FINAL REPORT

2018 Grizzly Bear Population Inventory – Bear Management Area 7

Prepared for

West Fraser, Millar Western Forest Products, Vanderwell Contractors, FRIAA and Alberta Environment and parks

January 2021
Final Report

Gordon Stenhouse, John Boulanger, Karen Graham, Isobel Phoebus, Cameron McClelland and Karine Pigeon

Citation: Stenhouse, G.B.[1], Boulanger, J.[2], Graham, K.[1], Phoebus, I.[1], McClelland, C.[1] and Pigeon K.[1]. 2021. Estimates of Grizzly Bear population size, density and distribution for the Alberta Swan Hills Population Unit (BMA 7). 65 pages

[1.] fRI Research Grizzly Bear Program, 1176 Switzer Drive, Hinton, Alberta

[2.] Integrated Ecological Research, Nelson, B.C.

fRI Research
Informing Land & Resource Management

Acknowledgements

This project would not have been possible without funding provided by West Fraser Timber, Millar Western Forest Products, Vanderwell Contractors, the Forest Resource Improvement Association of Alberta (FRIAA) and the Government of Alberta (Alberta Environment and Parks). We want to thank all our partners for seeing this project through to completion.

Thank you to all who helped with this project; it could not have been completed without the dedication of so many. Karine Pigeon provided strong leadership in overseeing all elements of the fieldwork for this project and her dedication and participation was instrumental to the gathering of genetic samples. We primarily would like to thank our field crews who drove, hiked and flew in all weather conditions including: Sean Murray, Erika Croken, Mercede Schindler, Lyndsey Stewart, Christine Kuntzemann, Damon Waselenchuk, Brianna Brandon, Lauren Skinner, Brian Smith, Ryan Ponich, Denyse Dawe, and Franco Alo. We would also like to thank Karen Graham for her considerable support in data management throughout the course of this project. Thank you to both Dan Wismer and Julie Duval for GIS support and to Cemil Gamas and Risa Croken for administration support. We would like to acknowledge Wildlife Genetics International in Nelson, B.C, and NIBIO lab in Svanhovd Norway for the laboratory DNA analysis portion of this study. We would like to thank our helicopter pilots Hans Nogel and Ian Tower for getting us to sites safely. We would further like to thank the volunteer efforts of Cala Jorgensen, Kevin Downing, Jim Castle, Curtis Stambaugh, Fauve Blanchard, and Callen Warren. Cam McClelland and Isobel Phoebus assisted with the preparation and assembly of this final report.

Foreword

This document represents the achievements and results from the 2018 grizzly bear population inventory project conducted in the Swan Hills Bear Management Area (BMA 7). The focus of this project was to complete a DNA inventory to provide the first population estimate for this BMA. These analyses required DNA laboratory results from genetic samples collected in 2018, however, project funding was on hold for over a year and a half. With funding provided in 2020, we were able to complete the genetic laboratory work, statistical analysis, and prepare this final report.

Executive Summary

In 2018, a collaborative project was undertaken between regional forest tenure holders and the Alberta Government (Alberta Environment and Parks) to provide the first assessment of the grizzly bear population in the Swan Hills Bear Management Area (BMA 7). Since the Swan Hills area has never had a DNA based population estimate, this project was intended to provide a base level for future comparisons to monitor population trends.

Using genetic samples gathered through non-invasive barbwire hair snagging, we sampled 9,800 km^2 of grizzly bear habitat with a grid sampling design over a 6-week period from May to July 2018. The study design used was based on previous knowledge of grizzly bears and habitats within BMA 7, combined with past experience and data from other spatially explicit capture-recapture grizzly bear population inventory work that our research team has undertaken in other provincial BMAs since 2004. This project provides the first estimates of grizzly bear abundance and density for the Swan Hills area.

During this inventory, we submitted 750 hair samples for DNA analysis. 507 of these were genetically determined to be black bears, 100 were from grizzly bears. From these grizzly bear samples, 93 grizzly bears were identified to the individual, with 39 unique bears identified (21 females and 18 males). The Swan Hills project had lower sampling efficiency compared to other projects conducted in Alberta. This was a result of the low proportion of grizzly bears detected in more than one sampling session, and a high proportion of new grizzly bears detected in the final sampling session. This low redetection frequency was anomalous when compared to other grizzly bear DNA mark-recapture projects performed in the province.

To confront sparse data from the BMA 7 project we used a meta-analysis approach to estimate density that used data from the adjacent BMA 2 survey that was conducted in 2008. This analysis suggested the density of grizzly bears to be 12.6 bears per 1,000 km^2 which resulted in an average estimated number of bears between 150 and 152 (CI=69–330) in core and secondary areas. However, the precision of estimates was low (CVs of 35–41%) and the low numbers of redetections was the primary factor for the poor precision of these estimates. Although we cannot fully explain the low redetection rates of bears in this study, it is likely that a high-density black bear population in this BMA could have influenced grizzly bear responses (i.e. attraction) to the sampling sites. Based on the large amount of black bear

hair identified, the presence of black bear hair at most sampling sites in all sessions, and supported by the identification of a large number of black bear scats, we feel such an effect is possible, although not fully understood.

We did see that the detection of family groups (4 cubs - in two family groups) in the last sampling period had an effect on population estimates by creating potential demographic closure within the analysis framework. When these four bears that were sampled together at one site, and identified as cubs through genetic analysis, were excluded from the analysis (mothers were retained), the population estimate decreased by 30 bears. This demonstrates the effect of potential demographic closure and the sparse nature of the data set on the population estimate. The population estimate of grizzly bears in the Swan Hills using the data set without the 4 cubs mentioned above (cubs identified only during the last session) is 118.6 bears (CI=62–226). As a result, the estimates from this project are relatively imprecise and should be interpreted with caution.

Given the high CV and lack of estimate precision found with BMA 7 data, we conducted an additional analysis where a similar detection function found for BMA 2 (2008) was applied to the Swan Hills data set The results of this analysis showed that when the cubs detected during the final sampling session were removed from the analysis and a similar detection rates for BMA 7 and BMA 2 were assumed, population estimates changed to 56 - 64 grizzly bears and densities were 3.5 - 5 bears per 1,000 km^2 with an increase in precision to a CV of 14%. These results, based on detection rates which were similar to those found in most other grizzly bear inventory work in Alberta, provided grizzly bear density estimates similar to what has been observed in other provincial BMAs.

Using the new Alberta grizzly bear genetic database, we did not find previous history on any of the 39 unique bears identified within this inventory, nor did we identify any offspring from the 10 grizzly bears that were captured and collared in 2005 and 2006 as part of other research efforts in BMA 7. This is in stark contrast to the 2018 BMA 4 inventory where 40% of the identified grizzly bears had a known history, as determined through genetic sampling. This may indicate elevated mortality rates in BMA 7 but we recognize that no ongoing grizzly bear collaring efforts have taken place in this area since 2006. We also did not detect any grizzly bear movement across Highway 43 during our sampling period. Genetic analysis of grizzly bears detected in BMA 7 clearly showed that these bears are from a genetically distinct population, suggesting no or very limited immigration.

The main challenge for the 2018 Swan Hills DNA inventory is low precision, resulting in wide confidence limits on population estimates. **For this reason, we suggest that these estimates be interpreted cautiously, and that the lower bound of the confidence limit of 62 bears be used for management purposes at this time. We note that the lower bound of the confidence limit (62) roughly corresponds to the population estimate of grizzly bears if a detection function similar to BMA 2 is assumed (56–64 bears).**

TABLE OF CONTENTS

List of Figures

LIST OF TABLES

Grizzly Bear DNA Spatially Explicit Capture-Recapture (SECR) Inventory for Bear Management Area 7

Introduction

As part of ongoing provincial grizzly bear recovery efforts, it has been widely recognized that there is a persistent need to determine population status and trend within the various provincial grizzly bear management areas. In the 2008–2013 provincial recovery plan, it was recommended that population inventory work be undertaken at five-year intervals within each of the 7 provincial BMAs (Bear Management Areas; Alberta Grizzly Bear Recovery Team, 2008). Although this has not taken place in every BMA, two BMAs (3 and 4) have had two DNA population inventories completed. For BMA 3 (Yellowhead), the first estimate took place in 2004 and the second in 2014 (Stenhouse et al., 2015), which found that the population had doubled in size during the 10-year time period. More recently, Stenhouse et al. (2020) also found the grizzly bear population in BMA 4 (Clearwater) had doubled in size between 2005 and 2018.

In an effort to determine grizzly bear population status in BMA 7 (Swan Hills), a collaborative project was undertaken between regional forest tenure holders and the Alberta Government (Alberta Environment and Parks) in 2018. Since BMA 7 never had a DNA based population estimate undertaken, this project was intended to provide a base level for future comparisons to monitor trends. This report details the results of our 2018 spatially explicit capture-recapture (SECR) based population inventory of grizzly bears in the Swan Hills BMA.

In 2009, management boundaries within the BMA were divided into core and secondary conservation areas (more recently combined as recovery zones; Alberta Environment and Parks, 2016) that provided guidance for the assessment of grizzly bear populations relative to habitat states and anthropogenic risks (Nielsen et al., 2009). The current primary management emphasis is on recovery of grizzly bears within these zones that consist of higher quality habitat with lower open all-weather road densities. The core and secondary conservation areas provide a management-based stratification of the BMAs, as well as a delineation of core habitat, that should harbor the highest densities of bears within BMAs (Nielsen et al., 2006). Therefore, sampling consideration of core and secondary areas was of primary consideration in the design of the BMA 7 2018 inventory with an emphasis being on estimation of densities within these areas. The study design for this project (see details in Appendix A) incorporated our current knowledge of the study area and resident bear populations, previously used spatially explicit capture-recapture methods, and relied on established DNA hair sampling methodologies that use non-invasive approaches.

The primary objectives of this BMA 7 inventory were to:

1. Provide an estimate of the current size and density of the grizzly bear population within this BMA.
2. Investigate possible movement of grizzly bears into and out of this BMA in relation to neighboring BMAs.
3. Determine if grizzly bears were crossing Highway 43 during the sampling period.

Study Area

The 2018 DNA inventory of BMA 7 consisted of a systematic sampling grid with 200, 7x7 km grid cells covering approximately 9,800 km^2 (Figure 1). Because population closure is an important assumption of our population estimators, we designed the sampling of the study area to minimize the movement of bears across the boundaries. Our study area encompassed almost all habitat designated as core and secondary grizzly bear conservation areas in BMA 7. The sampling area was bounded by Highway 43, Highway 2, and the Athabasca River providing relative closure surrounding the study area, with Lesser Slave Lake just to the north. Highway 33 and 32 ran right through the region.
The study area consists of upper and lower foothills, with elevations that ranged from 650 m to 1,450 m with a diversity of habitats throughout. Upland forests consisted of aspen (*Populus tremuloides*), Paper birch (*Betula papyrifera*), 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 grizzly bear foods 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 in the region are black bears (*Ursus americanus*), wolf (*Canine lupus*), and cougar (*Puma concolor*).

BMA 7 has various land-use activities including forestry with intensive logging, oil and gas exploration and development, and outdoor recreation. There are a few small parks and wildlands scattered within the BMA, but no significant protected areas. The land has been heavily developed by industrial activity, with a high density of roads in some areas. The landscape has a number of linear features including roads, pipelines, seismic lines, and all-terrain vehicle (ATV) trails. Access to the study area was primarily by vehicle and foot while some areas required helicopter support for access. Access was also dynamic in that weather events could change access type. Road access in dry conditions would at times require helicopter support during periods of heavy or prolonged rains.

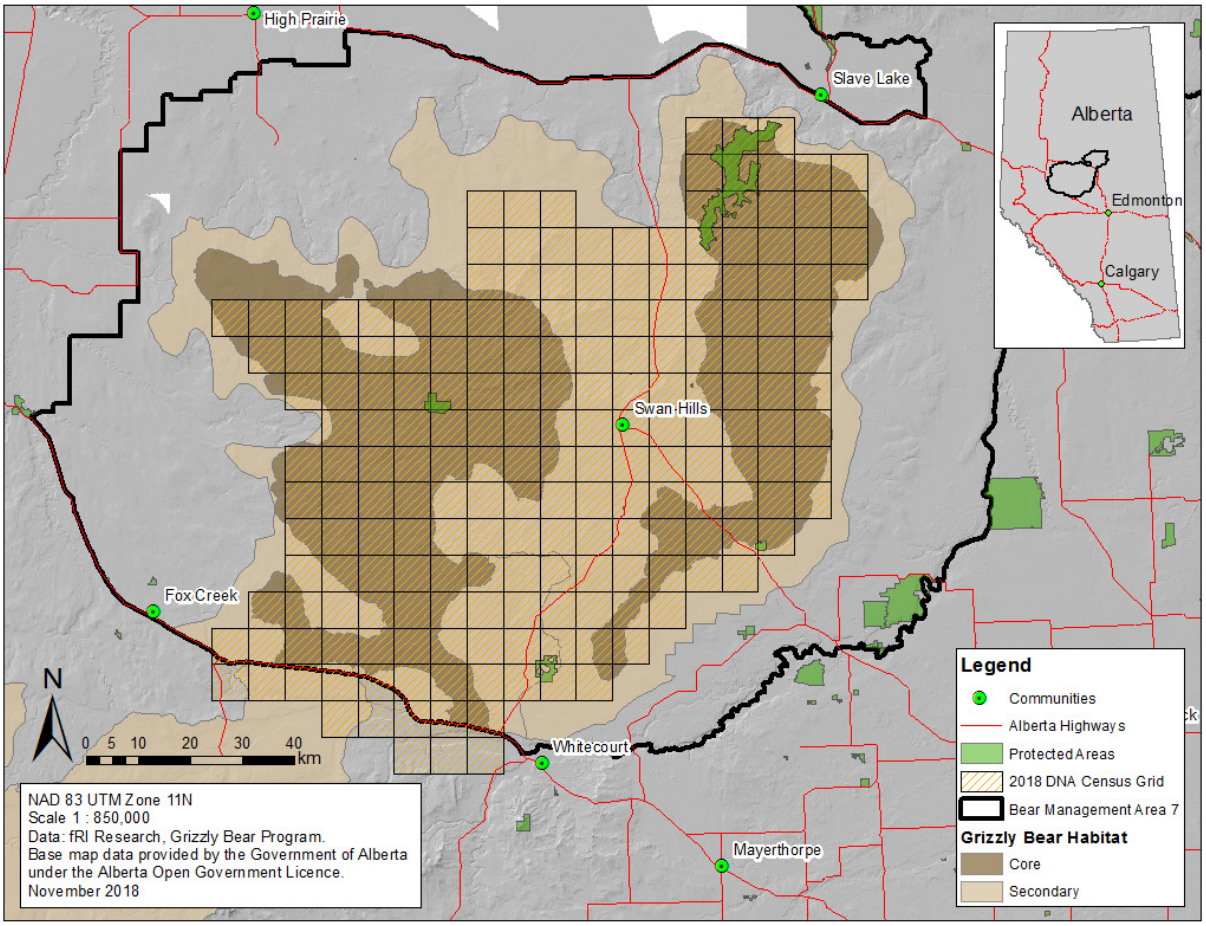

Figure 1. The Swan Hills Bear Management Area (BMA 7), including provincial lands, protected areas, core and secondary grizzly bear habitat areas, and the 2018 DNA census grid.

METHODS

Barb wire hair-snag sampling of grizzly bears in western Canada is generally based on a spatial sampling design that places one or more hair snag sites in each cell of an arbitrary square grid (Woods et al. 1999; Proctor et al. 2010; Boulanger, Nielsen, and Stenhouse 2018). This ensures sufficient spatial coverage while allowing some leeway 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.

During sampling design, funding partners expressed interest in learning more about the possible movements of grizzly bears across Highway 43 (Figure 2), which forms the southern boundary of BMA 7. To gather more data on this question, we established sampling grid cells on either side of this transportation corridor. There were 12 grid cells that were established to the south and north of Highway 43.

Field Data Collection

Site Selection

We selected site locations based on the 200-cell 7×7 km grid system (Figure 2). We designed the grid to reflect core and secondary grizzly bear conservation areas (Nielsen et al., 2009), and sampled every cell in the core areas, a reduced portion of the secondary areas, and an extended area on the southern side of Highway 43. The sampling design was similar to that employed in the 2014 BMA 3 population inventory (Boulanger and Efford, 2014; Stenhouse et al., 2015) and in the BMA 4 population inventory in 2018.

One hair snag site was placed in each grid cell. 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 (Boulanger and Efford, 2014; Stenhouse et al., 2015). We generated site locations in a geographic information system (GIS) prior to fieldwork using a grizzly bear resource selection function (RSF) model (Nielsen et al., 2002), aerial photographs, and expert opinion. Preference was given to areas of high RSF and reasonable access for field crews. In the field, we targeted site locations near riparian areas, linear clearings, natural meadows, and forestry cutblocks. Research has shown that placing sites in these areas is important for maximizing detection at fixed hair snag sites (Rovang et al., 2015). To minimize the risk of bear-human encounters and to address public safety concerns, sites were also placed at least 200 m from roads, pipelines, and heavily used seismic lines (i.e. ATV trails), and 500 m from facilities (e.g. wellsites, industrial camps, trapper cabins, campgrounds, or private homes).

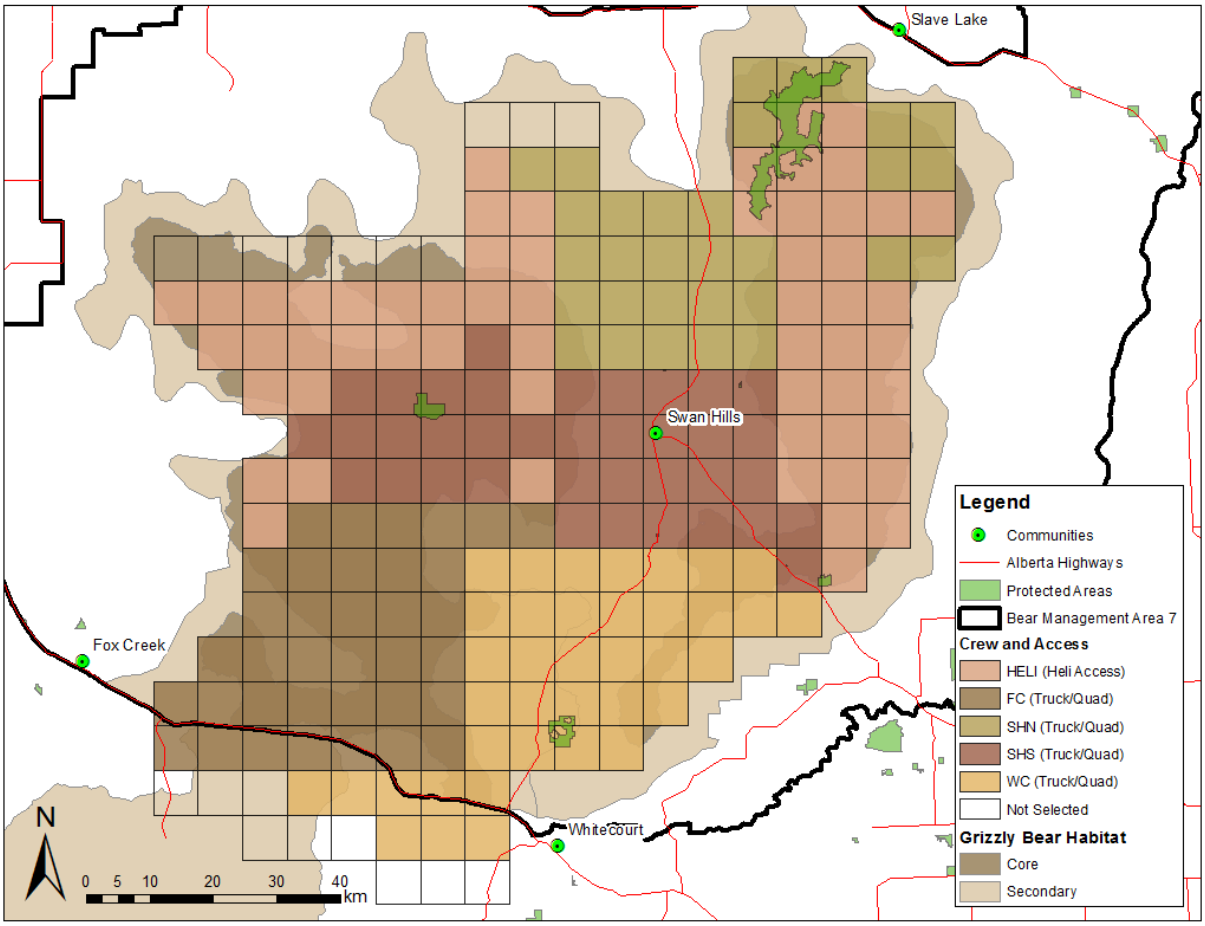

Figure 2: DNA sampling grid used in the grizzly bear population inventory of the Swan Hills Bear Management Area (BMA 7) in 2018 (200-cells) including crew areas and access.

Site Set-Up and Sampling

We built hair snag sites (corrals) using approximately 30 m of barbed wire strung around 3-6 trees at a height of 55 cm above ground following protocols adapted from previous studies (Boulanger et al., 2006, 2005; Woods et al., 1999). We constructed a scent lure pile in the center of corrals using branches, rotten wood, and other forest debris, topped with a thick layer of moss or other absorbent material available at the site. Corrals were large enough that the lure pile could be reached only when a bear crossed over or under the barbed wire. Uneven ground (low or high spots) below the wire was filled or obstructed to prevent bears from entering the corral without coming into contact with the wire. During site setup and every two weeks thereafter, we baited each site with 2.5 L of scent lure (2 L of aged cattle blood mixed with 500 mL of canola oil), topped with conifer branches to protect the lure from rain. Each site was set up with caution tape and a warning sign to deter the public from entering the sampling area.

Our field season consisted of 5 field sessions from May 22nd to July 25th 2018. Following our first shift of site set-up with no hair collection (Session 0), we checked sites for hair every 14 days for 4 sampling periods (Sessions 1, 2, 3, and 4; with hair collection). Once sites were set up, all sites were sampled each session except two cells (560 and 561) which were visited one day after Session 1 due to flooding, and two additional cells that were not visited at all during Session 1 (413 and 474).

Hair samples were collected and placed in paper envelopes. Each barb on the wire with hair was treated as a single sample that was placed into its own envelope. Hair samples on adjacent barbs were labelled as a group, and groupings were split by one or more empty barbs. Samples from the ground, trees, shrubs and the bait pile were considered as separate groupings. Samples on the wire (but not on a barb) were also a separate grouping, unless known to be immediately adjacent to a barb. Based on these designated groupings, we selected the best hair sample in each group.

During the field season, we implemented a sub-sampling protocol for hair samples which staff could identify as black bear hair with a high degree of confidence due to the high abundance of black bears at sites and the time required for sampling. As of June 20th 2018 (Session 2), barb groups with 2 or more adjacent black bear samples, regardless of the total number of samples at a site were sub-sampled. We selected the best sample for each set of three black bear samples within a barb group. All grizzly bear samples were collected, and any samples that were deemed as potential grizzly bear hair were collected.

We collected data regarding sample location on wires, 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 any remaining hair from the wire with a lighter to ensure that hair found during subsequent visits was from the correct sampling session. Throughout the field season, hair samples were stored with silica desiccant both in the field and in the office.

In this study bear scat samples were searched for at site or collected opportunistically to supplement hair results. Once all hair samples were collected, a 25 m radius from the site center was searched for bear signs (e.g. digging, anting, foraging on vegetation or berry bushes, beds, or scat). Any suspected bear scat found at hair snag sites was collected and documented with additional information (e.g., likelihood of the same bear for multiple scats, scat contents, etc.). Bear scat was sampled using a wooden sampling stick to collect 1 cm^3 of scat. Samples were stored in vials containing silica desiccant. Scat samples were also collected opportunistically during the walk to and from sites and while driving along roads within the grid sampling area. If scat samples were located on a road, the remaining scat was cleared off to prevent duplicate samples.

Sub-Selection of Samples for DNA Analysis

As is the case for most large-scale grizzly bear inventory projects, and because of budget constraints, it was not possible to genotype all hair samples collected during 2018. To select a sub-sample of hair for the DNA analysis, we followed a series of sub-selection criteria based on those previously used for DNA surveys in Alberta (Stenhouse et al., 2015). These sub-sampling criteria have been shown to result in a

minimal reduction of the number of individual bears identified. 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 at least one guard hair, or 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 further criteria were only applied to samples not excluded by the initial screening criteria. 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.

Scat samples were also sub-selected for DNA analysis. Bear scat found at hair snag sites, any scat found on the path to sites, and scat found on roads were selected for genetic analysis. Those samples excluded were samples collected during training and site set-up (session 0).

Lab Methods

In order to gather population estimates and supplement hair analysis results, while also comparing the population estimate capabilities of both method, both hair and scat samples were collected and sent to labs.

Hair samples were sent to Wildlife Genetics International, Nelson, Canada, for genotyping to identify species, gender, and unique individuals. Samples that did not contain sufficient material (no guard hair roots and less than 5 underfur hairs), that were of notably different species (ungulates), or that had a jet-black colouration from root to tip (associated with black bears) were not analysed. DNA was extracted using QIAGEN DNeasy Blood and Tissue kits following standard protocols (Paetkau, 2003a). The lab aimed to use 10 clipped guard hair roots, if available, or up to 30 whole underfur hairs, if needed to supplement guard hairs. Multilocus genotyping was used to analyze the DNA extracts with the established set of 8 ‘Alberta grizzly bear’ markers (7 microsatellites [G10B, G10H, G10J, G10M, G10P, G1A, G1D] plus a ZFX/ZFY sex marker) to identify unique individuals. The samples went through multiple passes and error checking during genotyping (Paetkau, 2003b). An individual was defined for each unique multilocus genotype using the 8-locus analysis to produce full genotypes. The sample that provided the best result for each bear had an additional 13 microsatellites run (CPH9, CXX110, CXX20, G10C, G10L, G10U, G10X, MSUT2, MU23, MU50, MU51, MU59, REN145P07), so each bear had a final

genotype consisting of 20 microsatellites plus a sex marker (Kendall et al., 2009; Paetkau, 2003a; Waits and Paetkau, 2005).

Scat DNA analysis was conducted at NIBIO (Norwegian Institute of Bioeconomy Research) in Ås, Norway. DNA was extracted from the samples, and a species-specific test was conducted to determine the species, identity, and gender of individuals using STR markers. Each sample then underwent a mitochondrial DNA (mtDNA) species-specific test to differentiate grizzly from black bear scat. For all samples identified as grizzly bear, genotypes were determined based on 12 STR markers (G10B, G10J, G10L, G1A, G1D, MU50, G10P, Mu23, Mu51, Mu59, G10X and G10U) and one sex-specific marker (BIK-F XY). Samples determined to have unique profiles were analysed using nine additional STR-markers (GIOH, G10M, G10C, REN145P07, CPH9, CXX20, MSUT2, MSUT6 and CXX110).

For both lab methods, individual profiles were compared with known individuals in the new provincial grizzly bear genetic database.

Analysis Methods

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

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 (Efford, 2019). 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. Therefore, there is no need to adjust for study-area size and closure violation as with previous closed models.

SECR methods model the 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. We conducted an initial analysis with sexes combined to determine the size of the mask needed to control bias in density estimates relative to study area size. We ran the esa.plot and suggest.buffer functions of the R package 'secr' for a g_0(sex), σ (sex) conditional likelihood model. These suggested a buffer width of 26 km to obtain unbiased estimates; estimation is also expected to be unbiased with a wider buffer but computation is then slower for a given spatial resolution. We ran subsequent analyses separately for male and female grizzly bears to test for variation in detection probability at the home range center and scale of movements.

Spatially explicit capture-recapture model fitting had three distinct phases:

1. Tests for temporal, behavioural, and individual 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. Fit strata-specific and other density covariate models, using the most supported model from step 2.

We used terrain ruggedness index (TRI) and canopy closure (CC) as site covariates and evaluated at two spatial scales as potential predictors influencing 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., 2004). In most cases, the site scale was used as a covariate for detection probabilities (g_0) and the home range scale was used as a covariate for the σ scale parameter. For this phase of the analysis, we assumed that grizzly bear 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)
CC	Percent canopy cover

Some sites were not sampled in all sessions and the resulting temporal variation was represented with a binary 'usage' matrix – a series of 1s and 0s for each site indicating the sessions in which it was active (1) or non-active (0). We used a discrete cell size (mask spacing) of 3 km for the habitat mask for all SECR 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 density with spacing of 3.5–2.5 km). Mask cells were categorized according the stratum of their centroid.

To estimate home range centers of the detected bears we used baseline SECR detection models. This approach takes into account the configuration of detectors relative to bear detections as well as modelled sources of variation in detection. It is therefore a better indicator of home range center than the mean locations of where individual bears were detected.

We used 7x7 km cells for our sampling grid with one hair snag site placed per cell. Core grizzly bear habitat and a relatively high proportion of the secondary habitat was sampled.

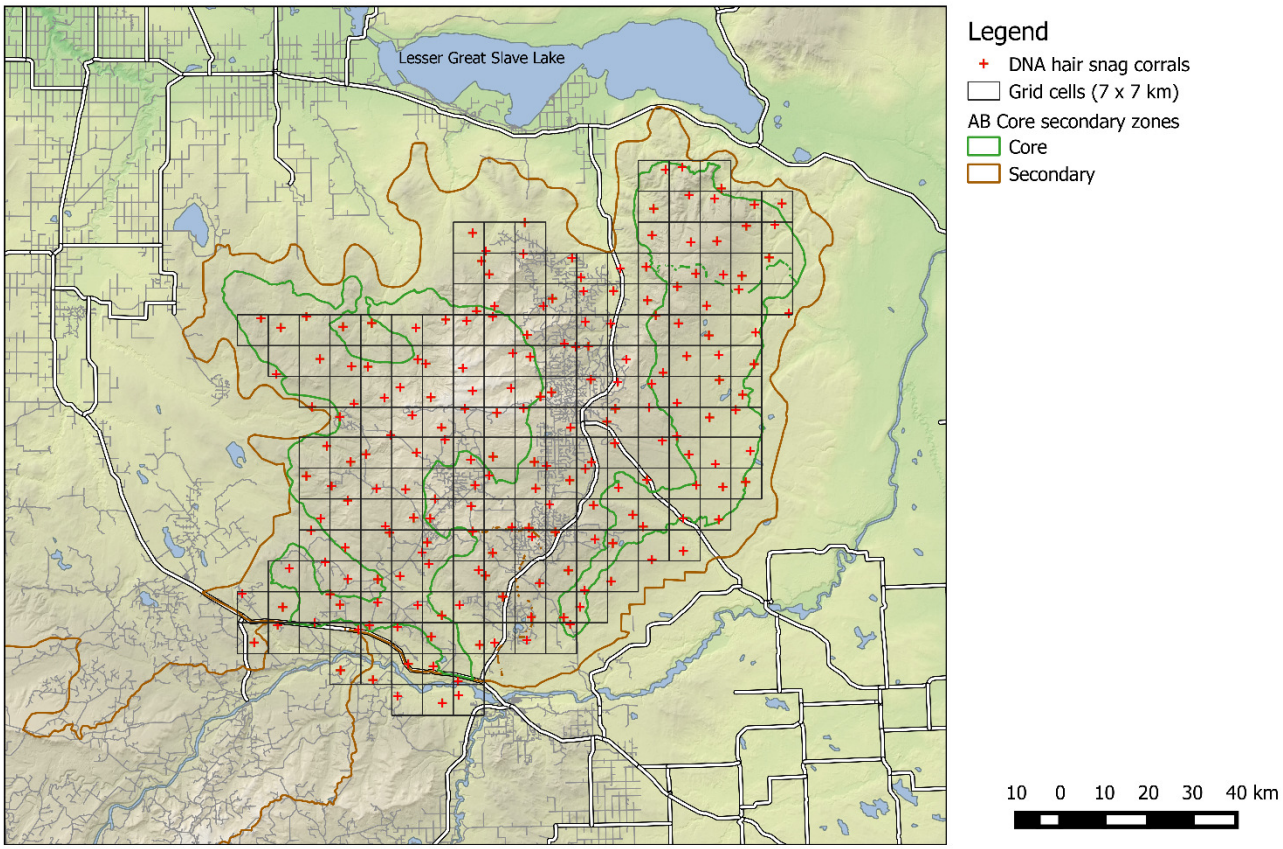

Figure 3: Layout of DNA sampling grids and DNA sites in Swan Hills (BMA 7).

We suspected that the sample size of detected bears available for estimates in the Swan Hills might be limited from past work in this area. Therefore, we also ran a meta-analysis estimation strategy that utilized data from the Grande Cache (BMA 2) inventory project (Figure 4). The BMA 2 survey occurred to the west of Swan Hills in 2008 utilizing a similar sampling design (Alberta Grizzly Bear Inventory Team, 2009; Boulanger et al., 2018). The meta-analysis strategy allows joint pooling of detection parameters with potential gains in estimate precision especially for sparse data sets (Boulanger et al., 2002). This approach tests the support of models with project-specific detection parameters versus models that pool detection parameters between projects.

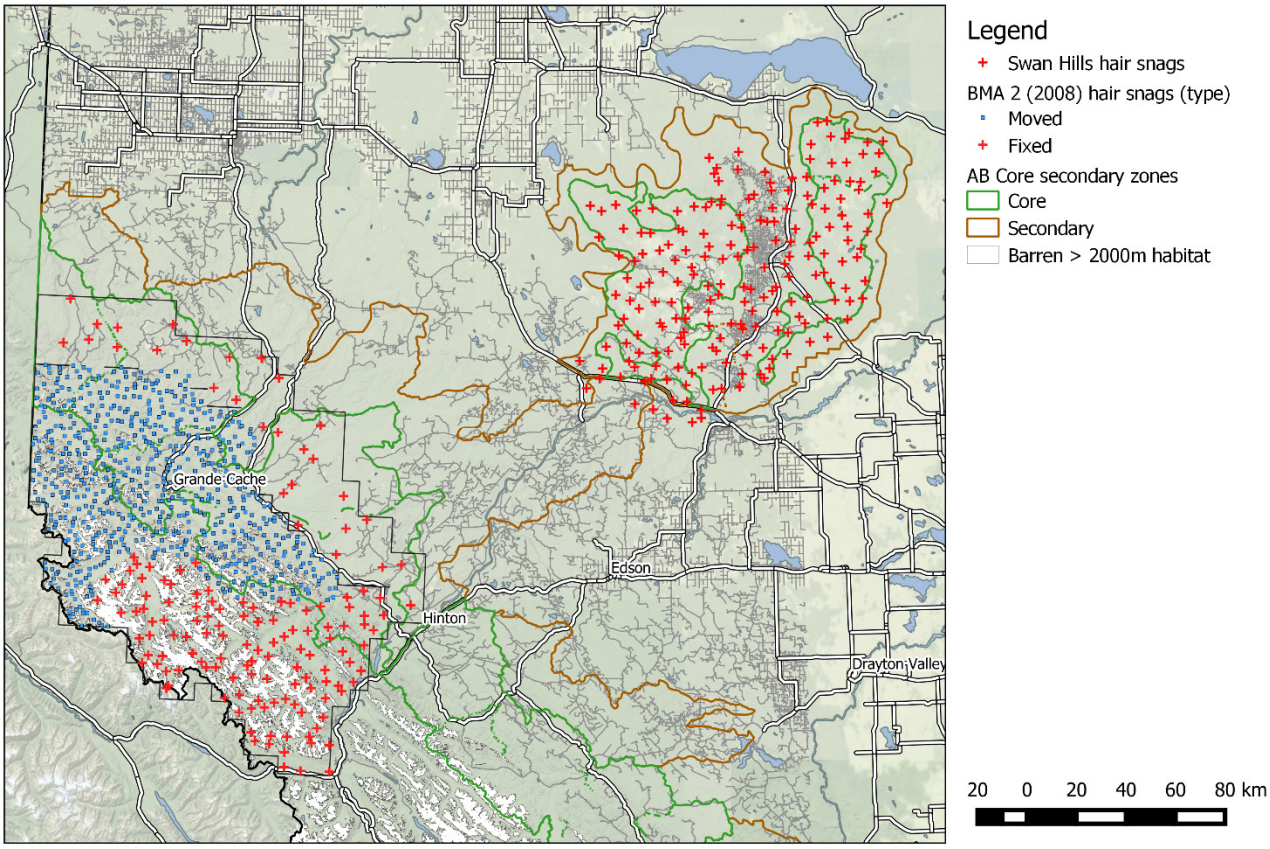

Figure 4: The Grande Cache (BMA 2: 2008) and Swan Hills (BMA 7: 2018) inventory sampling layouts.

We derived expected population size and density estimates from the most supported models for each sex. 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. We generated Log based confidence intervals on expected population size and density using formulas from Efford and Fewster (2013). The precision of SECR estimates is primarily related to the number of bears on the sampling grid and the number of recaptures during sampling (Efford and Boulanger, 2019). The precision of the estimate is indexed by the coefficient of variation (CV_d), which is the standard error of an estimate divided by the estimate. One central question in study design is whether precision of estimates are limited by the number of bears on the sampling grid or by the estimation of detection parameters, which relates to recaptures and the complexity of detection models. To explore this question, we dichotomized the precision of estimates into binomial variation caused by the number of bears detected on the sampling grid (CV_n) in contrast to the variance caused by the estimation of effective sampling area and related detection parameters (CV_a). These two components add up to the

CV of the density estimate using the equation $\mathrm{CV_d} = \sqrt{\mathrm{CV_n^2} + \mathrm{CV_a^2}}$ (Borchers and Efford, 2008; Efford, 2019; Huggins, 1991).

All spatially explicit analyses were done in package *secr* (Efford, 2014a) in the R statistical software (R Development Core Team, 2020). Map and data figures were produced using the *QGIS* program (QGIS Development Team, 2020) and *ggplot* (Wickham, 2009), and *ggmap* (Kahle and Wickham, 2013) R packages.

RESULTS

DNA Sample Extraction Rates from Hair and Scat

Of 6,767 collected samples, 750 hair samples were sent to the Wildlife Genetics International (WGI) lab for DNA analysis. Of these samples, 5% (39/750) were not analyzed because they were visually determined to be black bear or other species, and 8% (58/750) were not analyzed due to lack of sufficient materials. Of the 653 remaining samples analyzed, 93% (607/653) of the samples were successfully identified to the bear species level, with 17% (100/607) determined as grizzly bear and 85% (507/607) determined as black bear (*Ursus americanus*). Of the 100 grizzly bear samples, 93 samples successfully identified unique individuals, and determined to come from 39 unique grizzly bears (18 male and 21 female).

There were 205 scat samples collected by field crews during visits to hair sampling sites and we sent 168 of these samples to the lab. Of these samples, 133 (79%) were determined to be black bears, 10 samples (6%) were from grizzly bears and 25 samples (15%) were from other species. None of the 10 grizzly bear samples could be genotyped to the 7 markers required to identify individuals but all were found at sites where grizzly bear hair was collected. The large number of black bear scats is in line with the large amount of black bear hair collected at the barbwire hair snag sites.

Table 2: Extraction rate comparisons between hair sampling and scat sampling techniques for species and individual level analyses.

	Hair Sampling	Scat Sampling
Number of Samples Collected	6,767	205
Number of Samples Sent to the Lab	750	168
Number of Samples Analyzed	692	168
Percentage of Samples Identified to Bear Species	93% (607/653)	85% (143/168)
Percentage of Samples Determined Grizzly Bear	17% (100/607)	7% (10/143)
Percentage of Samples Determined Black Bear	85% (507/607)	93% (133/143)
Percentage of Grizzly Bear Samples Identified to Individual	93% (93/100)	0% (0/10)
Number of Individual Grizzly Bears	39	0

Sampling and Distribution of Bear Species in BMA 7

Of the 200 sites in BMA 7, 94% of sites had bear hair collected from them at least once during the hair collection sessions. One site only had grizzly bear hair while all other sites had either only black bear hairs, or black bear and grizzly bear hairs (Figure 5).

We found suspected bear scat at 17% of sites, while there was no scat found at 83% of sites (Table 2). Additional scat samples were encountered and collected along the path to hair snag sites, ATV trails, and roads within the study area (Figure 6).

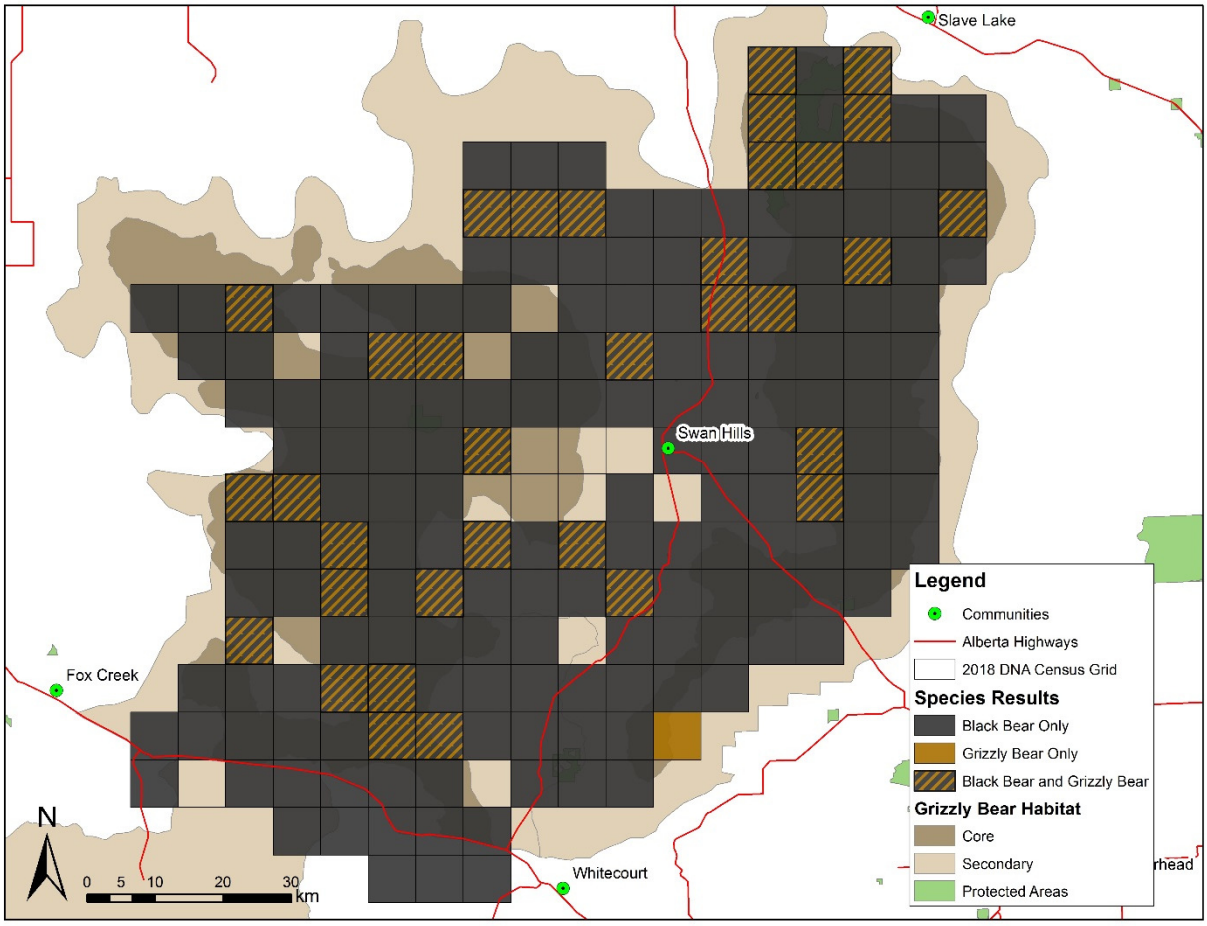

Figure 5: Bear species sample locations across the Swan Hills BMA (BMA 7). Black bear results include lab results and black bear samples that were not sent to the lab, but were identified with a 90-100% confidence level in the field. Grizzly bear results include all samples identified at the species and individual level from the lab.

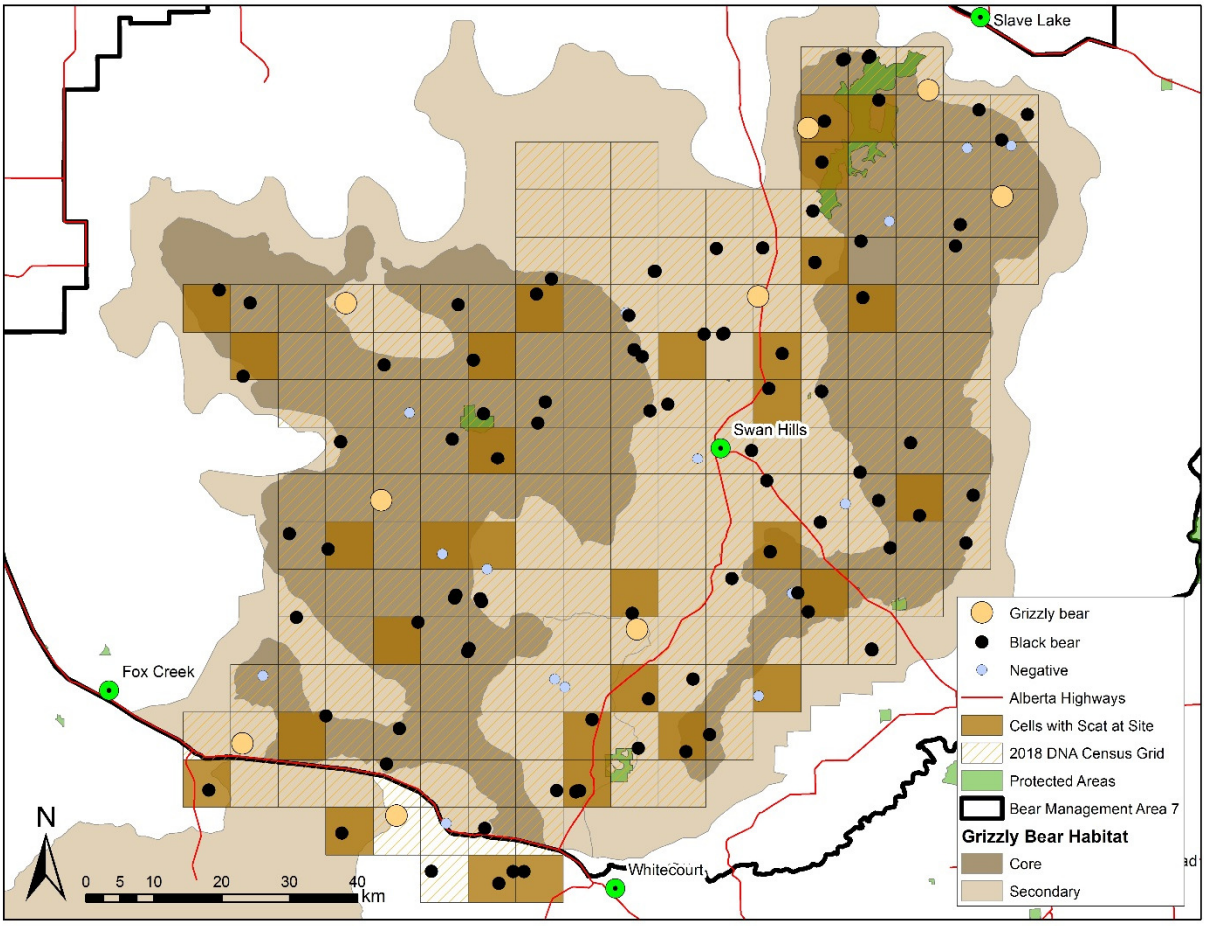

Figure 6: Location of scat samples, the bear species they represent, and the grid cells with scat samples found at hair snag sites in 2018 during the DNA inventory of the Swan Hills Bear Management Area (BMA 7). Negative samples indicate samples that were identified as neither black or grizzly bear.

Data Summary for Population Analysis – Hair

Overall, 39 grizzly bears (21 females and 18 males) were detected during this inventory. The number of bears detected increased in latter sessions, especially for females. We detected 5 bears in more than one session, with only one male detected in more than one session. The number of new bears detected was highest in session 4, suggesting that sampling efficiency was moderate to low (Table 3).

Table 3: Summary statistics for BMA 7 inventory.

Statistic	1	2	3	4	Total
Females + Males					
Animals detected (nj)	8	5	13	19	45
Newly detected (uj)	8	5	12	14	39
Total individuals detected (Mj)	8	13	25	39	39
Frequencies of detections (fj)	34	4	1	0	39
Unique detections	8	5	13	20	46
Detectors visited	5	5	13	13	36
Females					
Animals detected (nj)	2	3	10	11	26
Newly detected (uj)	2	3	9	7	21
Total individuals detected (Mj)	2	5	14	21	21
Frequencies of detections (fj)	17	3	1	0	21
Unique detections	2	3	10	11	26
Detectors visited	2	3	10	8	23
Males					
Animals detected (nj)	6	2	3	8	19
Newly detected (uj)	6	2	3	7	18
Total individuals detected (Mj)	6	8	11	18	18
Frequencies of detections (fj)	17	1	0	0	18
Unique detections	6	2	3	9	20
Detectors visited	4	2	3	8	17
Detectors employed	190	190	192	192	764

The low redetection frequencies and the relatively large number of new bears detected in session 4 was anomalous compared to other grizzly bear DNA mark-recapture projects (Figure 7). The curve of detections of new bears per session was low and as a result, 74% of bears detected in session 4 had not been previously detected (Figure 7). This contrasts with the 2018 BMA 4 grizzly bear inventory project results which found that 60% of bears detected in session 4 were new bears.

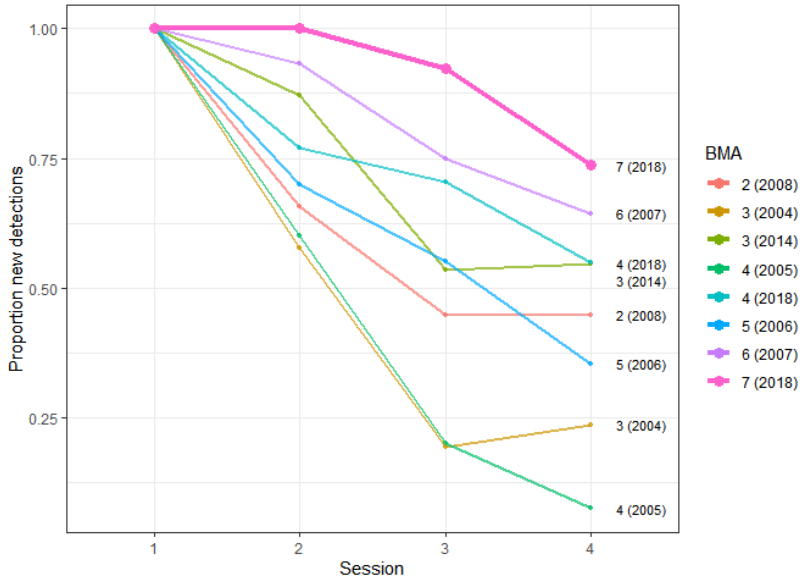

Figure 7: Comparison of the sampling efficiency of DNA inventory projects indicated by the proportion of new bears detected by session.

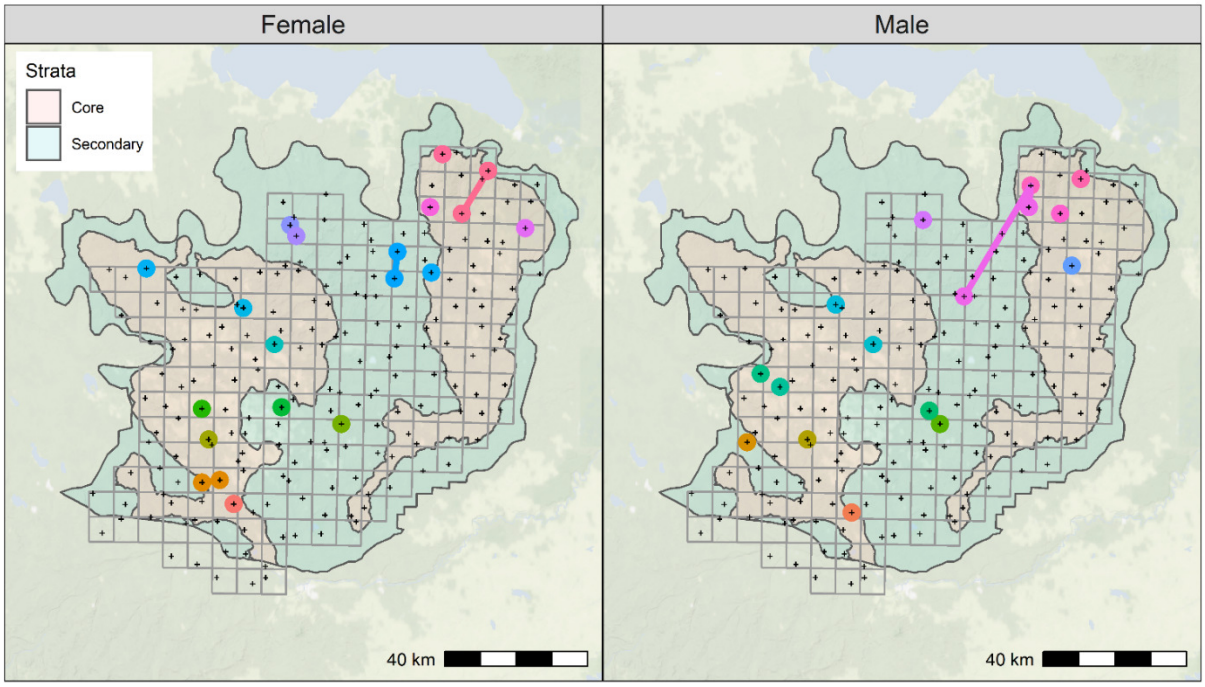

Figure 8: Detections and redetections for all sessions of male and female grizzly bears on the BMA 7 sampling grid. A line connects redetections.

The locations of detections and redetections of male and female bears suggests detections in both core and secondary areas with few movements detected (Figure 8).

A plot of detection frequencies per site (Figure 9) reveals two sites in session 4 where 3 bears were detected, indicating detection of potential family groups. In most other sessions, all sites detected single bears with the exception of one site in session 1 where 3 bears were detected.

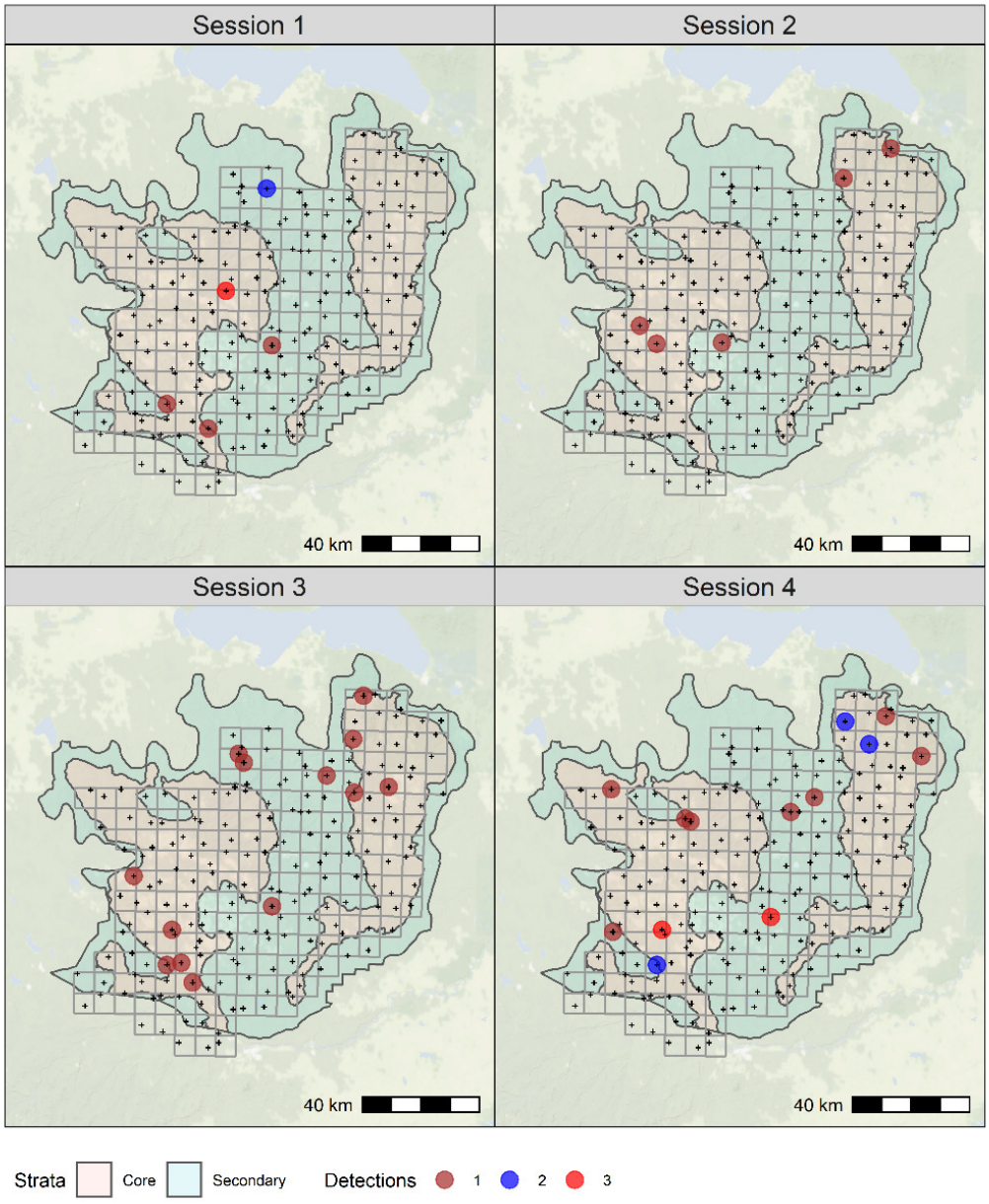

Figure 9: Spatial distribution of hair snag sites (+ signs) and frequencies of bears detected at sites for each sampling session.

One potential factor that may have reduced rates of detection of grizzly bears was the large proportion of sites that were visited by black bears during sampling (Figure 10). While visitation of sites by grizzly bears and black bears is expected to occur, the high visitation rates of black bears might have reduced the likelihood of obtaining grizzly bear hair if barbs on wires were already saturated with black bear

hairs. It is also possible that the high number of black bears at sites reduced the attractiveness of lures for grizzly bears, especially for females or family groups. The number of sites visited by black bears, as assessed by field identification of hair, was 93, 115, 130, and 153 sites of the 198-200 sites in each session. The proportion of sites visited by black bears therefore increased from 32% (64/198) to 58% (153/200) from session 1 to session 4. Overall, of 796 site visits, 573 had hair deposited on the hair snags. Of these 573 visits, 516 (90%) had occurrences of black bears as determined by field staff and/or genetic identification of hair samples.

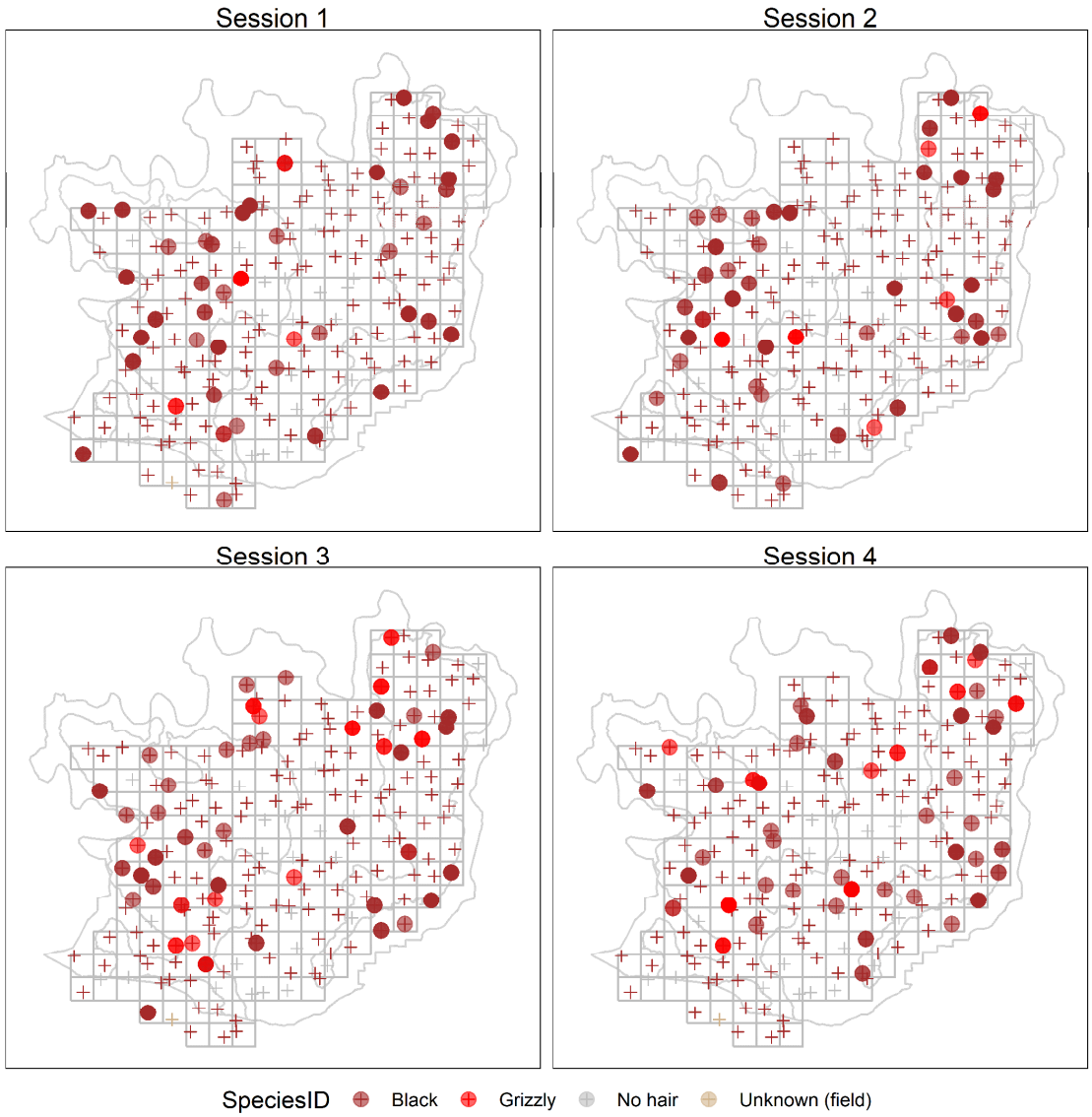

Figure 10: Occurrence of black bears as denoted by field detection of black bear hair (brown + signs) or genetic identification of grizzly bear hair (brown dots) in comparison to grizzly bear detections (red dots) by session. Grey + signs denote sites where no hair was detected. Unknown (field) pertains to hair detected at sites but not classified as black or grizzly bear. Note that only a subset of sites where black bears hair is detected are genotyped.

Another potential reason for the larger number of new bears detected in session 4 was the possible presence of cubs that may have displayed lower detection probabilities, in earlier sessions. Our parentage analysis found that 2 sites with 3 grizzly bear detections were likely family groups (Table 5). This potentially created a violation of demographic closure, which is the assumption that all bears in the study area are available for detection in all sessions (if cubs had 0 probability of detection in earlier sessions). If the family groups were not available for detection in previous sessions due to the low height of cubs relative to the barbed wire, or if only the mother of the family group was available for detection

in earlier sessions, then our estimates could be biased high. We cannot conclude definitively that cubs were not available, or whether these young were cubs of the year or yearlings (yearlings would have been more detectable because of their larger size), however, given the low redetection frequencies across sessions in the data set, we felt that this topic was worthy of further investigation. We note that spatially explicit methods confront geographic closure (bears moving in and out of the study area during sampling) but are not robust to violation of demographic closure. To assess sensitivity of estimates to this issue, we ran the most supported models with the cubs detected in session 4 included and excluded.

Table 4: Relationships between grizzly bears that were detected at the same site and session during the Swan Hills inventory. Of particular interest were potential cubs that were detected in session 4 and highlighted in red.

Names	Session	Relationship
221-258-2D-4 (m) 221-258-2H-4 (f) 221-258-1A-4 (mom)	4	Likely parent offspring Detected by both Parente and Relate Likely cubs-of-the-year
500-1014-2D-2 (m) 530-1061-1E-4 (m)	4	No relation in both Parente and Relate
161-134-1B-1 (f) 162-143-1C-3 (f)	4	Full siblings by Relate Could be 2-year-olds or independent young
227-288-1A-4 (mom) 227-288-1K-4 (F) 227-288-2L-4 (m)	4	Likely parent offspring Detected by both Parente and Relate Likely cubs-of-the-year
314-507-1D-1 (m) 314-507-1F-1 (f) 314-507-8F-1 (m)	1	Unclear; no relation in Parente but Relate shows 314-507-1F-1 (f) and 314-507-1D-1 (m) as parent offspring
466-944-2A-1(m) 466-944-2B-1 (m)	1	No relation
501-1019-1D-4 (m) 562-1098-2D-2 (f)	4	No relation

Stand-alone Analysis of Swan Hills

Lower sample sizes of male redetections (1 of 17 males was detected in more than one session) precluded sex-specific modelling. As an alternative, sex was modelled using a mixture-model approach that allowed us to incorporate sex-specific detection functions and allowed for estimation of sex-specific density using full-likelihood models.

Initial model selection focused on parsimonious detection models, followed by modelling the density variation within the sampled area. Models with trap-specific covariates were considered, however, sparse recaptures resulted in unstable estimates from these models and they were not considered further. However, these trap-specific covariates were considered again in the meta-analysis. Of all detection models considered, the model with sex-specific detection at the home range center and sex-

specific movement (σ) was supported, with σ increasing linearly with sessions (as symbolized by a *T* term; Model 1, Table 5). As a next step, we modelled density variation on the sampling area, however, none of the density surface models were more supported than the constant density model (presumably due to sparse data). A model with density varying by RSF score was tied for support, further re-affirming the delineation of the sampling area using core/secondary and RSF scores (Figure A1).

Table 5: Model selection for stand-alone analysis of Swan Hills BMA 7 data set. 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. A half-normal detection function was used for the analysis.

No	Density	Detection at HR center (g_0)	Scale (σ)	AIC_c	ΔAIC_c	w_i	K	LL
1	constant	sex	sex+T	470.14	0.00	0.26	7	-226.3
2	constant	sex+trend	sex	470.70	0.56	0.20	7	-226.5
3	RSF	sex	sex+T	470.94	0.80	0.18	8	-225.1
4	strata	sex	sex+T	471.94	1.80	0.11	8	-225.6
5	RSF+RISK	sex	sex+T	472.35	2.21	0.09	9	-224.1
6	RISK	sex	sex+T	472.51	2.37	0.08	8	-225.9
7	constant	sex+session	sex	474.61	4.47	0.03	9	-225.2
8	RSF*RISK	sex	sex+T	476.00	5.86	0.01	10	-224.1
9	constant	sex	sex	476.16	6.02	0.01	6	-230.8
10	constant	sex+sessions2&3	sex	476.82	6.68	0.01	7	-229.6
11	RSF	sex	sex	477.15	7.01	0.01	7	-229.8
12	constant	sex	sex+t23	477.28	7.14	0.01	7	-229.8
13	strata	sex	sex	477.51	7.37	0.01	7	-229.9
14	constant	sex+T	constant	479.14	9.00	0.00	6	-232.3
15	constant	bk+t	constant	479.69	9.55	0.00	5	-233.9
16	constant	t	constant	480.25	10.11	0.00	7	-231.3
17	constant	sex+bk	constant	481.58	11.44	0.00	6	-233.5
18	constant	sex+t	constant	482.73	12.59	0.00	8	-231.0
19	constant	constant	sex	482.82	12.68	0.00	5	-235.5
20	constant	constant	constant	482.85	12.71	0.00	4	-236.8

We estimated the locations of home range centers using the most supported model (Figure 11), revealing a relatively even spread of centers across the full sampled area with home range centers in both core and secondary areas. The actual locations were similar to detection locations given that few bears were recaptured.

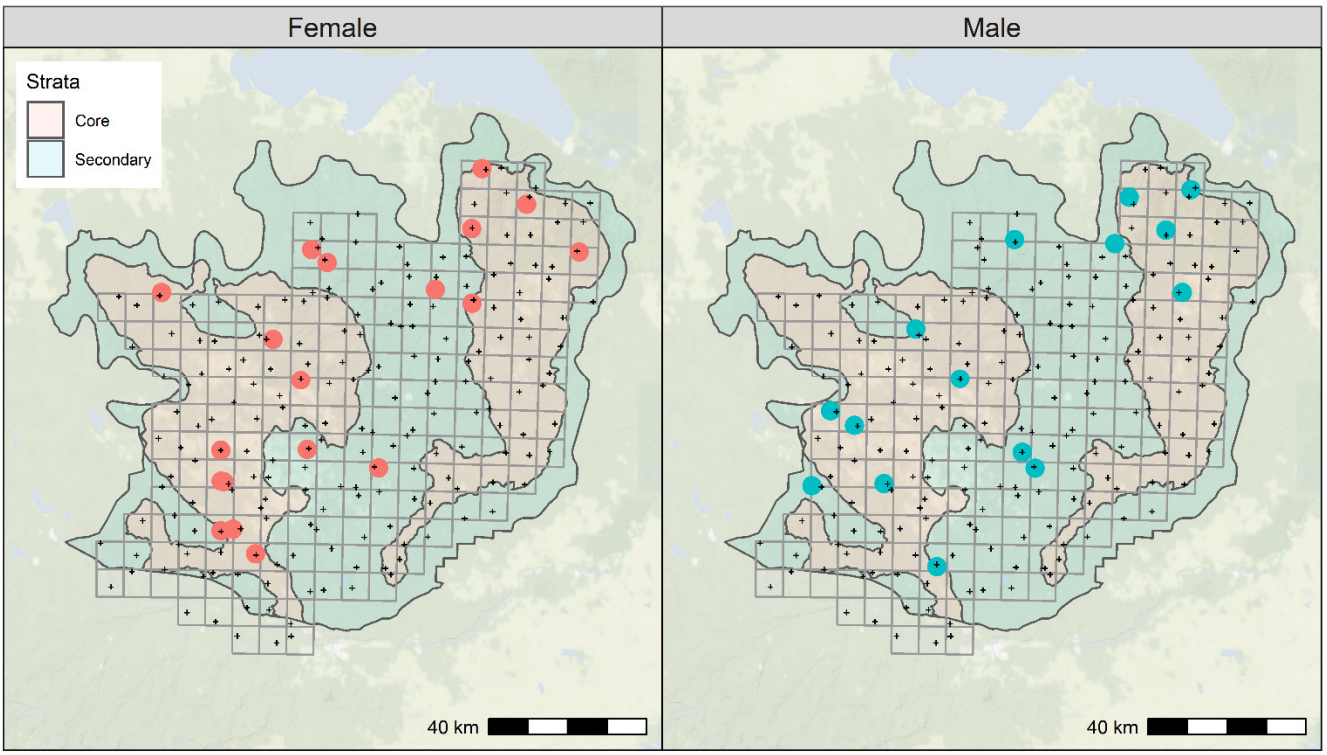

Figure 11: Estimated home range centers for female and male bears detected in the Swan Hills inventory.

Meta-analysis of Swan Hills and Grande Cache Data Sets

One of the challenges with the stand-alone analysis of Swan Hills was the low number of redetections, especially for males, that challenged valid estimation of scale of movement. The meta-analysis approach with BMA 2 allowed us to incorporate additional information from the BMA 2 data set, which could potentially refine detection parameter estimates for the Swan Hills. This approach also allowed a sensitivity analysis of estimates to detection by running a model that assumed similar detection functions for BMA 7 and BMA 2. We used a conditional likelihood approach was used for the analysis which allowed flexible modelling of sex-specific detection functions across the two BMA sampling areas. This approach does not directly estimate density but does allow density estimates as a derived parameter.

One of the key objectives of the meta-analysis was to develop models that would allow joint modelling of sex-specific detection functions across BMAs without the use of BMA-specific detection terms. If this could be achieved, the effect sample size used for detection would be the combined sample size of BMAs. To facilitate this, we used hair snag site covariates in the analysis, in addition to traditional covariates. We also considered covariates pertaining to whether a site was fixed or moved each session.

Of models considered, a model with BMA-specific detection at home range center with the additive effects of sex and canopy cover was the best model. Spatial scale (σ) was influence by terrain ruggedness index (TRI) of sites and sex (Table 6, model 1). A model that did not include BMA was less supported (Table 6, model 3).

Table 6: Model selection for meta-analysis 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. A half-normal detection function was used for the analysis.

No	Detection at HR center (g_0)	Scale (σ)	AIC_c	ΔAIC_c	w_i	K	LL
1	BMA+Sex+CC	Sex+TRI	4368.68	0.00	0.92	7	-2177.2
2	BMA+Sex	Sex+fix*Sex	4374.89	6.21	0.04	7	-2180.3
3	Sex+CC	Sex*TRI	4376.04	7.36	0.02	7	-2180.8
4	BMA+Sex+Fixsite	Sex	4378.55	9.87	0.01	7	-2182.1
5	BMA+Sex+Fixsite	Sex	4380.14	11.47	0.00	6	-2183.9
6	BMA+Sex	Sex+TRI	4383.62	14.94	0.00	6	-2185.7
7	BMA+Sex	Sex	4383.79	15.12	0.00	5	-2186.8
8	BMA+Sex	Sex	4383.79	15.12	0.00	5	-2186.8
9	BMA+Sex	Sex	4384.83	16.15	0.00	6	-2186.3
10	BMA+Sex	BMA+Sex	4385.60	16.93	0.00	6	-2186.7
11	BMA*Sex	BMA*Sex	4385.78	17.10	0.00	8	-2184.6
12	BMA+Sex	BMA+Sex	4386.73	18.06	0.00	7	-2186.2
13	Sex+CC	Sex+TRI	4388.01	19.34	0.00	6	-2187.9
14	Sex+CC	Sex	4396.24	27.56	0.00	5	-2193.0
15	Sex	BMA+Sex	4399.70	31.03	0.00	5	-2194.8
16	Sex	Sex	4416.80	48.13	0.00	4	-2204.3
17	Sex+fix	Sex	4418.86	50.18	0.00	5	-2204.3
18	constant	Sex	4467.35	98.67	0.00	3	-2230.6
19	Sex	constant	4546.88	178.20	0.00	3	-2270.4
20	constant	constant	4548.74	180.06	0.00	2	-2272.3

Plots of detection functions for BMA 2 and the Swan Hills from model 1 illustrate the large difference in detection at home range centers for BMAs with similar overall scales of movement (Figure 12). This result highlights the main distinction of the Swan Hills BMA, which is that bears were less likely to be detected regardless of trap placement. Covariates such as canopy cover also influenced detection of bears; however, the effect of site covariates could not explain differences in detection between BMA 2 and the Swan Hills.

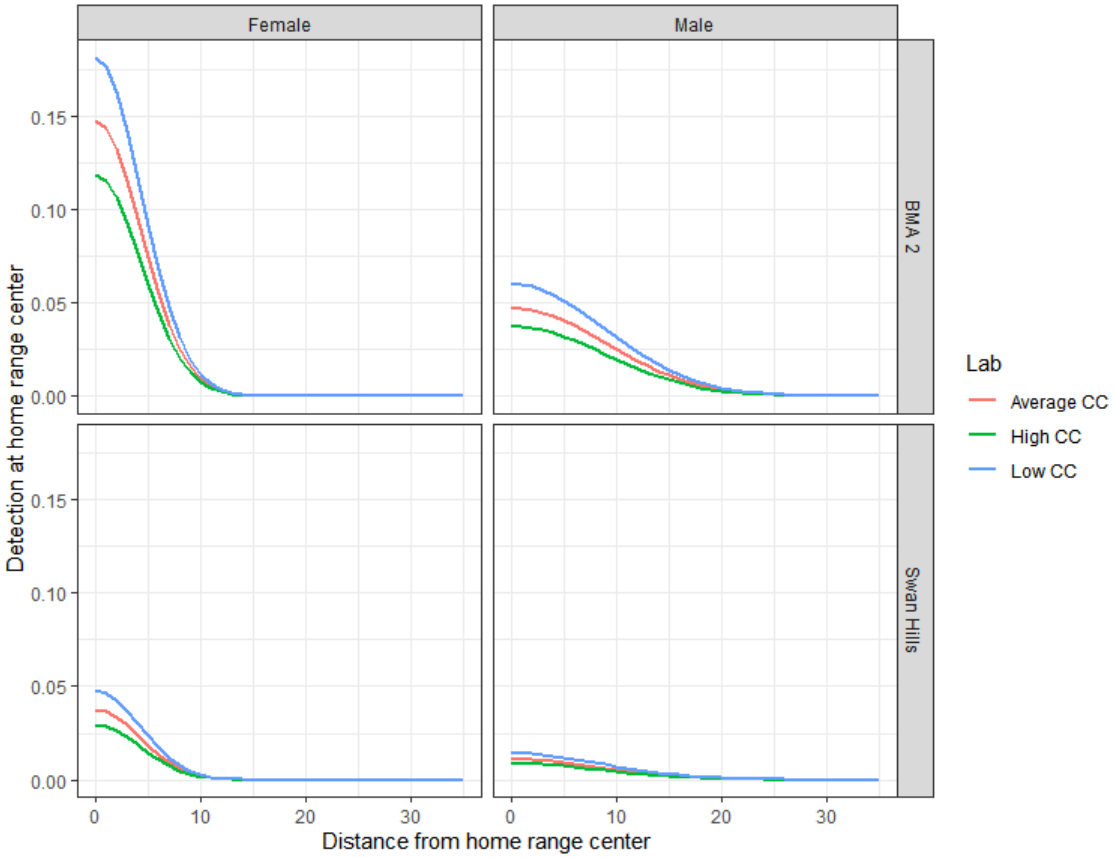

Figure 12: Detection functions from Grande Cache (BMA 2) inventory (2008) and Swan Hills (BMA 7) inventory in 2018.

Estimates of Density and Average Number of Bears in Core and Secondary Areas

We estimated the average numbers of bears by multiplying the estimated density by the area of core and secondary habitat (11,984 km^2) in the BMA 7 under the assumption that bear home range centers would be located in this area. Estimated home range centers, which all fell within the core and secondary area (Figure 11), along with gradients in bear habitat, suggest that this assumption was justified (Figure A1).

Estimates from the stand-alone and meta-analysis of grizzly bears resulted in a density of bears of 12.6 bears per 1,000 km^2, and a corresponding average estimated number of bears of 150–152 in core and secondary areas. The precision of estimates was low (CVs of 35–41%). The meta-analysis improved precision of estimates, especially for males, which had limited detections in BMA 7. Components of precision suggest, precision due to the number of bears detected CV_n was reasonable with CV_ns of 15–20%. The main factor reducing precision was the estimation of detection parameters (CV_a), which

ranged from 32–64%. Basically, the low numbers of redetections was the primary factor associated with low precision of estimates.

Table 7: Estimates for the Swan Hills BMA from the meta-analysis (with BMA 2) and for a stand-alone analysis. The full data set, including cubs detected in session 4 was used for estimates. Estimates were based on the most supported models from each analysis. Density is expressed as bears per 1,000km^2. Precision components pertain to the contribution of sample size of bears detected (CV_n), the estimation of detection parameters (CV_a) and the overall precision (CV_D).

Analysis/sex	Average bears in core/secondary area				Density (bears per 1,000km^2)				Precision components		
	Ave N	SE	Conf. Limit		Density	SE	Conf. Limit		CV_n	CV_a	CV_D
Meta-analysis											
Females	88.8	33.2	43.7	180.3	7.41	2.77	3.65	15.04	0.20	0.32	0.37
Males	61.6	23.6	29.9	127.1	5.14	1.97	2.49	10.60	0.21	0.32	0.38
Males+Females	150.4	51.9	77.9	290.2	12.55	4.33	6.50	24.22	0.15	0.31	0.35
Stand-alone analysis											
Females	68.3	27.2	32.2	144.9	5.70	2.27	2.69	12.09	0.20	0.35	0.40
Males	83.4	56.4	25.1	277.7	6.96	4.71	2.09	23.17	0.22	0.64	0.68
Males+Females	151.7	62.8	69.6	330.9	12.66	5.24	5.81	27.61	0.15	0.39	0.41

As noted earlier, we had a potential issue with demographic closure due to cubs that may have been detected in session 4 but likely had lower or no detection in earlier sessions. We removed these 4 cubs (Table 4) but retained the mother bears and re-ran the most supported models from each analysis. Removing the cubs from session 4 resulted in a reduction of overall estimates by approximately 30 bears, demonstrating the potential effect of demographic closure on these population estimates, and the sparse nature of the data set. Namely, when detection rates are low, individual detected bears have a high influence on estimates (Table 8 and Figure 13).

Table 8: Estimates for Swan hills with cubs detected in session 4 removed. Density is expressed as bears per 1,000km^2. Precision components pertain to the contribution of sample size of bears detected (CV_n), estimation of detection parameters (CV_a) to overall precision (CV_D).

Analysis/sex	Average bears in core/secondary area				Density (bears per 1,000km^2)				Precision components		
	Ave N	SE	Conf. Limit		Density	SE	Conf. Limit		CV_n	CV_a	CV_D
Meta-analysis											
Females	70.6	26.1	35.0	142.3	5.89	2.17	2.92	11.87	0.21	0.31	0.37
Males	48.0	18.2	23.4	98.6	4.01	1.52	1.95	8.22	0.22	0.31	0.38
Males+Females	118.6	40.2	62.1	226.4	9.90	3.36	5.19	18.89	0.15	0.30	0.34
Stand-alone											
Females	55.8	21.9	26.6	117.1	4.66	1.82	2.22	9.77	0.21	0.33	0.39
Males	64.3	42.7	19.6	210.2	5.36	3.56	1.64	17.54	0.23	0.62	0.66
Males+Females	120.1	48.1	56.4	255.9	10.02	4.02	4.70	21.36	0.16	0.37	0.40

Figure 13 provides a graphical interpretation of estimates and demonstrates the relative agreement of the meta-analysis and stand-alone estimates and the improvement of precision of the male estimate for the meta-analysis. Finally, the reduction in estimates by removal of cubs in session 4 is demonstrated in the context of overall certainty in estimates (as indicated by more narrow confidence limits).

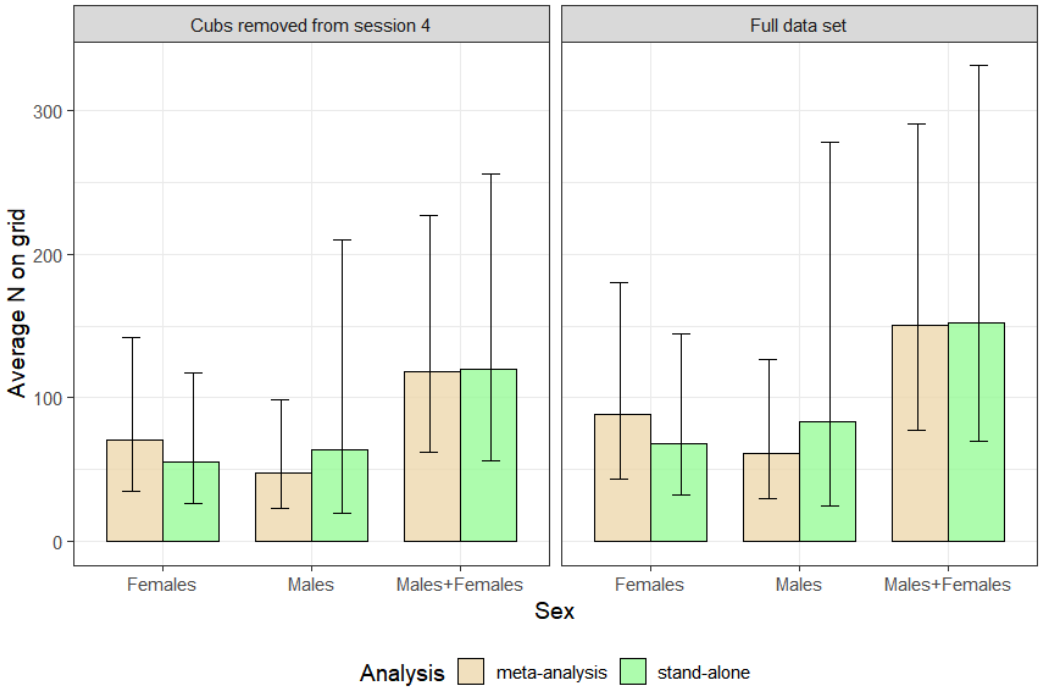

Figure 13: Comparison of estimates from the meta-analysis and the stand-alone analysis that included detection data from BMA 2.

One final estimate considered was from the meta-analysis where a similar detection function for BMA 2 and the Swan Hills was assumed (Table 6, model 3). More exactly, the model assumes that the differences in detection was primarily due to differences in canopy cover and terrain ruggedness in grid areas rather that BMA-specific differences. The support of model 3 was marginal for the full data set, however, support for this model increased when cubs in session 4 were removed (ΔAIC_c=2.68, w_i=0.20). The resulting estimates ranged from 56 to 64 bears and densities of 3.5 to 5 bears per 1,000 km^2 with a noted increase in precision. Figure 14 shows the range of density estimates from the meta-analysis.

Table 9: Estimates for Swan Hills from meta-analysis assuming similar sex-specific detection functions for BMA 2 and the Swan hills. Density is expressed as bears per 1,000km².

Analysis/sex	Average bears in core/secondary area			Density (bears per 1,000km²)			Precision components		
	Ave N	SE	Conf. Limit	Density	SE	Conf. Limit	CV_n	CV_a	CV_D
Full data set									
Females	37.7	7.0	26.3 54.2	3.15	0.59	2.19 4.52	0.17	0.07	0.19
Males	25.9	4.8	18.0 37.3	2.17	0.40	1.51 3.11	0.17	0.07	0.19
Males+Females	63.7	8.8	48.6 83.4	5.31	0.74	4.05 6.96	0.12	0.06	0.14
Cubs removed from session 4									
Females	33.3	6.4	22.9 48.5	2.78	0.54	1.91 4.05	0.18	0.07	0.19
Males	22.5	4.4	15.4 32.8	1.88	0.36	1.29 2.74	0.18	0.07	0.19
Males+Females	55.8	8.0	42.2 73.9	4.66	0.67	3.52 6.17	0.13	0.06	0.14

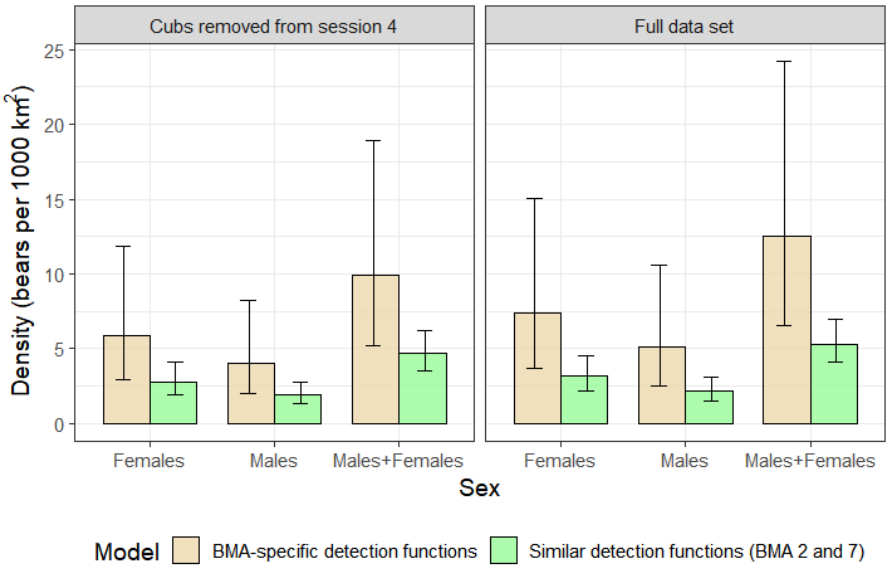

Figure 14: Estimates of density from the meta-analysis with and without session 4 cubs removed. In addition, estimates from a model that assumes similar detection functions for BMA 2 and Swan Hills are displayed.

Comparison of the Swan Hills Density with Other BMAs

The Swan Hills inventory had lower sampling efficiency than other DNA based inventories conducted in Alberta, as indicated by the low proportion of bears detected in more than one session and the comparatively high proportions of new bears detected each session (Figure 7). As a result, the precision of density estimates was lower (Table 9).

The estimated density for the Swan Hills is in the range of other BMAs sampled in Alberta (Figure 15). Two estimates are shown for Swan Hills; one with the full data set and one with session 4 cubs removed.

Table 10: Summary of most recent estimates from Alberta BMAs along with density estimates. Efficiency is the number of bears detected in more than one session divided by the total number of bears detected. Estimates from surveys prior to 2014 are summarized in Boulanger et al. (2018). The 2014 BMA 2 survey is summarized in Stenhouse et al. (2015) and the 2018 BMA 4 survey is summarized in Stenhouse et al. (2020).

BMA	BMA name	Year	Bears detected			Efficiency	Density				
			F	M	Total		Estimate	SE	Conf. Limit		CV
2	Grande Cache	2008	161	108	269	0.45	17.10	0.89	14.88	19.66	0.05
3	Yellowhead	2014	45	63	108	0.47	7.71	1.09	5.86	10.15	0.14
4	Clearwater	2018	29	36	64	0.28	9.23	1.35	6.25	13.67	0.15
5	Livingston	2006	45	40	85	0.42	9.98	1.07	7.43	13.41	0.11
6	Castle	2007	13	19	32	0.19	12.59	2.81	7.12	22.46	0.22
7	Swan Hills (full)	2018	21	18	39	0.13	12.55	4.33	6.50	24.22	0.35
7	Swan Hills (no cubs)	2018	21	18	39	0.13	9.90	3.36	5.19	18.89	0.34

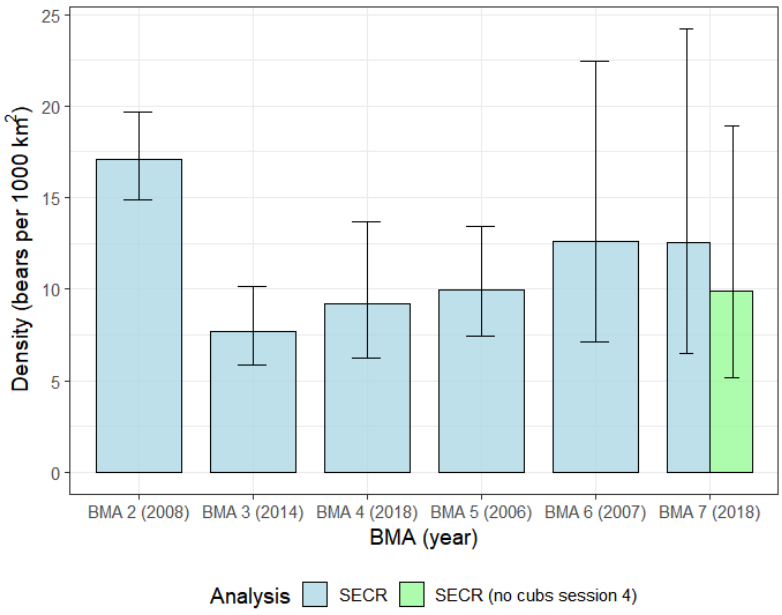

Figure 15: Estimated density from other BMAs compared.

Parentage and Detailed Genetic Analysis Results

The 39 genotypes found from the collected hair samples were compared with all available genetic samples of grizzly bears from across the province (WGI unpublished data; Graham and Stenhouse 2019) to determine if any of these bears were previously known. This analysis found that all genotypes were new bears, except for one that matched a bear from a "Swan River" 2018 project where the sample was collected within BMA 7 following our own sampling sessions.

A parentage analysis using software *Parente* was also performed by WGI as a way to check for possible errors in scoring. The program highlights perfect matches as mother-father-offspring triads and triads that mismatch at 1 or 2 markers. Any mismatched markers were then double-checked to ensure that an error was not made. In conducting this error check, we found one grizzly bear (G278), which had been previously captured and collared in the Grande Cache BMA in the spring of 2012 as an adult and again in 2017, who originated from parents in the Swan Hills BMA (Figure 17). No genetic matches were found for grizzly bears that were captured and collared in the Swan Hills area from 2005 to 2006 (n=10) as part of our long term research program. This compares to 10 bears in the BMA 4 2018 inventory that matched as previously known bears from a 2005 inventory effort (Stenhouse et al., 2020). We do know that, of the 10 previously collared research bears in the BMA 7, 3 died before the 2018 inventory and 1 bear was known to have left BMA 7, which would leave 6 previously known bears available for detection in 2018.

There were also no offspring detected within the 2018 sample of 39 individual bears from the known research bears monitored in 2005 and 2006 in BMA 7. This compares to 6 offspring from the 63 unique

grizzly bears found in BMA 4 also in the 2018 season. Both of these results; not finding any previously known bears or their offspring in 2018, is difficult to explain but may suggest that BMA 7 has lower grizzly bear survival rates compared to BMA 4 (Stenhouse et al., 2020), where both survival of known bears was seen along with reproductive output from genetic analysis. With 30% mortality of our collared research bears in BMA 7 after 2006 (when the spring hunt was suspended), we believe that bears in BMA 7 have low survival rates.

The Swan Hills population was also compared with the populations from neighboring BMAs (Grande Cache BMA 2 and Yellowhead BMA 3; Proctor et al., 2010). Using principle components analysis (PCA) software Genetix, the BMA 7 bears appeared to be genetically distinct from grizzly bears in the Grande Cache and Yellowhead BMAs (Figure 16). Interestingly, G278 who was captured in the Grande Cache BMA, clustered within the PCA with the BMA 7 bears, which further supports the interpretation of the genetic data that his parents were from the Swan Hills BMA.

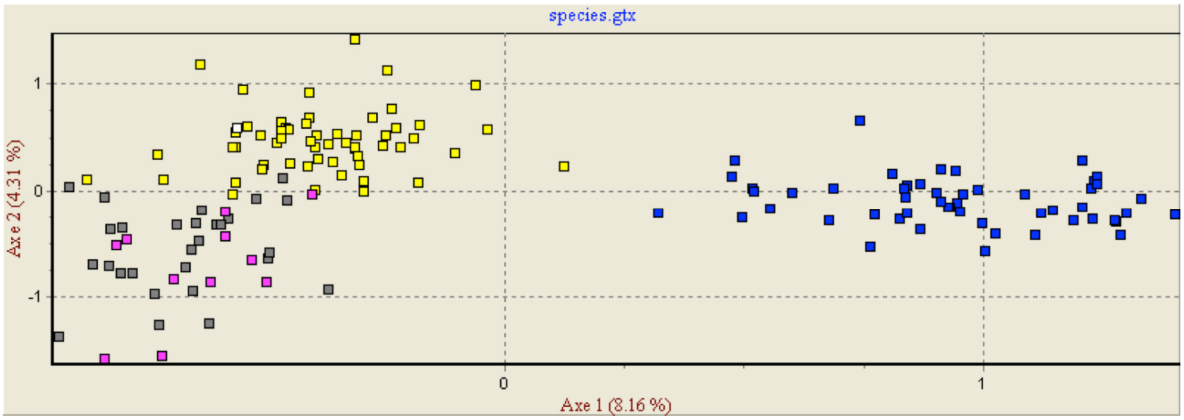

Figure 16: Principle component analysis of 6-locus genotypes from 53 black bears (blue) and 61 grizzlies (yellow) from BMA 3, alongside 39 individuals from BMA 7 that were either diagnosed as grizzly bears by their G10J genotypes (gray; n=28) or that have the non-diagnostic genotype 194.194 (pink; n=11).

Based on data from our long-term genetic database, we also determined that grizzly bears do disperse (emigrate) out of BMA 7, but we have no data suggesting that grizzly bears have immigrated into BMA 7 during the period of the provincial grizzly bear research and inventory efforts (1999–2020). Our dispersal cases are G278 (male) found in BMA 2 and from genetic analysis we believe his mother was from BMA 7 (Figure 17), and G202 (male) captured in BMA 7 as a yearling in 2005 and then redetected in BMA 3 in 2011 and 2014 in population inventory work (Figure 18).

Our results showed no detections of grizzly bears within the 12 cells or those adjacent in the north of Highway 43, suggesting that these habitats were not being used by grizzly bears. Thus, we concluded that during the sampling period in 2018, there was no movement of grizzly bears across this highway.

G278 Adult Male (red) and his likely Mother (yellow)

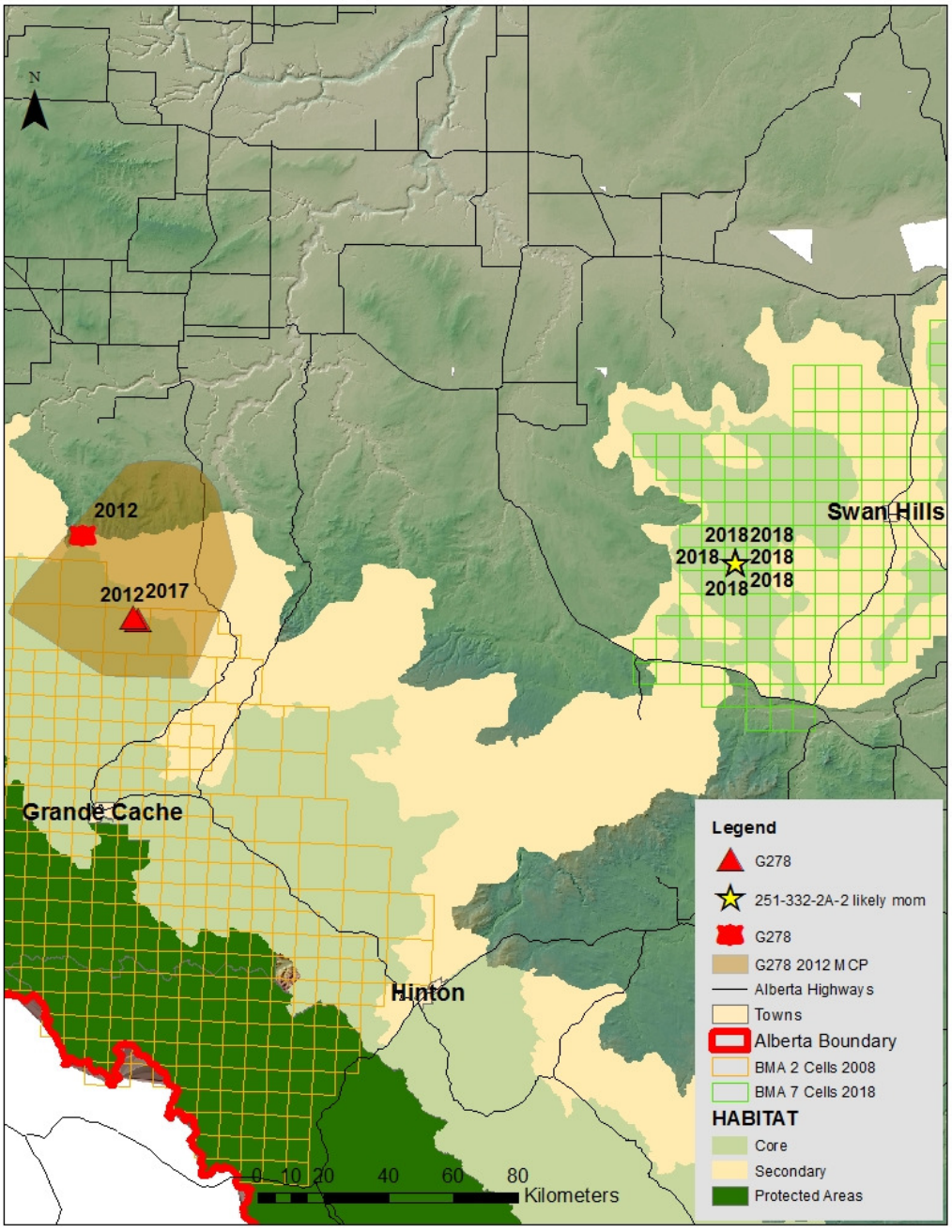

Figure 17: Demonstrating the location of G278 and his likely mother.

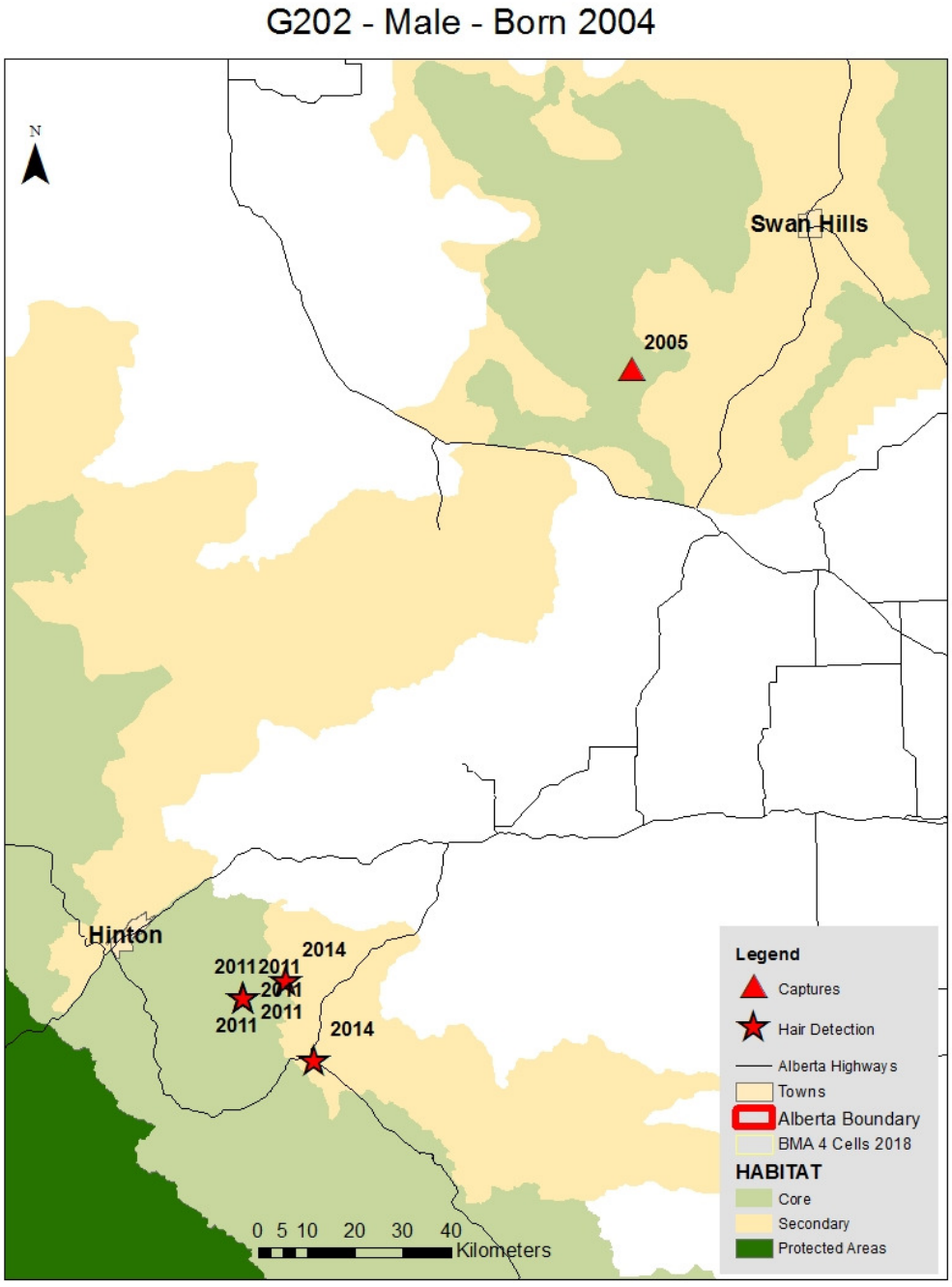

Figure 18: Demonstrates movement of G202 who was captured in the Swan Hills BMA (BMA 2) and then detected in the Yellowhead BMA (BMA 3).

DISCUSSION

This project provides the first estimates of grizzly bear abundance and density for the Swan Hills grizzly bear population unit (BMA 7). While DNA sampling was successful in detecting a moderate sample size of grizzly bears (39), the rates of detection falls below all other BMAs sampled in Alberta, despite the fact that similar sampling designs and methodologies were used during all inventories. We suspect that the large number and density of black bears in the area reduced our ability to detect grizzly bears and may have affected grizzly bear behaviour around the sampling sites. As a result, the estimates from this project are relatively imprecise and should be interpreted cautiously. We suggest that the lower bound of the confidence limit (62) be used for management purposes until higher precision can be obtained for grizzly bear population estimates in the area. We note that the lower bound of the confidence limit (62 bears) roughly corresponds to the estimate of bears if a similar detection function to BMA 2 is assumed (Table 8: 56–64 bears).

The main issue confronting estimates is lack of precision as indexed by wide confidence intervals. This means that if the project were repeated, a dissimilar estimate may result. In this context, discussion about potential biases is secondary to the issue of precision. We note that low detection rates, if they are similar across all sessions, should not inflate mark-recapture estimates. If detection rates are evenly low for bears, and they do not change after detection, then unbiased albeit imprecise estimates will result. However, factors such as demographic closure violation (addition of new bears into the sampled population such as young cubs suggested in session 4) can inflate estimates, which may have occurred if young cubs were detected in session 4 that were not available for detection in earlier sessions. Spatially explicit methods help confront geographic closure, the likelihood that some bears may be off the grid during sampling, by estimating a detection function that considers bear movement during sampling. However, SECR methods still assume demographic closure.

We note that the issue at hand with potential cubs in session 4 is not necessarily demographic closure but instead, the overall effect of low detection probabilities. Because detection rates were low, the reduction of the 4 potential cubs changed estimates by 30 bears. The reason for this can be thought of in terms of the basic mark-recapture estimating equation which is the number of bears detected (M) divided by their detection probability. When detection rates are higher (>=0.25), each detected bear will contribute about 4 bears to the estimate (1/0.25). When detection rates are lower (approximately 0.1-0.12 for Swan Hills), each bear contributes about 8-10 bears to the estimate (1/0.12) and therefore

the 4 cubs increase the estimate by about 30 bears. In most previous Alberta inventories, detection rates have ranged from 0.2-0.52 (Alberta Grizzly Bear Inventory Team 2008) and therefore, estimates have been more robust to the addition or subtraction of marked bears from the estimate. The general robustness of mark-recapture estimators when detection rates are higher is one of the prime reasons for the intensive sampling designs employed in the Alberta Inventories.

Behavioural response can potentially inflate estimates if bears become less inclined to visit a site and snag hair after initial visits. Behavioural response has been detected using site-specific detection models in other analyses, however, the overall magnitude of the behavioural response has not been high and often trap covariate models have had higher support than behavioural response models (Boulanger et al., 2018; Stenhouse et al., 2015). The challenge with the Swan Hills data set is that redetection rates were low and therefore the data set lacked power to sufficiently test for behavioural response or other more complicated forms of detection probability variation. The use of the meta-analysis allowed for enhanced modelling of scale of movement with a resulting increase in precision.

The issue with black bears potentially compromising detection of grizzly bears is difficult to investigate without having conducted genetic analysis of all black bear hair samples. Although we identified 507 black bear hair samples through lab results, we did not run genotypes to identify unique black bears, as this was not a focus of our project. However, these data do suggest a high density of black bears within the sampling area. We believe it is likely that this high density of black bears, reflected by the high number of black bear samples collected at sites, had an impact on both visits and revisits by grizzly bears. Grizzly bears could be avoiding sites where the presence of a high number of black bears was determined. It is also possible that visits by a large number of black bears to scent lure sites could have influenced the “attractiveness” of these sites to grizzly bears within the 10 day sampling period. Field observations did find that lure stations at sites that had significant black bear hair captures were largely destroyed at the end of the sampling period.

The issue of black bears interfering with sampling of grizzly bears could be investigated with data from BMA 1 where a large number of black bears were also identified. The question of whether heavy black bear use (or high density of black bears) of hair snag sites reduces the number of snags available for grizzly bears, compromises lures, or influences grizzly bear behaviour around sampling sites remains unanswered. Other studies of grizzly bears and black bears suggest segregation of species, however,

these studies occurred in mountainous areas with alpine terrain (Boulanger et al., 2016; Sawaya et al., 2012; Stetz et al., 2014). It is likely that there is less segregation in the Swan Hills given the relatively closed nature of the area without alpine habitats. If this is the case, measures such as reduction of session lengths or use of combined detection methods such as cameras, rub trees, scat and hair snags should be considered for future inventory efforts within this BMA.

Parentage analysis provides a potential way to identify cubs in DNA data sets. This approach was not developed in previous DNA inventories and often can be difficult to apply to large data sets. The question of whether cubs-of-the-year are detectable in DNA data sets was addressed in previous studies and it was suggested that cubs-of-the-year are likely more detectable in later sessions due to their larger size in late summer (Boulanger et al., 2004). It might be possible to further investigate this issue with other data sets if parentage analysis can be conducted. Still, the degree of bias caused by this issue is likely related to overall detection probabilities in the data set since, as mentioned above, high detection probabilities are more robust to 'missed bears'. Namely, if detection rates are high, addition or deletion of individual bears will likely not greatly affect overall estimates. However, when detection rates are lower, data sets become very sensitive to the addition or deletion of detections or redetections, which results in larger confidence intervals.

Given the lower detection rates obtained during this inventory, other detection (sampling) methods, such as systematically sampling roads for scat (Phoebus et al., 2020), rub trees (Kendall et al., 2019) and trail cameras could be used in unison with hair snags, to prevent low precision of estimates and overcome limitations of any single data source (Boulanger et al., 2008). Recent mark-resight approaches that use camera data and radio collared/individual natural marks also have promise to augment data sets and allow estimates of abundance (Efford and Hunter, 2018; Whittington et al., 2018). All of these potential modifications should be considered if further estimation of abundance in the Swan Hills BMA is to be pursued.

Literature Cited

Alberta Environment and Parks, 2016. Alberta grizzly bear (Ursus arctos) recovery plan. Edmonton, Alberta, Canada.

Alberta Grizzly Bear Inventory Team 2008, 2009. Grizzly Bear Population and Density Estimates for the 2008 DNA Inventory of the Grande Cache Bear Management Area (BMA 2). Report Prepared for Alberta Sustainable Resource Development, Fish and Wildlife Division.

Alberta Grizzly Bear Recovery Team, 2008. Alberta grizzly bear recovery plan 2008-2013, Alberta Species at Risk Recovery Plan No. 15. Alberta Sustainable Resource Development, Fish and Wildlife Division, Edmonton, Alberta. Edmonton, AB.

Borchers, D.L., Efford, M.G., 2008. Spatially explicit maximum likelihood methods for capture-recapture studies. Biometrics 64, 377–385. doi:10.1111/j.1541-0420.2007.00927.x

Boulanger, J., Cranston, J., Nielsen, S., Stenhouse, G., 2009. Estimation of grizzly bear population size for the Swan Hills management unit using DNA sampling and habitat-relative occupancy models. Report prepared for Alberta Sustainable Resource Development.

Boulanger, J., Efford, M., 2014. Design for the Yellowhead Unit 3 and Southern Jasper National Park 2014 Grizzly Bear DNA Inventory Project.

Boulanger, J., Kendall, K.C., Stetz, J.B., Roon, D.A., Waits, L.P., Paetkau, D., 2008. Multiple data sources improve DNA-based mark-recapture population estimates of grizzly bears. Ecol. Appl. 18, 577–589. doi:10.1890/06-1941.1

Boulanger, J., McLellan, B.N., Woods, J.G., Proctor, M.F., Strobeck, C., 2004. Sampling design and bias in DNA-based capture-mark-recapture population and density estimates of grizzly bears. J. Wildl. Manage. 68, 457–469. doi:10.2193/0022-541X(2004)068[0457:SDABID]2.0.CO;2

Boulanger, J., Nielsen, S.E., Stenhouse, G.B., 2018. Using spatial mark-recapture for conservation monitoring of grizzly bear populations in Alberta. Sci. Rep. 8, 1–15. doi:10.1038/s41598-018-23502-3

Boulanger, J., Proctor, M., Himmer, S., Stenhouse, G., Paetkau, D., Cranston, J., 2006. An empirical test of DNA mark – recapture sampling strategies for grizzly bears. Ursus 17, 149–158. doi:10.2192/1537-6176(2006)17[149:AETODM]2.0.CO;2

Boulanger, J., Stenhouse, G., Bradley, M., 2016. Estimates of population size and density of black bears from the 2014 South Jasper National Park DNA mark-recapture inventory.

Boulanger, J., Stenhouse, G., MacHutchon, G., Proctor, M., Himmer, S., Paetkau, D., Cranston, J., 2005. Grizzly bear population density estimates for the 2005 Alberta (proposed) Unit 4 Management Area inventory. Rep. Prep. Alberta Sustain. Resour. Dev. Fish Wildl. Div. 31 pp.

Boulanger, J., Stenhouse, G.B., 2014. The impact of roads on the demography of grizzly bears in Alberta. PLoS One 9. doi:10.1371/journal.pone.0115535

Boulanger, J., White, G.C., McLellan, B.N., Woods, J., Proctor, M., Himmer, S., 2002. A meta-analysis of grizzly bear DNA mark-recapture projects in British Columbia, Canada. Ursus 13, 137–152.

doi:10.2307/3873195

Calenge, C., 2006. The package “adehabitat” for the R software: a tool for the analysis of space and habitat use by animals. Ecol. Modell. 197, 516–519. doi:10.1016/J.ECOLMODEL.2006.03.017

Efford, M., 2015. secrdesign-sampling design for spatially explicit capture-recapture. R package.

Efford, M.G., 2019. Spatially Explicit Capture-Recapture Models. R package version 4.1.0., https://cran.r-project.org/web/packages/secr/secr.pdf.

Efford, M.G., 2014a. secr spatially explicit capture recapture models. R package version 2.8.1, http://CRAN.R-project.org/package=secr.

Efford, M.G., 2014b. Bias from heterogeneous usage of space in spatially explicit capture-recapture analyses. Methods Ecol. Evol. 5, 599–602. doi:10.1111/2041-210X.12169

Efford, M.G., 2011. Estimation of population density by spatially explicit capture-recapture analysis of data from area searches. Ecology 92, 2202–2207. doi:https://doi.org/10.1890/11-0332.1

Efford, M.G., 2004. Density estimation in live-trapping studies. Oikos 106, 598–610. doi:10.1111/j.0030-1299.2004.13043.x

Efford, M.G., Borchers, D.L., Byrom, A.E., 2009. Density Estimation by Spatially Explicit Capture–Recapture: Likelihood-Based Methods. Model. Demogr. Process. Mark. Popul. 255–269. doi:10.1007/978-0-387-78151-8_11

Efford, M.G., Boulanger, J., 2019. Fast evaluation of study designs for spatially explicit capture–recapture. Methods Ecol. Evol. 10, 1529–1535. doi:10.1111/2041-210X.13239

Efford, M.G., Dawson, D.K., Jhala, Y. V., Qureshi, Q., 2016. Density-dependent home-range size revealed by spatially explicit capture–recapture. Ecography (Cop.). 39, 676–688. doi:10.1111/ecog.01511

Efford, M.G., Dawson, D.K., Robbins, C.S., 2004. DENSITY: software for analysing capture-recapture data from passive detector arrays, Animal Biodiversity and Conservation.

Efford, M.G., Fewster, R.M., 2013. Estimating population size by spatially explicit capture-recapture. Oikos 122, 918–928. doi:10.1111/j.1600-0706.2012.20440.x

Efford, M.G., Hunter, C.M., 2018. Spatial capture-mark-resight estimation of animal population density. Biometrics 74, 411–420. doi:10.1111/biom.12766

Efford, M.G., Mowat, G., 2014. Compensatory heterogeneity in spatially explicit capture–recapture data. Ecology 95, 1341–1348. doi:10.1890/13-1497.1

Graham, K., Stenhouse, G.B., 2019. Alberta Grizzly Bear Genetic Dataset. fRI Research Grizzly Bear Program.

Huggins, R.M., 1991. Some Practical Aspects of a Conditional Likelihood Approach to Capture Experiments. Biometrics 47, 725. doi:10.2307/2532158

Kahle, D., Wickham, H., 2013. ggmap: Spatial Visualization with ggplot2.

Kendall, K.C., Graves, T.A., Royle, J.A., Macleod, A.C., McKelvey, K.S., Boulanger, J., Waller, J.S., 2019.

Using bear rub data and spatial capture-recapture models to estimate trend in a brown bear population. Sci. Rep. 9. doi:10.1038/s41598-019-52783-5

Kendall, K.C., Stetz, J.B., Boulanger, J., Macleod, A., 2009. Demography and Genetic Structure of a Recovering Grizzly Bear Population. J. Wildl. Manag. 73, 3–16.

Munro, R.H.M., Nielsen, S.E., Price, M.H., Stenhouse, G.B., Boyce, M.S., 2006. Seasonal and diel patterns of grizzly bear diet and activity in west-central Alberta. J. Mammal. 87, 1112–1121. doi:10.1644/05-MAMM-A-410R3.1

Nielsen, S.E., Boyce, M.S., Stenhouse, G.B., Munro, R.H.M., 2002. Modeling grizzly bear habitats in the Yellowhead ecosystem of Alberta: taking autocorrelation seriously. Ursus 13, 45–56.

Nielsen, S.E., Cranston, J., Stenhouse, G.B., 2009. Identification of priority areas for grizzly bear conservation and recovery in Alberta, Canada. J. Conserv. Plan. 5, 38–60.

Nielsen, S.E., Herrero, S., Boyce, M.S., MacE, R.D., Benn, B., Gibeau, M.L., Jevons, S., 2004. Modelling the spatial distribution of human-caused grizzly bear mortalities in the Central Rockies ecosystem of Canada. Biol. Conserv. 120, 101–113. doi:10.1016/j.biocon.2004.02.020

Nielsen, S.E., Stenhouse, G.B., Boyce, M.S., 2006. A habitat-based framework for grizzly bear conservation in Alberta. Biol. Conserv. 130, 217–229. doi:10.1016/j.biocon.2005.12.016

Paetkau, D., 2003a. An empirical exploration of data quality in DNA-based population inventories. Mol. Ecol. 12, 1375–1387. doi:10.1046/j.1365-294X.2003.01820.x

Paetkau, D., 2003b. An empirical exploration of data quality in DNA-based population inventories. Mol. Ecol. 12, 1375–1387. doi:10.1046/j.1365-294X.2003.01820.x

Phoebus, I., Boulanger, J., Eiken, H.G., Fløystad, I., Graham, K., Hagen, S.B., Sorensen, A., Stenhouse, G., 2020. Comparison of grizzly bear hair-snag and scat sampling along roads to inform wildlife population monitoring. Wildlife Biol. 2020. doi:10.2981/wlb.00697

Proctor, M., McLellan, B., Boulanger, J., Apps, C., Stenhouse, G., Paetkau, D., Mowat, G., 2010. Ecological investigations of grizzly bears in Canada using DNA from hair, 1995-2005: a review of methods and progress. Ursus 21, 169–188.

QGIS Development Team, 2020. QGIS Geographic Information System. Open Source Geospatial Foundation. http://qgis.org.

R Development Core Team, 2020. R: A Language and Environment for Statistical Computing. R Found. Stat. Comput., R Foundation for Statistical Computing. doi:10.1007/978-3-540-74686-7

Riley, S., Degloria, S., Elliot, S.D., 1999. A Terrain Ruggedness Index that Quantifies Topographic Heterogeneity. Int. J. Sci. 5, 23–27.

Rovang, S., Nielsen, S.E., Stenhouse, G., 2015. In the trap: detectability of fixed hair trap DNA methods in grizzly bear population monitoring. Wildlife Biol. 21, 68–79. doi:10.2981/wlb.00033

Sawaya, M.A., Stetz, J.B., Clevenger, A.P., Gibeau, M.L., Kalinowski, S.T., 2012. Estimating Grizzly and Black Bear Population Abundance and Trend in Banff National Park Using Noninvasive Genetic Sampling. PLoS One 7, e34777. doi:10.1371/journal.pone.0034777

Stenhouse, G., Boulanger, J., Efford, M., Rovang, S., Sorensen, A., Graham, K., McKay, T., 2015. Estimates of grizzly bear population size and density for the 2014 Alberta Yellowhead population unit (BMA 3) and south Jasper National Park, Weyerhaeuser Ltd., West Fraser Mills Ltd., Alberta Environment and Parks, and Jasper National Park.

Stenhouse, G., Boulanger, J., Phoebus, I., Graham, K., Sorensen, A., 2020. Estimates of Grizzly Bear Population Size and Density for the Alberta Clearwater Population Unit (BMA 4) in 2018 with Comparisons to 2005 Data.

Stetz, J.B., Kendall, K.C., Macleod, A.C., 2014. Black bear density in Glacier National Park, Montana. Wildl. Soc. Bull. 38, 60–70. doi:10.1002/wsb.356

Waits, L.P., Paetkau, D., 2005. Noninvasive genetic sampling tools for wildlife biologists: a review of applications and recommendations for accurate data collection. J. Wildl. Manage. 69, 1419–1433. doi:10.2193/0022-541X(2005)69[1419:NGSTFW]2.0.CO;2

Whittington, J., Hebblewhite, M., Chandler, R.B., 2018. Generalized spatial mark-resight models with an application to grizzly bears. J. Appl. Ecol. 55, 157–168. doi:10.1111/1365-2664.12954

Wickham, H., 2009. ggplot2: Elegant Graphics for Data Analysis. Springer New York.

Woods, J.G., Paetkau, D., Lewis, D., McLellan, B.N., Proctor, M., Strobeck, C., 1999. Genetic tagging of free-ranging black and brown bears. Wildl. Soc. Bull. 27, 616–627.

Worton, B.J., 1989. Kernel methods for estimating the utilization distribution in home- range studies. Ecology 70, 164–168. doi:10.2307/1938423

APPENDIX: DESIGN OF SWAN HILLS PROJECT

This appendix details work to design the Swan Hills sampling project.

METHODS AND RESULTS

Delineation of Target Study Area and Potential Stratification

Habitat models have been developed from a previous collared bear study for the Swan Hills BMA (Figure A1). From this model, core and secondary zones were developed based mainly on habitat value and road density. There is a rather abrupt cut-off in habitat quality outside of secondary areas and therefore it is likely that most home range centers are contained within the core/secondary areas, however, this boundary is not a “hard edge” and bears most likely venture into areas adjoining the secondary zone especially if the population is increasing. However, it is likely that the majority of home range centers occur in core and secondary areas.

It can be seen that the majority of the core and secondary areas have high habitat value, however, the central region has high road density and therefore it is categorized as secondary habitat. In the case of Swan Hills, it is not certain whether core and secondary areas will necessarily translate into expected densities of grizzly bears given that reasonable habitat occurs in secondary zones. In addition, forestry activities and road can potentially increase bear density by creating habitat (if mortality risk is managed) and therefore high road densities may not directly translate into lower bear densities. Density surface modelling of BMAs in Alberta suggested that RSF and Risk (road density) were associated with bear density in the adjacent Grande Cache (BMA 2), however, RSF alone was most associated with density in the Yellowhead (BMA 3) and Clearwater (BMA 4;Boulanger et al., 2018). The degree in which road density influences bears is a function of historic mortality as well as present management of road access and bear mortality risk (Boulanger and Stenhouse, 2014).

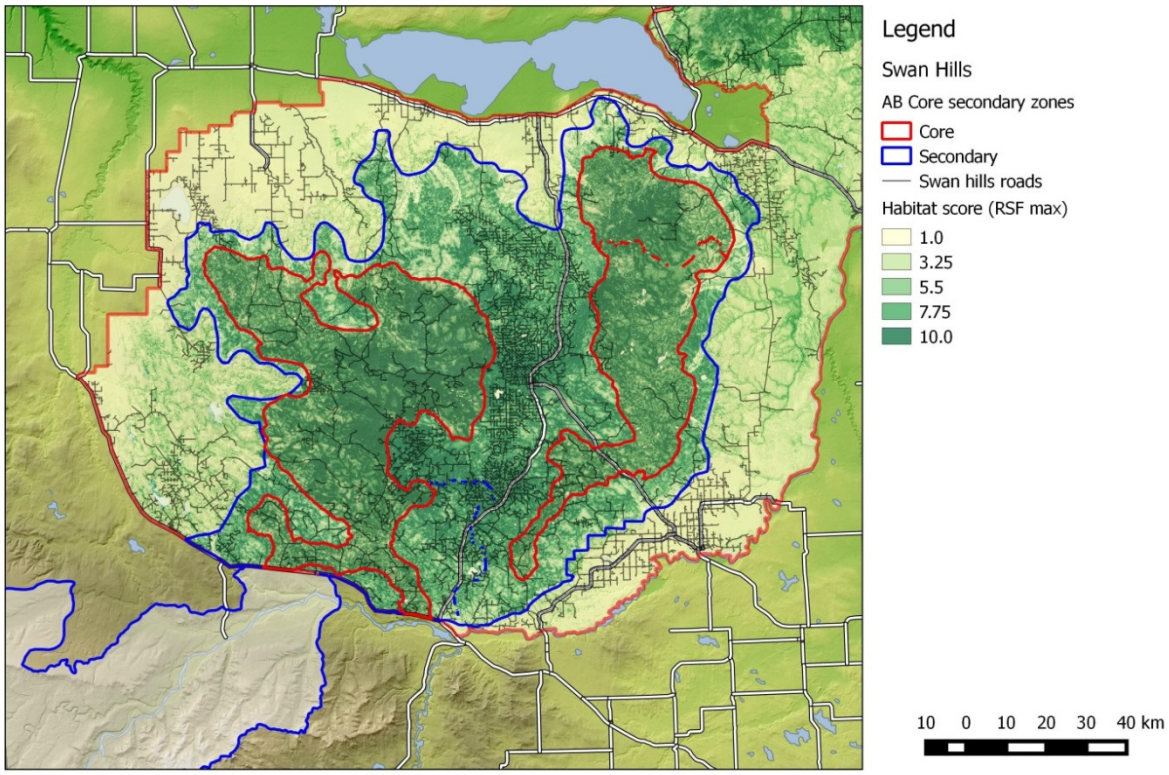

Figure A1: RSF habitat model scores for the Swan Hills and delineation of core and secondary areas.

Inference on Movement from Collared Bears

One of the challenges in designing the Swan Hills survey was the lack of previous data on movements of grizzly bears relative to other BMAs, which was required to determine optimal trap spacing. In addition, a question of interest was whether bear movements and potential densities were associated with the core and secondary areas within the BMA. A limited data set of collared bears from the Swan Hills was used to help answer these questions and inform the design of the Swan Hills DNA survey (Figure A2).

Seven bears were radio collared from 2005 to 2007 in the Swan Hills BMA. Individual paths and kernel home range areas (Worton, 1989) were analyzed for these bears using the *adehabitatHR* (Calenge, 2006) and *ggplot2* (Wickham, 2009) packages in program R (R Development Core Team, 2020). Data was only used for bears that had at least 10 locations for a given year.

The paths and kernel home range areas of collared bears (Figure A2) indicate that movements occur across core and secondary zones. It is possible that the distribution of collared bears was influenced by the location of collaring which did occur in the central, secondary area. However, even with limited data, it is apparent that bears traverse a reasonably large extent of bear habitat within the BMA which includes secondary and core areas. Therefore, stratification based on core and secondary zones, as was done in previous studies (Stenhouse et al., 2015), may not be optimal given that these zones may not predict bear density especially for secondary areas in-between the two core zones.

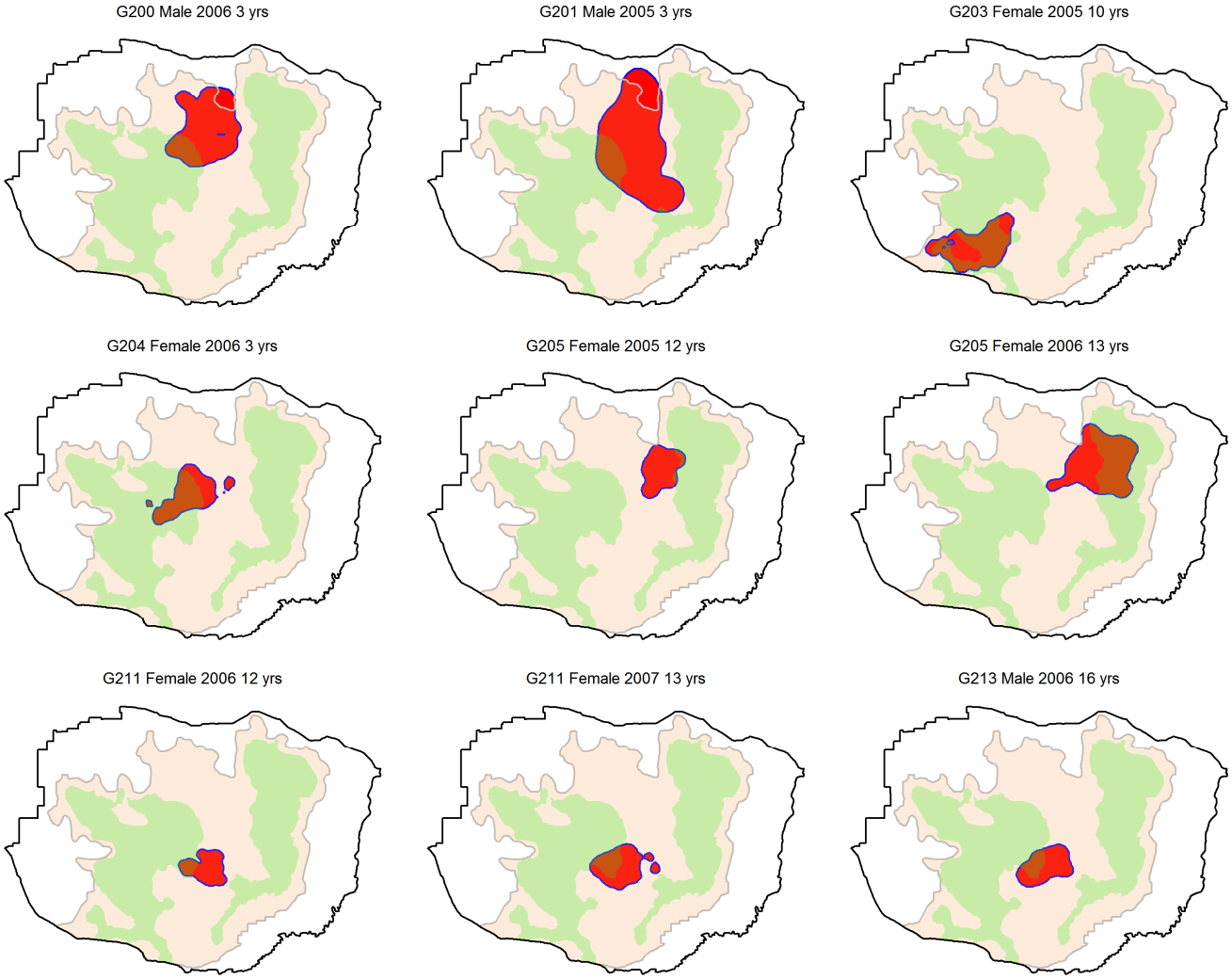

Figure A2: Collared bear kernel home range areas (red) for June and July relative to core (green), secondary (tan), and overall BMA 7 boundaries. The bear id, sex, year of locations, and age of bear is given above each figure.

A related question is whether the rather small area of habitat within the Swan Hills restricts movements and home range size. For this comparison, kernel 95% home range areas for June and July (when DNA sampling occurs) were estimated for the Swan Hills BMA and compared to adjacent BMAs (Figure A3). From this, it can be seen that the Swan Hills home range areas were relatively similar in size to other BMAs.

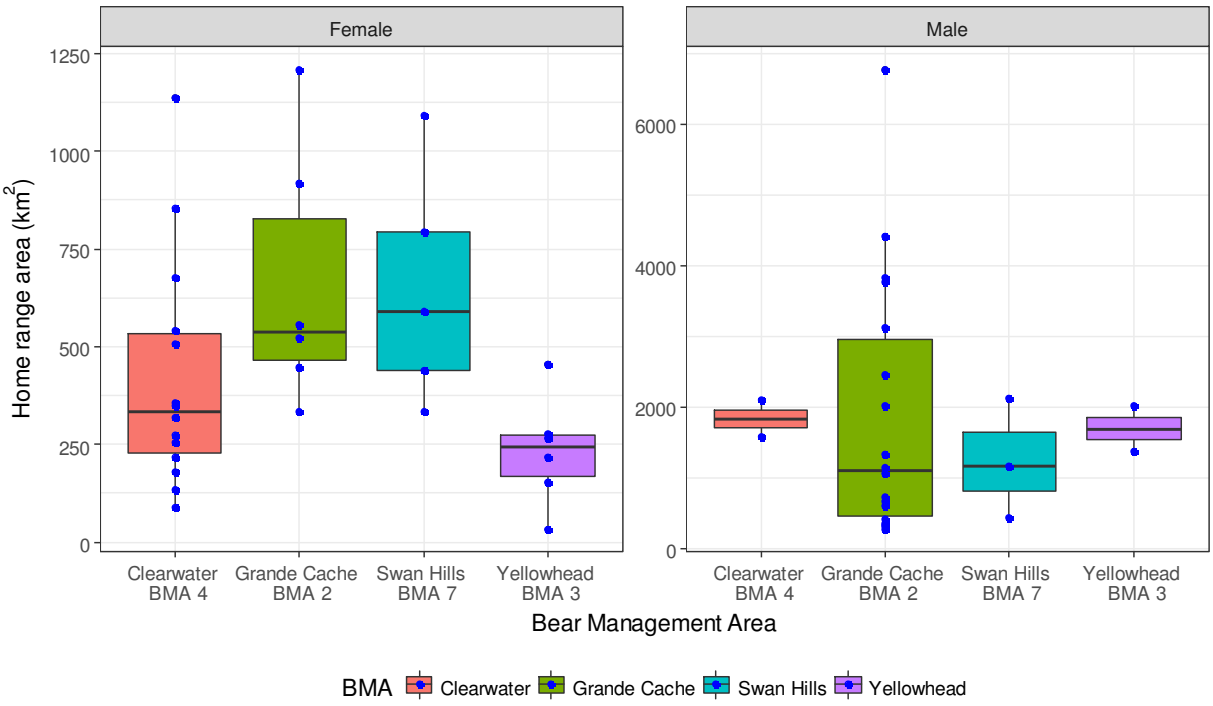

Figure A3: Boxplots of estimated June-July kernel home range areas for Swan Hills compared to other BMAs.

The collar analysis also documents the crossing of one male bear (G207,4 years old in 2005) crossing into the Swan Hills from the Grande Cache BMA. There was only one location of this male in Swan Hills BMA before it turned around and went back to the Grande Cache BMA. Therefore, data from this bear was not used in the analysis of home range size.

Simulation Methods

Previous DNA sampling has not occurred in Swan Hills, and likely ranges of spatially explicit parameters were derived from previous surveys conducted elsewhere in Alberta (Table 10). All previous surveys (conducted from 2004 to2008) utilized a systematic 7x7 km grid cell design with a single site per cell sampled for 4 sessions. In terms of study design, we were most concerned with detection and redetection of females which exhibit smaller home ranges than males and therefore simulation parameters were mainly based on females. In addition, a home range based estimate of the spatial scale parameter (σ) from previous collaring was derived. Table 1 also provides "rule of thumb" trap spacing guidelines (Murray Efford, per. comm.) which suggests a range of site spacing from 3.8 to 10.1 for females (using the lower 1.5 σ guideline). These guidelines, which should be verified by simulations, suggest the current spacing of 7 km used for Alberta projects is adequate and that it might be possible to increase site spacing if larger σ values can be assumed.

Table A1: Ranges of SECR parameters from previous studies in Alberta. Density is in bears per 1,000 km². Home range area (HRA) was estimated for Swan Hills (BMA 7) using a 95% kernel home range model (Figure A2) and converted to a σ value.

Parameter	BMA 2	3	4	5	6	7 (HRA)
Females						
Detection and HR center (g_0)	0.17	0.10	0.18	0.17	0.40	
Spatial scale (σ)	4369	6754	5782	4705	2547	4315
Density (bears per 1000 km²)	11.38	1.99	2.38	5.60	5.68	
Rule of thumb site spacing (1.5 σ) (km)	6.6	10.1	8.7	7.1	3.8	6.5
Rule of thumb site Spacing (2.5 σ)	10.9	16.9	14.5	11.8	6.4	10.8
Males						
Detection and HR center (g_0)	0.05	0.07	0.06	0.04	0.06	
Spatial scale (σ)	9119	10255	12749	12678	6158	5973
Density (bears per 1000 km²)	6.23	1.30	1.15	3.37	8.43	
Rule of thumb site spacing (1.5 σ) (km)	13.7	15.4	19.1	19.0	9.2	8.9
Rule of thumb site Spacing (2.5 σ)	22.8	25.6	31.9	31.7	15.4	14.9

An inverse relationship (Figure A4) can be seen between g_0 and σ (lower g_0 values correspond to higher σ values) as well a weaker relationship between density and σ (higher density values have lower σ values) as suggested in other studies (Efford et al., 2016; Efford and Mowat, 2014). For the main simulations we used the g0/σ values for females from the Grande Cache (g0=0.17/σ=4369) which used a σ value that was close to the home range area based estimated for BMA 7.

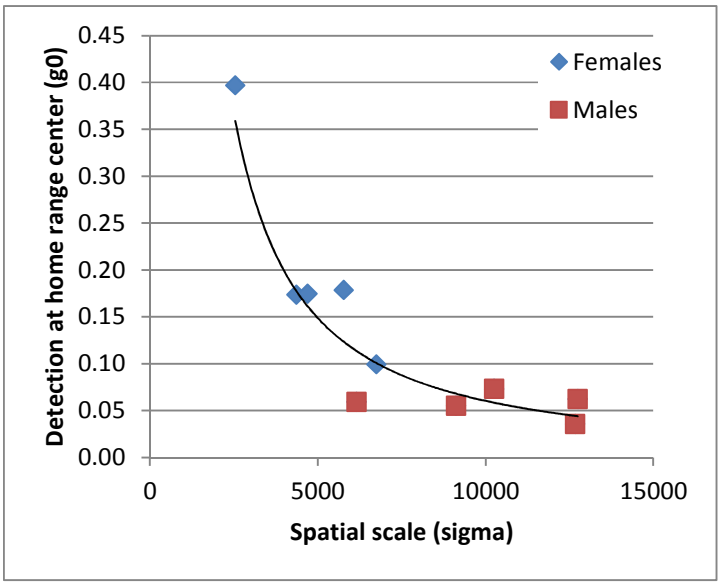

Figure A4: Relationship between detection at home range center (g_0) and spatial scale (sigma/σ) from Alberta DNA mark-recapture projects (Table 10). A power curve was fit to the data ($g0=10058\sigma^{-1.3}$) was fit to describe the relationship between g0 and σ. More direct parameterizations between g0 and σ are available (Efford et al., 2016; Efford and Mowat, 2014).

Previous estimates of abundance for the Swan Hill were based on RSF extrapolation of densities from other DNA studies. The estimate from this exercise was 23.2 (CI=5.9–70.9) bears. From this, we considered a range of 20 to 50 bears in the Swan Hills secondary and core areas. This translated into a density range of 0.84 to 4.19 bears per 1,000 km^2 if it is assumed that all home range centers are contained within the core and secondary area (11,937 km^2).

Simulations results were evaluated in terms of relative standard error (RSE) which is similar to the coefficient of variation. Namely, it is an estimate of standard error scaled by the point estimate therefore allowing comparison of precision across different levels of abundance. In addition, simulations were evaluated in terms of relative bias which is the difference between the point estimate and true value divided by the true value. Density was mainly used as the metric for comparison under the assumption that precision and bias of density would directly relate to estimates of population size. Population size in simulations would simply be the area of the SECR mask times the simulated density under the assumption that all simulated bears within the mask were part of the sampled population.

Designs Considered in Simulations

The main constraint on sampling was the relatively large area of the Swan Hills BMA which limited the number of total sites that could be employed. A target number of 200 sites sampled for 4 sessions was considered as a ball-park target for sampling intensity. The challenge in this context was that densities of bears were potentially low in the Swan Hills and bear distribution was likely to be spread out across all core, secondary, and peripheral areas. The requirement of equal access of all bears to all sites during

sampling is relaxed with SECR methods, however, sampling still needs to be representative of the landscape and habitat within the entire BMA.

There were two primary objectives to the Swan Hills inventory project. First, an estimate of abundance was desired for the BMA area. Second, an assessment of distribution of bears within the BMA is required to prioritize management of bear habitat areas within the BMA. Given these objectives, a systematic grid sampling design was mainly considered for sampling as opposed to stratified or subgrid designs. A stratified design was problematic given uncertainty of the distribution of bears within the BMA area (as discussed previously). An SECR sub grid design could potentially provide unbiased estimates of density and abundance but would give less inference on overall distribution of bear within the core and secondary areas.

The main aspects that varied in simulations were site spacing and the extent of the grid relative to the core and secondary areas (Figure A5). Four main designs were considered which sampled the main extent of the core and secondary area but with different cells sizes and trap spacing. For the *secr* package, evenly spaced sites were simulated which could be easily converted to a cell-based design used in previous DNA mark-recapture studies. Simulations were conducted in the *secrdesign* package (Efford, 2015) with further analysis using the *secr* (Efford, 2014a) package in program R.

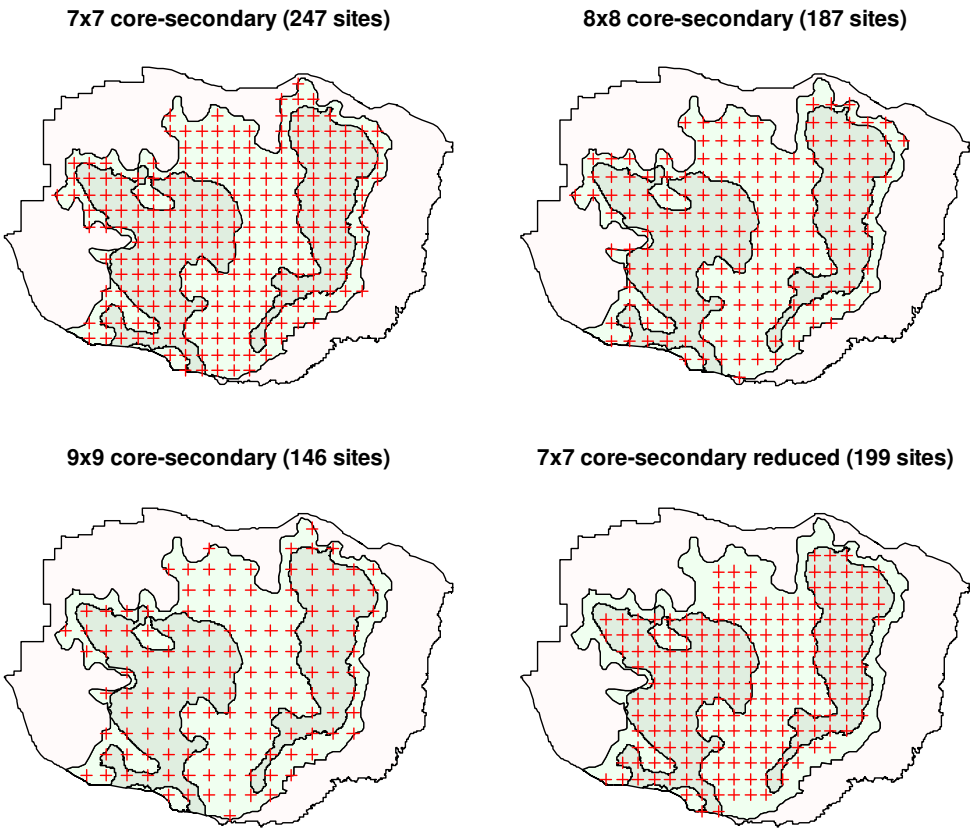

Figure A5: Designs considered in simulations with core (green) and secondary areas delineated. Each red + is a DNA site location.

Simulations assumed that all home range centers of bears were contained within the core and secondary areas (Figure A6). Bears could still traverse outside the core and secondary areas (as dictated by σ) as long as the home range center was within the core or secondary area. A similar density between core and secondary areas was assumed given the configuration of the core and secondary areas and likelihood, as indicated by radio collar data (Figure A2) that bear home ranges straddled both areas.

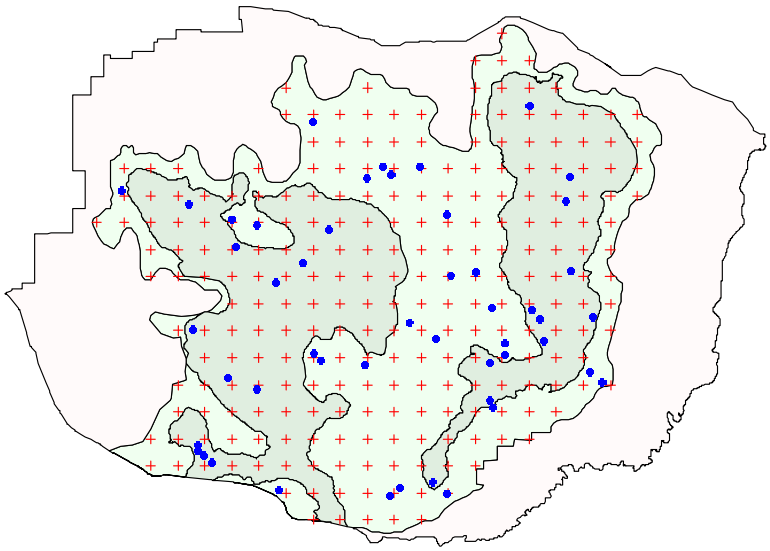

Figure A6: Exam e range centers (blue dots) in the re and secondary areas (based on σ values), however, home range centers were assumed to be within the core and secondary areas.

Simulation Results

Simulation results (Figure A6) suggest that only the 7x7 km cell designs achieved adequate precision across all simulated population sizes. The reduced site 7x7 km design achieved adequate precision; however, RSE was close to the threshold cutoff of 0.2 when population size was 20. The 8x8 km design achieved adequate precision, if the population size was above 28 bears. The 9x9 km cells size design only achieved adequate precision if the population size was close to 50 bears. Relative bias was within ±5% of estimates in all designs with nominal CI coverage for estimates.

Additional designs were considered, for example a 7x7 3 session design which achieved similar precision to the 8x8 km 4 session design (Figure A5). Designs which sampled outside of the core-secondary area achieved similar precision to designs, which sampled just the core/secondary area. This result was a partial artifact of the how the population was sampled, namely that all bear home range centers fell within the core/secondary area.

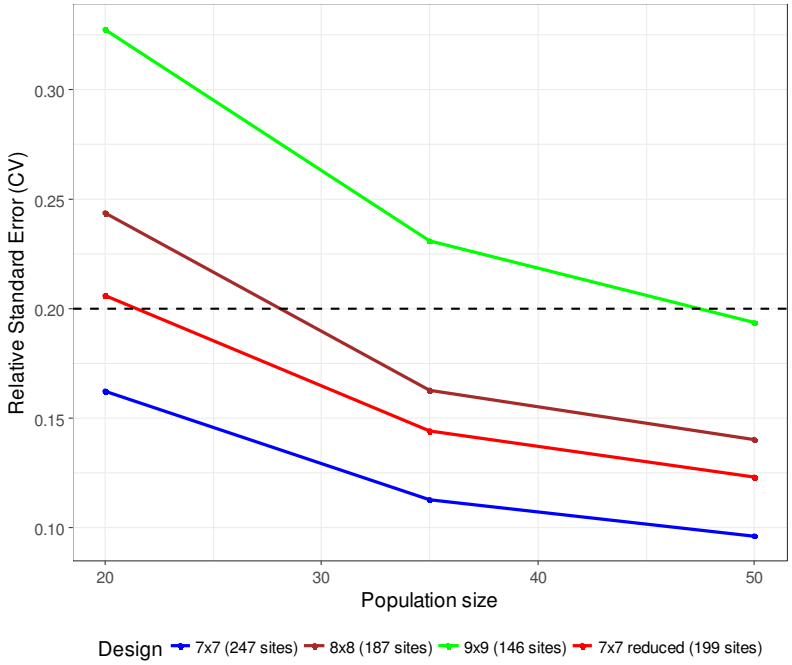

Figure A7: Female simulation results with RSE estimates each design (Figure 6) as a function of assumed population size. The population size (x-axis) is the population size simulated across the SECR mask (D=N/mask area).

One potential issue with the 7x7 km reduced design was that it did not fully sample the core and secondary areas therefore leading to potential bias if there was non-uniform densities within these areas. The most likely scenario in this case would be higher densities in the core compared to the secondary areas. To investigate this issue further, a set of simulations were run where the core area had twice the density of the secondary areas. Relative precision and bias of the 7x7 full core secondary and 7x7 reduced design was then compared.

Results suggested that precision was slightly improved for both designs when there were higher densities of bear in the core area (Figure A7). This was presumably due to more bears being resident on the grid (given that core areas were located in the central area of the BMA) which resulted in higher overall recapture rates.

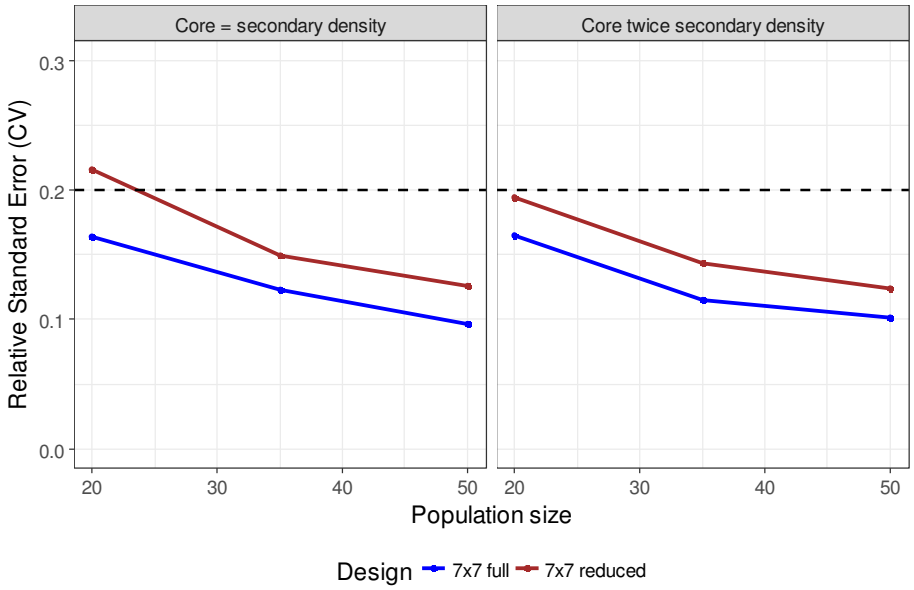

Figure A8: Relative standard error of the 7x7 km full and reduced designs with uniform and with the core density twice that of the secondary area.

Relative bias was within the ±5% levels for both designs across the population sizes simulated, suggesting that the lower coverage by the reduced design did not create a noticeable level of bias in overall estimates. The robustness of spatial mark-recapture to non-even densities has also been documented in previous studies (Efford, 2014b).

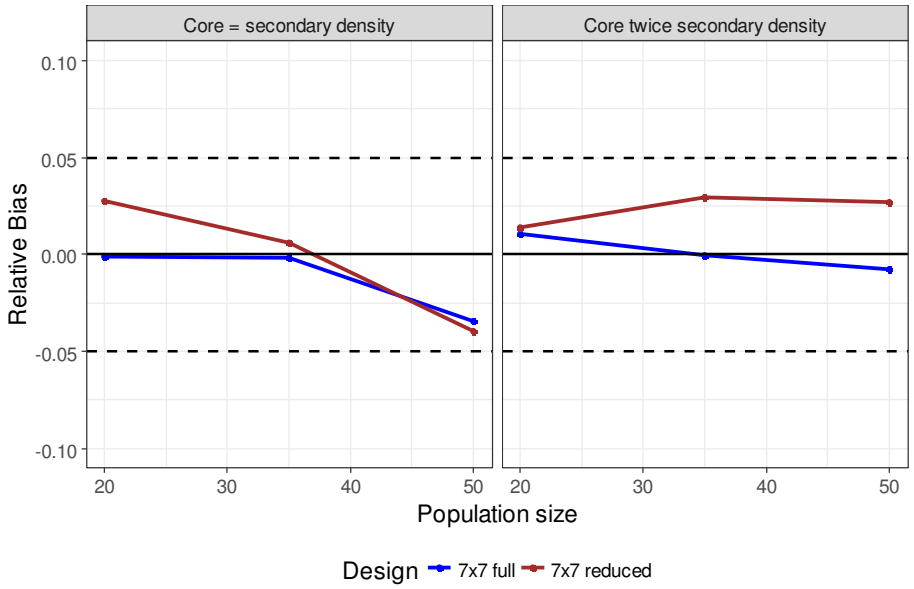

Figure A9: Relative standard error of the 7x7 km full and reduced designs with uniform and with the core density twice that of the secondary area.

As noted before, the actual design for sampling is easily converted to cell format (Figure A9). Below is a map with the 7x7 km reduced design with a cell rather than a site. These cells correspond to the full grid and are partially cross-referenced in terms of site access.

An additional study objective was to determine if bears were crossing the road in the southern part of the BMA. The current design could easily accommodate this objective by simply including the cells on the other side of the highway for the southern part of the grid. This would add 7 cells to the design, if every cell on the other side of the highways was sampled. Sites from these cells were not used for estimation but the information could be used to detect bears crossing the highway.

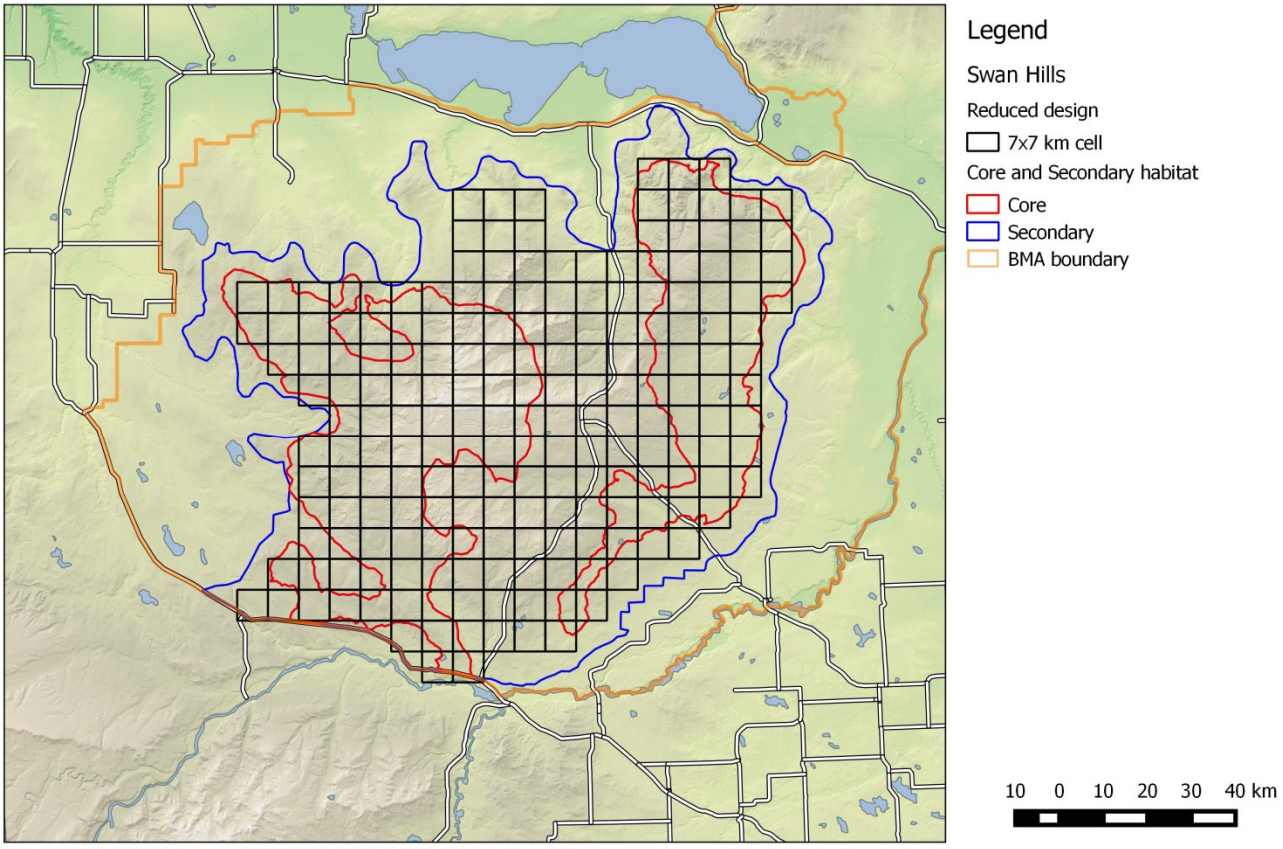

Figure A10: Reduced 7x7 km design with 199 cells relative to core and secondary boundaries.

Simulation Discussion

The results of the simulations conducted in this report highlight the relative risks of sampling smaller populations of grizzly bears. Namely, at lower population sizes, a larger degree of sampling effort is required to obtain enough initial captures and recaptures of bears to obtain precise estimates. Spatially explicit methods provide estimates of higher precision than closed models (Boulanger et al., 2018) for many grizzly bear data sets. However, there are still limits in terms of estimate precision that can be achieved when abundance is low.

The design of Swan Hills represents a trade-off between obtaining an adequate estimate of abundance while achieving adequate spatial coverage of bear habitat within the BMA given the limitations on the number of sites that can be employed. Smaller scale (7x7 km designs) potentially result in more recaptures of bears, therefore increasing precision, which is essential when population size is lower under the assumption that Swan Hills SECR parameters are similar to those from the Grande Cache BMA. Larger scale (8x8 km) designs are still reasonable especially if population sizes of bears are likely to be larger than 30 bears.

The reduced 7x7 km cell design achieved adequate precision with a reduced number of sites (compared to the full 7x7 km design), however, one risk with this design is that spatial coverage of bears in secondary areas was reduced which could bias results if the secondary area at the periphery displays markedly different densities than the other sampled areas. Simulation results suggest that the degree of bias caused by non-even densities was not large with either design simulated.

One of the main assumptions of simulations is that bear home range centers will occur in the core and secondary areas. This assumption could be further tested by sampling areas peripheral to the core and secondary area to assess if a substantial number of bears occur outside of this area. However, this would also require increasing the number of sites which may be problematic given that the designs that achieved adequate precision were above or close to the target number of 200 sites per session. Designs with lesser site intensity could be considered for adjacent areas; however, to incorporate these into estimates would require a stratified design given differences in site densities. As it stands, the proposed designs would be estimating the population size of bears that occur in core and secondary areas with the assumption that densities of bears (as indicated by locations of home range centers) will be very low in areas outside of the core and secondary.