

Draft Project Progress Report 2013

1. **NWRT Project Number:** 2-13-14

2. **Project title:** Estimation of population size for wolverines *Gulo gulo*, in the vicinity of Baker Lake, using DNA based mark-recapture method

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Note: This draft progress report provides a brief preliminary summary of the 2013 Baker Lake wolverine project DNA mark-recapture results. After 2014 hair samples results data will be combined for population analysis and will be presented in project final report in 2015.

Summary:

In Nunavut wolverine is listed both as furbearer (Schedule 5.2) animal and a big game (Schedule 5.1) under NLCA, and is an important cultural and economic resource for people. The Committee on the Status of Endangered Species in Canada (COSEWIC 2007) has listed the western Canada population, including Nunavut, as “Special Concern.” Potential cumulative direct and indirect effects from human development in tundra have escalated concerns about the species, and emphasize the need to estimate their abundance, monitor the trend, using Inuit hunters relevant skills and capacities and support a Total Allowable Harvest (TAH) decision. By involving local hunters, snagging hair samples and identifying individuals using DNA, the purpose is to use non-invasive sampling protocol to establish baseline wolverine population data (“natural” wolverine density in the areas with limited or no harvest pressure). In the spring of 2013, 209 baited posts wrapped with barbed wire were deployed in a 3,344 km² study area (4x4 km cells). The posts were visited using a snowmobile and checked 3 times at approximately 10-day intervals. A total of 871 samples (845 hairs and 26 scats) were collected at the posts. From these samples 17 (8F,9M) individual wolverines were identified through DNA hair analysis. During the 2014 sampling session 400 hair samples collected and submitted to genetics lab for analysis. Once the results of 2014 hair samples available, both years (2013 and 2014) data will be combined for population analysis and will be presented in project final report in 2015.

4. Project Objectives:

Our wolverine carcass collection program and this research proposal is designed to investigate the ecology and to estimate wolverines density and abundance in the Kivalliq region based upon a DNA sampling grid located near Baker Lake, Nunavut. The specific objectives are:

- To determine wolverine density;
- To establish baseline wolverine population data which can be used for population monitoring in the long term and to support a TAH decision;
- To determine wolverine landscape use and movements through genetic mark-recapture;

- To provide field work training and employment to HTO members and
- Increase collaboration between government and resource users.

5. Materials and Methods:

The proposed two year study was initiated in March 2013 on the mainland, 130 km northwest of Baker Lake, Nunavut (Fig 1). The study area covers 3,344 km² and was identified using elders/hunters knowledge about abundance, habitat use, harvest patterns and distribution of wolverines and their prey.

This study was designed to involve local hunters in the collection of samples. In the spring of 2013 three Baker Lake HTO members were hired to be part of the field work. A total of 209 bait posts were deployed in the centre of 4X4 km cells. Each hair snare bait post consists of ~ 1.6m long spruce post wrapped with barb-wire and anchored in packed snow. Bait (caribou meat) and a combination of commercial lures were attached on the top of the post. A GPS position of each bait post was recorded. Each post was visited 3 times at about 10-day intervals using snowmobiles. At each visit all visible hairs and wolverine scats were collected and the wood post was cleaned using a propane torch to remove any remaining hair. Each individual clump of hair was removed from the post and placed in labeled individual coin envelopes (post number, location on post and date) for storage. A fresh set of bait and lures was installed on each post after every check.

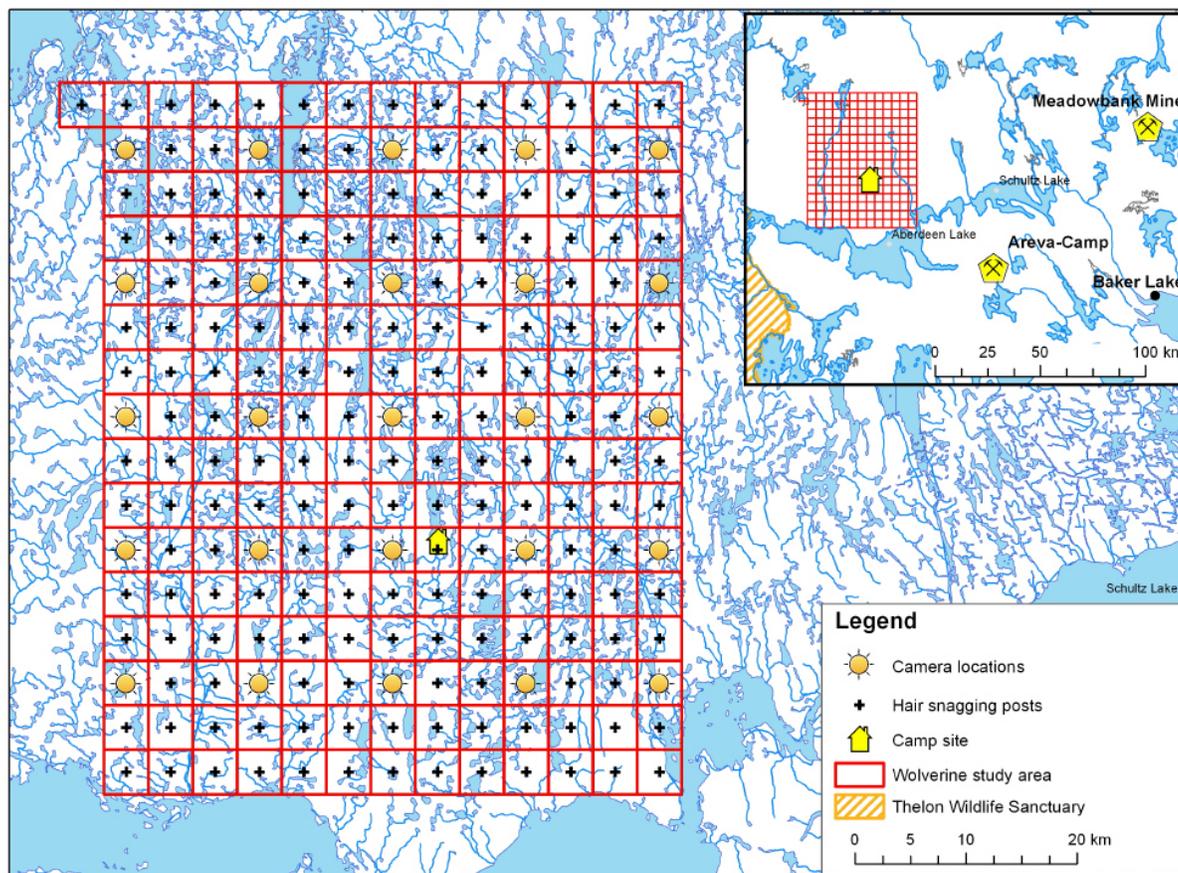


Fig. 1: Study area (3,344 km²) with 209, 4X4 km cells.

After the 3rd (last session) check, in early May 2013, posts were dismantled and stored at one location for next year use. A total of 25 motion triggered digital cameras (Reconyx PC-800 Hyperfire Professional IR) were installed at the sampling grid (Fig. 1), to document wolverine and other wildlife activity around the hair snagging post. Upon the end of the field season, the samples were sent to Wildlife Genetics International (WGI) Lab, Nelson, BC for individual wolverine identification.

WGI conducted genetic analyses on 871 samples (845 hairs and 26 scats) collected in spring 2013. Initially, we analyzed the single best sample per post per session, using a minimum quality threshold of 1 guard hair root or 5 underfur.

DNA was extracted from 284 samples (32%) using QIAGEN's DNeasy Tissue kits, following the manufacturer's instructions. The scat surface rubs were processed by clipping a $\sim 3\text{mm}^2$ piece of swab, and processing the clipping as if it were a tissue sample. The analysis of individual identity was based on a gender marker, plus the 7 microsatellite markers that have become standard for barren ground wolverine projects.

Spatially explicit mark-recapture methods (Efford 2004, Efford et al. 2004, Efford et al. 2007, Efford 2011a) were used to estimate density from the 2013 data. Spatially explicit methods model both the detections and redetections of wolverines at posts and the spatial configuration of posts on the landscape. The detection and redetection locations of wolverines on the grid allow a partial sample of where wolverines traversed both on and off the grid during sampling. Spatially explicit methods basically attempt to estimate the most likely spatial patterning of wolverines on the grid, and movements of wolverines on the grid, that resulted in the observed spatial capture detection histories observed on the grid. More precisely, the detection probabilities of wolverines at their home range center (g_0), spatial dispersion of movements (σ) around the home range center, and density are estimated. An assumption of this method is that wolverines home range can be approximated by a circular symmetrical distribution of use (Efford 2004). The actual shape and configuration of the sampling grid is used in the estimation process therefore accounting for the effect of study-area size and configuration on the degree of closure violation and subsequent density estimates.

For this analysis, a basic set of sex-specific secr models were run to assess sex-specific movement and detection rate parameters using program secr (Efford 2011b) in R (R_Development_Core_Team 2009). These estimates were then used to assess sampling efficiency and wolverine movements. Density and superpopulation estimates were then derived from the most supported secr

model. These were assessed in terms of precision as well as whether the number of wolverines in the area was sufficient for monitoring purposes.

6. Project Schedule:

Considering the relatively low density of wolverines on the eastern mainland (Kivalliq) more than a single year of study was proposed to obtain estimates of suitable precision. To intensify the initial sampling effort we conducted multiple sampling sessions (3 sessions) each year, for two years.

Estimation of population size for wolverines <i>Gulo gulo</i> , in the vicinity of Baker Lake, using DNA based mark-recapture method			
Output or Step	Start Date	End Date	Person days
Wood posts and barb wire	Completed	Already on the site	
Community consultations	Completed		
Delivery of fuel and gear to camp location	Completed	Completed	
Deployment of posts, and hair capture sessions (3 sessions)	Completed	Completed	
Collection of samples from harvested animals			On Going
Genetic and data analysis, Report preparation	May 2014	Nov 2014	40
2nd year report to DOE, NWMB, HTOs	Nov 2014	Jan 2015	20

7. Preliminary results/discussion:

Here we provided a brief summary of the 2013 wolverine project DNA mark-recapture results for annual progress report to NWMB. Once the results of 2014 hair samples available, both years (2013 and 2014) data will be combined for population analysis and will be presented in project final report in 2015.

Seventeen wolverines (8F, 9M) were detected in 2013 sampling. The number of unique individual detected per session was 8, 8, and 14 in sessions 1, 2, and 3 (Table 1).

	Sessions			Total
	1	2	3	
Individual detected	8	8	14	30
Unmarked detected	8	2	7	17
Detection frequencies	9	3	5	17
Cumulative detections	8	10	17	17
Post detections	55	62	94	211
Detectors visited	55	61	93	209
Detectors used	210	210	210	630

The number of unique posts visited by individuals was high for many wolverines. For example, the number of unique session/post visitation for individual 1-A08-B3 was 51. Looking at a map of detections per individual (Fig 2, right) shows a lot of within-grid movement for some individuals. Individuals detected fewer times were often on the edge of the grid indicating that their home range only partially overlapped the grid. Seven individuals had more than 10 detections during sampling.

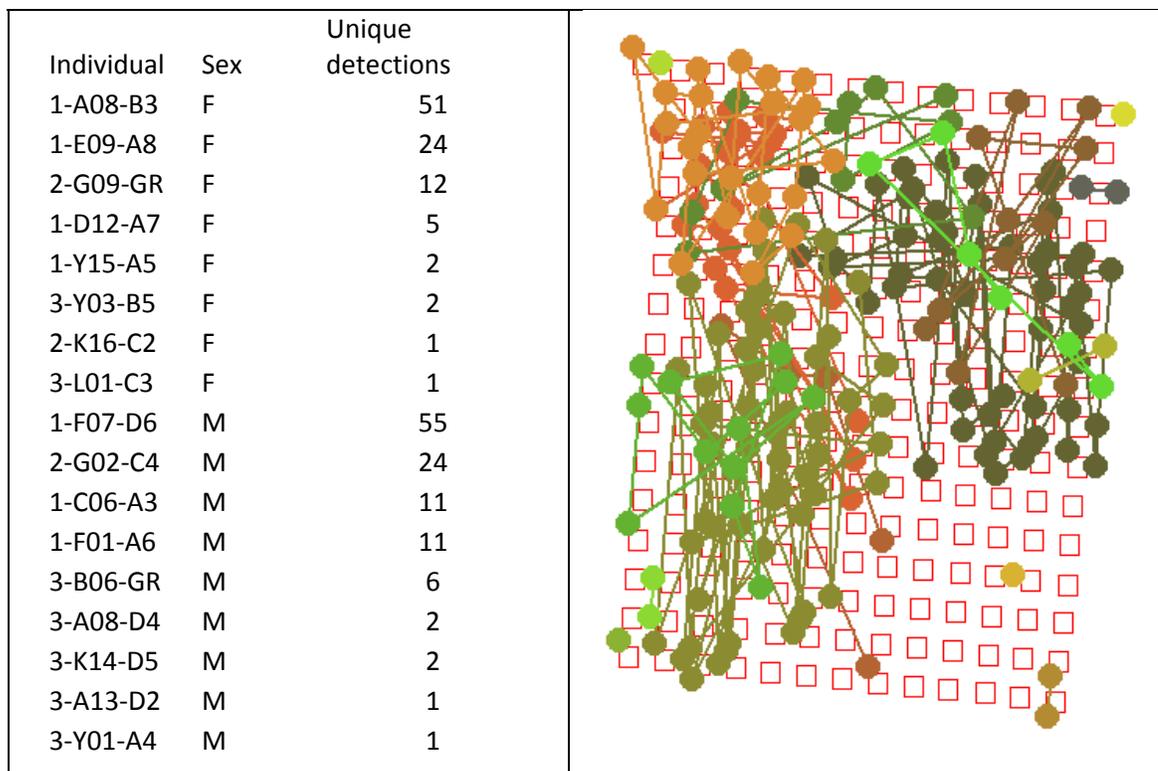


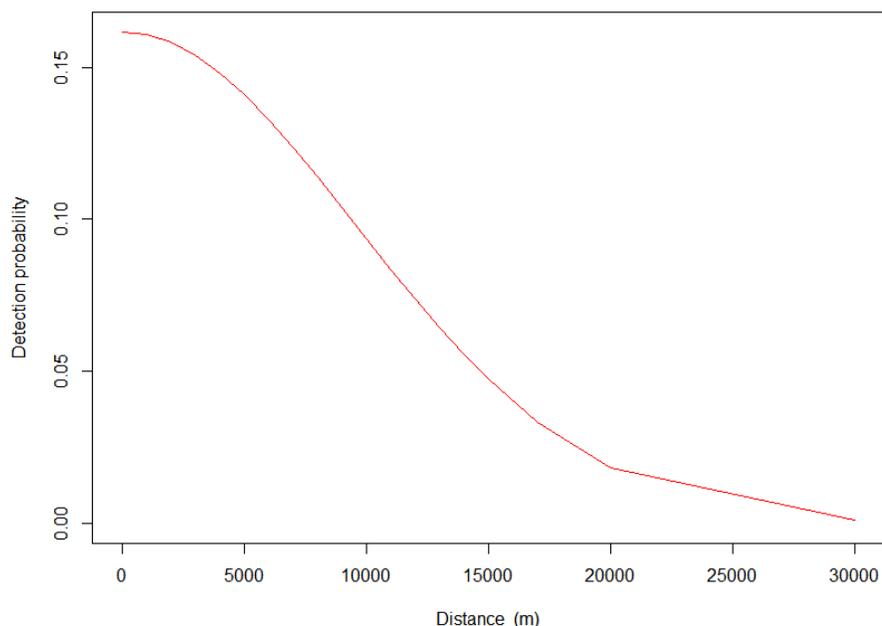
Fig. 2: Detections per individual on the grid during 2013 sampling.

Secr model selection indicated similar detection rates (g_0) and movements (σ) at the home range center for male and female wolverines. A buffer on the study area of 31.4 km was used for secr analyses as indicated by the `suggest.buffer` function.

Table 2: Model selection for secr. Akaike Information Criteria (AICc), the difference in AICc values between the i th model and the model with the lowest AICc value (Δ_i), Akaike weights (w_i), number of parameters (K) and model deviance are presented.

Model	AICc	dAICc	AICcwt	npar	logLik
$g_0(.) \sigma(.)$	1265.7	0.00	0.65	2	-630.43
$g_0(.) \sigma(\text{sex})$	1268.5	2.79	0.16	3	-630.33
$g_0(\text{sex}) \sigma(.)$	1268.5	2.83	0.16	3	-630.35
$g_0(\text{sex}) \sigma(\text{sex})$	1271.9	6.23	0.03	4	-630.30

Plotting the detection function for the constant g_0/σ model indicates detection probabilities of 0.16 in the home range center and detection probabilities >0 at distances up to 25km from the home range center.



Estimates of sex-specific detection and g_0 model also suggest similar detection and movements for male and female wolverines.

Table 3: Estimates of detection at home range center (g_0) and movement (σ) from model $g_0(\text{sex}) \sigma(\text{sex})$.

Sex	Parm	estimate	SE	CI	
Males	g_0	0.17	0.03	0.12	0.23
	Sigma (m)	10026.87	1653.90	7272.84	13823.78
Females	g_0	0.16	0.03	0.10	0.23
	Sigma (m)	9497.59	936.77	7831.78	11517.71

Estimates of density suggest relatively low densities of wolverines with marginally acceptable precision of pooled sex estimates. The average number of wolverines on the study area at one time was 7.19 which compares to the superpopulation size of 17 wolverines, which is the number of wolverines detected. This result basically suggests that all the wolverines that traversed the

study area were detected and that many (approximately 10) wolverine home ranges only partially overlapped the study area and 7 of the wolverines were “residents”. The closed model Mt superpopulation estimate is included for comparison, but the CV estimate is most likely negatively biased due to heterogeneity variation.

Table 4: Estimates of density (wolverines per 1000km²), average number of wolverines on study area (Ave N), superpopulation of wolverines on grid and surrounding area (Super N) from secr using estimate of effective study area of 7,911 km², and superpopulation from the Darroch closed model estimator (Otis et al. 1978).

Parameter	Estimate	SE	lcl	ucl	CV
Density	2.15	0.38	1.52	3.03	17.7%
Ave N	7.19	1.27	5.10	10.13	17.7%
Super N (secr)	17	3.00	17.00	23.97	17.7%
Super N (Mt)	18	1.32	17.00	25.00	7.3%

In the spring 2014 field work, a total of 400 samples (390 hairs and 10 scats) were collected and submitted to WGI for analysis.

Despite smaller sample sizes, estimates of density and Ave N had marginally acceptable precision due to the higher detection rates of wolverines as indicated by the large number of redetections for wolverines, especially those that were residents. Another year (2014) of sampling will improve the precision of estimates once the data will be used together.

The number of multiple detections at posts clearly demonstrates that the 4x4 km cell size is more than adequate to ensure detection of wolverines. The detection probability plot suggest detection rates are greater than 0 at distances up to 32 kilometers from the home range center. The study area could be increased by increasing cell size to 5x5 which would also increase the number of wolverines available for detection.

8. Reporting to Communities/resource users:

Preliminary results from first year (2013) study have been presented on October 29, 2013 at the Kivalliq Wildlife Board (KWB) AGM meeting, on November 18, 2013 to Baker Lake Hunters and Trappers organization (HTO) and on September 25, 2014 to Arviat HTO.

Field Team:

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Timothy Evviuk	Baker Lake HTO member
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Literature cited:

Efford, M. 2004. Density estimation in live-trapping studies. *Oikos* 106:598-610.

Efford, M., D. L. Borchers, and A. E. Byrom. 2007. Density estimation by spatially explicit capture–recapture: likelihood-based methods. Pages 255-269 in D. L. Thompson, E. G. Cooch, and M. J. Conroy, editors. *Modelling demographic processes in marked populations*. Springer, New York.

Efford, M., D. K. Dawson, and C. S. Robbins. 2004. DENSITY: software for analysing capture-recapture data from passive detector arrays. *Animal Biodiversity and Conservation* 27:217-228.

Efford, M. G. 2011a. Estimation of population density by spatially explicit capture-recapture analysis of data from area searches. *Ecology* 92:2202-2207.

_____. 2011b.

Otis, D. L., K. P. Burnham, G. C. White, and D. R. Anderson. 1978. Statistical inference from capture data on closed animal populations. *Wildlife Monographs* 62:1-135.

R_Development_Core_Team. 2009. R Foundation for Statistical Computing, Vienna, Austria.