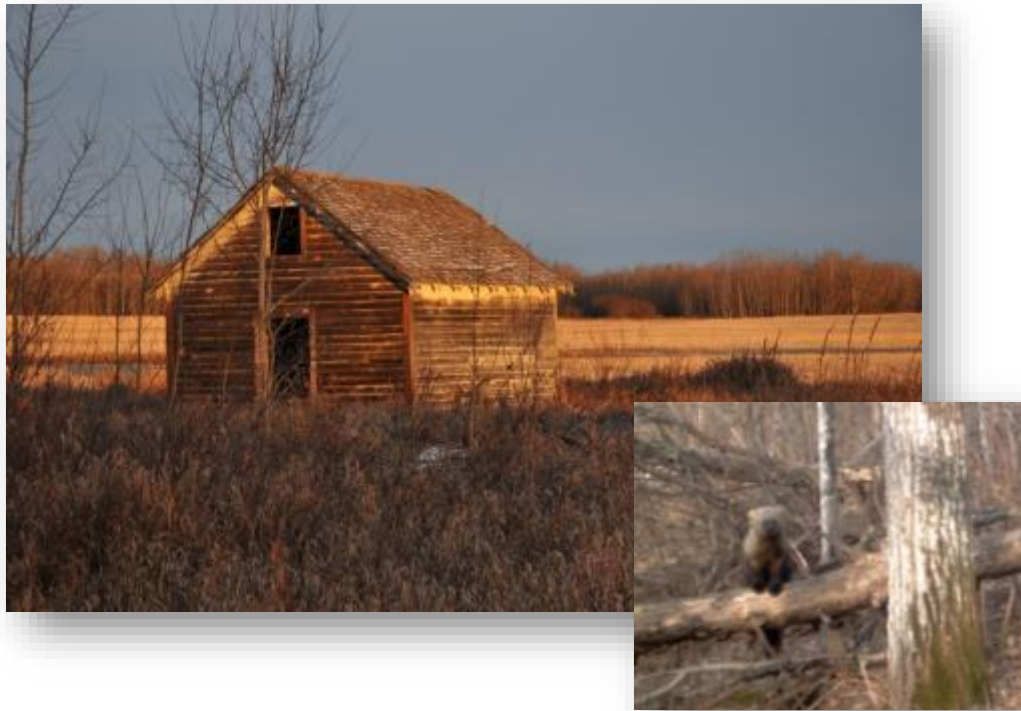

MORaine MESOCARNIVORES PROJECT: 2016-2017 REPORT TO LANDOWNERS AND VOLUNTEERS

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MAY 24, 2017

EXECUTIVE SUMMARY

The *Moraine Mesocarnivores Project* (MMP) investigates the degree to which the network of protected areas, private woodlots, and developed land within the mixed-use landscape of central Alberta's heartland maintains mammalian diversity, and whether this landscape is connected to forested areas in the west and north. Our goals are to (1) measure mammal diversity and statistically relate this to landscape structure, and (2) test for connectivity within and among protected areas by examining the movement and genetic structure of fisher (*Pekania pennanti*) populations.

In November 2013 we deployed 64 sampling points in a systematic design and sampled mammal species occurrence using non-invasive genetic tagging *via* hair trapping, and camera trapping. In 2014-2015 we conducted genetic analysis on these hair samples. From November 2015 through March 2016, we repeated hair trapping and camera trapping; we also live-trapped and GPS-collared 14 fisher individuals. Most recently, in 2016-2017, we (i) examined fisher genetics to understand how the forested heartland is connected to distant forested areas in the boreal forest and Rocky Mountains; (ii) examined how camera data of fisher occurrence represents actual fisher movement, as a guide to large-scale monitoring; (iii) mapped fisher movement pathways in relation to natural and anthropogenic landcover, to understand how development facilitates (or impedes) their movement, and hence persistence; and (iv) began analysis of the mammalian community – from wolves to weasels – across this landscape. The final analysis, and the final reporting of this project, is our goal for the upcoming year. This report contains two preliminary publications from this project, which are being submitted to the journal *Biological Conservation* and to *Ecological Applications*, and has been presented in several public and academic lectures.

As this work comes together, please feel free to contact either myself (fstewart@uvic.ca), or Jason (Jason.fisher@innotechalberta.ca), at any point with questions about this research. You can also keep up to date on project results and happenings by visiting the project website: www.mesocarnivore.weebly.com.

We very much appreciate your enthusiasm and support of this project to date, and look forward to delivering ongoing results as this project comes to a close.

Best, Frances

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1.0 INTRODUCTION AND MOTIVATION

Biodiversity is declining worldwide and increasing human footprint is the primary driver (Vitousek et al. 1997, Sanderson et al. 2002, Leu et al. 2008). Alberta is a special case of this global problem. A diversity of economic opportunities - forest harvesting, agriculture, and petroleum extraction – generate a diversity of disturbance patterns in Alberta, where the rate of forest loss is one of the highest on the planet, eclipsing even the Amazonian rainforest (Global Forest Watch Canada 2014). Years of rapid development have radically changed the Alberta landscape. For example, the Alberta boreal forest is now a novel landscape, without analog historically or geographically (Pickell et al. 2013, Pickell et al. 2014, Pickell et al. 2015). The effects of wholesale habitat change on Alberta's biodiversity remain largely unknown. This is true even of "Alberta's Heartland", the mixed forest and prairie region in central Alberta.

The persistence of wildlife populations on Alberta's landscape are entirely dependent on how well that landscape functions (Wiens 1992, Wiens et al. 1993), which in turn depends on the degree of habitat fragmentation it has sustained from landscape development (Fahrig 1999, Fahrig 2001, Fahrig 2002, 2003). In central Alberta, fragmentation stems from development in multiple sectors: agriculture, petroleum extraction, rural residential properties, and transportation infrastructure. The cumulative effects of these impacts on biodiversity in the region remain, surprisingly, largely unknown. Alberta's Land Use Framework (LUF) assumes that a mix of protected areas (PAs) and remaining habitats within the "working landscape" will together support wildlife populations. This pivotal assumption in the LUF remains untested, and we know nothing about the thresholds of human impact that will permit, or prevent, wildlife populations from remaining on the landscape.

The *Moraine Mesocarnivores Project* tests new ideas about the biodiversity, connectivity, and conservation value of small protected areas in a landscape with cumulative effects of multiple impacts. We are examining the diversity and distribution of mammal species within a matrix of PAs and private land in central Alberta, with natural habitats contiguous with areas of significant anthropogenic disturbance. We will use a combination of field, laboratory, and statistical methods to understand the diversity on the PAs, their value relative to the surrounding "working" landscape, and the connectivity between protected areas, which is so vital to maintaining persistent wildlife populations.

2.0 INVESTIGATING ASSUMPTIONS OF ALBERTA'S LAND USE FRAMEWORK: LANDSCAPE CONNECTIVITY BETWEEN ALBERTA'S HEARTLAND, THE NORTHERN BOREAL FOREST, AND THE ROCKY MOUNTAINS

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2.1 PREFACE

This section is based on a paper conducted under the *Moraine Mesocarnivores Project*. One of the primary goals of the MMP is to scientifically investigate whether the primary assumptions of Alberta's Land Use Framework holds true: the Green (forested) Zones of Alberta are functionally connected to one another although the land between them is highly developed for agriculture and other sectors. We had the unique opportunity to test this assumption by examining the genetics of the fisher (*Pekania pennanti*) population on Alberta's Cooking Lake Moraine. This population had been extirpated long ago, and then was reintroduced, bringing a genetic "dye marker" experiment that lets us examine how those genes spread through Alberta. This research was a national collaborative effort; this paper is tentatively accepted (pending revisions) in *Biological Conservation*.

2.2 ABSTRACT

Reintroductions are a common biological conservation tool for restoring lost biodiversity around the globe and across taxa. However, rarely is the probability of recolonization explicitly examined when considering reintroduction. Performing post-hoc genetic tests between reintroduced and adjacent

populations documents the success rate for these two management strategies and may provide surprising results about species recolonization ability. We use the fisher (*Pekania pennanti*), one of North America's most commonly reintroduced species, as a model to conduct an evaluation of reintroduction success. We assessed 15 microsatellite loci to determine the genetic contribution of reintroduced individuals to an ostensibly successfully reintroduced population in central Alberta, Canada. Principle component analysis and Bayesian statistical methods converged with confidence on one result: assayed individuals were descended from adjacent native Albertan populations, not putative founders from eastern Canada. These results indicate that reintroduction was a suboptimal management strategy as fishers have naturally recolonized central Alberta. A review of fisher reintroduction literature reveals potentially similar patterns: a large proportion of contemporary individuals appear to be the result of recolonization events. This rare test has broad implications on conservation as it suggests 1) over-confidence in reintroductions, perhaps resulting in significant expenditure of financial and human capital on initiatives of modest, if any, benefit, and 2) underestimation in species' ability to disperse and (re-) colonize, highlighting limits to our understanding of functional connectivity. Importantly, obtaining genetic samples from reintroductions with even minute probabilities of recolonization will allow for objective comparison, publication, and evaluation of the most effective conservation methods.

Abbreviations: CLM – Cooking Lake Moraine, WW – Willmore Wilderness, NA – Northern Alberta, MB – Manitoba, ON - Ontario

2.3 INTRODUCTION

Reintroduction – the attempt to re-establish a species in part of its native range (Pavlik 1996; IUCN 1998; IUCN/SSC 2013) remains a popular management method in conservation biology after a century of use (Hayward & Sommers 2009; Seddon et al. 2014). Considerable contemplation is given to reintroductions as a conservation tool across taxa: in 2016, the Species Survival Commission Reintroduction Specialist Group of the World Conservation Union (IUCN) lists 52 ongoing case studies encompassing invertebrates, fish, amphibians, reptiles, birds, mammals, and plants (Soorae 2016). The rate of reintroductions being conducted each year is increasing (Seddon et al. 2007), reflecting the conservation community's growing confidence in the strategy compared to other management options. Successful reintroductions are loosely defined as 'establishment of a self-sustaining population' (Seddon

1999; but see Beck et al. 1994; Sarrazin & Barbault 1996) and are most commonly observed in North America, Australia, and New Zealand (Fischer & Lindenmayer 2000). Often less consideration is given to the real probability for natural recolonization. Many reintroductions are performed in systems perceived to be highly isolated; however, natural recolonization is possible in many areas that demonstrate some form of contemporary, or importantly future, functional connectivity to adjacent populations (Karieva 1990). With both landscape and climate change altering the occurrence and distribution of biodiversity (Maxwell et al. 2016) the possibility of natural recolonization should be prioritized for many mobile species (Rout et al. 2013).

Context about the dynamics of reintroduced populations may be gleaned from the invasion biology literature. Species invasions and reintroductions are characterized by initiation and expansion stages prior to establishment (Shigesada & Kawasaki 1997; Armstrong & Seddon 2007). Invasive (or exotic) species rarely establish following a single introduction (Shigesada & Kawasaki 1997). In reintroductions, the probability of establishment can be greatly increased with planning and relies on a suite of limiting factors such as habitat availability and quality, predation, parasitism, and duration in captivity (Seddon et al. 2014). Invasion biology recognizes the ‘Tens Rule’ where 10% of introduced species establish and a further 10% of these spread (Jeschke & Strayer 2005). Reintroduction biology recognizes that roughly 20% of reintroductions have been self-described as “successful” (Griffith et al. 1989; Seddon et al. 2014); one might expect this rate may be inflated, and question why conservation efforts are being spent on reintroduction compared to other management techniques that address the mechanisms that lead to extirpation in the first place.

“Success” is a contested term in reintroduction biology. Definitions vary with project objectives, life history of the species, and the temporal scale of observation (Griffith et al. 1989; Beck et al. 1994; Sarrazin & Barbault 1996; Seddon 1999; Haskins 2015; Robert et al. 2015). The IUCN provides guidance (IUCN 1998; IUCN/SSC 2013), however no definition enjoys a consensus. There are no standards for comparison, and specifically no threshold for discriminating the successful establishment of reintroduced individuals from recolonization events (Robert et al. 2015); just because a species is present in a reintroduction location does not equate to a successful reintroduction. We define ‘reintroduction success’ as an instance where the reintroduced genetic lineage is maintained in the contemporary population. Using this definition, we question whether reintroduction success is as high as the 20% currently documented (Seddon et al. 2014). Do conservation biologists overestimate

reintroduction success, and perhaps underestimate the frequency with which species naturally recolonize former ranges? To distinguish between reintroduction and recolonization success, reintroduction events need to be tested using genetic assessments within a critical time limit; too long and the results will be ambiguous due to accumulation of mutations and/or genetic drift (Nei et al. 1975), and too short risks false declaration of success.

As an example of this larger issue for conservation biologists globally (Olding-Smee 2005), we re-assessed a fisher (*Pekania pennanti*) reintroduction to Alberta's Cooking Lake Moraine (CLM) previously deemed "successful" (Badry et al. 1997; Proulx & Genereux 2009; Proulx & Dickson 2014). The loss of fisher from 40% of its historic range has stimulated frequent reintroduction attempts, making it an attractive model to investigate the probability of reintroduction versus recolonization success (Lewis et al. 2012; Powel et al. 2012). Between 1990 and 1992, twenty fisher were opportunistically reintroduced to the CLM from Steinbach, Manitoba and Bancroft, Ontario, after being held in captivity at Vegreville, Alberta (Badry 1994; Proulx et al. 1994; L. Roy, R. Toews, and J. Bowman pers com.). The CLM is an area where all evidence indicated the fisher was locally extirpated, due to overexploitation and land-use change, for a minimum of 50 years (Badry et al. 1997). Fishers have frequently been reported by landowners within the CLM since 2007 (Pybus et al. 2009), but between 1997 and 2007 no confirmed records exist. The CLM is a forested island surrounded by matrix of unsuitable agricultural habitat; extant fisher are widely hypothesized to be functionally isolated from adjacent Albertan populations. The distinct genotypic signatures of Manitoba, Ontario, and native Alberta (Kyle et al. 2001) provide an opportunity to assess the degree of reintroduction vs. recolonization success by comparing alleles between reintroduction source populations, adjacent Albertan populations, and contemporary CLM samples. With an extant population, we test three non-mutually exclusive hypotheses about the outcome of the CLM reintroduction; 1) a successful reintroduction, wherein the genetic signature of one or both source populations (Ontario and Manitoba) is present within contemporary CLM samples, 2) re-stocking, wherein an undetected population was occupying the CLM prior to reintroduction as indicated by unique alleles within CLM samples that do not appear in any other sampled population, or 3) natural recolonization, wherein contemporary fisher individuals are most closely related to animals from adjacent Albertan populations, without genetic evidence of Ontario or Manitoba fishers.

2.4 METHODS

We investigated the ancestry of the contemporary CLM fisher population by comparing microsatellite genotype signatures against four possible candidate source groups: two adjacent Albertan populations and the two reintroduction source populations (Figure 1). We consolidated the most recently collected samples from each population (2000 – 2014).

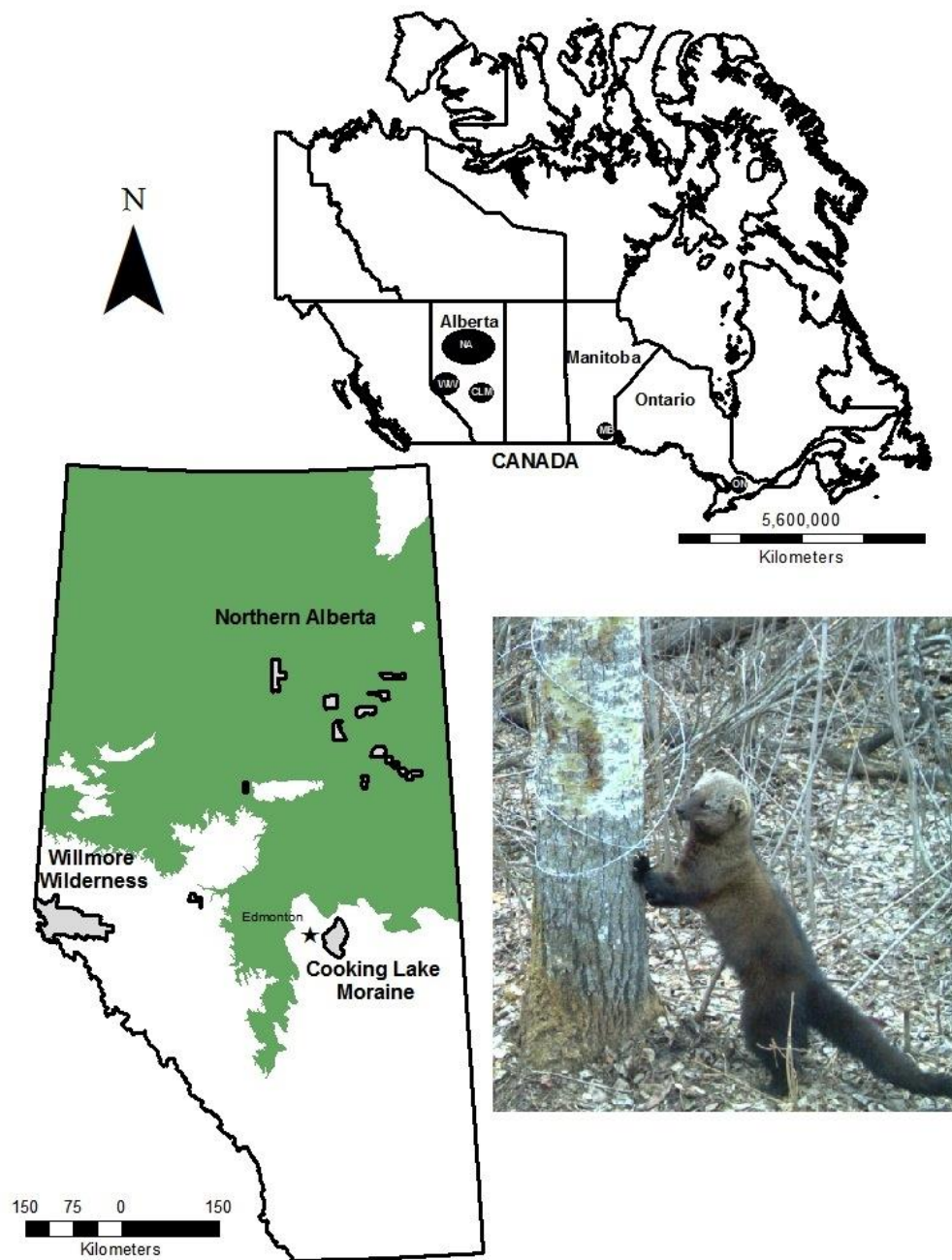


Fig. 1. Fisher DNA samples were collected from 64 sample sites across Alberta's Cooking Lake Moraine (CLM) and compared to four candidate source populations; two adjacent populations in Alberta (Willmore Wilderness in the Rocky Mountains and scattered trap lines throughout Northern Alberta) and reintroduction source populations (Manitoba and Ontario) to assess the success of a 1990/1992 fisher reintroduction. Alberta's boreal forest is highlighted in green and a fisher is depicted at a CLM

sample site. CLM = Cooking Lake Moraine, NA = northern Alberta, WW = Willmore Wilderness in the Rocky Mountains, MB = Manitoba, ON = Ontario.

Samples from reintroduction source populations were donated from the original trap-lines sampled in Steinbach, Manitoba (2014 skin; R. Toews pers. com.) and Bancroft, Ontario areas (2000 – 2003 muscle; sensu Carr et al. 2007, J. Bowman pers. com). CLM fisher DNA samples were collected from 64 stratified-random, non-invasive baited hair traps (sensu Fisher et al. 2011, 2013) in the winters of 2014 and 2016. Fisher populations adjacent to the CLM were sampled via muscle samples donated from fur-harvested individuals in Alberta's boreal forest north of Edmonton (2014), and isolated fisher DNA samples recovered from baited hair traps in Alberta's Willmore Wilderness (Figure 1) in the Rocky Mountains (2006 - 2008; Fisher et al. 2011, 2013). All research was performed under the Canadian Council for Animal Care Guidelines (University of Alberta permit #AUP00000518).

We extracted DNA from samples using the QIAGEN DNeasy Blood & Tissue Kit® and protocol (Hilden, Germany). We excluded hair samples that did not contain at least 1 guard hair root or 5 underfur hairs. Muscle and skin samples comprised a ~3 mm³ clipping. Samples that produced weak or no amplification were analyzed a second time for confirmation, after which we culled 22.8 % (87/381) of samples that failed on both attempts. A 15-microsatellite array was used to identify individuals and quantify genetic differentiation between individuals. Primers were developed by Duffy et al. 1998 (Ggu101 and Ggu216 in wolverine), Dallas and Piertney 1998 (Lut604 in Eurasian otters), Davis and Strobeck 1998 (Ma-1, Ma-2 and Ma-19 in American marten, and Ggu7 in wolverine), Jordan et al. 2007 (MP144, MP182, MP055, MP114, MP175, MP227 and MP247 in fisher), and Fleming et al. 1999 (Mvis72 in mink and ermine). PCR reactions were performed in a volume of 15 µL containing 50 mM KCl, 160 µM dNTPs, and 0.1 % Triton X-100, with primers and Taq polymerase optimized to permit co-amplification (Paetkau et al. 1998). PCR thermal cycling ran in a Perkin Elmer 9600 with an initial denaturing step of 94°C for 1:20 min, 40 cycles of annealing and extension following 94°C for 20 s, 54°C for 25 s, and 72°C for 10 s, followed by 1:05 min at 72°C. Microsatellite error-checking followed Paetkau (2003) published protocol of reanalyzing mismatching markers in pairs of genotypes that are very similar.

We used three statistical methods to determine the most probable ancestry of contemporary CLM genotypes. First, we compared genetic differentiation between groups using F_{ST} (Wright 1943), the probability of identity by descent based on allele frequency variation. F_{ST} values range from 0-1, with probability of identity by decent increasing as the value approaches zero. We determined F_{ST} , and whether these values were significantly different than zero in the hierfstat package. We determined the

most probable grouping of samples by genotype-based relationships by qualitatively observing whether sample locations clustered on a biplot with a PCA (Genetix; Belkhir et al. 2004), and quantitatively using MCMC maximum likelihood clustering algorithm (Structure; Hubisz et al. 2009) as well as an assignment test (GeneClass2; Piry et al. 2004). Finally, allele occurrences across sampled populations were screened for any CLM alleles diagnostic of reintroduction or recolonization (Table 1).

2.5 RESULTS

Both PCA and MCMC identified three distinct provincial clusters (Alberta, Ontario and Manitoba; Figure S1; Figure 2). Neither method suggested CLM samples were distinguished from Northern Alberta or Willmore Wilderness samples. Study areas contained 40 unique identified individuals from the CLM, 19 from Willmore Wilderness, 34 from Northern Alberta, 29 from Ontario, and 25 from Manitoba (Table S1). Within Albertan samples, F_{ST} was just 0.04 between the Willmore Wilderness and the other two study areas, but just 0.02 (marginally greater than zero) between northern Alberta and the CLM. The highest F_{ST} (greatest genetic differentiation) when comparing Alberta samples to other provinces was between Ontario and the Willmore Wilderness ($F_{ST} = 0.14$; Table S2).

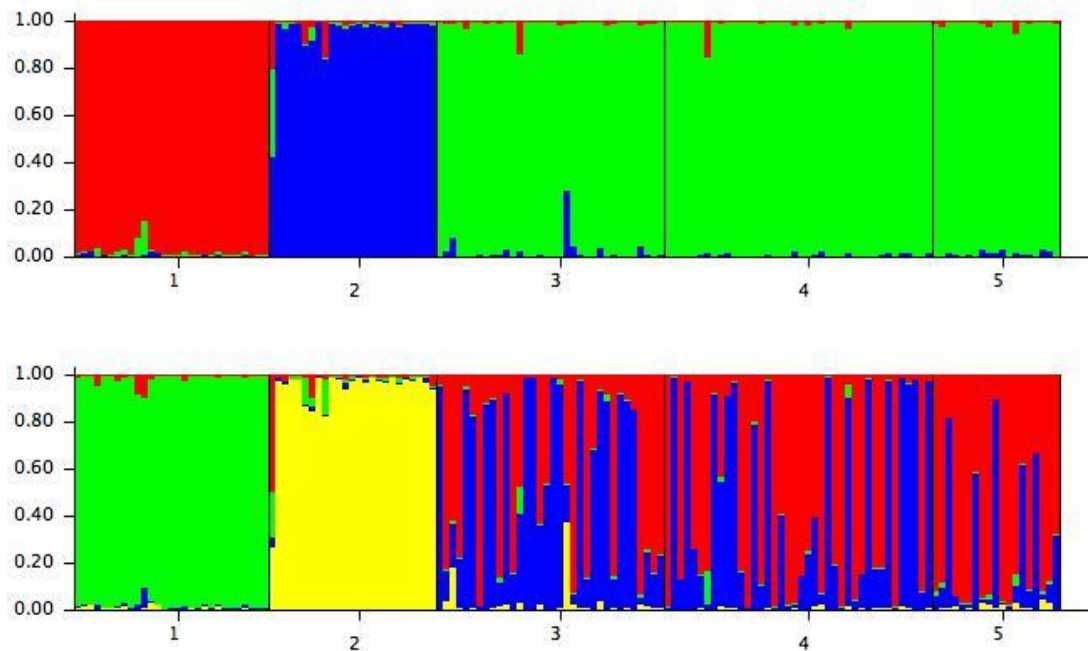


Fig. 2. The probability of population structuring when 3 (upper; $k = 3$), or 4 (lower; $k = 4$), populations are assumed across fifteen-locus fisher (*Pekania pennanti*) genotype data. Each vertical line represents the probability of population assignment for an individual. Multiple runs under the same conditions

converged, and further increases in k did not produce plausible clusters nor did they increase the likelihood meaningfully (likelihoods rose sharply with each step from $k = 1$ through $k = 4$; Figure S2). The populations are: 1 Ontario; 2 Manitoba; 3 northern Alberta; 4 Cooking Lake Moraine; and 5 Willmore Wilderness in the Rocky Mountains. In either situation, Cooking Lake Moraine samples are most closely related to samples from northern Alberta and the Willmore Wilderness.

Only 2 of 109 alleles (173 at Ma-2, and 136 at Lut604) were indicative of reintroduction success; they were found only in the CLM, Ontario, and Manitoba populations. These alleles occurred in few animals in the CLM but are common in Ontario samples (Table 1). We tested individual origins using the software GeneClass2 (Piry et al. 2004); no CLM individual showed a statistically meaningful departure from expectation for pure Alberta ancestry (lowest p -value = 0.05 which is not significant after correcting for small sample sizes). There were no alleles unique to the CLM, indicating that re-stocking is unlikely. Together, these results provide strong support for recolonization of the CLM from northern Alberta and Willmore Wilderness areas rather than successful reintroduction of founder individuals from Ontario or Manitoba.

2.6 DISCUSSION

Contemporary fisher samples from the Cooking Lake Moraine (CLM) show no significant genetic trace of reintroduced individuals. Some reintroduced individuals remained close to release locations for up to several months after reintroduction (Badry 1994). However, our data suggest few if any F1 individuals survived. Instead it appears that recolonization by Albertan individuals is responsible for the current presence of fisher on the CLM landscape. This result is not uncommon; a review of all fisher reintroductions (Lewis et al. 2012; Powell et al. 2012), demonstrates that 8/17 (47%) of reintroductions have been given a different reintroduction status once genetic testing for reintroduction success was performed (Table 2). Generally, reintroduction success is therefore lower than expected, but recolonization success may be higher.

Cryptic recolonization has been observed in other commonly reintroduced mammals. In a similar example, Kruckenhauser and Pinsker (2004) review multiple Alpine Marmot (*Marmota marmota*) reintroductions and demonstrate that three contemporary Austrian populations are more closely related to proximal Austrian populations than putative founder individuals from France – evidence for recolonization across the Austrian Alps. Mirroring this result, Hicks et al. (2007) conclude that dispersal is much higher in Elk (*Cervus elaphus*) than previously believed because of the

astoundingly high genetic diversity within, and low genetic divergence between, western North America's reintroduced populations. Statham et al. (2012) document the unanticipated continental recolonization of native Red Fox (*Vulpes vulpes*) compared to the perceived reintroduction success from European sources. Such examples highlight that many reintroductions are sub-optimal conservation strategies when compared to the ability of species to naturally recolonize historic ranges. Rather, facilitating functional connectivity may be a more effective conservation goal.

Caveats

Genetic data from populations that have undergone a bottleneck effect, such as reintroductions, must be collected within a limited period to avoid errors arising from mutation and/or genetic drift (Nei et al. 1975). Within the CLM samples, two alleles suggested ancestry of eastern fishers (Table 1), but they may have been the result of a single microsatellite mutation (Waits & Paetkau 2005). Longer microsatellites mutate more frequently and rates can vary from 10^{-3} to 10^{-4} per locus per generation (Ellegren 2000). Ideally, genetic samples should be collected at multiple time points from reintroduction, source, and adjacent populations to document drift and mutation rates.

Post translocation genetic data does not distinguish the exact date, route, or mechanism by which individuals disperse and recolonize former ranges. However, our genetic analysis has reduced the possibility of reintroduction success from eastern populations, yet a contemporary population still exists. We can conceive two possible mechanisms to explain contemporary occurrence of fisher on the CLM: 1) "horse-power" reflecting unknown (and unsanctioned) translocation, and 2) "paw-power" reflecting multiple routes of natural dispersal.

Our genetic analyses found eight of 109 alleles diagnostic of recolonization from northern Alberta. We find it unlikely two of these alleles (MP182 175 and Mvis72 258) could be explained by a mutation because they do not match the microsatellite allele sequence for that loci (Table 1). These alleles are therefore truly diagnostic, and suggest that dispersal happened recently and quickly across a long distance; it is unlikely that these alleles are the result of independent parallel mutations within each Albertan population. Fishers use areas of high forest cover compared to what is available (Badry 1994; Koen et al. 2007; LaPoint et al. 2013; Koen et al. 2014). Dispersal may happen through unsuitable habitat if distances are small and within a home territory (LaPoint et al. 2013); average dispersal distances are typically less than 30 km for either sex (6 – 29 km; Aubry and Raley 2006; Lofroth et al. 2010). For fisher, dispersal distance from either the North Saskatchewan River or the southern edge of

Alberta's boreal forest to the CLM is large and was previously believed to be unattainable (Badry et al. 1997; Proulx & Genereux 2009). However, mustelids can demonstrate amazing feats of dispersal. Carr et al. (2007) demonstrate that fisher recolonized eastern Ontario from the Adirondack Mountains – on the other side of the St. Lawrence River – and one case of wolverine (*Gulo gulo*) dispersal exists between the Rocky and Sierra Nevada Mountain Ranges (Moriarty et al. 2009). We cannot reliably distinguish between “horse-power” and “paw-power” mechanisms of provincial recolonization, but find a necessarily large-scale successful unsanctioned release unlikely. This research demonstrates that recolonization may be an important aspect of range stability. Given equal opportunity, landscape management that facilitates connectivity and natural recolonization may ultimately be a better use of conservation resources than reintroductions, at least in landscapes with proximal populations.

2.7 CONSERVATION IMPLICATIONS

If cryptic recolonization is misinterpreted as reintroduction success, it implies that our concept of functional connectivity may be flawed. Functional connectivity is a species-specific concept, and describes how genes, individuals, or populations move through a landscape (Goodwin 2003; Garroway et al. 2008; Luque et al. 2012; Rudnick et al. 2012). However, if individuals are recolonizing areas that were previously perceived to be functionally disjunct from the rest of the species range, then individuals (and their genes) are moving through landscape features more readily than predicted. We therefore recommend conservation biologists not underestimate the ability of species to recolonize former ranges. There may be situations where connectivity is detrimental to establishing populations, however, if there is even a small chance of natural recolonization we recommend investing the time and money into non-invasively sampling the genetic signatures of both reintroduced individuals and proximal populations across a series of time intervals. These genetic measurements inform landscape resistance modeling (Cushman et al. 2006; McRae et al. 2008; Rudnick et al. 2012; Zeller et al. 2012; Koen et al. 2014, 2016; Elliot et al. 2014), and translocation evaluation (Bowman et al. 2016) including the need for assisted colonization in response to climate change (Rout et al. 2013). Such emerging applications in landscape genetics and wildlife management have applicable ramifications on future biodiversity through corridor and conservation area planning (Spear et al. 2005; Balkenhol et al. 2009; Schwartz et al. 2010). The accurate quantification and perception of functional connectivity, which can be empirically documented through recolonization events, is paramount for decision making and implementing the best conservation management techniques.

Our results from the CLM fisher reintroduction (Table 1), fisher reintroduction genetics in general (Table 2), and a sample of mammalian reintroduction events from the literature demonstrate the importance of employing genetic data for comparing reintroductions and recolonizations as optimal conservation strategies. We recommend that given the large amount of money, political capital, public buy-in, and hard work invested in reintroductions – in addition to the great conservation importance of their outcomes – that if recolonization is even minutely probable, reintroduction be treated as a conservation experiment, with genetic samples obtained and analyzed from all animals, non-invasive samples obtained from proximal and source populations, and results published that generate and disseminate an objective conclusion about reintroduction vs. recolonization success. Documenting the relative success of reintroductions and recolonizations across varying degrees of functional connectivity helps conservation biologists understand the efficacy of these conservation tools, thereby saving valuable conservation funds. Alternative conservation approaches – such as landscape management to facilitate functional connectivity – may be more effective long term, and moreover fix some of the very problems that led to extirpation in the first place.

2.8 ACKNOWLEDGMENTS

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3.0 CHALLENGES AND OPPORTUNITIES IN USING CAMERA-TRAP DATA FOR SPECIES AT RISK AND BIODIVERSITY MANAGEMENT

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3.1 PREFACE

Management decisions that effectively maintain biodiversity require information on how species relate to their environment. Scientists gather this information in multiple ways (Scott et al. 2002, Williams et al. 2002). One rapidly expanding mode of gathering species data across large landscapes is through camera trapping (Burton et al. 2015, Steenweg et al. 2016). Many Albertan agencies (government, industry, NGOs, academia) have invested heavily in camera trapping over the last decade, and it promises to be a major platform for research in the future. Though an effective species sampling tool, scientists are still working to understand how camera traps sample populations, what these data mean, and how the information can be used. In this research, we used camera data and movement data from one species (fishers, *Pekania pennanti*) to better understand what camera data represent for species' use of the landscape, and how we can use this knowledge to better inform future biodiversity monitoring. This chapter is from a manuscript that has been submitted to the journal *Ecological Applications* in May 2017.

3.2 ABSTRACT

Animals move across space and through time. Biologists sample these dynamic point processes by collecting observations of species occurrence, where the data density has the potential to be biased by the observation method. These species occurrence data (SOD) – including presence-absence or count data – provide the foundation for much ecological research and conservation management. An increasingly popular method for collecting SOD of terrestrial mammals is camera trapping. These data are collected from stationary points, but result from the interaction between these points and the

dynamic location and movement of individuals on the landscape. Biologists attempt to analyze these interactions and their detection probability through species distribution and occupancy modeling. These models involve movement assumptions that are rarely tested or explicitly stated. To determine whether SOD better reflects species location or movement, we compared individual locations and movements from 14 GPS collared fisher (*Pekania pennanti*) with fisher occurrence across an array of 64 stationary camera traps. We compared a suite of generalized linear models and occupancy models to determine the relative contributions of species location and movement to SOD, occupancy, and detection probability across three temporal resolutions. We demonstrate that SOD, occupancy, and detection probability are more closely associated with variance in species locations (movement) than the cameras' proximity to those locations, despite the temporal resolution investigated.

Synthesis and application: SOD are used globally for inferring ecological processes, species interactions, and understanding biodiversity shifts associated with climate and landscape change. Movement must receive greater consideration when planning, conducting, and interpreting these data to correctly infer ecological process driving data patterns. We discuss the ecological implications of our current misunderstanding of SOD, and make recommendations for future monitoring programs.

3.3 INTRODUCTION

Animals move to obtain resources and avoid competition and predation. This dynamic space-time process makes it difficult to determine exactly where individual animals are, and when; whether individuals over-lap in their space-use; and how cumulative individual locations defines the species' distribution. Biologists study these concepts by collecting animal point locations through time, where the realized locations of individuals is a thinned point process assumed, but rarely tested, to be unbiased by the observation method (Royle et al. 2014). With rapid and observable biodiversity declines and shifts in species distributions in the face of landscape and climate change (Maxwell et al. 2016), the collection and interpretation of data that accurately reflects species occurrence is a leading conservation priority (Nichols and Williams 2006, Steenweg et al. 2016).

High resolution animal locations, and inferred animal movements, have traditionally been documented through telemetry or tracking techniques (Kays et al. 2015). Telemetry is an expensive method that collects detailed individual location information but lacks the ability to document population or species changes across large spatial and temporal extents. The exciting development and rapid use of remote camera traps (CTs) allows these issues to be addressed by collecting species

occurrence data (SOD) across very large spatial and temporal scales (Burton et al. 2015), but they lack the high resolution of individual movement patterns that can be derived from radio- or GPS-telemetry. This trade-off in data resolution is acknowledged in terrestrial animal ecology, but the influence of this trade-off on the thinned point process is rarely tested. Instead the trade-off has been incorporated as assumptions inherent in statistical models that utilize data from stationary survey methods, such as CTs.

CTs provide time-series SOD in the form of presence-absence or count data for inference of distribution (Liu et al. 2011), occupancy and detectability (MacKenzie et al. 2006, Burton 2012), abundance and density (Gardner et al. 2010, Chandler and Royle 2013), habitat selection (Fisher et al. 2011), and ecological processes. Estimations derived from SOD assume that variation in species occurrence at the point in space represents variation in individuals' locations and movement through time (Turchin 1998); but they implicitly assume individuals are distributed uniformly over some region, randomly move into the range of the observation apparatus, and are detected by it. Rarely do researchers using SOD data (such as CT surveys) state the assumed relationships between measured SOD variables (such as relative species abundance) and inferred ecological process (such as movement) but this area of inquiry represents one of the most important areas for CT survey improvement (Burton et al. 2015). Several studies attempt to incorporate movement data into SOD estimates by either combining telemetry and SOD datasets (Royle et al. 2009, Popescu et al. 2014) or by using occupancy models to estimate detection probability, wherein movement is inferred from variation in the detection histories (MacKenzie and Kendall 2002, MacKenzie and Nichols 2004). However, the question remains: Does SOD better reflect the geographic location of mobile species in space and time, or where species move in space and time?

As a simple way to examine this question and test the assumptions inherent in SOD, one dataset representing individual locations and movement could be used to predict variation in SOD recorded by another. This is an examination of the thinned point process wherein 'true data' – location and movement data – explain a sub-sample of those 'true' data – the frequency of species detections – at a fixed point. Species location and movement data relative to CTs can be quantified as the mean (i.e. average geographic location), and standard deviation (i.e. variation in locations, or inferred movement) of distances between GPS fixes and each CT (Figure 1). We refer to these hereafter as 'GPS metrics' and use them to ask two questions; 1) do GPS metrics account for variation in SOD collected from stationary

surveys, such as CTs (Figure 1), and 2) is this relationship affected by the temporal resolution of summarized SOD (survey, monthly, or weekly occurrences)?

We use location data collected from fisher (*Pekania pennanti*) GPS-telemetry paired with SOD collected from a CT array overlapping collared fishers to examine whether individual locations in space and time, and variation in those locations (movement), explain the frequency of SOD across three temporal data resolutions (survey, monthly, and weekly occurrences). We expect the frequency, and probability, of animal detections to be more closely related to animal movement than to the geographic location of animals and for this relationship to increase in strength with temporal resolution from survey to weeks. CT studies to date rely on SOD collected from CTs being representative of animal locations in space and time, make implicit assumptions about movement, and infer ecological processes there from (Burton et al. 2015). We seek to explicitly quantify the contribution of animal movement (variation in locations) to this relationship and demonstrate how the inference of ecological process would change if movement, rather than locations, is the best predictor of SOD.

3.4 MATERIALS AND METHODS

Fisher are a medium-sized (2.2-7.0 kg) Mustelid native to northern North American forests from the western Cordillera to the eastern seaboard (Powell 1982). They have moderate body and home range size (Lindstedt et al. 1986) representative of mammal species investigated in previous CT surveys (Burton et al. 2015), making them a reasonable model for evaluating location and movement contributions to CT SOD. Fisher occurrence was sampled in the central east region of Alberta, Canada, an area known as the Cooking Lake Moraine (CLM; Figure 2) which supports a diverse mammal community (F. Stewart and J. Fisher, unpublished data). This 1,056 km² landscape of rolling knob and kettle topography is dominated by small wetlands, with trembling aspen (*Populus tremuloides*), balsam poplar (*Populus balsamifera*), and scattered pockets of spruce (*Picea glauca* and *P. mariana*). It is a patchwork of exurban development, agriculture, protected forested areas, and privately owned green space.

We deployed 64 camera trap (CT) sites in a 4 x 4 km² systematic grid cell array across the CLM (Figure 2). At each site the camera photographed the area surrounding a tree baited with ~5 kg of beaver meat and a commercial scent lure (O’Gorman’s™ Long Distance Call). Fisher occurrence at each CT was recorded using Reconyx™ infra-red cameras (models PC900 and PC85). CTs were deployed from December 16th 2015 through April 4th 2016 and checked once monthly. We quantified CT SOD as fisher

presence/absence during the whole survey duration (0/1), and counts of fisher presence across each month (December through March; 0 – 4), and weeks (December through March; 0 – 15).

We live-trapped and GPS-collared 14 fisher individuals from November 2015 through April 2016. Animals were captured in covered cage traps (Tomahawk 109 live-trap, Tomahawk, WI), sedated with a combination of ketamine (100 mg/ml, 12mg/kg) and midazolam (5 mg/ml, 0.3 mg/kg), vital rates monitored, and fitted with GPS tracking collars (E-obs Collar1A; Grünwald, Germany). Collars contained a GPS microchip, a tri-axial accelerometer and ultra-high frequency transmitter for telemetry and data download. The GPS was programmed with a 5-minute fix schedule when the animal was moving greater than 10 cm/s. We retrieved data from 10 animals (5 male:5 female).

All data were collected under Canadian Council of Animal Care permits approved by InnoTech Alberta (2070M-A02/048/15-P01), and the University of Alberta (AUP00000518) Animal Handling and Care Committees.

3.5 STATISTICAL METHODS

We ask whether the location and movement of fishers is related to frequency of detection of (generic) fishers – not specific individuals. Therefore, we calculated summary statistics of the distances between all GPS fixes and each CT (Figure 1); we measured the mean, standard deviation, minimum, and maximum distance (m) between all GPS collar fixes and each CT site using the Generate Near Table tool in ArcGIS 10.4.1 (Environmental Systems Research Institute, Redlands, CA). We refer to these values as our ‘GPS metrics’. The mean GPS metrics represent the average fisher locations relative to CTs. The standard deviation GPS metrics represent the variation in fisher locations (ie. species movement) relative to CTs. We tested for correlations between GPS metrics to avoid using confounding variables in our statistical models. We conducted two separate analyses to investigate; 1) the relationships between SOD, species location, and species movement and, 2) the influence of detection probability on these relationships.

The effect of movement and temporal resolution on species occurrence data

We hypothesized that (naïve) species occurrence data (SOD) is more closely related to animal movement than the geographic location of animals. To test this hypothesis we regressed SOD against GPS metrics using generalized linear models in R (R foundation for statistic computing 2017) to quantify the contribution of species location and movement to SOD. We expected that a negative relationship between the minimum GPS metric and SOD would be the result of a sampling artifact – fisher must be

close to the CT to be detected, but this is not particularly biologically informative. If SOD is reflective of animal locations, then we expect a negative relationship between SOD and the mean GPS metric: animals close to a CT are most likely to be photographed, whereas animals far from a CT are less likely. If SOD is reflective of animal movement, then we expect a negative quadratic relationship between SOD and the standard deviation (variation) of GPS metrics: high or no variability in animal locations may result in few CT photographs, whereas intermediate variation in animal locations should result in more CT photos.

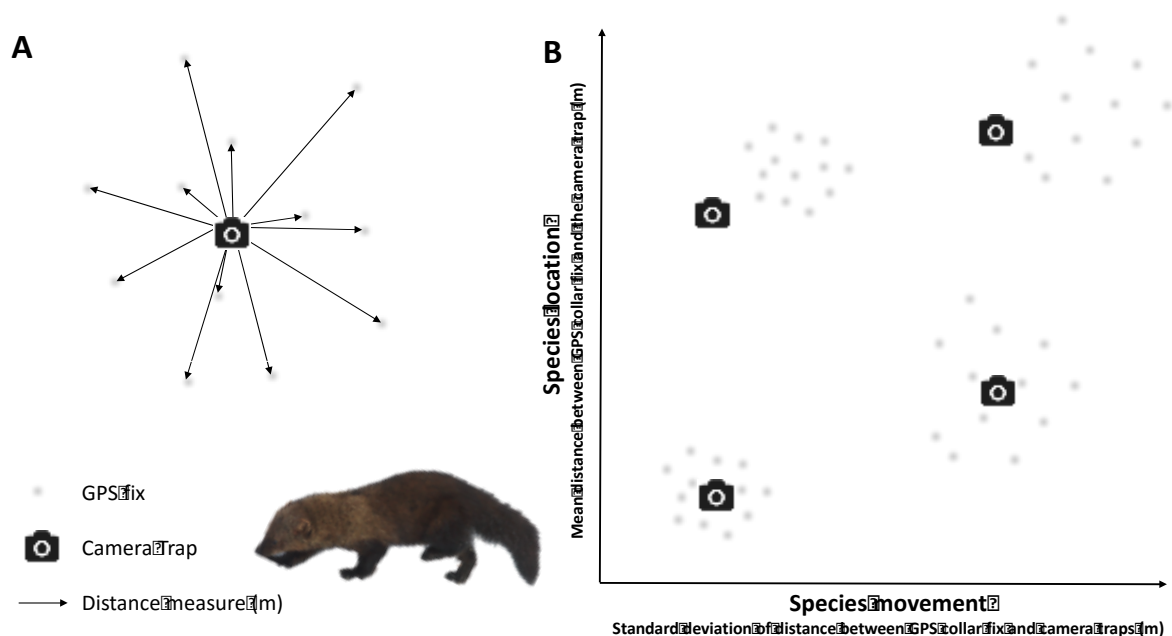


Figure 1. Species occurrence data is the result of species location and movement. To tease apart the relative contributions of these two predictors, the minimum, mean, maximum, and standard deviation of the distance between a camera trap and GPS fixes can be measured (A), and regressed against SOD. If mean distances and standard deviations are small, then the GPS data are clustered around the camera trap and will likely result in a detection, while large mean distances and standard deviations demonstrate dispersed data and likely result in no detection (B).

To investigate the effects of temporal resolution on these relationships, we competed suites of models representing the above two predictions with SOD measured as survey presence absence (0/1), monthly counts (0-4), or weekly counts (0-15). Survey presence/absence data were modelled using a binomial link function in R. Monthly count data required a multinomial regression in the R package nnet (Venables and Ripley 2002), and weekly count data was poisson distributed. Suites of models within each temporal resolution were competed using Akaike information criterion (AIC; Burnham and Anderson 2002). Results are presented as mean \pm standard error unless otherwise specified.

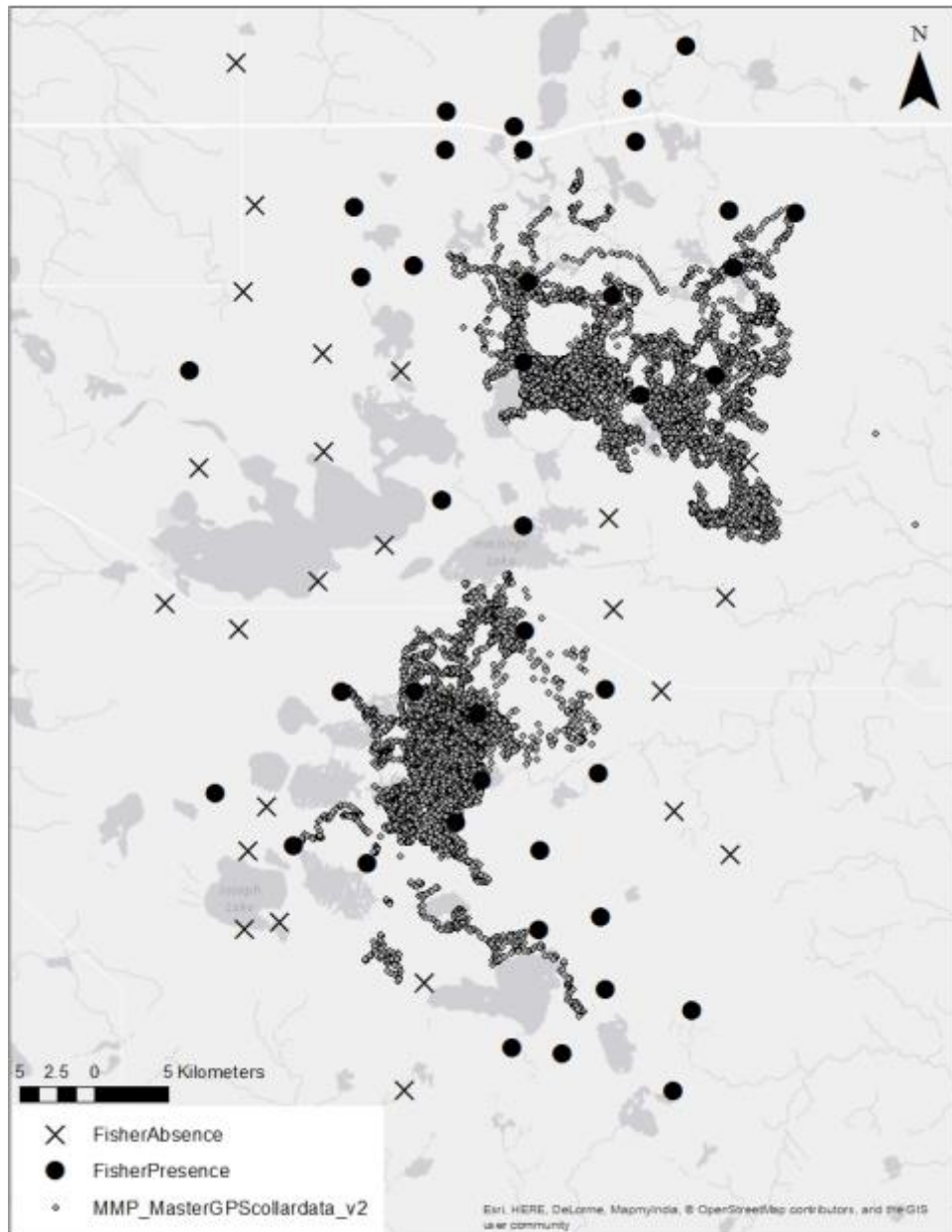


Figure 2. Fisher GPS fixes from 10 individuals are overlaid on the spatial distribution of camera trap sites deployed through winter 2015/2016 on Alberta’s Cooking Lake Moraine.

The effect of movement and temporal resolution on detection probability

We hypothesized that the probability of animal detections is more closely related to animal movement than it is to animal geographic location. To test this hypothesis we used an occupancy modeling framework to quantify the contribution of animal locations and movement to species site occupancy and detection probability (Mackenzie et al. 2006). Occupancy models use serial detection

non-detection data (a series of zeros and ones that represent species absence and presence at each study site across multiple site surveys) to quantify the probability that species absence is not a false-absence (i.e. detection probability; p). Species occupancy (Ψ) – the probability of a site being occupied by a species – is adjusted by the detection probability. Detection probability can vary among surveys (MacKenzie et al. 2006). Obtaining the serial detection/non-detection data needed for these models requires study sites to be visited multiple times and at regular intervals. We competed a null model, $\Psi(.)p(.)$, against models with all possible combinations of our GPS metrics as either occupancy (Ψ) and/or detection probability (p) covariates. We expected models involving animal movement (standard deviation GPS metric) as a detection covariate to outperform models involving animal locations (mean GPS metric) as a detection covariate.

To investigate the effects of temporal resolution – or how frequently a site is visited within an occupancy framework – on occupancy and detection probability, we competed two suits of models where species detection histories were composed of either four monthly (i.e. 0101) or 15 weekly (i.e. 01100101110101) detection non-detection histories. All occupancy models were performed in PRESENCE software v11.7 (Hines 2006) and competed in an AIC framework (Burnham and Anderson 2002). Results are presented as mean \pm standard error unless otherwise specified.

3.6 RESULTS

Sixty-four cameras were deployed for a total of 102 days (6,528 trap days), and collected 95,128 photos from December 2015 through early April 2016. Of these photos 12,156 were of fisher, with 2,032 clearly containing collared individuals. From 10 GPS-collared individuals we obtained a total of 28,088 fixes, with $2,808 \pm 1,137$ fixes per individual. GPS fixes were on average $15,188 \pm 1,281$ m away from any CT (Figure 2). Microsatellite analysis from hair samples collected throughout the study revealed that at least 32 fisher occupied the CLM during the winter of 2015/2016 (Stewart et al. in revisions). We therefore obtained GPS information from 31% of the minimum known population. Mean, standard deviation, minimum, and maximum GPS metrics were all highly correlated. We therefore did not include more than one GPS metric as a predictor variable within each of our below models.

The effect of movement on species occurrence data

Fisher SOD were best explained by GPS metrics representing animal movement (standard deviation GPS metric), rather than location relative to the camera (mean GPS metric). As predicted, a

quadratic relationship with movement out performed all linear relationships. Fisher geographic location (mean GPS metric) was never a better predictor than the null model (Figure 3).

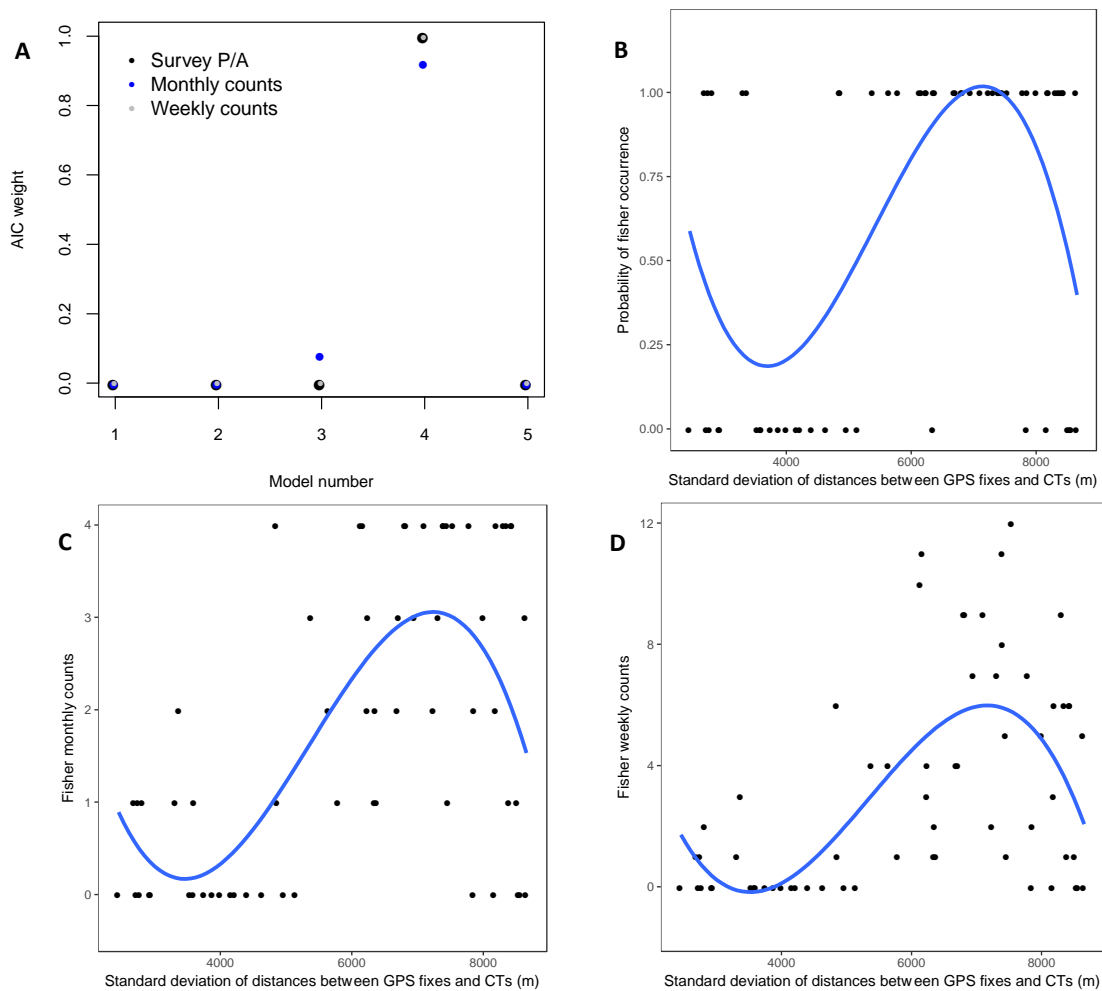


Figure 3. Generalized linear models across three temporal resolutions all demonstrate that the standard deviation of the distances between GPS collar fixes and camera traps best predict the probability of species presence absence, monthly counts, and weekly counts. Models presented in panel (A) include fisher SOD as the response variable, with predictors of: 1- null model, 2 – mean GPS metric, 3 – standard deviation GPS metric, 4 – standard deviation quadratic GPS metric, and 5 – mean GPS metric. Panels (B) through (C) demonstrate the top model from panel (A) of each temporal resolution.

The effect of movement on detection probability

Fisher detection probability was best explained by GPS metrics representing animal movement (standard deviation GPS metric), rather than geographic location relative to the camera (mean GPS metric). Fisher were observed on 43 CTs, which translates to a naïve occupancy estimate of 0.67 (43/64 sites). We competed a total of 45 monthly, and 45 weekly, models involving all possible combinations of

GPS metrics as both occupancy (Ψ) and/or detection probability (p) covariates. Top models all involved our movement GPS metric as detection probability covariates, and only involved our geographic location GPS metric as an occupancy covariate when movement was also a detection covariate.

The effect of temporal resolution on species occurrence data and detection probability

The direction of SOD relationships predicted by animal movement were consistent across all temporal resolutions (survey, monthly, and weekly; Figure 3). As predicted, relationships measured at the weekly temporal resolution were stronger than relationships measured at either the monthly or survey temporal resolutions. Modeled occupancy of fisher at sites across the CLM varied slightly with temporal resolution (monthly: $\Psi = 0.68$, $p = 0.65$; weekly: $\Psi = 0.64$, $p = 0.32$). AIC ranking of occupancy models differed between monthly and weekly temporal resolutions, however, top models always involved the standard deviation GPS metric as an occupancy and/or detection probability covariate. For monthly frequencies of fisher detections, detection probability is not dependent on survey-specific fisher movement (ER = 3.87), and fisher occupancy varies with the maximum GPS metric (ER = 70.1). For weekly frequencies of fisher detections, detection probability is dependent on survey-specific fisher movement (ER = 1.96), and fisher occupancy varies with movement (ER = 9.3).

3.7 DISCUSSION

Species movement, rather than species location, best predicts species occurrence data (SOD). This relationship holds despite temporal resolution of the data (survey presence-absence, monthly counts, or weekly counts; Figure 3). The average location of species relative to the survey device does help to explain site occupancy when combined with a species movement covariate, however, the detection probability is strongly influenced by solely the movement variability of the species (Table 2). Together, these results provide strong evidence that the thinned point process associated with collecting SOD from camera traps (CTs) better represents where species move, rather than the assumed prediction of where species are.

Movement will vary across individual, population, species, and landscape characteristics. Here we present movement variations from a mammal representative of the species encompassed in camera trap (CT) studies to date (Burton et al. 2015), however, we recognize that the relative influence of movement on species occurrence data will differ between studies and species investigated. This is an important point to consider when interpreting SOD from multiple studies; the ecological processes and inferred implications derived from each study may differ. To generate more robust conclusions on the

relationship between SOD and movement variation, we recommend that the analyses presented here be repeated in other systems.

We utilized occupancy models to quantify the contributions of species location and movement to detection probability. However, we knowingly make several common violations of occupancy assumptions: closure and site independence (McKenzie et al. 2006). The fisher population studied here demonstrates high genetic connectivity with adjacent provincial populations (Stewart et al., in review), but it is unlikely that dispersal between populations occurred during our winter study period, or that juveniles were detected (Powel 1982) on our CTs; therefore, we assume this population to be closed for the period investigated here. CTs were not independent within this study as fisher GPS tracks overlapped multiple camera sites, and multiple fisher have been detected through non-invasive genetic tagging at many camera locations (F. Stewart and J. Fisher, unpublished data). We do not anticipate the effects of these violations to be greater than the benefits of estimating movement and location contributions to detection probability, as presented here.

Using attractants in CT studies is common with bait and scent lures composing 22.9% and 9.0% of CT studies to date, respectfully (Burton et al. 2015). If bait is evenly distributed on the landscape it should not have a significant effect on species habitat use or movement patterns any more than temporal variability in natural food sources. Here, we do not anticipate the bait to have drastically affected the movement ecology of CLM fisher as individual GPS tracks spanned multiple CT sites, GPS tracks displayed intrasexual territoriality as is common for this species (Powell 1982), and preliminary spatial capture-recapture models (Burgar et al. in prep) demonstrate similar population density as other fisher studies (Powell et al. 1994; Koen et al. 2007; Popescu et al. 2014). However, results may vary when comparing studies with baited surveys to studies without baited surveys, and one explanation may be the presence and type of bait used.

3.8 IMPLICATIONS FOR ECOLOGY

Wildlife surveys commonly aim to monitor more than one species. CTs, in particular, are explicitly used for this purpose; a quarter (26.2%) of studies to date use CT images to estimate the density of multiple species (Burton et al. 2015). Our results suggest that using a single CT sampling design for obtaining SOD from multiple species may result in inaccurate inference of ecological process, as SOD varies with species mobility. For example, within one study investigating mesocarnivore occurrence on camera traps, the relative abundance of coyote (*Canis latrans*) may be inferred as being

higher than American marten (*Martes americana*) because more photos of coyote than marten were obtained. Although the space-use of both species relies on many factors, coyote generally have larger territories, longer step lengths, and move more within a single day than marten. Given our results presented here, the greater movement variability of coyotes is the most likely explanatory factor for inferred increases in coyote relative abundance when compared to marten.

The probability of species detection in multi-species surveys is also likely to vary with species movement. In the above example, we would expect that coyote detection probability would be greater than fisher detection probability, not because of differences in species density or abundance as is commonly highlighted in the literature (Royle et al. 2013), but because of differences in the movement ability of both species. This concept needs to be extended across all species monitored within a multi-species survey, and receive much greater consideration when interpreting and modeling SOD.

Using data collected from past species surveys, whether from CTs or other stationary methods, involves movement considerations for data interpretation. However, incorporating movement considerations in future CT studies will greatly enhance our understanding of what each species SOD actually represents. We demonstrate that SOD is best predicted by a negative quadratic relationship with species movement variability. This relationship suggests that the number, and spacing of CTs will need to correspond with not only the amount of movement that a typical species displays, but the variability of within-species or within-study movement. Ideally, the number and spacing of camera traps hits the peak of this negative quadratic relationship – too few or too many camera traps, or traps that are spaced too wide or too closely together, will underestimate SOD. As such, species with small variation in movement may require more CT sites in close clusters, while species with larger variation in movement will dispersed CTs. CT site placement and density could be scaled by species home range size or average step length. The discussion of these concepts are beginning within the scientific and management literature (Pease et al. 2016), however we strongly endorse their quick implementation.

Movement and location data, as shown here, provides the ability to inform spatial density models, which assume a negative logarithmic relationship between the probability of detection and the centre of habitat use (a.k.a. “activity centre”; Royle et al. 2013). Spatial capture-recapture models (and species occurrence data in general) make the explicit assumption that “thinning” between actual process (animal locations) and observed process (camera detection rates) happens with distance between the animal locations and the camera. Here, we tested that assumption with our mean GPS

metric and found that distance tells only part of the story, and not the biggest part – the dispersion of animal locations matters most. Most CT studies estimate density from capture-recapture methods (Burton et al. 2015), and our results presented here therefore have profound implications on future density estimations.

3.9 RECOMMENDATIONS FOR FUTURE MONITORING PROGRAMS

Future CT research, and monitoring programs in general, need to place increased consideration into the movement ecology of the focal species(s) prior to survey deployment. The results presented here suggest that obtaining SOD and the probability of detection varies with species movement rather than species average geographic location. For multi-species surveys, we recommend that grid cell size vary with the smallest expected home range, that species with either very small or very large home range size receive a disproportionate number of survey stations relative to species with intermediate home range size within each study, that landscape fragmentation and resistance values be considered when estimating species home range size, and that acknowledgement of the probability of detection varying with home range size be considered an important aspect of CT deployment and data analysis. Including multiple bait types to increase the detection probability of multi-species surveys, group subset clusters of cameras to obtain relative detections between species of large and small home ranges, or use species-specific survey methods for each species within a multi-species survey may increase detection probability for each target species. For example, using baited camera traps may be appropriate for elusive species (e.g. wolverine (*Gulo gulo*)), but may not reflect the abundance or density of conspicuous species within the study area (e.g. snowshoe hare (*Lepus americanus*)). Live-trapping, snow tracking, plate tracking, or GPS collaring may be more appropriate for conspicuous species. After data collection, researchers should report the correlation value of SOD, and detection probability (p), with expected species home range size(s) to justify the link between survey deployment and species life-history within their study.

Modeling projections for biodiversity response to shifts in landscape and climate are based on SOD, and assume to reliably predict where species occur. We demonstrate that these projections may be more closely related to species movement rather than species location. This result has profound implication on how we interpret SOD collected from stationary surveys, distribution model projections and the inferred ecological processes that govern these systems, and ultimately how to anticipate species response to landscape and climate change. We advocate for increased consideration around

movement assumptions when deploying SOD field methods, when interpreting SOD, and when incorporating SOD into models of distribution, occupancy (MacKenzie et al. 2006), abundance, and density (Royle et al. 2013). Ultimately, movement ecology of the target species(s) needs to be prioritized when quantifying biodiversity from stationary methods.

3.10 ACKNOWLEDGEMENTS

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4.0 MAMMALAN BIODIVERSITY IN CENTRAL ALBERTA'S HEARTLAND

4.1 PREFACE

This component of the *Moraine Mesocarnivores Project* is the core objective of the study. Alberta's Land Use Framework (LUF) – the central piece of policy for land-use planning to conserve biodiversity – explicitly assumes that most of Alberta's biodiversity will be maintained on "working landscapes". These landscapes are mosaics of forested protected areas, semi-forested private lands, agriculture, transportation, petroleum extraction, and residential infrastructure. This central assumption of the LUF has never been explicitly tested. The Cooking Lake Moraine is, in many ways, a landscape-scale model of the many interacting land-uses in Alberta, and an ideal place to test these assumptions. Our goal was to examine how multiple mammal species were distributed across this landscape, and how their relative abundance and persistence related to its diverse kinds of land-use. This component is the last to completed, and will be finished in 2017-2018.

4.2 INTRODUCTION

Conserving biodiversity and ecological integrity is a primary purpose of parks and protected areas (PAs) worldwide, though there is great variability in how well PAs are achieving this goal (Parrish et al. 2003). In Alberta, Canada, the "working landscape" has been impacted by agriculture for over a century; forest harvesting for over fifty years; and more recently by rural residential development, and petroleum exploration and extraction. Each resource sector is accompanied by marked increased in road and trail access. The cumulative effects of multiple forms of development are widespread across Alberta, contributing to declines of woodland caribou (Sorensen et al. 2008, Hervieux et al. 2013), range contraction of wolverines (Fisher et al. 2013), and a suite of other ecological impacts (Schneider et al. 2006). Growing landscape impacts necessitated a provincial strategy to plan for land-use with a goal of maintaining biodiversity - Alberta's Land-use Framework¹ (LUF). Protected areas are a key component of the LUF, which is designed to balance environmental sustainability with economic opportunity.

¹ https://www.landuse.alberta.ca/Documents/LUF_Land-use_Framework_Report-2008-12.pdf

The LUF assumes that Alberta biodiversity will be maintained by a combination of PAs and the working landscape, functioning together to sustain viable wildlife populations and biotic communities. However, this assumption only holds if (1) PAs and adjacent patches of working landscape are functionally connected – operating together to support animal populations; and (2) large intact landscapes and PAs are functionally connected over large scales to allow immigration and emigration, and hence gene flow, among populations (Pulliam 1988, Pulliam and Danielson 1991, Dunning et al. 1992, Goodwin and Fahrig 2002). These assumptions have never been tested for Alberta, but are crucial to maintaining ecological integrity and biodiversity of a landscape.

The biodiversity value and conservation role of the many small protected areas common throughout Alberta – in addition to protected parcels owned by NGOs – has always been controversial. Most small PAs are embedded within mixed-use landscapes – patchworks of forested, protected areas, small-scale agriculture, rural residential areas, and natural fragments on private land. How valuable are these PA islands for maintaining biodiversity and ecological integrity?

In fact, increasing evidence shows they can be extremely valuable, particularly when patches of natural habitats are connected with one another. It is true that habitat fragmentation and loss adversely affect the persistence of many wildlife species (Andren 1994, Fahrig 1997, 2003). However, habitat fragmented is not always lost. Mixed forested and agricultural landscapes can support viable and persistent wildlife populations in woodland patches within agricultural landscapes (Middleton and Merriam 1983, Henderson et al. 1985, Bennett et al. 1994), provided habitat patches remain sufficiently connected for wildlife species (Taylor et al. 1993). In fact, agricultural habitat may actually provide complementary or supplementary resources to species living in wooded patches (*i.e.*, prey), facilitating their persistence (Dunning et al. 1992, Fisher and Merriam 2000). Just as importantly, emerging research shows that protected areas can act as catalysts for integrated conservation between government and private lands in mixed-use landscapes (Miller et al. 2012). Both ecologically and socially, small protected areas may be significant, even essential, in maintaining biodiversity in mixed-use landscapes.

Measuring all biodiversity is a daunting task but mammals are a useful biodiversity indicator. Mixed-use landscapes may be particularly suited to mammalian mesocarnivores – mid-sized mammalian predators, such as marten, fishers, foxes, coyotes, lynx, and raccoons – which may persist in forest landscapes with a degree of agricultural incursion or fragmentation. Working landscapes often have reduced or absent top predator populations (such as bears and wolves). In the absence of top predators,

mesocarnivores are released from predation and competition, and their populations can increase (Prugh et al. 2009, Terborgh and Estes 2010). Moreover, fragmented landscapes often support diverse small-mammal populations, which provide abundant prey for mesocarnivores. Where wooded patches are large enough to provide breeding habitat, but are interspersed with “novel” agricultural patches that provide a resource subsidy, fragmented forest landscapes may support persistent populations of mesocarnivores. The landscape features allowing species’ persistence is both landscape and species-specific (Fisher et al. 2005), preventing generalities from other parts of the continent. In western Canadian landscapes, we know little about mesocarnivore species persistence in fragmented, mixed-use forest-agricultural systems, but this information is vital to evidence-based decision-making designed to maintain ecological integrity within small protected areas.

We seek to help supply this information by examining the diversity, distribution, and connectivity of mesocarnivores on the Cooking Lake Moraine in central Alberta: a matrix of protected areas, private land with natural habitats, and areas of significant anthropogenic disturbance. We ask several related questions:

1. What mesocarnivore species occupy this mixed natural-agricultural system?
2. What landscape elements – including natural and anthropogenic features – positively or negatively affect mammal occurrence and diversity?
3. How functionally connected are PAs within this landscape? Can animals move among disjunct PAs to form functional home ranges?
4. How functionally connected is the CLM to other forested landscapes to the west and north, separated by intensive development? Specifically, are fishers (*Pekania pennanti*) occurring on the Moraine more genetically related to re-introduced ancestors from Ontario and Manitoba, or is there evidence of genetic contribution from adjacent landscapes indicating functional connectivity?

4.3 METHODS

Study Area

The Cooking Lake Moraine is approximately 1,500 km² of primarily aspen forest with patches of white spruce, open meadows, and small permanent water bodies (Pybus *et al.* 2009; Patriquin 2014). This (relatively) intact and heterogeneous complex sits in a matrix of agricultural land. Our study area covers the moraine and its agricultural environs, an area over 1,060 km² in size. The moraine is, to a

large degree, spatially disjunct from tracts of contiguous forests to the north and west. Several parks and protected areas cover this landscape, limiting development and human activity (Figure 1). As such,

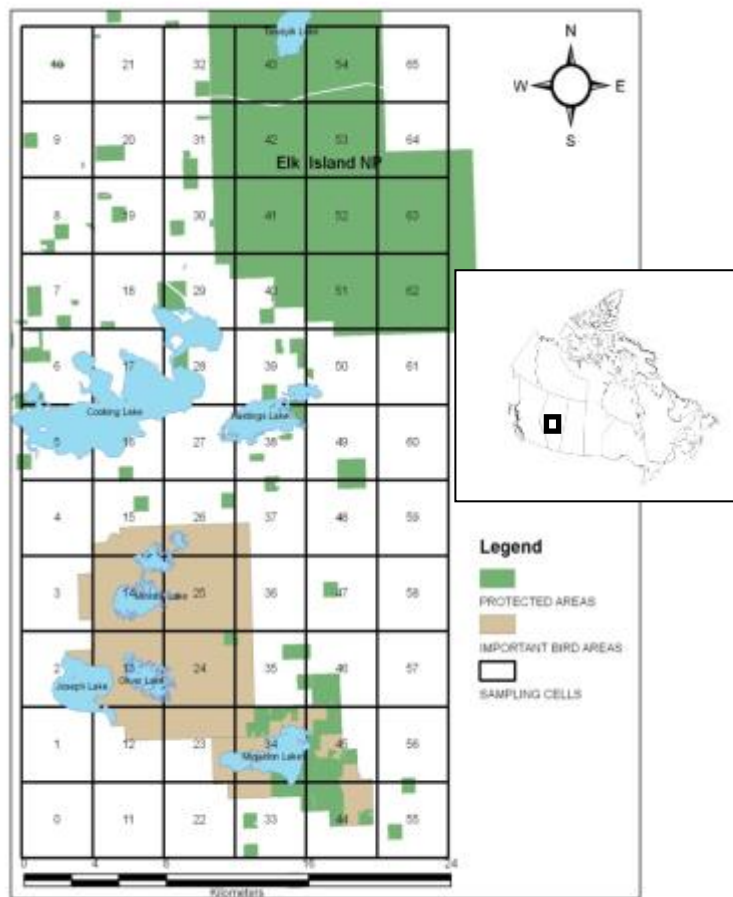


Figure 1. Mesocarnivore diversity is being sampled within a systematic design on the Cooking Lake Moraine area of Alberta, Canada. 66, 4km x 4km sampling cells were designated in GIS. Within 64 of these cells, a sampling site was subjectively placed within a forested area a minimum of 1-ha in size.

the CLM may be an important source of biodiversity for the entire region. Elk Island National Park, within the moraine, is a fenced park with large populations of ungulates, wolves, coyotes and other mesocarnivores, as well as diverse bird and plant communities. This Park, together with the many provincial protected areas and conservation properties (*i.e.*, ACA, DU, ABFG, EALT and NCC) on the moraine, support high biodiversity, but an empirical, multi-species analysis of the composition of the mammalian community has not been conducted.

Species sampling

Mesocarnivore occurrence is being surveyed using a multi-method approach (Nichols et al. 2008) involving a combination of non-invasive genetic tagging (NGT) (Waits and Paetkau 2005) *via* hair

sampling and infra-red remote cameras (IRCs) (O'Connell et al. 2011). This double-method sampling has proven effective for mammals elsewhere in Alberta (Fisher et al. 2011, Fisher et al. 2012, Fisher et al. 2013) and has a high probability of detecting mesocarnivores, including fishers (Fisher and Bradbury 2014). Hair samples for NGT were collected using Gaucho barbed wire wrapped around a tree baited with beaver fat and O'Gorman's scent lure. At each station, we also deployed one Reconyx™ infrared-triggered digital camera. Cameras are placed *ca.* 6-10 metres from the tree such that the camera's detection cone and field of view includes the NGT hair trap and the area surrounding it. DNA from collected hairs have been extracted and analysed to identify species using mitochondrial DNA (mtDNA), which is then compared against a DNA reference library of all known mammal species in the region. For fishers, individuals and gender are identified using microsatellite (nuclear DNA) analysis. Individual capture histories can be used in mark-recapture models to estimate population sizes and densities.

NGT provides unique information, but may underestimate species' occurrence. Absence of hair may result from (1) an absent individual, or (2) a present, but undetected individual. Such imperfect detection has ramifications for estimates of species occupancy, density, and habitat use (MacKenzie et al. 2002, MacKenzie et al. 2006). To maximise detectability, we are surveying mesocarnivore occurrence using camera traps and hair traps. Cameras are triggered by heat-in-motion and are set to take a series of 5 photographs at each detection event. Images containing human activity are permanently deleted immediately; following this, all other images are being triple-redundant stored for analysis. Images are analysed and summarised for species presence, creating a serial detection-nondetection dataset for each site. Camera data on the mesocarnivore community will inform landscape-scale species-distribution models.

4.4 RESULTS

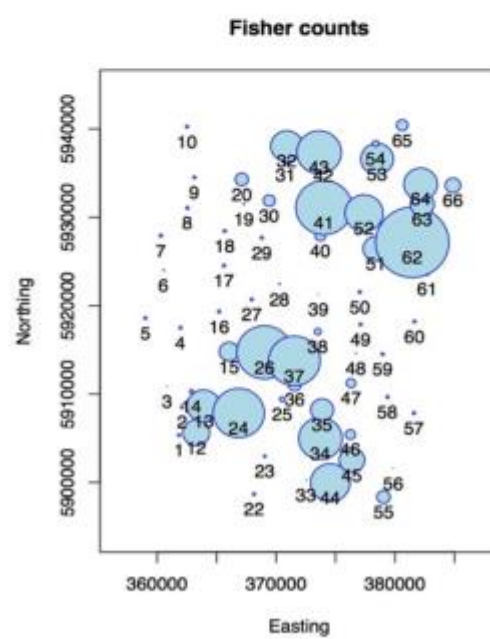
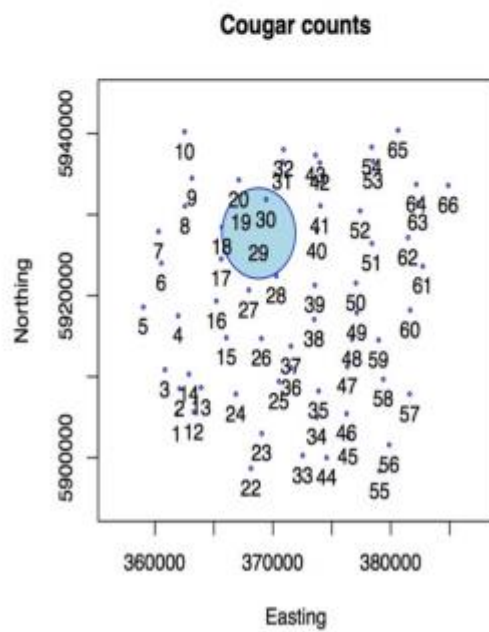
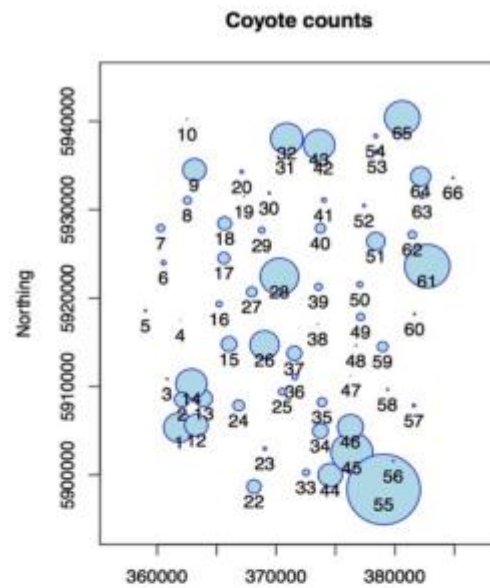
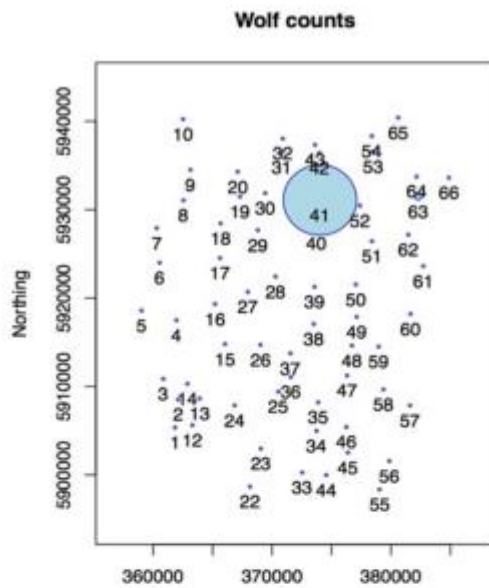
We deployed a total of 64 sampling sites across the Cooking Lake Moraine and sampled them monthly from November 2013 to June 2014, and this year from November 2015 to April 2016. We have collected 230,118 photos and 750 hair samples across the study area.

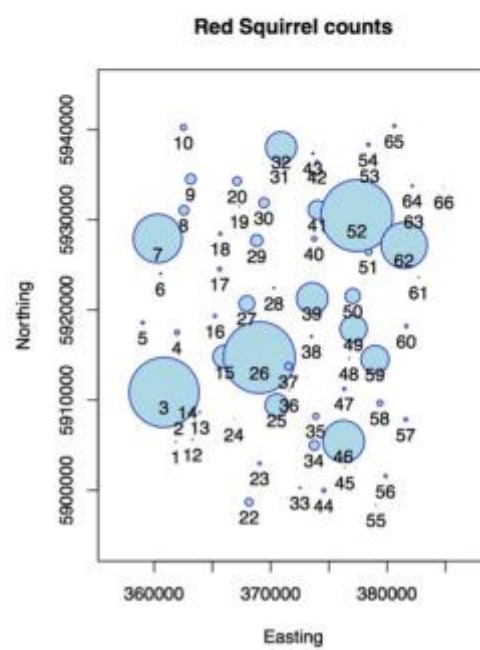
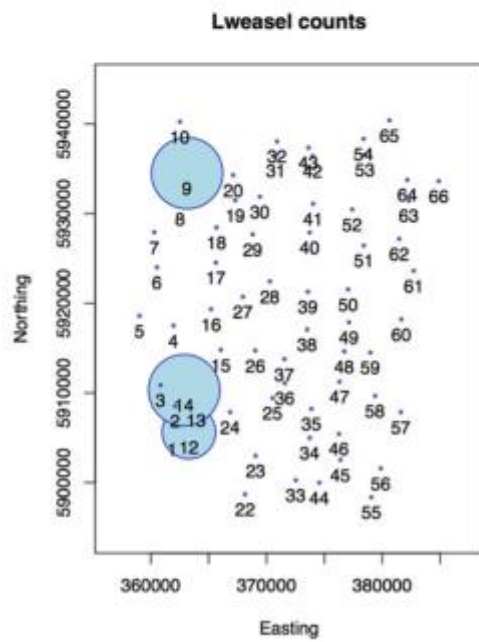
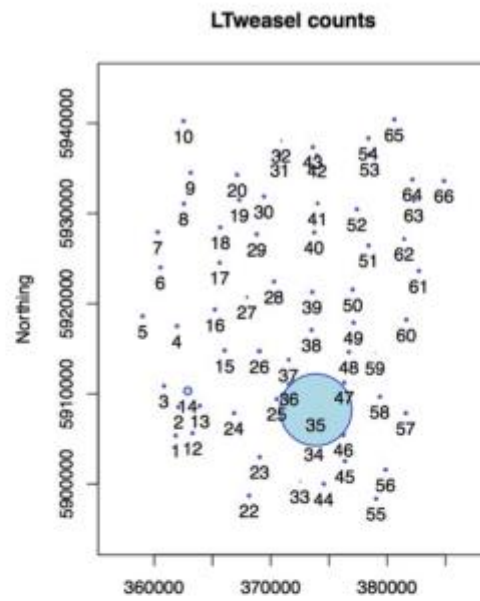
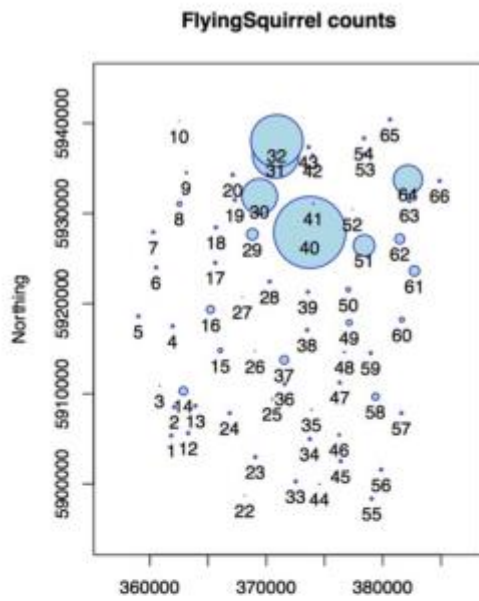
4.4.1 Mammal communities

Moose (*Alces alces*), white tailed deer (*Odocoileus virginianus*), mule deer (*Odocoileus hemionus*) red fox (*Vulpes vulpes*), coyote (*Canis latrans*), wolf (*Canis lupus*), least (*Mustela nivalis*), short-tailed (*Mustela erminea*) and long-tailed (*Mustela frenata*) weasels, porcupine (*Erethizon dorsatum*), striped

skunk (*Mephitis mephitis*), wood bison (*Bison bison athabasca*), elk (*Cervus canadensis*), black bear (*Ursus americanus*), striped skunk (*Mephitis mephitis*), cougar (*Puma concolor*), and domestic animals such as the domestic dog (*Canis lupis familiaris*) were also detected, illustrating that mammalian diversity is high across this landscape.

We used R statistical software to generate bubble plots of relative abundance for each species (Figure 3). The distribution and relative abundance of each species varied widely across the study area.





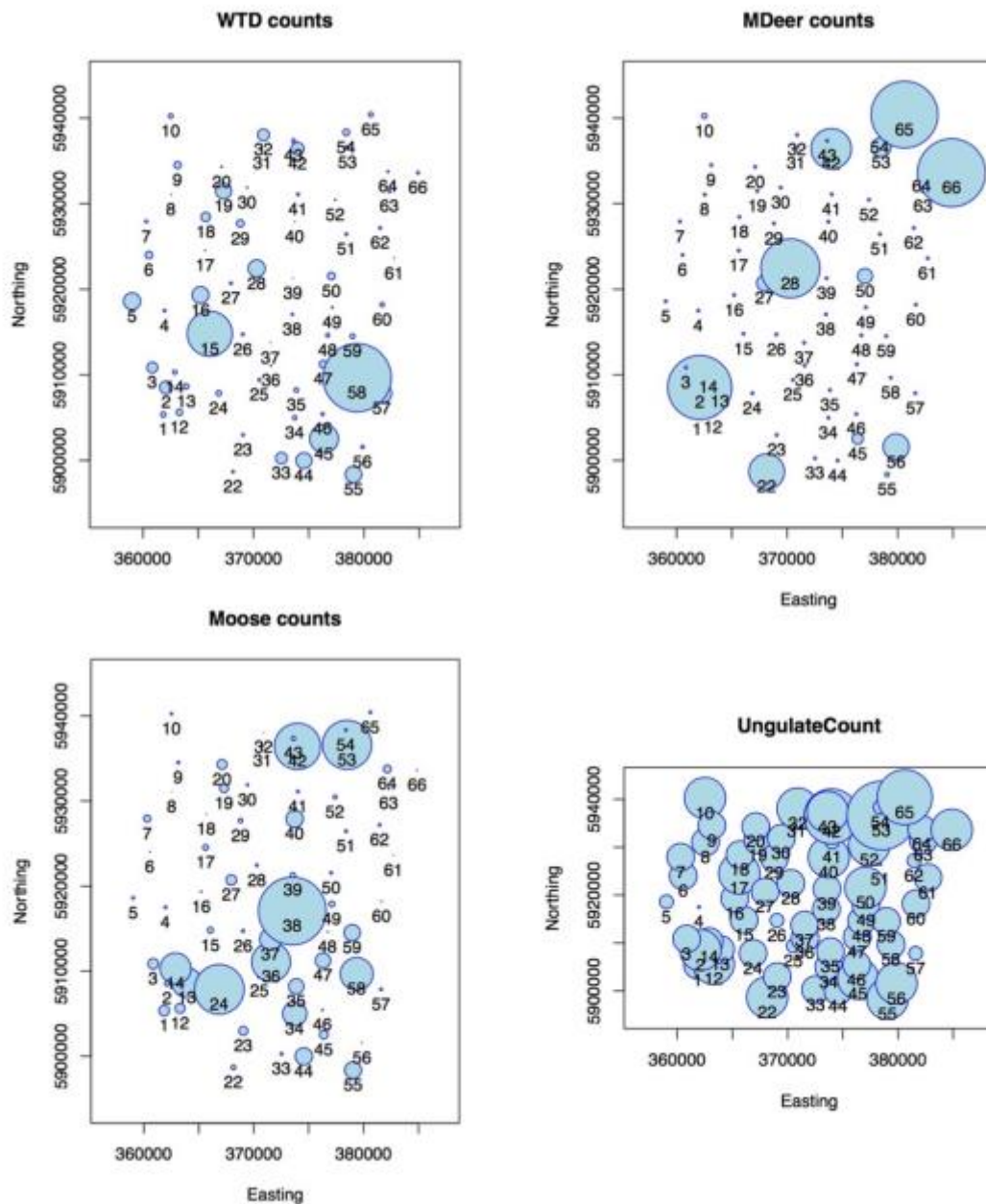


Figure 3. The distribution of mammals varied markedly across this mixed-use landscape. Each dot is a camera trap. The numbers of observations of each species are scaled to the size of the bubble around each site, as a visual index of relative abundance. Large carnivores were very rare, whereas mesocarnivores were abundant and widespread. Moose and both deer species occupied much of the landscape, suggesting the importance of different natural and anthropogenic features in maintaining this community.

4.4.2 Fisher occupancy

Camera surveys, like any survey, are challenged by the possibility of false absences: failing to detect a species that is, in fact, present. To assess the reliability of camera data, we must first estimate the probability of detecting that species if it is present at a site (MacKenzie et al. 2002). The frequency of repeated species detections at a camera can be used much like a mark-recapture history to estimate this probability of detection. Given this probability, we can correct for potential false absences and thus more accurately estimate the probability that fishers occupied a site during a sampling period. This *probability of site occupancy* takes into account missed detections, and because it describes the *likelihood* that a fisher uses a site, it is a more ecologically meaningful measure of a species' site-use than simply presence or absence, which is an all-or-none measure. Detectability and occupancy are estimated using hierarchical occupancy models (MacKenzie et al. 2006), which are gaining widespread use for examining species' distributions ranging from wolverines (Fisher et al. 2013) to salmon (Fisher et al. 2014a) and grizzly bears (Fisher et al. 2014b).

Occupancy is not a static measure; it is expected to change through time (MacKenzie et al. 2003). For example, sites without fisher can become occupied in the following season, whereas sites with fishers in one season may have no fishers in the next season, as they die, or emigrate to better habitat. Examining how occupancy changes among seasons helps us better understand the influence of environmental conditions on fisher distribution.

We used multi-season occupancy models (MacKenzie et al. 2003; MacKenzie et al. 2006) for a preliminary assessment of detectability and occupancy of fishers from 2014 camera data; we are currently sorting 2016 data and will conduct another assessment with both 2014 & 2016 data. We assumed that each month of camera sampling represents a distinct and independent survey. We assumed that fisher occupancy could change between seasons, however, as individuals give birth, die, immigrate or emigrate between patches. We therefore divided the sampling period into 4 seasons, with 2 monthly surveys within each: Nov-Dec (autumn), Jan-Feb (winter), Mar-Apr (breeding), and May-Jun (kit emergence). Each season is assumed to be closed to changes to occupancy at the species level – that is, fishers will not disappear completely from a site, appear if absent, within each season, but can change between seasons. The assignment of seasons here is somewhat arbitrary and can change to suit species biology.

We also assumed the probability of detecting a fisher on camera – given it is present – could stay the same, vary among surveys or seasons, or vary monthly within seasons. Finally, we tested whether fishers were more likely to occupy sites within protected areas or outside protected areas. We ran a model with each set of assumptions, and ranked each model by its AIC score (Akaike's Information Criterion) – a measure of how well each model fit the data³⁴. AIC scores weights were normalised to sum to 1.0 to create AIC weights, analogous to the probability that a model best explained the data, compared to other models in the set.

In the coming year, landscape structure will be quantified from available GIS data. We will use a combination of occupancy modelling (MacKenzie et al. 2002; 2006) and generalized linear modelling (Faraway 2004) to examine relationships between species occurrence and habitat features. Multiple competing hypotheses will be represented as multiple statistical models, which we will rank (Burnham and Anderson 2002) based on how well



each model fits the data. The best-supported models indicate those natural landscape features and agricultural patches that best explain mesocarnivore occurrence on the moraine, and model parameter estimates will allow us to map the probability of occurrence of species across this landscape.

The probability of detecting fishers within a month-long camera survey (given they were present at a site; p) varied across time. The probability of fisher occupancy was also highly variable across the study area. The best-supported model, which carried almost all of the weight of evidence ($AIC_w = 0.9997$), indicates that p was different for each monthly survey (Table 1). There was a low probability of detecting fishers on cameras at the onset of the study, in November and December. This probability improved throughout the winter, peaking in February and March. Detectability in May and June was very low.

Table 1. Selection of competing occupancy models of fisher distribution, each with different assumptions about probability of detection and fisher occupancy. The best-supported model is highlighted.

Detectability varies:	Occupancy varies:	AIC	Δ AIC	AIC weight	Model Likelihood	# parameters
Constant	Constant	472.45	89.97	0.00	0.00	3.00
Seasonally	Constant	428.63	46.15	0.00	0.00	6.00
Among survey months	Constant	398.54	16.06	0.00	0.00	10.00
Within seasons	Constant	474.37	91.89	0.00	0.00	4.00
Constant	Protected areas	461.44	78.96	0.00	0.00	4.00
Seasonally	Protected areas	409.20	26.72	0.00	0.00	7.00
Among survey months	Protected areas	382.48	0.00	1.00	1.00	11.00
Within seasons	Protected areas	463.38	80.90	0.00	0.00	5.00
Constant	Seasonally	469.33	86.85	0.00	0.00	6.00
Seasonally	Seasonally	458.00	75.52	0.00	0.00	9.00
Among survey months	Seasonally	457.81	75.33	0.00	0.00	13.00
Within seasons	Seasonally	471.32	88.84	0.00	0.00	7.00

After accounting for imperfect detectability, there was a significant difference in fisher occupancy inside and outside of protected areas. Fishers were ~ 4.5 times more likely to occur at camera sites within protected areas ($\psi = 0.76$, s.e. = 0.11) than sites outside of protected areas ($\psi = 0.16$, s.e. = 0.07). There was no evidence that fisher occupancy varied among seasons, and their distribution was stable throughout the study period. These are preliminary models without spatial covariates derived from GIS data, and with assumptions about seasons and surveys that deserve scrutiny (Burton et al. 2015). These models will be supplemented with data from the 2015-2016 field season, and with data quantifying anthropogenic and landscape features, to yield final results of fisher and competitor mesocarnivore species occupancy across the CLM across two years.

4.4.2 Fisher movement

We live-trapped and GPS-collared 14 fishers. Of these, we obtained GPS telemetry locations from 10 (5 males, 5 females) individuals. From these limited observations we cautiously see that fishers moved

widely around the landscape and may use undisturbed forest as activity centres and "stepping stones" across areas of developed or naturally unforested landscape (Figure 3). We also see that fisher avoid large open areas, such as those that are found as grazing areas in Cooking Lake/Blackfoot Recreation area. These results are observational and preliminary, however, utilizing the statistical technique of step selection functions (Thurfjell et al. 2014) we will quantify the proportion of used to unused habitat types. This analysis will quantify the type of habitat features required to support fisher populations, the distance between ideal habitat features, whether fisher reside within the centre or along the edge of habitats, and the speed to which fisher can travel through different habitat types – all crucial information for ensuring Alberta's landscapes "work" to maintain persistent biodiversity.



Figure 3. Movement path of Fisher male "M01", overlaid on Google Earth imagery, shows the complex network of movements over a two week period. The width of the figure represents 6km.

4.5 DISCUSSION AND FUTURE DIRECTIONS

The plan for 2017-2018 is to publish sections 2.0 and 3.0 of this report, and to explore the data and complete analyses of section 4.0. Section 4.0 will comprise two of Frances' Ph.D. thesis chapters, and will complete the writing of her thesis. This April she will start the analysis of step selection

functions of fisher GPS collar data (Section 4.4.3), and by August she will be finalizing the mammal community and fisher occupancy work (Section 4.4.1 and 4.4.2).

These chapters will be submitted to *Ecography* and *Journal of Applied Ecology*, respectfully, once written. This will guarantee at least 4 scientific articles to be published out of this work, with potential collaborations being currently developed that would all the data to used and published under other cutting edge research questions.

Frances will be continuing to provide regular public presentations on this work and gets regular invites as a guest lecturer; all of this allows for this community involved research to be disseminated through public, academic, and government institutions.

4.5.1 Community Involvement

We have contacted over 50 landowners and received the support of 26 of them for this project. The support of private landowners has been very encouraging throughout *The Moraine Mesocarnivore Project*, and the project has been the focal point for community discussions about conservation and developing greater connection and discussion facilitation between locals. We also incorporated seven CSL (Community Service Learning) students from Augustana Campus, University of Alberta, to help us input data from camera pictures and complete some basic fieldwork in throughout our 2014 & 2016 field seasons. We have engaged *Friends of Elk Island Society* in this project, and they have eagerly assisted with camera deployment and checking (see <http://www.elkisland.ca/conservation-research/mesocarnivore-monitoring>), public communication through organizing a once yearly public talk, and advertising and promoting this research to the Edmonton community. We have also engaged the *Beaver Hills Initiative*, securing financial and in-kind (GIS data) support, and their help in engaging their membership with outreach activities. Environment Canada, Ontario MNR, Trent University, and Manitoba DNR have all helped procure samples for this project. The University of Victoria has provided genetic laboratory space free of charge.

This work to date was presented three times at the annual meeting of the FEIS to an audience of ~70 people each time; the Alberta Trail Rider's Association; the Friends of Cooking Lake / Blackfoot Provincial Recreation Area; the Strathcona All Horse Association; University of Augustana's Conservation

Biology course; and InnoTech Alberta offices in Vegreville. We received very positive feedback from the local community, with dozens of people offering their time for fieldwork in both 2014 and 2016. One of the things we like best about this research is the opportunity to involve local Albertans in ecological research in their own backyards.

4.6 PRELIMINARY CONCLUSIONS

We have developed fantastic relationships and close bonds to many of the local landowners, FEIS volunteers, Alberta Park and Parks Canada staff, and Augustana campus students throughout this project. Engaging the local community in our research was a primary objective of *The Moraine Mesocarnivore Project* and we have done so with their staunch support. Frances continues to track citizen fisher sightings through the project webpage (www.mesocarnivore.weebly.com), regularly reminds associations such as the Edmonton Area Land Trust, Beaver Hills Initiative, Alberta Parks, and Nature Conservancy of Canada to ask their Twitter followers to send sightings her way. She has received over 40 citizen science sightings of fisher throughout the province of Alberta, and is plotting them in Google Earth to observe their distribution.

The Moraine Mesocarnivore Project was a central facet of the successful and recent biosphere nomination of the Beaver Hills – Canada’s newest Biosphere (<http://www.beaverhills.ca/conservation/biosphere-nomination/>). We hope to continue to provide valuable research for the conservation of this landscape, and the conservation of similar landscape throughout Canada. We will continue to communicate and converse with the public regarding the findings of *The Moraine Mesocarnivore Project*. The local landowners love to better understand how their property is facilitating local biodiversity and provincial connectivity throughout Alberta’s heartland.

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