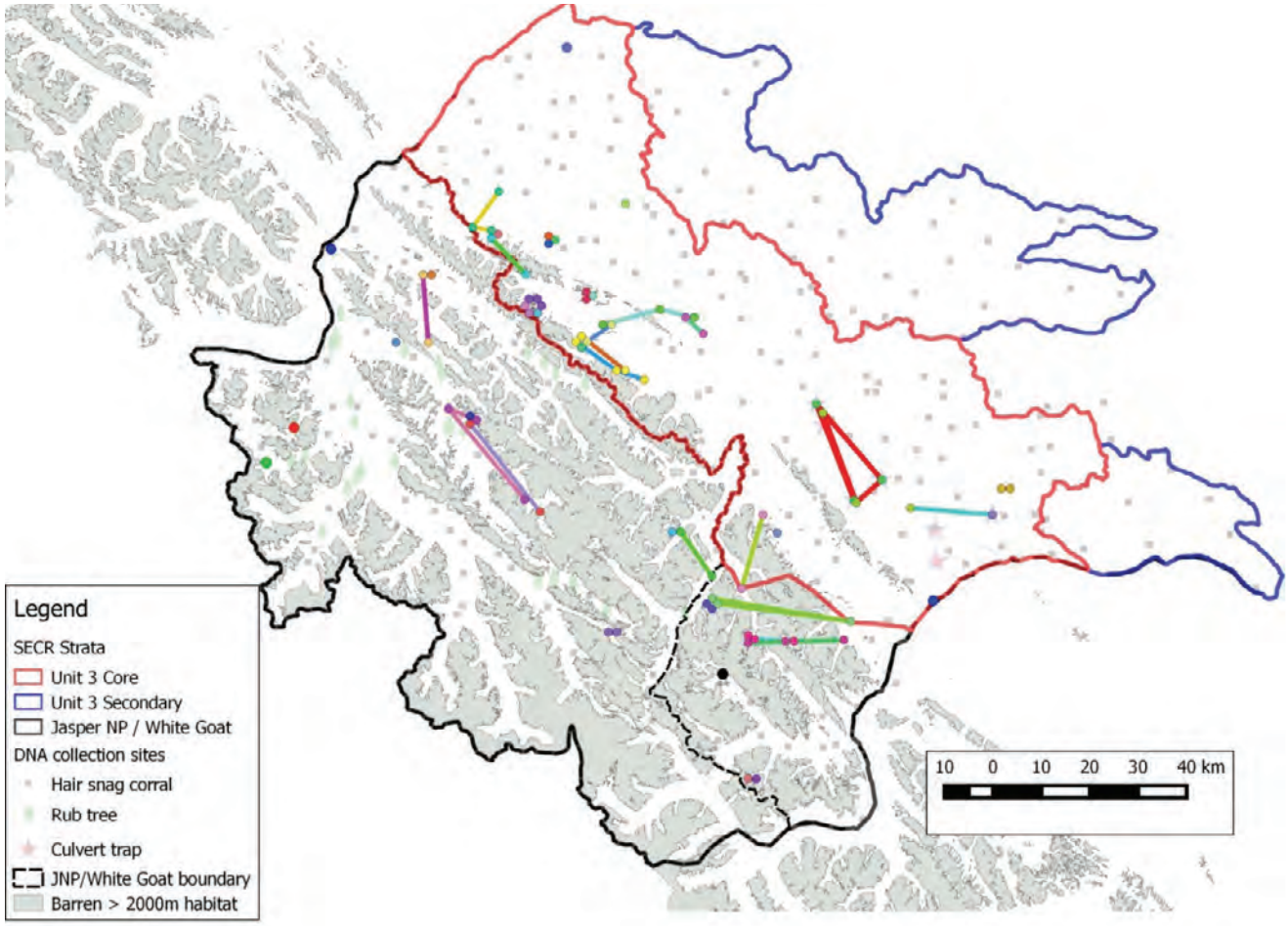


Figure 12. Approximate movement paths of females based on detections during the DNA inventory. The actual path is approximate, given that the sequence of detections is not known. Symbols for multiple detections at single sites are offset to facilitate interpretation.

Model selection efforts initially focused on identifying base variation in detection at home range center (g_0) and scale of movement (σ). From the suite of models considered , the model with temporal variation in detection probabilities (g_0) in session 5 (denoted as t5) was most supported (model 12). Models with behavioural response due to habituation to fixed hair snag sites (termed b_{HS} in models 18-20) were not supported. In the second phase, site covariate models were considered. Of these, the model where g_0 varied with canopy cover, whether a site was a rub tree or hair snag (model 2) was substantially more supported than other site covariates such as terrain ruggedness (model 5) and distance from stream (model 8). In the last phase of model selection, the strata-specific density model was more supported than models which assumed homogenous density across the sampling grid (model 1). The strata-specific model assumed similar responses of detection probabilities to canopy closure across all strata.

Table 6. Female SECR model selection results. Site covariate acronyms are listed in Table 1. AIC_c = sample size adjusted Akaike Information Criterion, ΔAIC_c = the difference in AIC_c between the model and the most supported model, AIC_c weight = w_i, K = the number of model parameters, and log-likelihood (LL) are given. Baseline constant models are shaded for reference with covariate models.

No	Model	AICc	ΔAICc	wi	K	LL
	Strata-specific density					
1	g0(CC+RT+t5A) σ (.)	708.0	0.00	1.00	7	-344.0
	Site covariate models (uniform density)					
2	g0(CC +RT+t5) σ (.)	719.8	11.81	0.00	6	-352.8
3	g0(CC +t5) σ (.)	723.1	15.03	0.00	5	-355.8
4	g0 (CC) σ (.)	731.4	23.38	0.00	4	-361.2
5	g0 (TRI+t5) σ (.)	743.1	35.09	0.00	5	-365.8
6	g0 (RT+t5) σ (.)	741.8	33.80	0.00	5	-365.1
7	g0 (t5) σ (dstream)	747.9	39.89	0.00	5	-368.2
8	g0 (t5+dstream) σ(.)	747.4	39.34	0.00	5	-367.9
9	g0 (t5) σ (.)	748.3	40.24	0.00	4	-369.6
10	g0 (t5) σ (CC)	750.8	42.76	0.00	5	-369.6
11	g0 (t5) σ (TRI)	750.7	42.66	0.00	5	-369.6
	Base models (uniform density)					
12	g0 (t5) σ (.)	748.3	40.28	0.00	4	-369.6
13	g0 (t) σ (.)	750.3	42.28	0.00	7	-366.6
14	g0 (T) σ (.)	755.6	47.58	0.00	4	-373.3
15	g0 (.) σ (h2)	760.9	52.88	0.00	3	-377.2
16	g0 (.) σ (.)	763.2	55.18	0.00	4	-377.1
17	g0 (b) σ (.)	763.3	55.28	0.00	4	-377.1
18	g0 (RT+bHSB) σ (.)	766.0	57.98	0.00	6	-375.9
19	g0(RT+bHS) σ(RT+bHS)	766.3	58.28	0.00	9	-371.6
20	g0(.) σ(RT+bHS)	767.7	59.68	0.00	6	-376.7

[A]denotes specific detection rates for session 5

[B]denotes a behavioural response specific to hair snag sites

The detection function from model 2 suggested that bears were the most detectable in session 5 (Figure 13, black line) compared to other sessions (red line) for hair snags. Females were the least detectable at rub trees (green line).

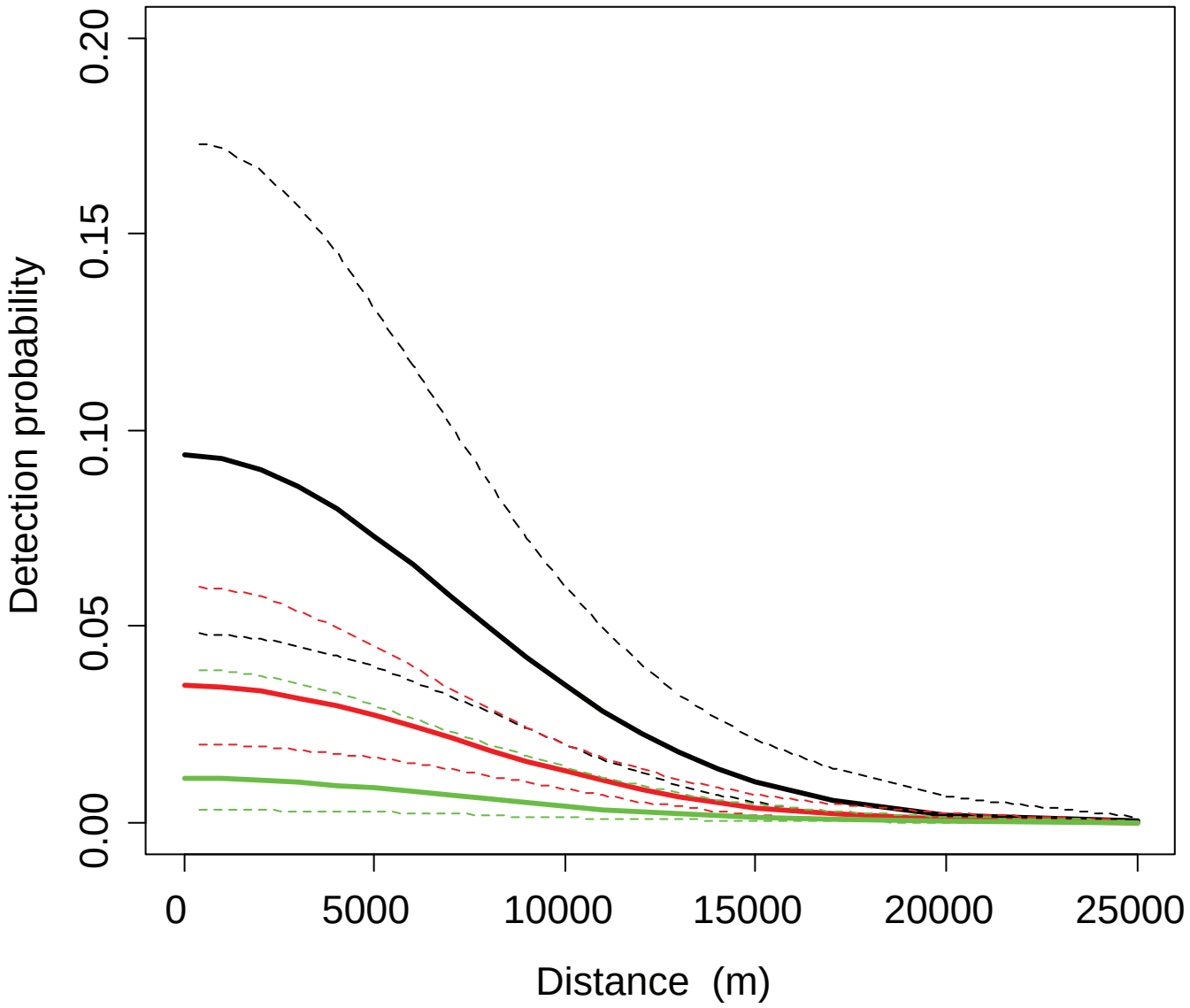


Figure 13. Detection functions for detection at hair snags in session 5 (black line), detections at hair snags in sessions 1-4 (red line), and rub trees averaged across sessions (green line) from model 2 (Table 6). Canopy cover was set at mean levels. Dashed lines are confidence limits on predictions.

A plot of the detection function at various canopy cover levels (Figure 13a) suggest that bears were had lower detection probabilities in sites with high canopy cover (Figure 14a, green line) compared to areas of low canopy cover (black line). The distribution of sites relative to canopy cover (Figure 14b) suggests that most sites were in moderate canopy cover with detection rates indicated by the red line in Figure 14a.

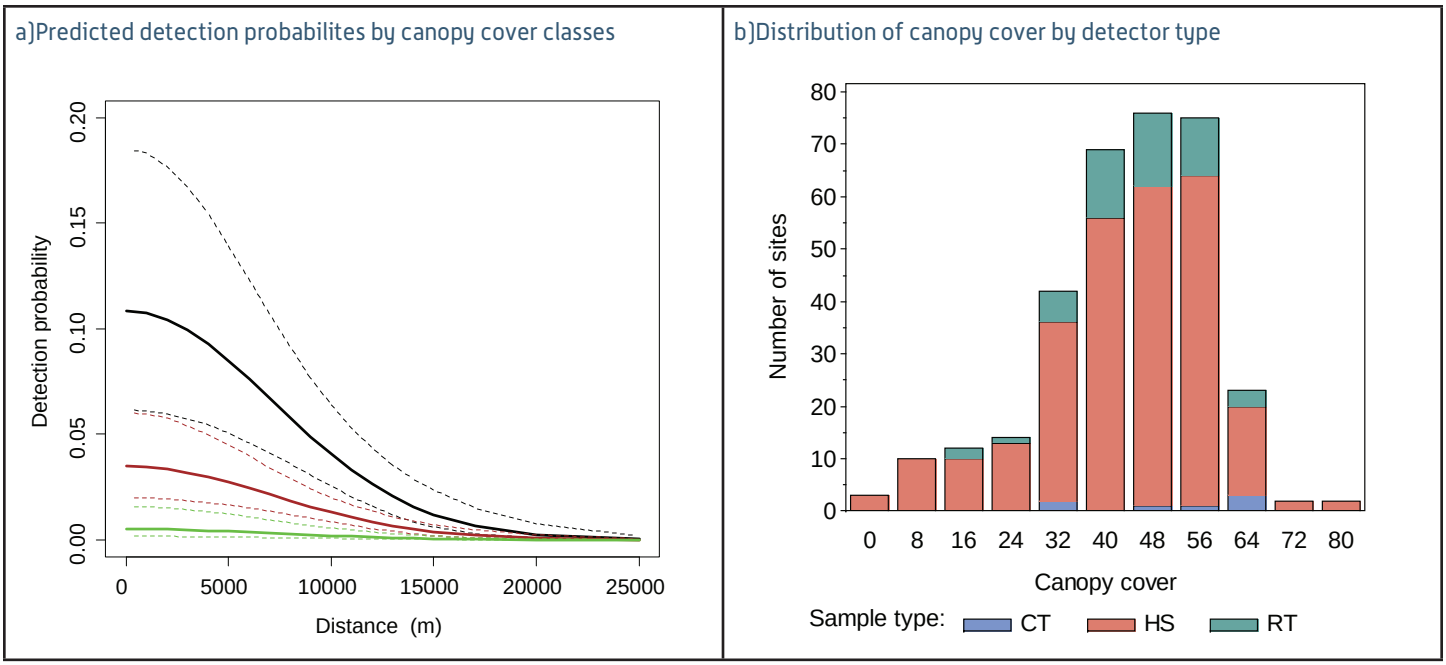


Figure 14. Detection function for model 2 (Table 6) at various levels of canopy cover (a). Green line is for highest observed canopy closure (81%); red line is for mean canopy closure (43%) and black line is for lowest canopy cover (1%, black line). The distribution of canopy cover by site type is given on the right graph (b).

Expected population size and density estimates were produced for the strata specific density model (Table 6, model 1). Estimates were not possible for the secondary stratum, given that no female bears were detected in this stratum. Estimates for individual stratum were not very precise, however, the overall estimate for the entire Yellowhead area had acceptable precision as defined by a coefficient of variation of less than 20% (Pollock et al 1990) (Table 7).

Table 7. Estimates of expected population size and density for females on the 2014 Yellowhead Ecosystem sampling grid. Estimates are from model 1 (D(strata) g_0(CC+RT+t_5) σ(.)) in Table 6. Estimates were not possible for the secondary stratum since no female bears were detected.

Strata/area	**Expected population size**					**Density**			
	Estimate	SE	Conf. Limit		CV	Estimate	SE	Conf. Limit	
BMA 3									
Core	34.4	8.5	21.4	55.4	24.6%	5.45	1.34	3.39	8.77
Secondary									
Total	34.4	8.2	21.7	54.5	24.6%	3.48	0.83	2.20	5.53
Jasper	28.0	6.7	17.6	44.4	23.9%	6.55	1.57	4.13	10.40
White Goat	5.4	1.3	3.4	8.5	23.9%	6.55	1.57	4.13	10.40
Entire population unit	67.7	11.0	49.3	93.0	16.3%	4.53	0.74	3.30	6.23

3.2.2. Males (2014)

For male grizzly bears, lower numbers were detected in sessions 1 and 5 (Table 8); however, this could have been due to the lower number of active detectors in sessions 1 and 5. The number of new bears detected declined as the sessions progressed, and only 3 new males were detected in session 5 suggesting minimal immigration of new bears during the August (session 5) berry season. Capture frequencies, or the number of sessions in which individual males were detected, suggested reasonable detection rates with males being detected in up to 4 different sessions.

Table 8. Summary statistics for detections of males in the Yellowhead Ecosystem 2014 sampling grid. Detections were pooled across detector types.

Statistic	Session(j)					
	1	2	3	4	5	Total
Detections (nj)	14	31	27	21	13	106
Unmarked (uj)	14	26	10	10	3	63
Cumulative marked (Mt+1)	14	40	50	60	63	63
Frequencies (fsessions)	33	21	5	4	0	63
Total site visitsA	18	42	32	25	15	131
Detectors visited	15	35	26	19	13	107
Detectors available	194	281	314	315	121	1225

[A]Includes multiple visits to different sites within single sessions.

Movements of males based upon detections and redetections demonstrated extensive movement and movements across stratum boundaries (Figure 15). Most notable were the movements on the boundary of the core and Jasper/White Goat strata. Most movements were less than 50 kilometers in total, across all sampling sessions.

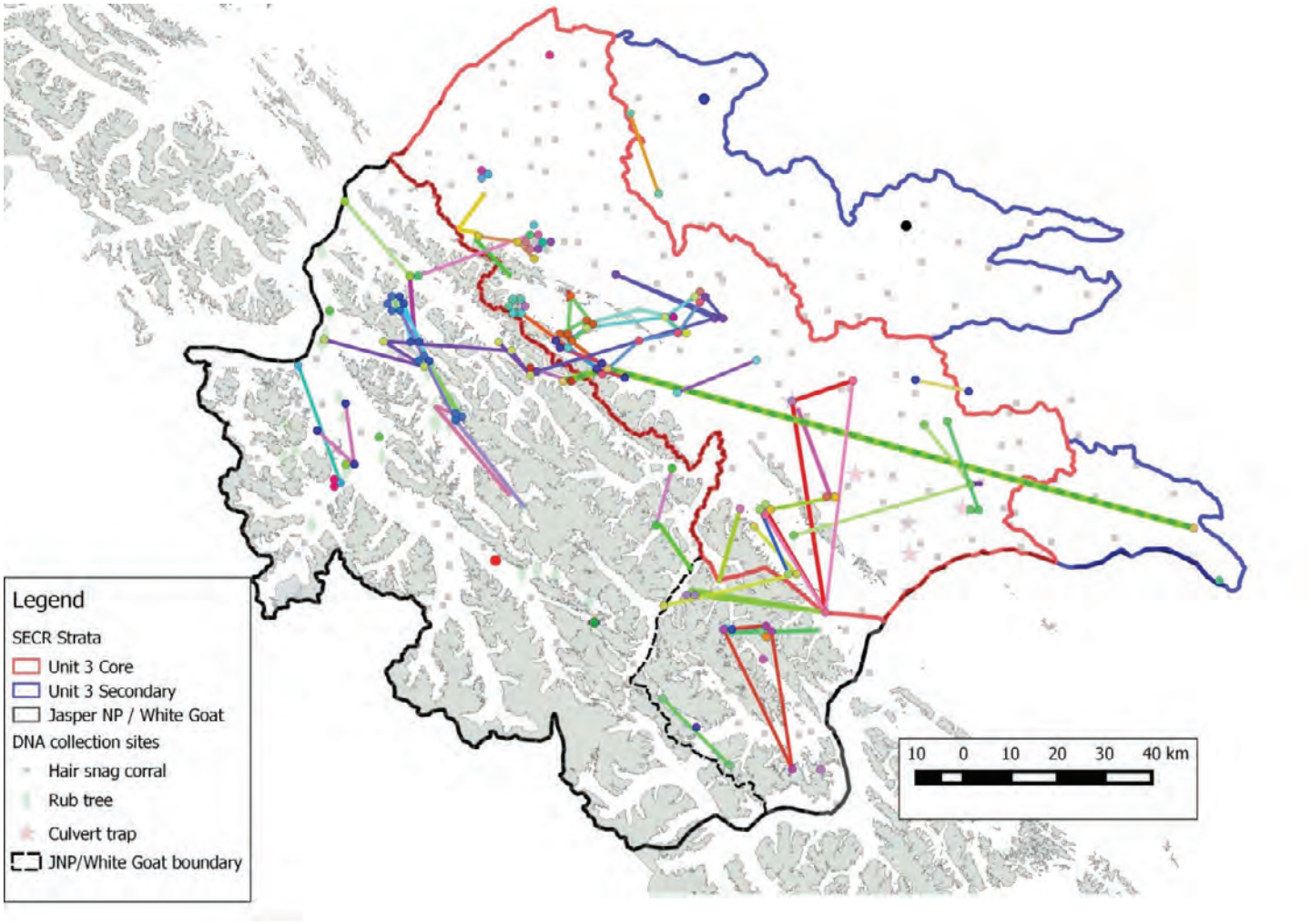


Figure 15. Approximate movement paths of males based on detections during the DNA inventory. The actual path is approximate given that the sequence of detections is not known. Symbols for multiple detections at single sites are offset to facilitate interpretation. A movement of 127 kilometers is highlighted with a hashed green line.

One movement (by male id 343-1A-2) of 127 kilometers occurred between sessions 3 and 4; genotypes for these detections were confirmed based on analysis to a larger number of loci for each sample. This movement is denoted by a hashed line in Figure 14. This movement was an outlier compared to all other movements, as illustrated by plotted detection functions with and without this movement included (Figure 16). The density estimates with the outlier movement data included was 3.46 bears per 1000 km^2 (SE=0.4, CI=2.77-4.22), versus an estimate of 3.85 (SE=0.44, CI=3.07-4.83) when the outlier data were included (baseline $g_0(.)$ $\sigma(.)$ model). We therefore excluded this movement from the spatially explicit model analysis, given the sensitivity of SECR estimates to movement distances. Spatially explicit models, as well as most mark-recapture methods, assume that the "target population" of bears have stationary home ranges, and that the sample of bears does not include a large proportion of "transient" bears. This assumption allows a defined population and density estimate. By incorporating movement data, spatially explicit models allow further assessment of this assumption and how it might affect estimates.

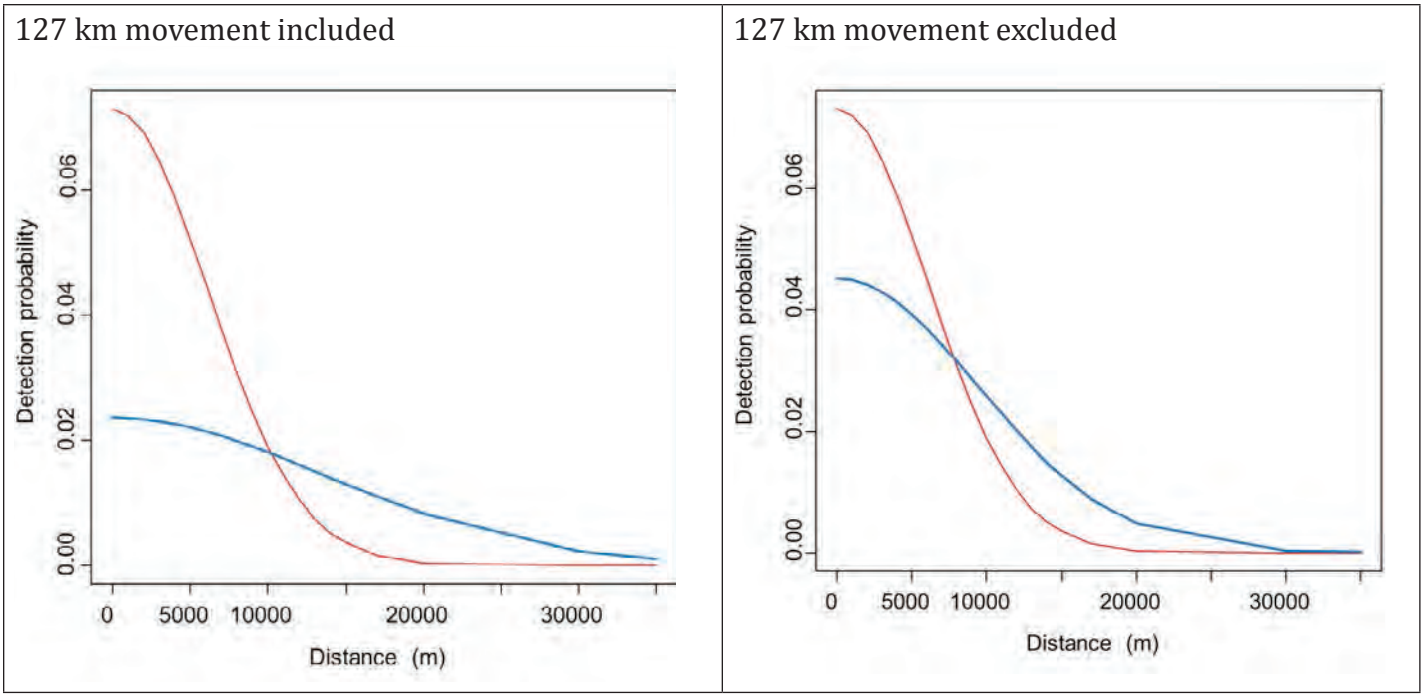


Figure 16. Effect of inclusion and exclusion of outlier 127 kilometer movement on spatially explicit detection function estimates. Male detection functions are indicated by the blue line. Female detection function lines are in red for reference purposes.

Model selection for male grizzly bear data was conducted in three stages. In the first stage, a base model was fitted which tested for general forms of detection probability and σ variation. Behavioural response and time variation in detection probabilities were not supported. A model with constant detection probabilities at home range center and linear trends in scale of movement (Table 9: model 13). Site covariate models were fitted in the second stage. Many of the site covariate models were more supported than the baseline model (models 8 and 15), including models with terrain ruggedness (model 8),canopy closure (models 2-4), and rub trees (models 3 and 5) affecting detection probabilities (g_0). Terrain ruggedness (models 5 and 6) and canopy closure (model 7) affected scale of movement (σ). Of these, a model with canopy closure influencing g_0 with linear trends in scale of movement (σ) was more supported (model 2) . Strata was then added as a covariate for density; this variable also increased the overall support as indicated by a lower AIC_c score (model 1), further suggesting stratum-specific densities within the Yellowhead sampling grid.

Table 9. Male SECR model selection results. Site acronyms are given in Table 1. AICc = sample size adjusted Akaike Information Criterion, ΔAICc = the difference in AICc between the model and the most supported model, AICc weight = wi, K = the number of model parameters, and log-likelihood (LL) are given. Baseline constant models are listed twice and shaded for reference with covariate models.

No	Model	AICc	ΔAICc	wi,	K	LL
	Strata-specific density					
1	g0(CC) σ (T)	1245.2	0	0.96	7	-615.7
	Site covariates models (uniform density)					
2	g0 (CC) σ (T)	1252.8	7.6	0.02	5	-620.9
3	g0 (CC+RT) σ (T)	1254.7	9.5	0.01	6	-620.6
4	g0 (CC) σ (.)	1255.6	10.4	0.01	4	-623.5
5	g0 (RT) σ (TRI+T)	1257.6	12.3	0.00	6	-622.0
6	g0 (.) σ (TRI+T)	1259.1	13.9	0.00	5	-624.0
7	g0 (.) σ (CC+T)	1266.7	21.5	0.00	5	-627.8
8	g0 (TRI) σ (T)	1275.8	30.5	0.00	5	-632.4
9	g0 (.) σ (T)	1276.7	31.5	0.00	4	-634.0
10	g0 (RT) σ (T)	1277.5	32.2	0.00	5	-633.2
11	g0 (dstream) σ (T)	1278.7	33.4	0.00	5	-633.8
12	g0 (.) σ (dstream+T)	1279.0	33.7	0.00	5	-634.0
13	g0 (RT+bhs) σ (T)	1281.5	36.3	0.00	8	-631.4
	Baseline models (uniform density)					
14	g0 (.) σ (T)	1276.7	31.5	0.00	4	-634.0
15	g0 (.) σ (.)	1278.1	28.9	0.00	3	-635.8
16	g0 (T) σ (T)	1278.6	33.4	0.00	5	-633.8
17	g0 (.)σ (t)	1280.4	35.1	0.00	7	-632.2
18	g0 (t) σ (.)	1280.9	35.6	0.00	7	-632.4
19	g0 (t) σ (t)	1284.1	38.9	0.00	11	-628.5

Plots of the detection function from model 2 (Figure 17) revealed that detection probabilities of bears were highest at sites with low canopy closure, a similar result to females (Figure 14). Scale of movement decreased slightly over the sampling sessions.

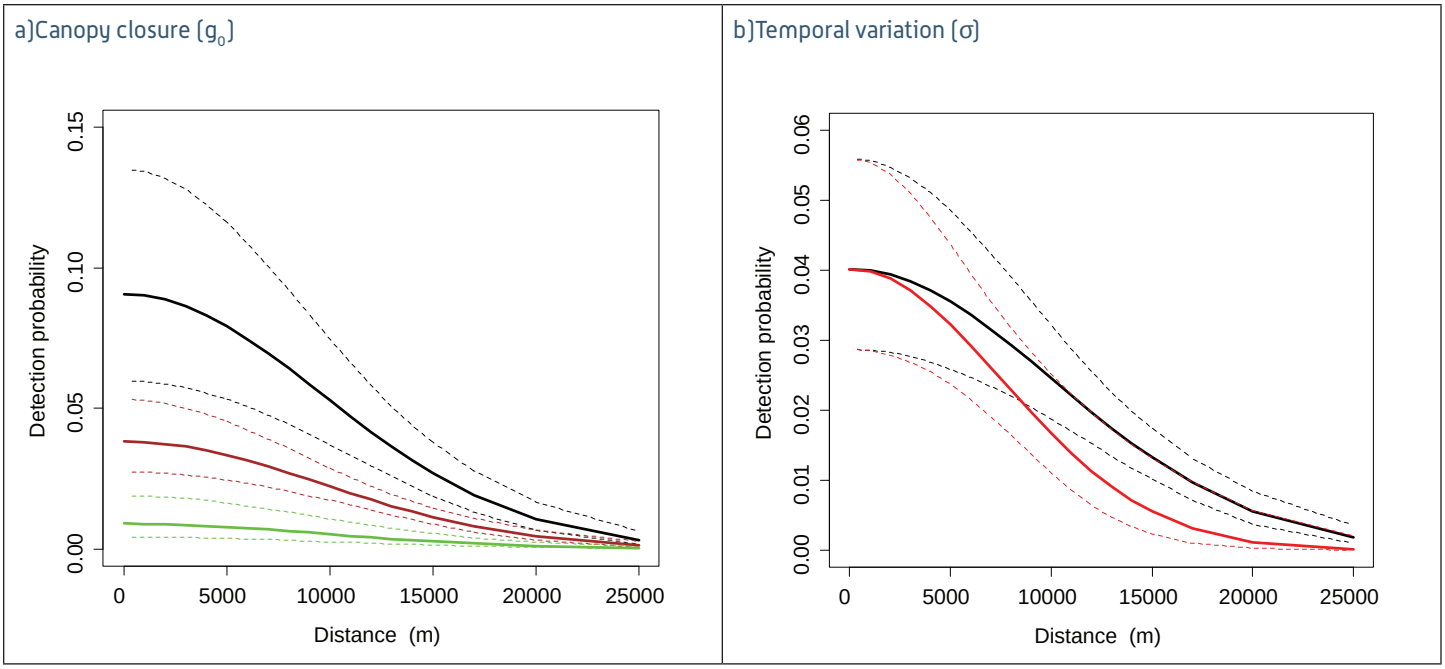


Figure 17. a) Detection function on highest observed canopy closure (81%); green line, mean canopy closure (43%, brown line) and minimal canopy closure (1%, black line). B) Temporal variation in σ in session 1 (black line) and session 5 (red line) with canopy closure at mean levels.

Estimates of expected population size were reasonably precise (CV<20%) for most strata with the exception of the secondary stratum (Table 10).

Table 10. Estimates of expected population size and density for males on the 2014 Yellowhead Ecosystem sampling grid. Estimates are from model 1 (D(strata) g0(CC) σ (T)) in Table 9.

Strata/area	Expected population size					Density (bears per 1000 km2)			
	Estimate	SE	Conf. Limit		CV	Estimate	SE	Conf. Limit	
BMA 3									
Core	35.8	6.38	25.3	50.6	17.8%	5.66	1.01	4.00	8.02
Secondary	4.1	2.4	1.4	11.9	58.8%	1.15	0.68	0.39	3.34
Total	39.9	6.65	28.8	55.2	16.7%	4.04	0.67	2.92	5.59
Jasper	26.0	5.18	17.7	38.3	19.9%	6.10	1.21	4.15	8.98
White Goat	5.0	0.99	3.4	7.4	19.8%	6.11	1.21	4.15	8.99
Entire population unit	70.9	7.78	57.2	87.8	11.0%	4.74	0.52	3.83	5.88

3.2.3. Combined Estimates for Males and Female Bears

Table 11 provides combined estimates for male and female bears for the 2014 Yellowhead population unit (from Tables 7 and 10). Precision was better for combined estimates, compared to sex-specific estimates, with all coefficients of variation < 20%, other than the secondary stratum.

Table 11. Combined estimates of male and female bears on the Yellowhead Ecosystem DNA sampling unit based on estimates in Tables 7 and 10.

Strata/area	Detected	Expected population size					Density (bears per 100 km2)			
		Estimate	SE	Conf. Limit		CV	Estimate	SE	Conf. Limit	
BMA 3										
Core	61	70.2	10.6	52.3	94.3	15.1%	11.12	1.68	8.28	14.92
Secondary	5	4.1	2.4	1.4	11.9	58.8%	1.15	0.68	0.40	3.35
Total	66	74.2	10.6	56.2	98.0	14.2%	7.53	1.07	5.70	9.93
Jasper	29	54.0	8.5	39.8	73.2	15.7%	12.66	1.98	9.33	17.17
White Goat	18	10.4	1.6	7.6	14.1	15.6%	12.66	1.98	9.34	17.16
Entire unit	108	138.6	13.5	114.6	167.7	9.7%	9.28	0.90	7.67	11.22

3.2.4. An Estimate for the Entire Jasper National Park

We also completed a spatially explicit analysis for the north JNP, reanalyzing data that was collected during the DNA inventory in 2008 (Boulanger 2015). The analysis of Boulanger (2015a) used density surface modelling to partition and estimate density and expected population size in sub-regions of the 2008 BMA 2/JNP sampling grid (Alberta Grizzly Bear Inventory Team 2009). A model that predicted density of the 2008 DNA grid using resource selection function based habitat scores and RISK scores (Nielsen et al. 2004, Nielsen et al. 2006) was used for this analysis. This model, combined with spatially explicit detection models, estimated 34 females and 26 males for North Jasper (Table 12). Under the assumption that densities have remained constant in northern Jasper since 2008, a total of 113 bears was estimated for the entire area of JNP. However, this estimate should be interpreted with caution, given the uncertainty in status of the grizzly bear population in north JNP since 2008. For example, this estimate will be biased if the population in north JNP experienced a decline or increase in abundance since 2008. Given this, it is not appropriate to estimate a confidence limit on the overall estimate since it would not include the statistical uncertainty in trend between 2008 and 2014.

Table 12. Comparison of expected population size and density estimates from the 2014 and spatially explicit analysis of the 2008 BMA 2/ Jasper inventory (Boulanger 2015).

Sex	SECR model		Expected population size					Density (bears per 1000 km2)			
	Density	Detection	Estimate	SE	Conf. Int.		CV	Estimate	SE	Conf. Int.	
North JNP (2008)											
females	RSF*Risk	g0(CC) σ (TRI)	34	3.5	27.5	41.3	10.4%	11.89	1.24	9.69	14.58
males	RSF	g0(TRI) σ(.)	26	2.0	22.0	30.0	7.9%	9.07	0.71	7.77	10.58
South JNP (2014)											
females	Stratum	g0(CC+RT+t5) σ (.)	28	6.7	17.6	44.4	23.9%	6.55	1.57	4.13	10.40
males	Stratum	g0(CC) σ (T)	26	5.2	17.7	38.3	19.9%	6.10	1.21	4.15	8.98

A previous estimate for JNP was based on extrapolation of reference area densities using RSF modelling (Boulanger et al. 2011); results from the 2004-2008 DNA inventory projects were used to derive RSF models, which were then applied to extrapolate densities from the DNA grids to adjoining park areas. The extrapolation produced an estimate of 109 (CI=64-173) bears for JNP.

3.3. Reanalysis of 2004 DNA BMA 3 Population Inventory Data Using Spatially Explicit Methods

The 2004 BMA 3 inventory employed an intensive sampling design: each cell included a fixed sampling site which was sampled for four sessions, along with a site that was moved to a new location during each of sessions 2 through 4 (Boulanger et al. 2005, Boulanger et al. 2006). This entire data set was considered in the SECR reanalysis of the 2004 data, since SECR models consider site location as well as whether or not a session was active (Figure 18). A 'fix' covariate was used to test for differences in detection between fixed and moved sites. Sampling in 2004 overlapped much of the 2014 core strata and the western section of the 2014 secondary strata.

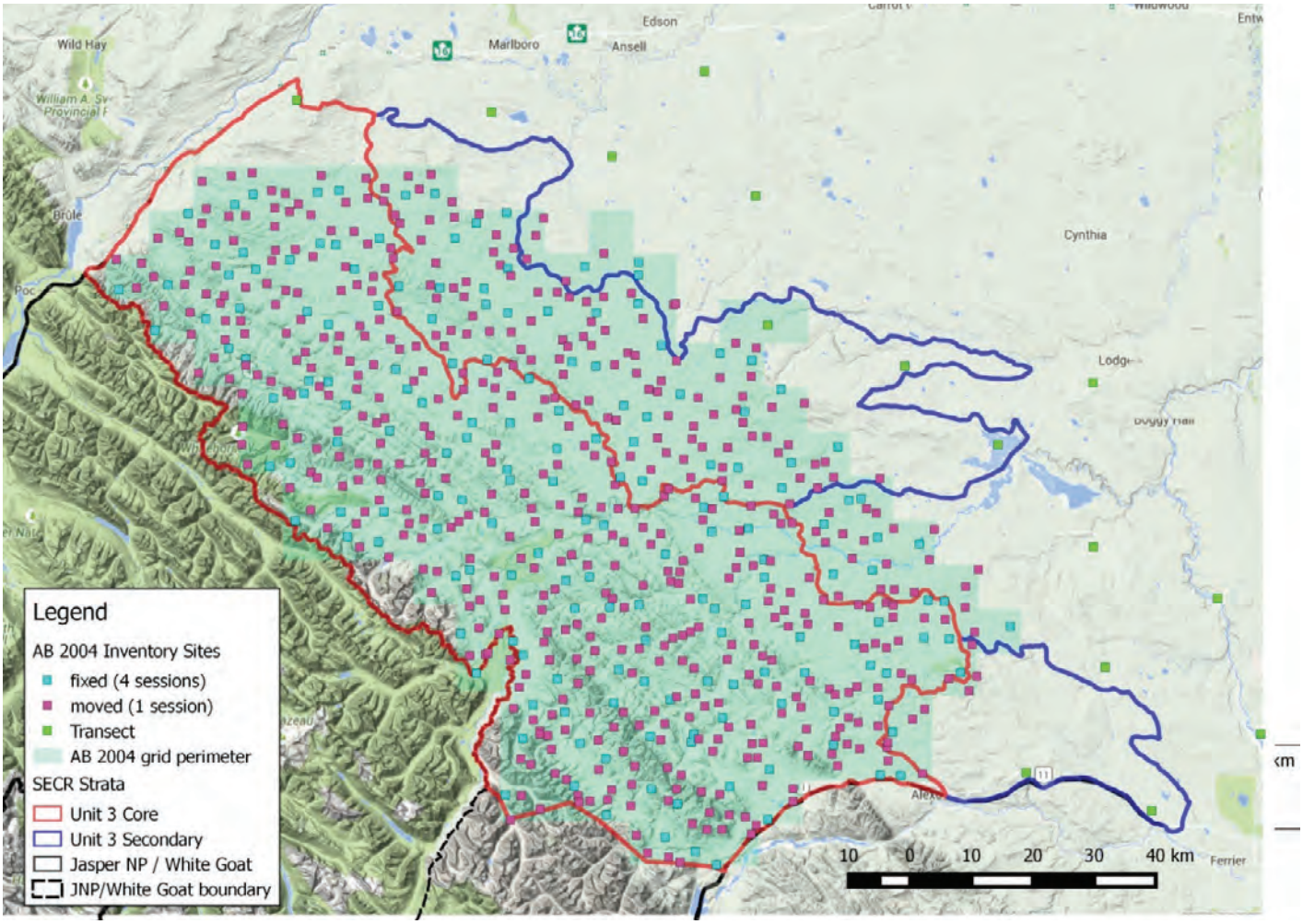


Figure 18. Locations of hair snag sites sampled during the 2004 BMA 3 DNA mark-recapture inventory. Moved sessions were only in place for a single session whereas fixed sites were in place for all 4 sessions.

Overall, 44 bears (24 females and 20 males) were detected during the 2004 DNA Inventory (Figure 19). Of these, mean locations for 3 males and 2 females fell within the 2014 secondary stratum, with the rest occurring in the core stratum. In the 2014 reanalysis of 2004 data, 23 females and 35 males were detected within the core 2004 grid. Sampling intensity in 2014 was lower, especially in the secondary area (Figure 6); therefore, the best comparison is of spatially explicit estimates rather than numbers of bears detected.

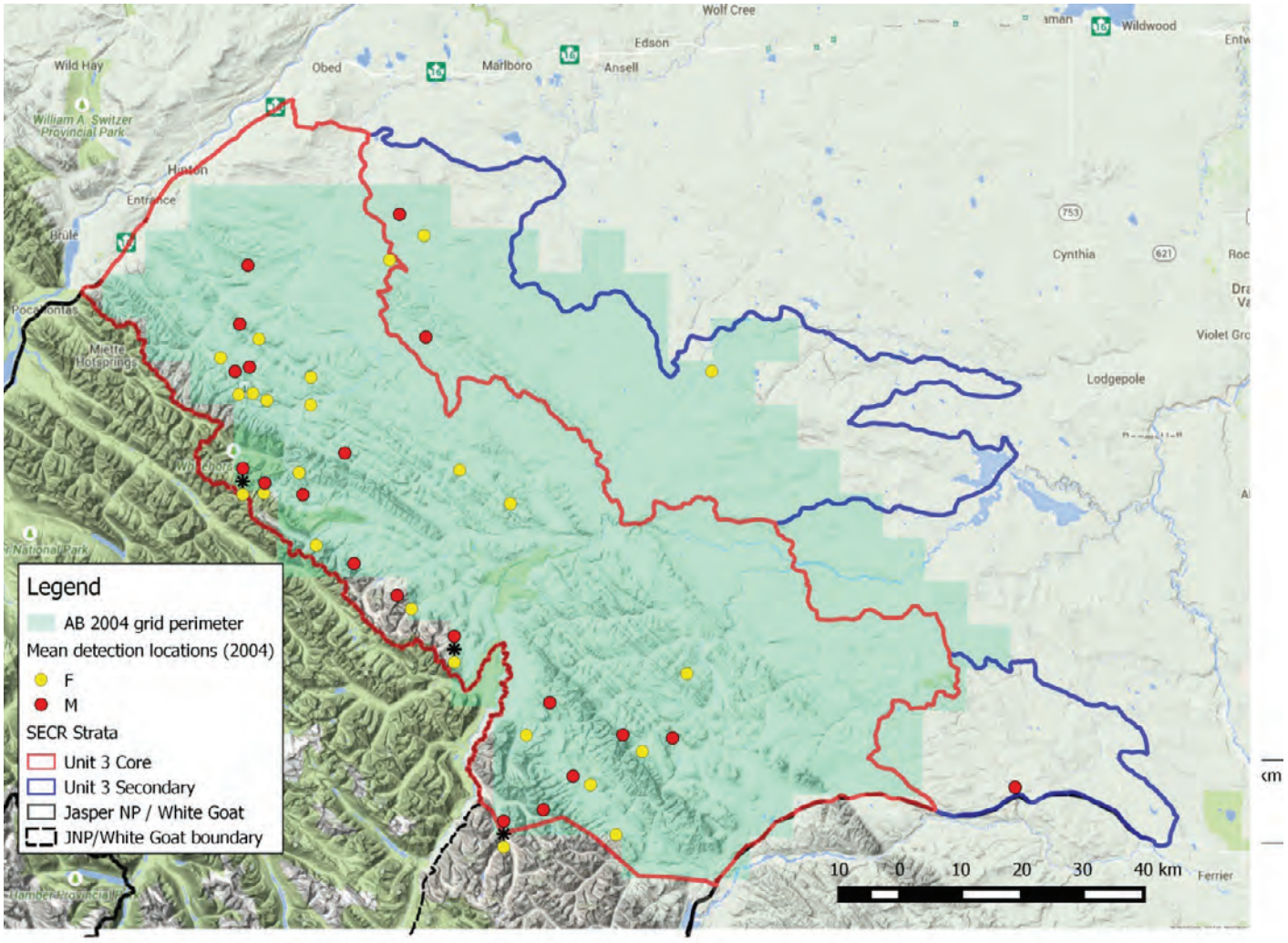


*Figure 19. Mean detection locations of bears for the 2004 BMA 3 DNA mark-recapture inventory with the 2004 grid and 2014 SECR strata shown in reference. Not shown are locations of transect sites in 2004 that did detect one male bear in the southwest corner of the sampling grid. Multiple mean detection locations at single locations are offset with a * denoting the central location.*

3.3.1. Females

Detections of females were lowest in the first and last sampling sessions. Low detections in the first session may have been due to a lower number of active sites (Table 13). The number of new bears detected declined with session, suggesting that sampling was effective in detecting most of the bears on the sampling grid. In addition, as indicated by detection frequencies, the majority of bears were detected at least twice during sampling.

Table 13. Summary statistics for detections of females in the 2004 BMA 3 sampling grid.

Statistic	Session(j)				
	1	2	3	4	Total
Detections (nj)	7	16	16	9	48
Unmarked (uj)	7	11	4	2	24
Cumulative marked (Mt+1)	7	18	22	24	24
Frequencies (fsessions)	10	7	4	3	24
Total site visitsA	13	23	18	15	69
Detectors visited	12	21	14	15	62
Detectors available	188	365	349	360	1262

[A]Includes multiple visits to different sites within single sessions.

Detections and movements were primarily distributed on the western edge of the sampling grid with a few movements into the secondary strata (Figure 20). There was also a single detection in the central part of the secondary strata.

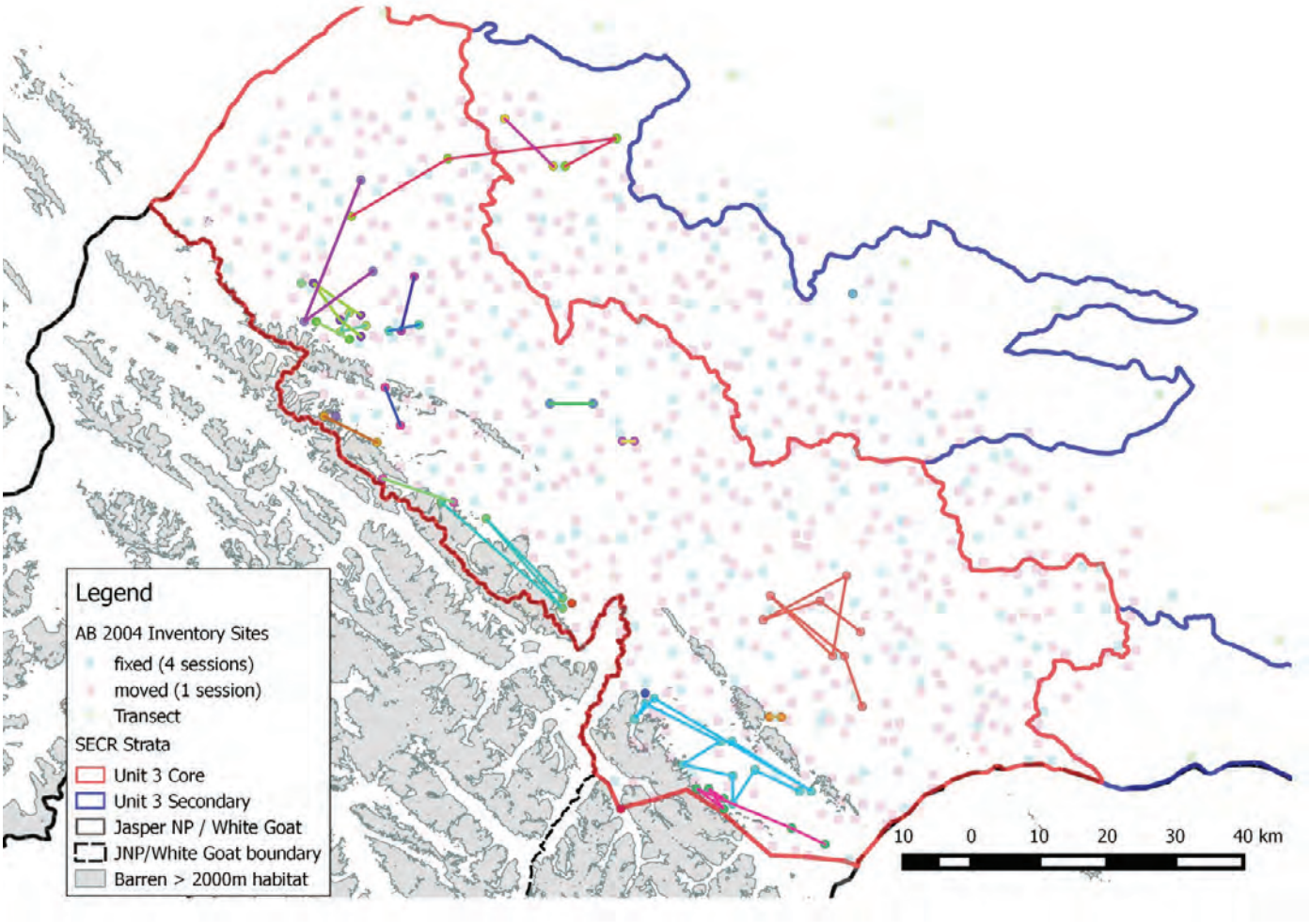


Figure 20. Approximate movement paths of females based on detections during the 2004 BMA 3 DNA inventory. The actual path is approximate given that the sequence of detections is not known. Symbols for multiple detections at single sites are offset to facilitate interpretation.

Base model selection did not detect any variation in detection at home range center or scale of movement (Table 14, Model 11). Of site covariate models, a model with detection probability at home range center being positively associated with terrain ruggedness was most supported (Model 2). A model with fixed sites displaying lower detection rates also showed some support compared to a constant parameter model (Models 3 and 5). A model with strata-specific densities (Model 1) was most supported further demonstrating different densities between core and secondary strata.

Table 14. Female SECR model selection results for the 2004 BMA 3 Inventory. AIC_c = sample size adjusted Akaike Information Criterion, ΔAIC_c = the difference in AIC_c between the model and the most supported model, AIC_c weight = w_i, K = the number of model parameters, and log-likelihood (LL) are given. Baseline constant models are shaded for reference with covariate models.

No	Model	AICc	AICc	wi,	K	LL
	Strata model					
1	g0(TRI) σ (.)	645.7	0.00	0.64	5	-316.2
	Site covariate models					
2	g0 (TRI) σ (.)	648.1	2.38	0.19	4	-319.0
3	g0(fix+TRI) σ (.)	649.7	4.00	0.09	5	-318.2
4	g0 (TRI) σ (TRI)	649.8	4.14	0.08	4	-318.3
5	g0 (fix) σ (.)	663.8	18.14	0.00	4	-326.8
6	g0 (.) σ (.)	664.4	18.75	0.00	3	-328.6
7	g0 (.) σ (CC)	664.6	18.89	0.00	4	-327.2
8	g0 (CC) σ (.)	666.3	20.57	0.00	4	-328.1
9	g0 (stream) σ (.)	667.2	21.50	0.00	4	-328.5
10	g0 (.) σ (CC)	667.2	21.54	0.00	4	-328.6
	Base model					
11	g0 (.) σ (.)	664.4	18.75	0.00	3	-328.6
12	g0 (T) σ (.)	664.9	19.21	0.00	4	-327.4
13	g0 (.) σ (T)	666.6	20.88	0.00	4	-328.2
14	g0 (b) σ (.)	667.2	21.47	0.00	4	-328.5
15	g0 (.) σ (t)	667.2	21.54	0.00	6	-325.1
16	g0 (T) σ (T)	667.5	21.78	0.00	5	-327.1
17	g0 (t) σ (.)	671.6	25.93	0.00	6	-327.3

The 2014 SECR reanalysis of the 2004 data resulted in an estimate of expected population size of 21.6 females for the 2004 sampling grid. This estimate for the entire 2004 grid was close to the sum of the separate estimates for the core and secondary strata (Table 15). The terrain ruggedness covariate for g_0 had minimal effect on estimates.

Table 15. Female expected population size and density estimates from spatially explicit mark-recapture analysis of the 2004 BMA 3 data. Estimates are from model 1 in Table 14.

Strata	Expected population size					Density			
	Estimate	SE	Conf. Limit		CV	Estimate	SE	Conf. Limit	
2004 sampling grid	21.6	3.5	15.7	29.6	16.2%	2.53	0.41	1.85	3.47
SECR strata									
core	19.3	3.4	13.8	27.1	17.4%	3.05	0.53	2.18	4.28
secondary	2.5	1.8	0.7	8.7	70.0%	0.71	0.50	0.21	2.46
Total	21.8	3.6	15.9	30.0	16.3%	2.21	0.36	1.61	3.04

3.3.2. Males

Summary statistics indicate that detections were relatively even across sampling sessions, however, the number of active detectors was less for the first session. The number of marked bears declined for each session suggesting that sampling was relatively effective (Table 16).

Table 16. Summary statistics for males detected in the 2004 BMA 3 Inventory.

Statistic	Session(j)				
	1	2	3	4	Total
Detections (nj)	13	10	10	8	41
Unmarked (uj)	13	4	1	2	20
Cumulative marked (Mt+1)	13	17	18	20	20
Frequencies (fsessions)	9	2	8	1	20
Total site visitsA	20	21	17	9	67
Detectors visited	17	18	15	7	57
Detectors available	188	365	349	360	1262

Distributions of detections and movements demonstrated that most males were detected on the western part of the sampling grid with only single detections of bears in the secondary strata (Figure 21). If compared with the 2014 spatial data (Figure 10), it is apparent that many of the bears detected on the 2004 sampling grid may have had home ranges that overlapped Jasper and White Goat in the west.

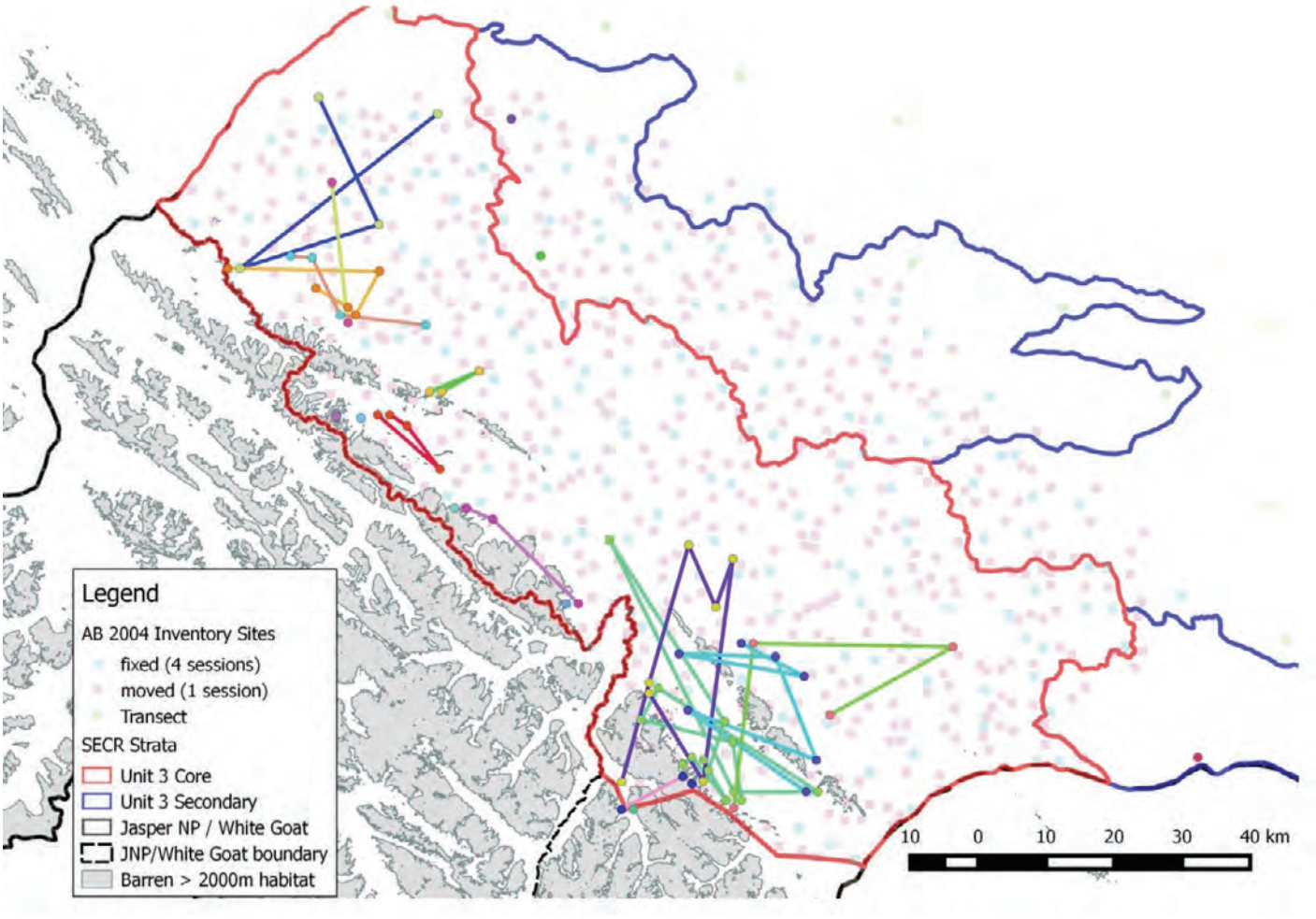


Figure 21. Approximate movement paths of males based on detections during the 2004 BMA 3DNA inventory. The actual path is approximate given that the sequence of detections is not known. Symbols for multiple detections at single sites are offset to facilitate interpretation.

Baseline model selection revealed linear trends (symbolized by *T*) in scale of movement (σ; Table 17, model 9) as with the 2014 data (Table 9). Terrain ruggedness influenced scale of movement with substantially more support than baseline models (model 2). A strata (core and secondary strata) model was most supported (model 21).

Table 17. Male SECR model selection results for the 2004 BMA 3 3 Inventory. AIC_c = sample size adjusted Akaike Information Criterion, ΔAIC_c = the difference in AIC_c between the model and the most supported model, AIC_c weight = w_i, K = the number of model parameters, and log-likelihood (LL) are given. Baseline non-covariate models are shaded for reference with covariate models.

No	Model	AICc	AICc	wi,	K	LL
	Strata model					
1	g0 (.) σ(T+TRI)	628.5	0.00	0.62	6	-305.54
	Site covariate models					
2	g0 (.) σ(T+TRI)	629.5	1.01	0.37	5	-307.12
3	g0 (TRI) σ(T)	639.0	10.51	0.00	5	-312.37
4	g0 (.) σ(T+CC)	640.6	12.06	0.00	5	-313.15
5	g0 (.) σ(T)	646.9	18.39	0.00	4	-318.12
6	g0 (CC) σ(T)	647.5	18.97	0.00	5	-316.6
7	g0 (.) σ(T+dstream)	650.1	21.60	0.00	5	-317.92
8	g0 (dstream) σ(T)	650.5	22.01	0.00	5	-318.12
	Baseline models					
9	g0 (.) σ (T)	646.9	18.39	0.00	4	-318.1
10	g0 (T) σ(.)	657.9	29.34	0.00	4	-323.6
11	g0 (.) σ (T+fix)	649.5	21.00	0.00	5	-315.5
12	g0 (fix+T) σ (.)	660.4	31.89	0.00	5	-323.1
13	g0 (.) σ (t)	654.5	25.96	0.00	6	-321.3
14	g0 (b) σ (.)	661.7	33.16	0.00	4	-325.5
15	g0 (t) σ (.)	664.9	36.36	0.00	6	-323.2
16	g0 (t) σ (t)	666.8	38.26	0.00	9	-315.4
17	g0 (.) σ (.)	669.2	40.72	0.00	3	-330.8

The estimate of expected or average population size was 14.4 for male bears for the Alberta 2004 grid area (Table 18).

Table 18. Male abundance and density estimates from spatially explicit mark-recapture analysis of the 2004 BMA 3 data.

Strata	Expected population size				Density (bears per 100 km2)				
	estimate	SE	Conf. Limit		CV	Estimate	SE	Conf. Limit	
AB04 DNA grid	14.4	2.4	10.4	19.9	16.7%	1.69	0.28	1.22	2.34
SECR strata									
core	13.2	2.5	9.2	19.1	18.8%	2.09	0.39	1.45	3.02
secondary	2.0	1.6	0.5	8.0	82.7%	0.55	0.46	0.14	2.27
Total	15.2	2.6	10.9	21.1	16.9%	1.54	0.26	1.11	2.14

3.3.3. Combined Estimates for Males and Females in 2004

The combined estimate of bears for reanalysis of the 2004 data set was 37 bears for the core and secondary area and 36 bears for the DNA sampling grid (Table 19).

Table 19. Combined sex abundance and density estimates from spatially explicit mark-recapture analysis of the 2004 BMA 3 data from estimates of females (Table 15) and males (Table 18).

Strata	Abundance					Density (bears per 100 km2)			
	estimate	SE	Conf. Limit		CV	Estimate	SE	Conf. Limit	
AB04 DNA grid	36.0	4.2	28.6	45.3	11.8%	4.22	0.50	3.36	5.32
SECR strata									
core	32.5	4.2	25.3	41.8	12.9%	5.14	0.66	4.00	6.61
secondary	4.5	2.4	1.7	12.0	53.5%	1.26	0.68	0.47	3.38
Total	37.0	4.4	29.3	46.6	11.9%	3.75	0.45	2.97	4.73

3.3.4. Comparison of 2004 SECR Estimates with 2004 Closed Model/Telemetry Estimates.

The SECR estimate for the 2004 DNA grid area was 36 bears (males and females, CI=29-45). This is lower than the previous estimate of 42 bears (CI=36-55), which was derived from closed models corrected by proportion points on the grid (using radio collared bears) (Boulanger et al. 2005). However, the confidence intervals of these two estimates overlap; therefore, this difference should be interpreted with caution.

3.4. Comparison of 2014 and 2004 Estimates

3.4.1. Spatially Explicit Estimates of Expected (average) Number of Bears on the Sampling Grid.

Estimates from spatially explicit models for the 2004 sampling grid (Figure 16) were compared to assess the relative change in expected or average number of bears on the sampling grid between 2004 and 2014 (Table 20).

Table 20. Comparison of spatially explicit estimates of expected (average) number of bears on the 2004 BMA 3 DNA sampling grid between 2004 and 2014.

Year/sex	Bears detected	Expected N	SE	Conf. Limit		CV
2004						
females	24	21.6	3.5	15.7	29.6	16.2%
males	20	14.4	2.4	10.4	19.9	16.3%
pooled	44	36.0	4.2	28.6	45.3	11.8%
2014						
females	23	33.7	8.1	21.1	53.7	24.1%
males	35	37.6	6.2	27.3	51.8	16.4%
pooled	58	71.3	10.2	53.9	94.2	14.3%

A graphical representation of the estimates and confidence intervals from Table 20 is given in Figure 22.

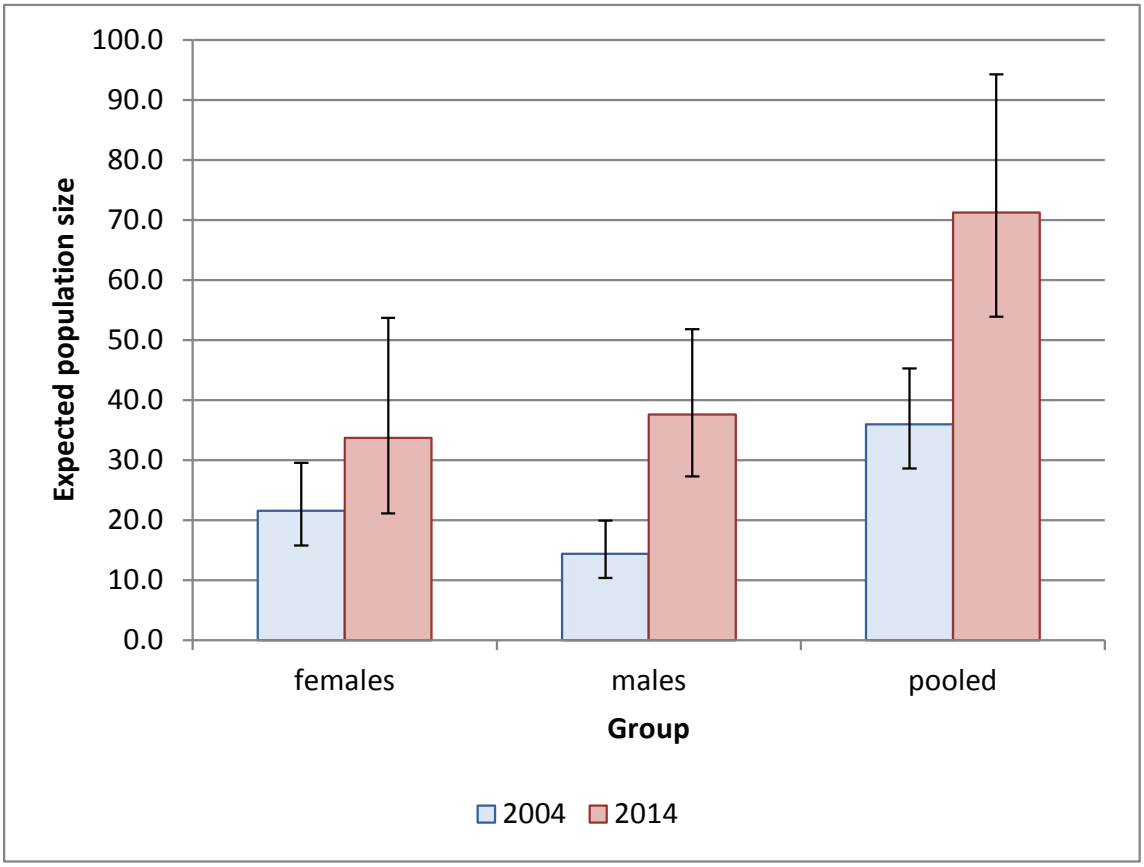


Figure 22. Comparison of spatially explicit estimates of expected (average) population size for the 2004 BMA 3 DNA sampling grid area in 2004 and 2014.

Estimates from the ratio of the 2014 and 2004 estimates (gross change) were scaled for a yearly interval to estimate yearly rates of change. Yearly rates of population change were estimated at 1.05 and 1.11 for females and males respectively, for a pooled average rate of change of 1.07 (Table 21).

Table 21. Estimates of gross change (ratio of estimates in 2014 and 2004) and yearly change based on spatially explicit estimates of average population size.

Sex	Gross change		Yearly change			
	Estimate	SE	Estimate	SE	Conf. Limit	
females	1.56	0.45	1.05	0.14	0.76	1.33
males	2.61	0.61	1.10	0.19	0.72	1.48
pooled	1.98	0.37	1.07	0.12	0.84	1.30

The pooled rate of change is compared to previously published estimates, as well as other hypothetical rates of change in Figure 23. The estimate of lambda of 1.04 pertains to estimated rates of increase for the Northern Continental Divide Ecosystem (2004-9; (Mace et al. 2011)) as well as Banff National Park and Kananaskis (1994-2002; (Garshelis et al. 2004)). The estimated rate of change calculated in our analysis was higher than most previously published bear studies. As discussed later, one factor that most likely influenced the rate of change was the addition of at least 30 relocated bears to the Yellowhead BMA over the last 10 years. Future analyses will consider factors influencing the observed trend including relocated bears, known mortalities, and radio collar-based survival rates.

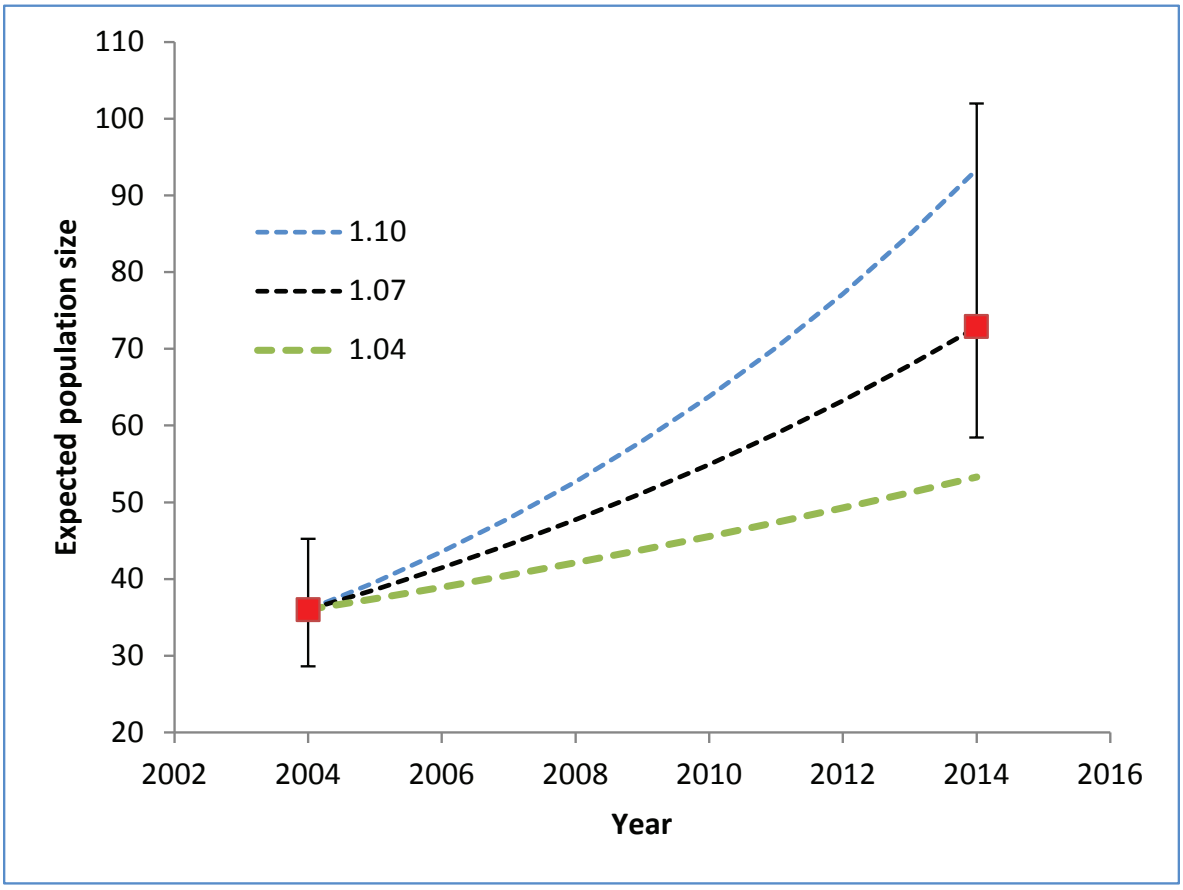
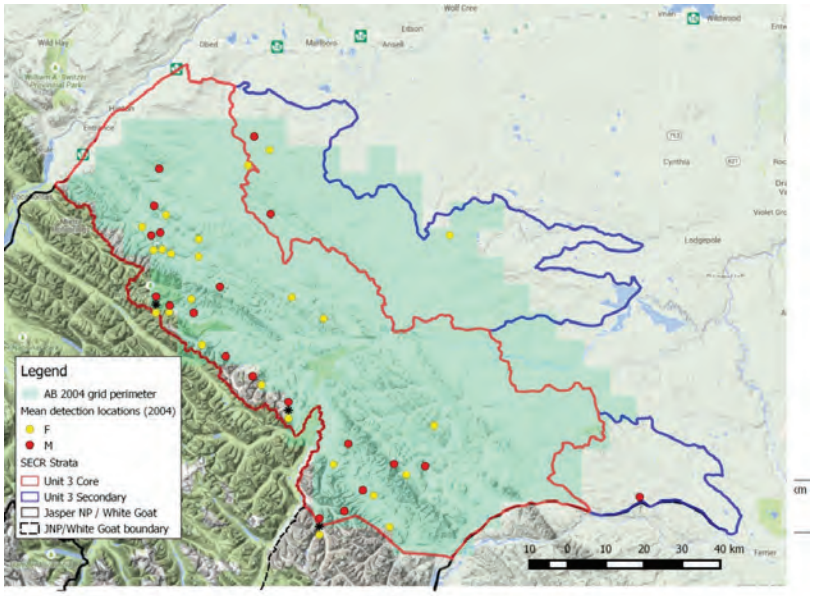


Figure 23. Annual rates of population change in comparison to the estimate rate of change (1.07). The estimate of estimated rate of change of 1.04 pertains to estimated rates of increase for the Northern Continental Divide Ecosystem (2004-9; (Mace et al. 2011)) as well as Banff National Park and Kananaskis (1994-2002; (Garshelis et al. 2004)).

3.4.2. Comparison of Spatial Distribution Between 2004 and 2014

Figure 24 provides a comparison of the spatial distribution of detections in 2004 and 2014. This comparison should be interpreted cautiously given the higher degree of sampling effort, especially in secondary areas, in 2004. The main differences in distribution between 2004 and 2014 are an increase in bears in the central and southeast core area, and around the Cadomin mine in 2014 as compared to 2004.

2004 distribution of mean detections



2014 distribution of mean detections

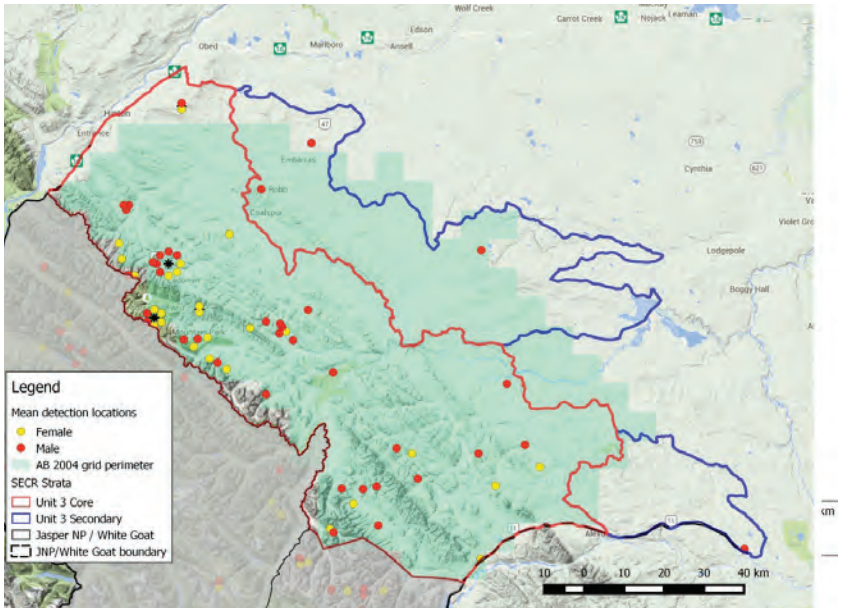


*Figure 24. Comparison of mean detections of bears from the 2004 and 2014 inventory of BMA 3. Multiple mean detections at single sites are indicated by a concentric ring with the site location denoted by a *.*

An upcoming density surface modelling exercise will provide further inference on differences in distribution and factors influencing distribution.

3.5. Wildlife Camera Results

Results from wildlife cameras in selected grid cells indicated that we were successful in gathering samples from bears visiting these sites. The majority of photos within these cells were of black bears, and grizzly bear hair was collected at all sites and sessions where photos showed a grizzly bear had visited the hair snag site.

Table 22. The number of cameras operating, the total number of photos taken, and the number of photos containing a black bear and grizzly bear for each DNA session.

DNA Session	No. Cameras Set Up	No. Cameras Sampled	Total Photos	Black Bear Photos	Grizzly Bear Photos
0	-	-	-	-	-
1	43	-	-	-	-
2	+4	43	630	491	12
3	+3	47	401	260	1
4	-	50	290	145	5

4. Discussion

Estimates from the 2014 grid suggests the population of grizzly bears in BMA 3 has increased between 2004 and 2014, with an estimated rate of population increase of approximately 7% (CI=-16%-30%), which is higher than commonly seen in most interior grizzly bear populations in North America (Garshelis et al. 2004, Schwartz et al. 2005, Mace et al. 2011). The reasons for population increase are unclear, and additional investigation is required to determine whether management actions have contributed to this rate of increase. The provincial grizzly bear hunting moratorium that was put in place in 2006 has played a role in reducing overall human caused mortalities over the past 8 years.

There are a number of additional pieces of information (datasets) that need to be considered when evaluating the observed increase in population size within BMA 3. First it should be recognized that as a result of management actions related to "problem bear management", enforcement officers have relocated 30 bears to this BMA during the period 2004-2014. This represents approximately 3 bears per year over this 10 year period. At this time we have not pursued further analysis to determine what role this population augmentation may have played in population increase, however, we recommend that this analysis be undertaken in order to make refinements in management practices to support recovery efforts. In addition, new DNA data sets obtained from a scat collection project undertaken within BMA 3 in the fall of 2014 may further refine DNA-based estimates. Further analysis of these datasets is now underway.

Other studies, have also suggested an increasing population within BMA 3, including results from a smaller sampling grid in the vicinity of Hinton (Rovang 2013). The 2013 analysis estimated a yearly rate of increase of 1.06 (CI=0.93-1.19), using a Pradel trend model that compared bears detected on the 2011 grid with those from the 2004 grid. A similar analysis combining detections of individual bears on DNA grids each year between 2004 and 2014 collaring effort, and translocated bear data, will provide a more precise and definitive estimate of trend.

Spatially explicit methods provided a way to obtain robust population estimates with less sampling effort, through the use of fixed rather than moved sites and by allowing a stratified sampling approach. For example, precision of estimates for bears on the BMA 3 grid were similar (Table 20) in 2004 and 2014, even though the 2014 grid used only fixed sites, as well as reduced trap density in secondary areas (Figures 6 and 18). This type of stratification can be employed in future population inventory work to reduce overall project costs.

The use of site covariates in spatially explicit analyses provides a new way to model heterogeneity variation in individual bear detection probabilities caused by placement of site in various habitats. In general, it may be easier to select site locations in non-homogenous forest (lower canopy cover) or in mountainous areas (higher terrain ruggedness), since a heterogeneous landscape is more likely to contain features or micro-habitats optimal for site placement. Not surprisingly, detection of bears is associated with these site covariates given the relative ease of finding optimal areas for site placement . In addition, in some analyses, scale of movement is influenced by terrain ruggedness, as indicated by smaller grizzly bear home range sizes in mountainous areas (Schwab 2003).

Spatially explicit analysis resulted in lower estimates of abundance for the 2004 sampling grid as compared with the original closed model approaches used in 2004, however, this difference could be due to sampling variation. Of particular note, the SECR reanalysis suggested that the expected population size of male bears was only 14 bears, even though 20 bears were detected on the grid in 2004. This was due to the fact that many bears were detected on the eastern edge of the grid, resulting in many bears with partial home ranges on the grid. The 2004 data also included many detections on the eastern border, resulting in uncertainty in male residency on the grid. The closure correction estimate for 2004 was based upon a limited sample size of bears. A potential analysis that could refine the 2004 estimate would be the use of the cumulative sample size of bear locations to provide a better closure-corrected 2004 estimate which could be compared with the 2004 SECR estimates.

The current analysis assumes that densities in each stratum are homogenous. It is more likely that densities vary as a function of habitats and proximity of roads (which influence survival rates) (Boulanger and Stenhouse 2014). Spatially explicit estimates are robust to variation in densities across sampling grids (Efford 2014a); therefore it is likely that strata-specific estimates of density and expected population size will also be robust. Future analyses will utilize density surface modelling (Royle et al. 2013, Efford 2014a, Boulanger 2015) to explore factors that affect larger-scale density across the sampling grid and provide a spatial representation of density variation.

This report has provided the first documented example of an expanding grizzly bear population in Alberta through the use of DNA inventory techniques and SECR methodologies, showing the value and importance of well designed, repeat inventory efforts. These data will be essential in discussions on population recovery targets and review of the provincial status assessment for this species. In addition, the estimate for south Jasper represents the first population estimate for this area, and forms a strong and important foundation for status monitoring and genetic databases.

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