**Wildlife Restoration OPERATING GRANT
FINAL PERFORMANCE REPORT**

ALASKA DEPARTMENT OF FISH AND GAME
DIVISION OF WILDLIFE CONSERVATION
PO Box 115526
Juneau, AK 99811-5526

Alaska Department of Fish and Game
Wildlife Restoration Grant

GRANT NUMBER: AKW-B-R2-2020 Amendment #1

PROJECT NUMBER: 4.38

PROJECT TITLE: Kenai Peninsula brown bear population demographics

PERIOD OF PERFORMANCE: July 1, 2019 - June 30, 2021

PERFORMANCE YEAR: July 1, 2020 - June 30, 2021

REPORT DUE DATE: August 27, 2021

PRINCIPAL INVESTIGATOR: Sean Farley

COOPERATORS: Jeff Selinger

Authorities: 2 CFR 200.328
　　　　　　　2 CFR 200.301
　　　　　　　50 CFR   80.90

I.   PROGRESS ON PROJECT OBJECTIVES DURING PERFORMANCE YEAR

OBJECTIVE 1: Determine the finite rate of change (lambda) for the Kenai brown bear population. Accomplishments: There are 21 collars being monitored. Figure 1 and Table 1 show vhf and capture locations for the reporting period. Demographic data have been updated and calculations run for 1995-2005 and 2006-2021, however the 2021 data reflect productivity only to spring 2021.

The map depicts current spring 2021 locations and the table contains spring 2021capture locations.

DATE	Bear ID	LAT DEG	LAT MIN	LON DEG	LON MIN	Sex	Est Age
26-May-21	380	59	49.17	150	37.57	F	Adult
26-May-21	353	60	45.82	149	36.44	F	Adult
25-May-21	383	60	18.672	150	13.737	F	Adult
24-May-21	393	60	11.97	149	57.741	F	Adult
24-May-21	388	60	21.917	149	31.896	F	Adult
24-May-21	385	60	35.016	149	56.354	F	Adult
24-May-21	327	60	18.672	149	59.342	F	Adult

OBJECTIVE 2: Complete data analysis on differential reproductive fitness of Kenai brown bears.

Accomplishments: Previous analyses demonstrate that the population of brown bears on the Kenai Peninsula has lower levels of genetic diversity relative to most other brown bear populations in Alaska and rejected the hypothesis that the Kenai brown bear population is partitioned into northern and southern populations on the Kenai Peninsula proper (Jackson et al. 2008). During 2020-2021, we compared fragment data of 14 nuclear microsatellite and sequence data from Kenai brown bears with homologous data from brown bears of 10 nearby populations (mainland Alaska, insular/peninsular south central and south coastal Alaska (including Montague Island), and western Alaskan). We also compared levels of genetic diversity at MHC Class II DQB exon 2 genes, which functions in adaptive immune response and is thought to be under balancing selection and thus is expected to show high levels of allelic diversity.

All markers showed relatively decreased levels of genetic diversity in Kenai Peninsula brown bears. All measures of population differentiation ($\chi2$ distribution of alleles, F-statistics, and Bayesian analyses of population structure) for all three marker classes show the Kenai brown bear population is genetically isolated from the 10 nearby western Alaska brown bear populations. Prior genetic analyses show that brown bear populations elsewhere in Alaska appear to be highly regionally structured, and that structure appears to be female-biased. However, our preliminary assessment Kenai Peninsula brown bears show a genetic signature of a recent demographic bottleneck that warrants additional investigation. A

Analysis of the microsatellite loci as well as preliminary data from a panel of unfiltered 150 autosomal single nucleotide polymorphism (SNP) loci, uncovered a signal of differentiation between brown bears occupying habitats east of the foothills of the Kenai Peninsula, and those occupying western Kenai Peninsula habitats. Preliminary analyses of the MHC Class II DQB exon 2 gene demonstrated alleles differentially partitioned between western and eastern Kenai Peninsula brown bear as well.

However, the SNP markers need filtering to select the most appropriate SNPs for future analyses and to determines applicability for use with lower-quality DNA sources such as hairs and swabs. Thus, we are currently filtering the 150 autosomal SNPs originally identified from sequence reads collected as part of a whole genome sequencing collaboration (Miller et al. 2012) and an additional 48 SNPs (derived from the brown bear X-chromosome). Filtering criteria include determining SNP usefulness in more granular population genetics studies, including Close Kin Mark Recapture (CKMR) studies and the tracking of female lineages.

A concomitant study to measure vital rates of Kenai Peninsula brown bears hints at differential reproductive success playing a significant role in population health. The SNPs we are examining will help determine whether Kenai brown bears show variance in reproductive output that may impact intergenerational evolutionary trajectories and contribute to the decreased levels of genetic diversity in brown bears in the Kenai Peninsula evident from nuclear microsatellites, the MHC Class II DQB exon 2 data and the mitochondrial genome

Jackson, J.V., S. L. Talbot, and S. Farley. 2008 Genetic characterization of Kenai brown bears (*Ursus arctos*): Microsatellite and mitochondrial DNA control region variation in brown bears of the Kenai Peninsula, south central Alaska. Can. J. Zool. 86(7):756-764.

Miller, W., S. C. Schuster, A. J. Welch, A. Ratan, O. C. Bedoya-Reina, F. Zhao, H. L. Kim, R. C. Burhans, D. I., Drautz, N. E. Wittekindt, L. P. Tomsho, E. Ibarra-Laclette, L. Hererra-Estrella, E. Peacock, S. Farley, G. K. Sage, K. Rode, M. Obbard, R. Montiel, L. Bachmann, Ó. Ingólfsson, J. Aars, T. Mailund, Ø. Wiig, S. L. Talbot and C. Lindqvist. 2012. Polar and brown bear genomes reveal ancient admixture and demographic footprints of past climate change. Proceedings of the National Academy of Sciences: doi: 10.1073/pnas.1210506109

OBJECTIVE 3: Develop a model predicting demographic vigor of Kenai Peninsula brown bears.

Accomplishments: A manuscript under development has been in holding status due to Covid-19 pandemic closures of the laboratory and restricted work from collaborators.

OBJECTIVE 4: Attend conferences and training, write and present papers.

Accomplishments: No conferences were attended.
Provided input as associate editor for Canadian J. Zoology. Reviewed multiple manuscripts for Journals.

II.   SUMMARY OF WORK COMPLETED ON PROJECT TO DATE.

Litter size and survival, female survival, and lambda calculation results are presented below

Number of Cubs by Fate and Age: 1995-2005						
	Age of Cubs					
	0	1	2	3	4	Grand Total
Sum of Survived	152	87	85	2	0	326
Sum of lost	57	63	0	0	0	122
Sum of Unknown	20	18	2	0	0	40
Total	231	168	87	2	0	488
Maximum Survival	0.72	0.58	1	1		To weaning
Minimum Survival	0.66	0.52	0.98	1		

Number of Cubs by Fate and Age: 2006-2021*						
	Age of Cubs					
	0	1	2	3	4	Grand Total
Sum of Survived	174	167	148	42	5	536
Sum of lost	125	43	4	0	0	172
Sum of Unknown	7	3	3	0	0	13
Total	306	213	155	42	5	721
Maximum Survival	0.58	0.79	0.97	1	1	To weaning
Minimum Survival	0.57	0.78	0.95	1	1	

Number of Litters by Litter Size and Age of Cubs: 1995 - 2005

	Age of Cubs					
Litter Size	0	1	2	3		Grand Total
1	14	11	8	0		33
2	54	49	23	1		127
3	33	20	11	0		64
4	3	0	0	0		3
Grand Total	104	80	42	1		227
Mean Litter Size	2.24	2.11	2.07	2.00		2.11

Number of Litters by Litter Size and Age of Cubs: 2006-2021*

	Age of Cubs					
Litter Size	0	1	2	3	4	Grand Total
1	37	45	27	6	1	115
2	69	42	40	9	2	160
3	43	28	16	6	0	93
4	1	0	0	0	0	1
Grand Total	150	115	83	21	3	372
Mean Litter Size	2.05	1.85	1.87	2.00	1.67	1.89

*2021 Data collected up to June 2021

Mean adult female survivorship:

Year span	mean	s.d.	Range
1995-2005	0.938	0.050	(0.857 – 1.00)
2006-2021	0.933	0.049	(0.821 – 1.00)

Population finite rate of increase (lambda): **

Year span	
1995-2005	1.039
2006-2020	1.06

**lambda calculated using Vortex 10.5.0.0
8/25/2020

III.   SIGNIFICANT DEVELOPMENT REPORTS AND/OR AMENDMENTS.

The Covid-19 pandemic has severely curtailed progress.

IV.   PUBLICATIONS

None

V.   RECOMMENDATIONS FOR THIS PROJECT.

Extend data collection on adult females and young until 2024 to cover one more litter generation and to recover from the time lost to Covid-19. During that time begin a transition to following 2 and 3 yr old bears with expandable collars to determine survival rate after weaning.

Continue efforts to identify maternal lineages of Kenai Peninsula brown bears and construct a genealogical lineage for at least 3 generations removed from present. Explore that dataset for indicators of reproductive success (e.g., home range location, heritability).

Use genetic relationship (first and second order relatives) to estimate population size. Augment data sample size by conducting one season of spring biopsy collection. Samples could be used for traditional mark-recapture calculations as well as possible application of close-kin mark-recapture.

Date: 9/3/2021