POPULATION TREND ANALYSIS FOR BOREAL CARIBOU IN SK2 CENTRAL USING NON-INVASIVE CAPTURE-RECAPTURE ANALYSIS (2007 – 2019)

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SUMMARY

Boreal caribou populations were listed as threatened under the *Species at Risk Act* in 2003 and a national recovery strategy was developed by Environment and Climate Change Canada in 2012. At the time, there had been no population assessment of Saskatchewan's Boreal Plain (SK2) caribou conservation unit and it was assessed "as likely as not" to be self-sustaining, based on a high level of disturbance resulting in only 57% undisturbed habitat. A threshold of 65% undisturbed habitat is expected to provide a 60% probability of population persistence.

The large size of SK2 (109,717 km^2) made range assessment and range planning difficult, so in 2015, three smaller caribou administration units within SK2 were delineated: SK2 East, SK2 Central, and SK2 West. The SK2 Central area covers 36,052 km^2. Saskatchewan committed to assess caribou population status, and in 2017, the province initiated a 3-year population monitoring program for the SK2 Central in a study area covering 16,092 km^2. Fecal-DNA based capture–recapture methods were used to estimate population sizes and population rate of change from 2017-2019.

The results for the population analysis show a significant decline in both female and male caribou numbers in the SK2 Central study area from 2017-2019 and since 2007 when assessed for the smaller Prince Albert Greater Ecosystem (PAGE) area.

The SK2 Central results for females show a statistically non-significant increase from 2017 to 2018 (lambda = 1.2) followed by a significant decrease between 2018 and 2019 (lambda = 0.7), with the decrease largely accounted for by the low survival rate (55%). Population size estimates for females were 103 in 2017, and 89 in 2019. For the males, a steady decline in abundance was observed over the 3 years (lambda = 0.66) with population size estimates of 78 in 2017, and 36 in 2019 for the study area. The total population estimate is 125 (112-160) animals for 2019 in the study area.

The results for the PAGE area over the 2017 to 2019 period are comparable, although the population is approximately 60% the size of that of the SK2 Central study area; demographic trends are less clear due to lower precision in the estimates. Population size estimates for females were 63 in 2017, and 50 in 2019 and estimates for males were 50 in 2017, and 27 in 2019.

The PAGE results for the 2007 to (2017-2019) time period points to a long-term loss rate of females, averaging around 7.5% per year (lambda = 0.927) and for males around 1.5% per year (lambda = 0.984). The MARK RD analysis indicates the loss rate for both sexes in recent years is much higher, around 30% per year (lambda = 0.71). The population size estimates for females were 137 in 2007, and 50 in 2019 and for males, estimates were 39 in 2007, and 27 in 2019.

Caribou in the SK2 Central study area are generally found in the remaining large, relatively intact areas with suitable habitat (Priadka et al. 2019, McFarlane et al. 2021). The remaining habitat areas are largely disconnected and the short and long term declining population trend clearly indicates that they are not sufficient to maintain a self-sustaining caribou population. Additional efforts to reduce the human-caused disturbance footprint should be made, as identified in the *Range Plan for Woodland Caribou in Saskatchewan, Boreal Plain Ecozone – SK2 Central Caribou Administration Unit*.

INTRODUCTION

Boreal forests are experiencing increasing rates of anthropogenic disturbances from petroleum, timber, and agricultural industries (Venier et al. 2014, Allred et al. 2015, Pickell et al. 2015). Across Canada, boreal caribou have declined range wide due to predation facilitated by human activities and anthropogenic habitat loss, but also to fire, hunting, and poaching (Alberta Woodland Caribou Recovery Team 2005, Environment Canada 2012 & 2020, Northrup and Wittemyer 2013, Hervieux et al. 2015). Reduction in population sizes throughout most of the range in Canada prompted the federal listing of boreal caribou as threatened in 2003 and also identified the need to derive accurate estimates of population sizes and trends (COSEWIC 2002 & 2003), especially within ranges heavily impacted by habitat loss.

An estimate of caribou abundance and trend is not available for the Saskatchewan's Boreal Plain (SK2) caribou conservation unit. In the federal boreal caribou recovery strategy (Environment Canada 2012), the SK2 caribou conservation unit was assessed "as likely as not" to be self-sustaining, based on a high level of disturbance resulting in only 57% undisturbed habitat. A threshold of 65% undisturbed habitat is expected to provide a 60% probability of population persistence. The large size of SK2 (109,717 km^2) makes range assessment and range planning difficult, so in 2015, three smaller caribou administration units within SK2 were delineated: SK2 East, SK2 Central, and SK2 West. The SK2 Central area covers 36,052 km^2 and in 2017, Saskatchewan committed to assess caribou population status. A 3-year population monitoring program was put in place for a study area within SK2 Central covering 16,092 km^2 using fecal-DNA based capture–recapture methods to estimate population sizes and population rate of change.

Here, we summarize the results of the surveys and use a robust design (Pollock et al. 1990) modeling framework to estimate both open and closed population parameters. We used data from 2017-2019 to model encounter rate (p) and apparent survival rate (φ or phi) and then to estimate sex-specific populations sizes (N) and rates of population change (λ). We used the robust design models in MARK with Pradel models for the primary periods and closed captures models for the secondary periods. The robust design models produced estimates of all 4 parameter sets (p, φ, λ, and N). We then compared the 2017-2019 population size estimates to those generated in 2007 for the Prince Albert Greater Ecosystem, a portion of the SK2 Central study area, following the same sampling methods. These results are critical to the provincial conservation efforts and the implementation of the Range Plan for Woodland Caribou in Saskatchewan – SK2 Central.

METHODS

Sampling design

Aerial surveys consisted of transect lines flown systematically 3-km apart across the SK2 Central study area using fixed-wing aircraft to locate caribou cratering activities. The surveys were done twice a year (February and March) in 2017, 2018 and 2019; amounting to approximately 10,000 km flown each year. Following the aerial surveys, cratering sites were accessed by helicopter and fecal samples were collected following the protocol outlined in Hettinga et al (2012). We compared the results from these surveys to the population size estimate obtained from a survey completed in 2007 over the Prince Albert Greater Ecosystem area (PAGE) in using data from SK2 Central study area that aligned with the PAGE survey area (Figure 1). The PAGE survey was done by helicopter between January and March 2007.

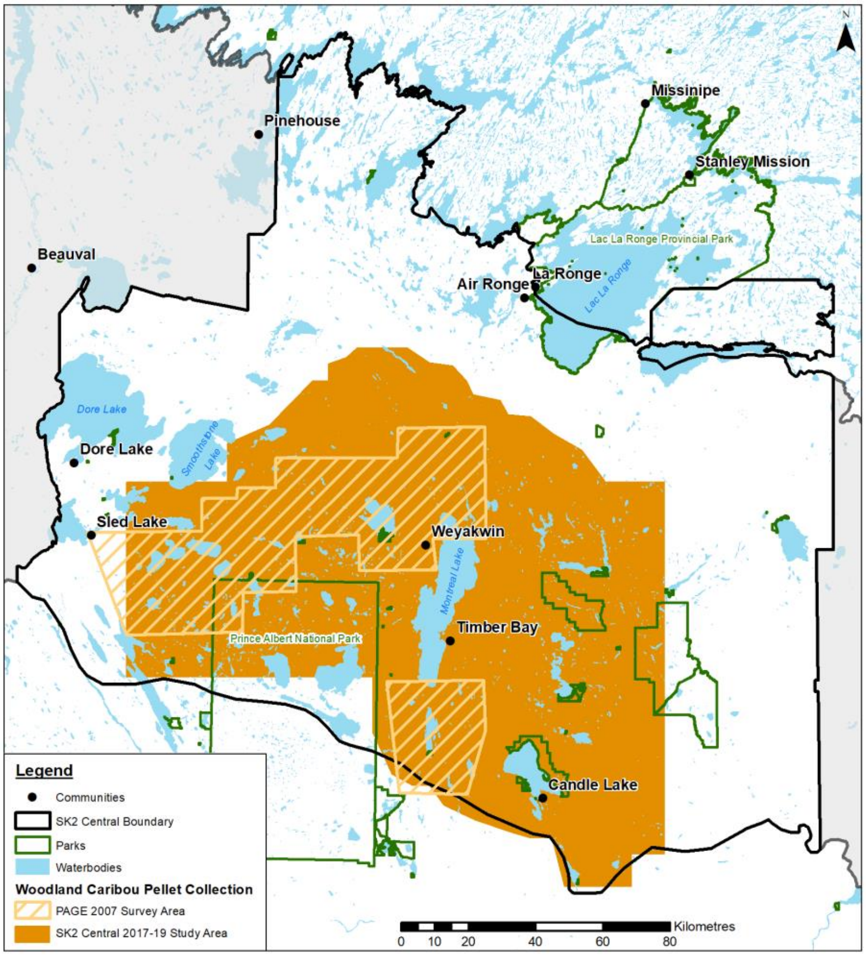

Figure 1. SK2 Central and PAGE study areas

Microsatellite Amplification and Genotyping

We processed fecal pellets for DNA analysis by gently swishing fecal pellets in lysis buffer to remove the outer mucous layer containing sloughed intestinal cells for DNA extraction. This protocol yields equal or higher concentrations of template DNA and lower levels of polymerase chain reaction (PCR) inhibitors than the previously-implemented fecal swabbing protocol (modified from Ball et al. 2007). We amplified DNA samples at 9 variable microsatellite loci markers (RT1, RT5, RT6, RT7, RT24, OHEQ, FCB193, BM888, and NVHRT16, Bishop et al. 1994, Wilson et al. 1997, Roed and Midthjell 1998, Cronin et al. 2005) and chromosome specific loci (Zfx/Zfy) to generate individual-specific genetic profiles. We labeled forward primers with HEX, 6-FAM (Integrated DNA Technologies), or NED (Applied Biosystems) and amplified loci in 2 multiplex and 3 singleplex reactions. To further minimize inhibitors, equalize peak heights, and improve allele morphologies, we used PCRboost (Biomatrica) in PCR. We ran samples on an ABI 3730 in two panels due to the number of loci with overlapping size ranges.

Capture History

We created capture histories of genetic profiles for both study areas by identifying genotypes observed at each sampling period and clustering groups of samples demonstrating the same individual-specific profile. We used ALLELEMATCH software (Galpern et al. 2012) to cluster multilocus genotype data and identify unique genotypes and potential genotyping errors. We retained samples that amplified at ≥5 loci and re-amplified apparent unique genetic profiles represented by a single sample using two independent scorers to confirm unique individual identities (Hettinga et al. 2012). An error rate per locus was calculated using these re-amplification results (see McFarlane et al. 2020 for more details).

Population Trend Analysis

Population demographics were estimated using capture-recapture (CR) analysis of the capture histories as implemented in version 8.2 of program MARK (White & Burnham 1999). The sex of each animal was designated in its capture history through the use of a sex-specific genetic marker, so estimates by sex can be identified, and tests for sex effects on parameters can be performed using the group features of MARK. The CR analysis was performed using robust design (RD) modeling (Pollock et al. 1990), which combines features of both closed and open population models into a single model consisting of the 3 primary periods (years 2017, 2018, and 2019) with each primary period having 2 secondary samples (within-year winter surveys, spaced 40-48 days apart). The population is assumed to be closed within years. The model is open to gains and losses from the last sampling occasion in the year (usually in March) to the first sampling occasion in the next year (in January or February) to account for annual recruitment and mortality as well as immigration/emigration. We used the closed capture models of Otis et al. (1978) as implemented in MARK for the secondary period estimates. These models assume that each animal has the same probability of capture on any given sampling occasion, but capture probabilities are allowed to vary among sampling occasions and with sex (Williams, Nichols & Conroy 2002). Captures are assumed to be independent within and between sample times. The

Otis et al. models include a behavioural model that allows the capture rate of animals to depend on its sighting history within the same year: animals at the second survey can have a capture rate of *c* if they were seen at the first survey but a different rate, *p*, if not seen. Testing if p=c can determine if there is trap-happiness or trap-avoidance, a violation of the equal catchability assumption that can seriously bias abundance estimates.

Population demographic metrics for the open primary intervals, including survival (φ or Phi), population rate of change (λ Lambda or Lam), and recruitment (*f*), were estimated in program MARK using Pradel models (Pradel 1996) for the open intervals. Survival (φ_i) is the probability that an individual, alive at the end of the surveys in year *i*, is alive and available for capture in the year *i*+1 surveys. The RD models assume that survival is independent for all animals in a group at time *i*, but survival rates can vary with time (*i*) or group (sex). Recruitment (f_i) is the ratio of new animals in the population at year *i*+1 (i.e. including births or immigration into the population from the previous year (*i*) sampling period) relative to the initial population N_i. The population rate of change is the ratio of next year's abundance to this year's and is a function of both φ and *f* ($\lambda_i = \varphi_i + f_i$), and indicates whether populations are increasing ($\lambda > 1$), decreasing ($\lambda < 1$), or stable ($\lambda = 1$). MARK normalises these rates to annual rates to permit meaningful testing of time effects.

MARK uses information from both the open and closed models to estimate the capture rates *p*, and these, as with the demographic parameters, may be assumed to differ with time and sex group: $p(g * t)$; or vary with time but the same for both sexes: $p(t)$; or constant over time but differing with group: $p(g)$; or constant with both time and group $p(.)$. This is the notation used to specify the models used (Table 2). The approach in MARK is to fit a battery of models incorporating different group and time effects in the capture and demographic parameters, and to then rank the models using AICc (Akaike Information Criterion corrected for sample size; Akaike 1973; Burnham & Anderson 2002). Models rank higher if they have a higher likelihood and if they use fewer parameters. If several of the top models are very close in AICc ranking, it is common practice to form estimates by using a weighted average of a parameter across models, using the AICc weights. This causes some inflation in the parameter CV and wider confidence intervals but helps reduce model bias by not putting all one's eggs in a single "best model" basket.

Likelihood Ratio Tests (LRTs) are used to test specific hypotheses by comparing a general model versus one involving hypothesized restrictions; e.g. a test of no sex effect on capture rate might involve the models:

$$\text{Phi}(g^*t)\ \text{Lam}(g^*t)\ p(g^*t) \text{ vs } \text{Phi}(g^*t)\ \text{Lam}(g^*t)\ p(t)$$

Similarly a test for no time or sex effect on survival or lambda might compare

$$\text{Phi}(g^*t)\ \text{Lam}(g^*t)\ p(g^*t) \text{ vs } \text{Phi}(.)\ \text{Lam}(.)\ p(\text{g}^*t)$$

RESULTS

SK2 Central Study Area (2017-2019)

Sampling

The surveys of the SK2 Central study area yielded 364 samples in 2017, 288 samples in 2018 and 393 in 2019; the number of unique genotypes identified on each survey varied between 61 and 111 for a total of 215 unique genotypes (83 males and 132 females; Table 1, Figures 2 and 3).

Table 1. Genotyping results for boreal caribou samples collected in SK2 Central in 2017-2019.

Year	Survey	Sites sampled	Number of samples	Number of unique genotypes	Number of male unique genotypes	Number of female unique genotypes
2017	T1	31	244	111	41	70
2017	T2	15	120	69	27	42
2018	T3	23	159	76	27	49
2018	T4	22	129	61	31	30
2019	T5	23	160	69	21	48
2019	T6	28	233	78	17	61

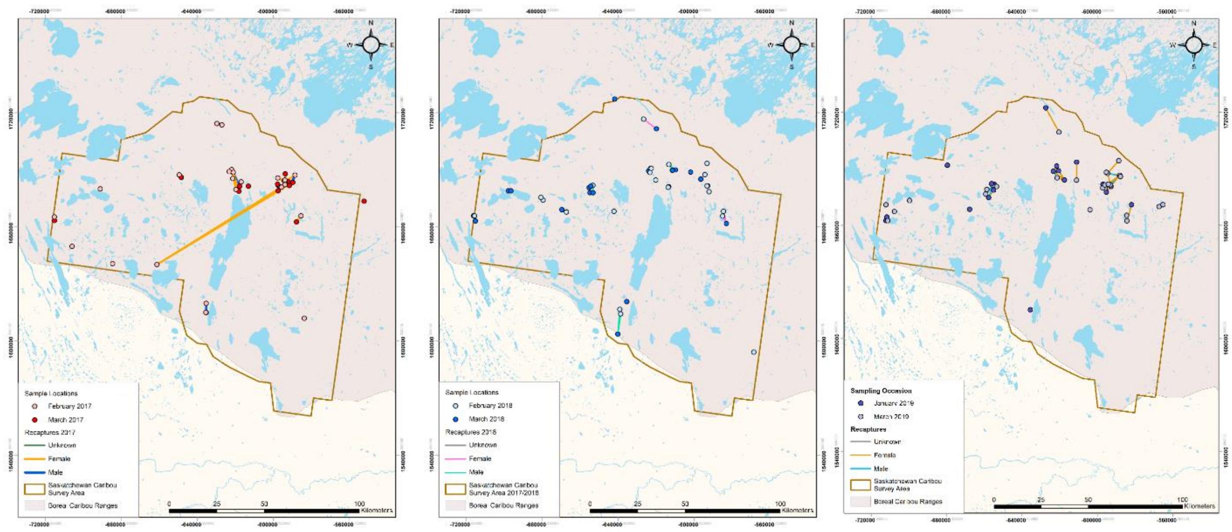

Figure 2. Capture and recapture locations for each survey (2017-2019) in the SK2 Central study area.

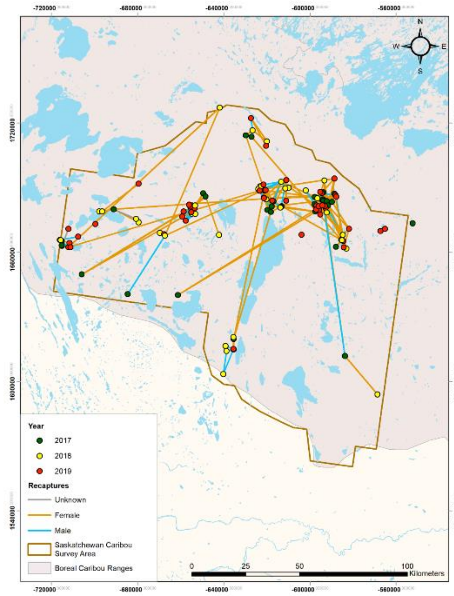

Figure 3. Capture and recapture locations of unique genotypes in the SK2 Central study area over the 3-year period (2017-2019).

Population Models for SK2 Central Study Area

A systematic exploration of time and group (sex) effects on p, φ and λ with special concentration on p (Table 2) was carried out. Behavioural models $p \neq c$ were assessed but all such models failed to converge (overparameterised, not enough data to estimate c). There appear to be strong time and sex effects on *p* (Figure 4) although the sex effect seems to be entirely due to the capture rate of females at the second survey in 2018 where the capture rate was very low (significantly lower than that of the males) and significantly below what would be predicted by the effort expended. If it weren't for this one sample, a model with *p*(*t*) and/or an effort model would have fit the capture rate data well. A model with *p*(*t*) for the other 5 occasions was assessed, but it had little effect on the estimates on *N*, φ and *λ* or their precision. As a result, a general capture model *p*(*g*t*) was used to obtain estimates for *N*, *λ*, and φ (Figure 5, 6, and 7).

The *N* and *λ* estimates (Figure 5 and 6) for females present an increase over 2017-18 with $\lambda > 1$ (though not significantly so) and $\lambda < 1$ over 2018-19 (significantly less than 1) with the corresponding response in *N*(F): increase of 20% from 2017 to 2018 followed by a huge 50% decrease between 2018 and 2019. Males however don't show the increase in abundance in 2018. Instead, they have the same *λ* in both intervals and hence a steady log linear decline in abundance over the 3 years. This decrease is largely accounted for by the low survival rate (survival rates of 0.55 for females in 2018-2019 and for males in both periods). The female recruitment rates (Figure 8) are the number of new female recruits, per female alive at time *i*, that survive and are in the population at time (*i*+1). The identity $\lambda = \varphi + f$ holds for both the "general" and "best" models. The estimates (with 95% CI) presented in Figures 4 (*p*), 5 (*N*), 7 (Phi), and 8 (*f*) are from the best model (#1 in Table 2) but those in Figure 6 (Lam) are from the general model (#2 in Table 2) to show support for the restriction Lam(F1,.) used to obtain the best model.

Closure Tests for the SK2 Central Study Area

A test of closure within years was done by fitting a CJS model as implemented in MARK (this fits the {φ (*g*t*) *p*(*g*t*)} model without taking account of the robust design sampling structure, but does allow for the different time intervals between samples). This model was then compared with the same one in which the φ are constrained to be 1.0 within years (between event 1 and event 2 in 2017, etc.) using a LRT. The test passed with strong significance indicating no apparent violation of closure within years. Similarly, use of a Pradel model fixing the *f* to be 0 within years gave strong support for no new entries within years. Simultaneously fixing both φ to be 1.0 and the *f* to be 0 within years in the Pradel model also gave an LRT result that strongly supported closure.

Model Selection and LRT Summary, SK2 Central

The top model is one using *p*(*g***t*) and where φ and *λ* are constant over time and sex except for females in the first interval, designated by (F1,) in Table 2. The CJS closure model also showed strong support for this model for φ. When a LRT is used to see if *p*(*t*) can be used instead of the more general *p*(*g***t*) [model #4 vs model #1] the test is highly significant indicating a significant sex effect; so the reduced model *p*(*t*) cannot be used. There is a huge drop in AICc weight from model 1 to model 2, so there is no point in doing model averaging. Also, an LRT of model 1 vs model 2 shows that the reduced model, where female *λ* and φ at time 1 is different from those rates for other times and sex groups, is strongly supported by the data.

Table 2. Robust design model exploration of time and group (sex) effects on apparent survival (phi), population growth (lam) and capture probability (p) from the capture-recapture data obtained from non-invasive DNA sampling in SK2 Central.

#	Model	AICc	Delta AICc	AICc Weights	Num. Par	-2ln (Likelihood)
1	{Phi(1F,.) Lam(1F,.) p(g*t) p=c PIM}	-604.8	0.000	0.945	22	-651.063
2	{Phi(g*t) Lam(g*t) p(g*t) p=c PIM}	-598.5	6.289	0.041	26	-653.691
3	{Phi(g*t) Lam(t) p(g*t) p=c PIM}	-595.2	9.594	0.008	24	-645.907
4	{Phi(1F,.) Lam(1F,.) p(t) p=c PIM}	-593.8	10.950	0.004	16	-627.035
5	{Phi(g*t) Lam(g*t) p(t) p=c PIM}	-591.9	12.840	0.002	20	-633.824
6	{Phi(t) Lam(t) p(g*t) p=c PIM}	-590.0	14.736	0.001	22	-636.327
7	{Phi(t) Lam(g*t) p(g*t) p=c PIM}	-586.5	18.234	0.000	24	-637.267
8	{Phi(t) Lam(t) p(t) p=c PIM}	-584.8	20.008	0.000	16	-617.977
9	{Phi(.) Lam(.) p(t) p=c PIM}	-584.4	20.320	0.000	14	-613.383
10	{Phi(t) Lam(.) p(t) p=c PIM}	-583.5	21.306	0.000	15	-614.534
11	{Phi(g) Lam(g) p(g) p=c}	-583.4	21.350	0.000	12	-608.109
12	{Phi(.) Lam(t) p(t) p=c PIM}	-582.7	22.085	0.000	15	-613.755
13	{Phi(t) Lam(g*t) p(t) p=c PIM}	-581.5	23.315	0.000	18	-618.990
14	{Phi(.) Lam(.) p(g) p=c}	-572.5	32.304	0.000	10	-592.950
15	{Phi(t) Lam(t) p(g) p=c}	-569.1	35.640	0.000	12	-593.820
16	{Phi(g*t) Lam(g*t) p(g*t) c(g*t) PIM fail}	2.0	606.78	0.000		0.000
17	{Phi(t) Lam(t) p(t) c(t) } PIM fail}	2.0	606.78	0.000		0.000

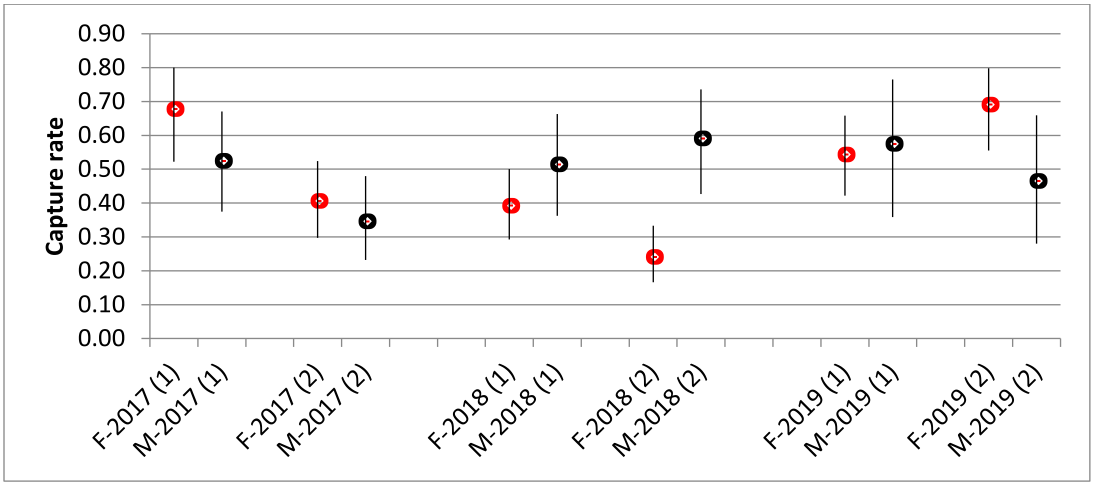

Figure 4. Capture rates from best model (#1 in Table 2) for male and female boreal caribou in the Central study area (2017-2019).

Population size estimates for females were 103 in 2017, and 89 in 2019 (Figure 5). For the males, with population size estimates of 78 in 2017, and 36 in 2019 for the SK2 Central study area. The total population estimate in 2019, for the SK2 Central study area is 125 (112-160) animals.

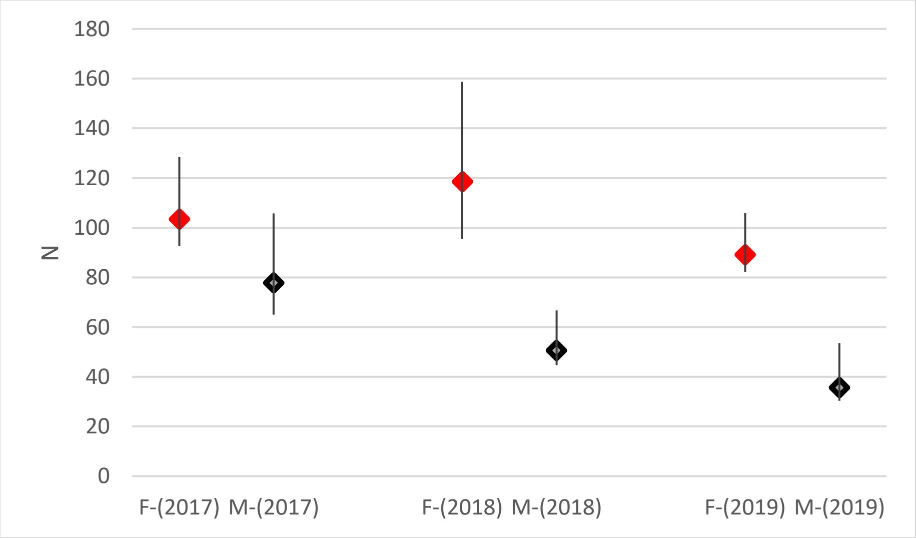

Figure 5. Abundance estimates (N) from best model (#1 in Table 2) for male and female boreal caribou in the SK2 Central study area (2017-2019).

The SK2 Central results for females show a statistically non-significant increase from 2017 to 2018 (Lambda = 1.2) followed by a significant decrease between 2018 and 2019 (Lambda = 0.7), with the decrease largely accounted for by the low survival rate of 55% (Figure 6). For the males, a steady decline in abundance was observed over the 3 years (λ =0.66).

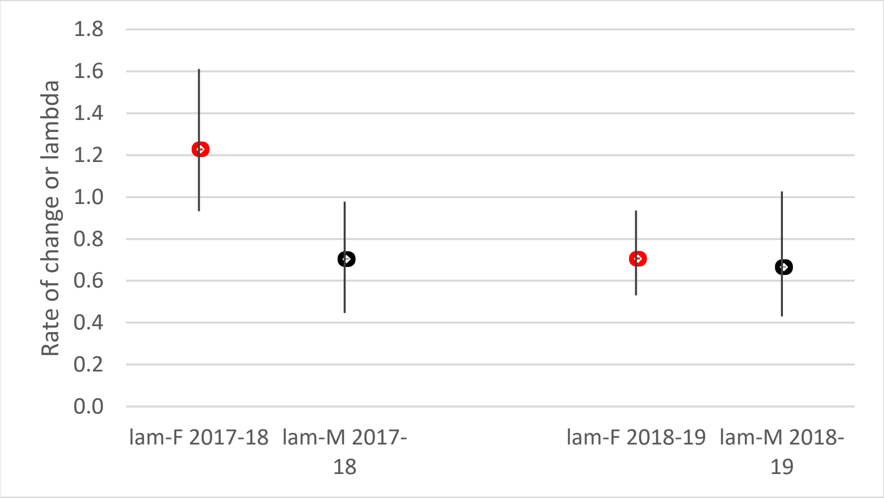

Figure 6. Lambda estimates from general model (#2 in Table 2) for male and female boreal caribou in the SK2 Central study area (2017-2019).

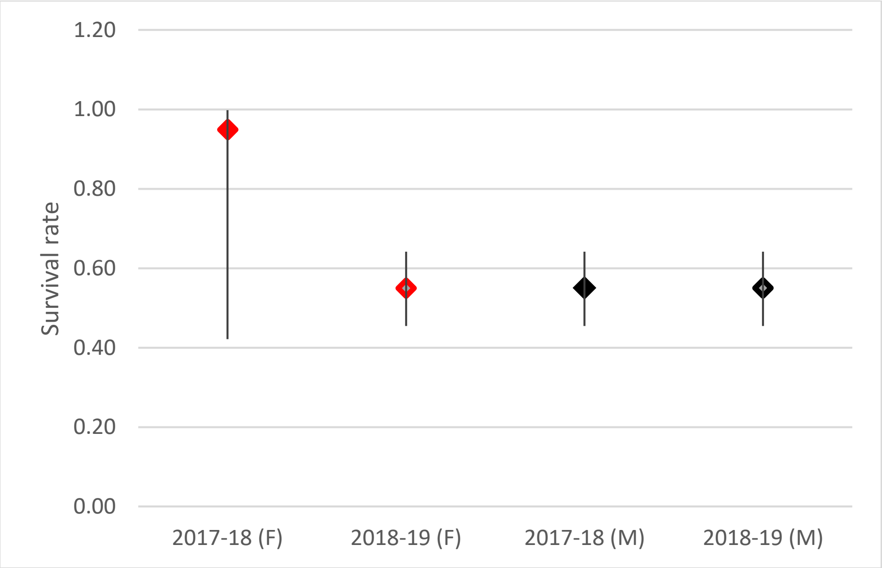

Figure 7. Survival rates from best model (#1 in Table 2) for male and female boreal caribou in the SK2 Central study area (2017-2019). Note that the last 3 estimates and their confidence intervals are all the same due to model constraints.

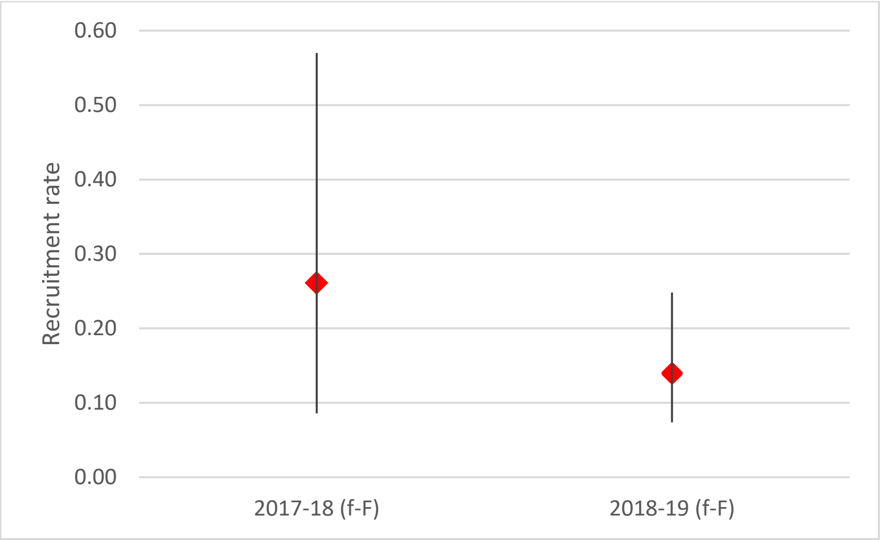

Figure 8. Recruitment rates for male and female boreal caribou in the SK2 Central study area (2017-2019).

Prince Albert Greater Ecosystems (PAGE) Study Area (2007-2019)

The PAGE is about 4443 km^2 or about 28% the size of SK2 Central study area (Figure 1). In total, 86 unique genotypes were sampled in 2007; 26 males and 60 females. The overall recapture rate was 31% (Table 3).

Table 3. Genotyping results for boreal caribou survey in the PAGE (2007).

Year	Number of unique genotypes	Number of recapture
Feb 2007	49	
March 2007	54	17

*total number of samples collected: 290; number of unique genotypes: 86 (26 males and 60 females)

Long-term Population Trend Analysis for the Prince Albert Greater Ecosystems Study Area

The models tested for the PAGE area (2017-2019) were the same models used for SK2 Central 2017-2019. The main difference between the PAGE subset and the SK2 Central area is that it is a smaller area but although capture rates were comparable to those in the large SK2 Central area, the precision was much lower for the PAGE. Consequently, the AICc algorithm in MARK selects as top models many heavily constrained models (e.g. no time and/or sex effects on p, ϕ or λ) because the low precision does not rule out such equality constraints and the number of model parameters is much reduced. The best SK2 Central model (#1 in Table 2) ended up with a rank of #4 in the set of models fit to the PAGE data, but the 3 heavily constrained models that ranked above it were all rejected by LRTs relative to the general model (#2 in Table 2) which ranked at #13 in the PAGE set. An LRT supported the restrictions of the best model relative to the general model, so we adopted the same best and general models for the PAGE subset as for the SK2 Central data. This also facilitates comparisons between the 2 areas.

In the best model, the estimated λ for the first group (λ (F,1)=1.12 (0.22) is not significantly different from stability (λ =1.0) but the common λ for the remaining cohorts is significantly less than 1.0: λ =0.71 (0.09) indicating a population where both sexes are in decline (Figure 9). *N* estimates declined over the 3 years from 2017 to 2019 from approximately 63 to 50 for females and from 50 to 27 for males (Figure 10).

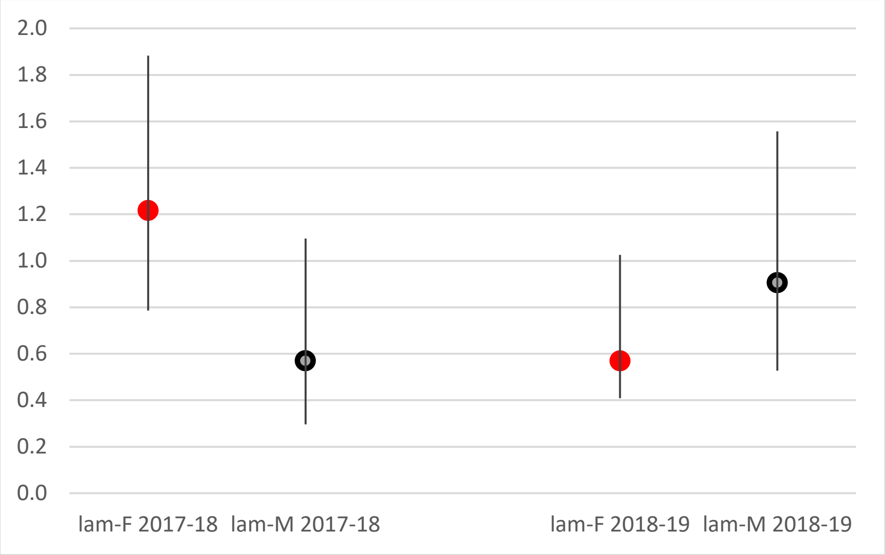

Figure 9. Lambda estimates from the general model for male and female boreal caribou in the PAGE area (2017-2019). The equality of the last 3 rates is less clear here than for the SK2 Central data (Figure 5) but is nevertheless supported by LRTs.

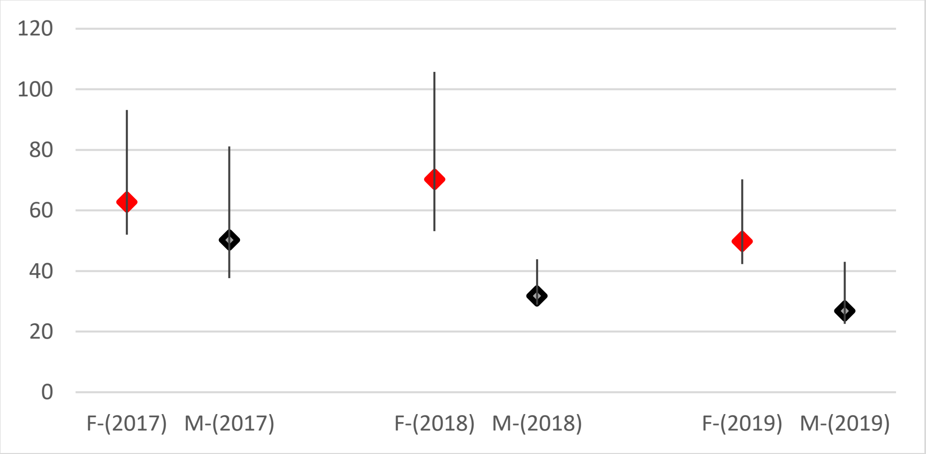

Figure 10. Abundance estimates of male and female boreal caribou in the PAGE area (2017-2019) using the best model.

Long-term Trend Analysis (2007-2019) in the PAGE

The long-term loss rate (blue lines in Figure 11) of females averaged around 7.5% per year (λ =0.927), 1.5% per year for males (λ =0.984), but for both sexes, the MARK RD analysis indicates the loss rate for both sexes in recent years (red lines) is much higher at around 30% per annum (λ = 0.71). This means a great reduction in abundance, to less than 100 animals currently found in the PAGE area.

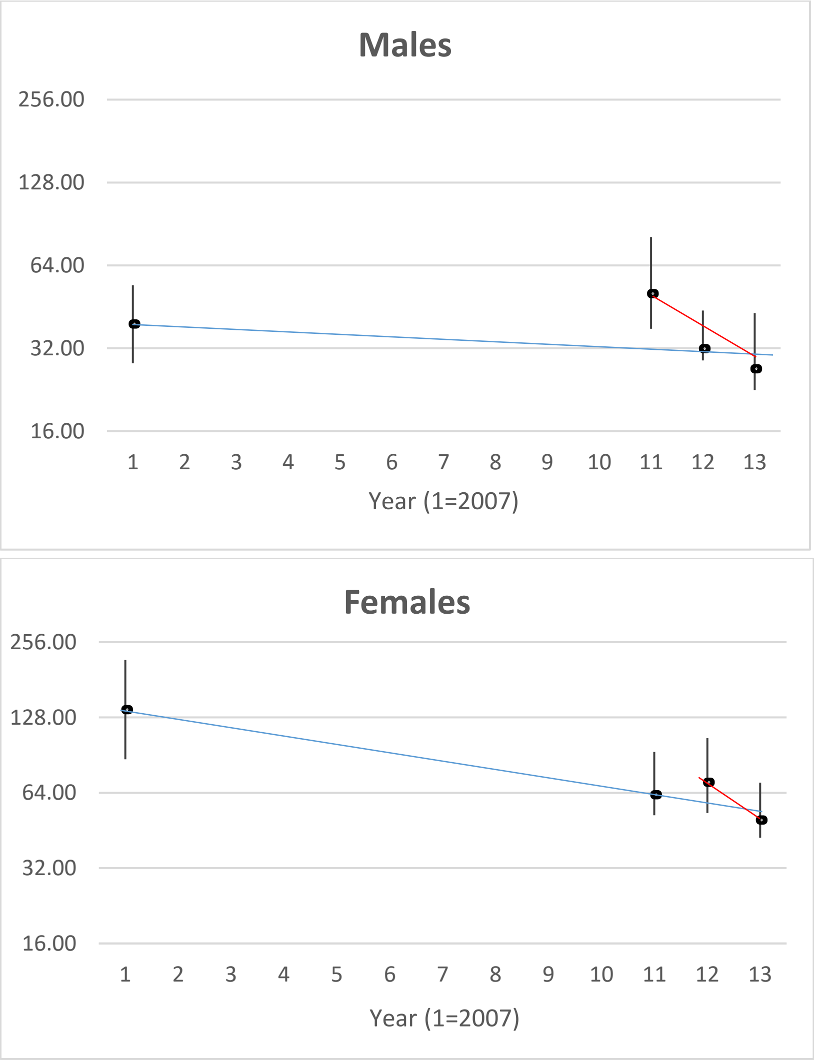

Figure 11. Change in caribou abundance (males and females) over the PAGE area between 2007 and 2017-2019. The 2007 (year 1) estimates (SE) are: Males 39 (6.5) Females 137 (32) Total 188 (31). The 2019 (year 13) estimates are: Males 27 (4.5) Females 50 (6.5) Total 80 (9.2).

CONCLUSIONS

The results for the population size and trend analysis show a significant decline in both female and male caribou numbers in the SK2 Central study area from 2017-2019. Analysis in the smaller Prince Albert Greater Ecosystem (PAGE) area shows that the decline is longer term and has been occurring since at least 2007.

The SK2 Central administrative unit is highly fragmented as a result of resource extraction, transportation and recreational corridors and wildfire. In 2015, the disturbance footprint (human-caused disturbance with a 500m buffer and wildfire area) resulted in only 57% undisturbed habitat (Saskatchewan Ministry of Environment 2019). Caribou in the SK2 Central are generally found in the remaining large, relatively intact areas with suitable habitat (Priadka et al. 2019, McFarlane et al. 2021). The remaining habitat areas are largely disconnected and the short and long-term declining population trend clearly indicates that they are not sufficient to maintain a self-sustaining caribou population in SK2 Central. These results align with the *Amended Recovery Strategy for the Woodland Caribou (Rangifer tarandus caribou), Boreal Population, in Canada (2020)*, which links habitat disturbance to caribou population status, and indicates that caribou ranges with 65% undisturbed habitat have only a 60% probability of population self-sustainability. Additional efforts to reduce the human-caused disturbance footprint should be made, as identified in the *Range Plan for Woodland Caribou in Saskatchewan, Boreal Plain Ecozone – SK2 Central Caribou Administration Unit* (Saskatchewan Ministry of Environment 2019).

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