

**Alaska Department of Fish and Game
State Wildlife Grant**

Grant Number: W-33 **Segment Number:** 11
Project Number: 14.26
Project Title: Estimating wolf populations in Southeast Alaska using noninvasive DNA sampling
Project Duration: July 1, 2009–June 30, 2014
Report Due Date: September 1, 2013
Principal Investigators: David Person and Kris Larson
Cooperators: USFS Tongass National Forest, Rocky Mountain Genetics Laboratory
Work Location: Prince of Wales Island and Ketchikan, Alaska

I. PROGRESS ON PROJECT OBJECTIVES DURING LAST SEGMENT

OBJECTIVE 1: Our objective is to devise a protocol that enables us to estimate wolf numbers in GMU 2.

Due to difficulties collecting a sample size of wolf (*Canis lupus*) feces sufficient to estimate wolf abundance within our study area, we substantially modified this project. During autumn 2012, we deployed several hundred hair traps (Ausband 2011) at scent post stations systematically located throughout our study area on Prince of Wales Island (POW). Each scent post was marked with an abundance of lure intended to induce wolves to roll on the hair traps and leave hair. Hair was collected and used for DNA extraction and analyses. In addition, scats will be collected at scent post stations and preserved in ethanol for DNA extraction.

II. SUMMARY OF WORK COMPLETED ON JOBS IDENTIFIED IN ANNUAL PLAN THIS PERIOD

JOB/ACTIVITY 1: Collection of wolf hair and tissue

We deployed 183 hair traps distributed among 37 sampling nodes. We established 9 nodes that overlapped the home ranges of wolves within the Staney Creek drainage, 17 that overlapped the much larger Honker Divide group area, and 11 that overlapped the area used by the Ratz Harbor wolves. We were able to check all traps 3 times during November, but could not locate all of the traps in December owing to snow. We generally had 2 teams checking nodes, and they could do a complete survey of nodes within 3 days.

Wolves visited and left hair at 14 (38%) of 37 nodes. Some nodes and boards were visited several times. We also collected one scat adjacent to a hair trap. Photos at nodes showed wolves investigating hair traps and rubbing and rolling on the boards. They also

showed some hair traps were rubbed by several wolves during a single visit, thus some traps may have had hair from >1 wolf. We also observed several wolves investigating traps but not rubbing. Indeed, of 7 events photographed, wolves were observed rubbing in 3 events and not rubbing in 4 events. However, in some of those events where wolves were observed investigating traps but not rubbing, we obtained hair samples from other boards out of view of the cameras at the nodes. Conversely, we did not get hair samples from all of the boards on which wolves were photographed rubbing. Wolves dug up several boards, rubbed on them, carried them off, and then rubbed on them again. Consequently, we often found hair traps many meters away from the trap beds after being visited by wolves.

By midwinter, 125 wolf samples collected had been sent to the U. S. Forest Service (USFS) Rocky Mountain Genetics Laboratory (Dr. Mike Schwartz) in Missoula Montana for genotyping. The genetic samples consisted of 67 from hair boards distributed in the POW study area during autumn, 1 sample from a road-killed wolf, 7 samples from the captured wolves, 10 samples from Gravina Island (bear, from sampler prototype tests in midsummer), and 40 late winter samples from harvested wolves on POW.

JOB/ACTIVITY 2: Extracting DNA from hair and tissue and genotyping wolves

Of 77 non-invasive samples from the hair traps, 3 samples did not contain hair. The remaining 74 samples were analyzed for species using the control region of mitochondrial DNA. This mitochondrial region does not distinguish between wolves and dogs (*Canis familiaris*) and therefore, samples are recorded as wolf/dog. Sixty-two samples (83.8%) were successfully identified to species: 45 wolf/dog, 16 black bear (*Ursus americanus*), and one hair sample was mixed black bear and wolf/dog.

DNA was evaluated from 7 radiocollared and 41 harvested wolves using a suite of microsatellite DNA markers used on wolves previously in the western North America. Ten loci were variable in this wolf population and also amplified consistently in non-invasively collected DNA samples. The 10 microsatellite panel gave us an acceptable cumulative probability of identity (PID) = 4.35×10^{-7} (1 in 2,298,317 chance that we are calling two samples the same when they are actually from different individuals).

Of the 45 samples identified as wolf/dog, 28 (62%) produced quality DNA for individual identification and 2 others yielded genotypes representing mixed individuals. From these samples, 16 unique individuals were identified (11 wolves and 5 putative dogs). Eight samples (representing 5 individuals) were listed as suspected dog based on the photos obtained from the cameras at these stations. While we didn't have domestic dogs from Alaska in the dataset, these individuals contain alleles across five of the microsatellite loci that we did not observe in our known wolf samples (study animals and harvested tissues). We conducted a PCA analysis using microsatellites from the harvested wolves, the putative wolves identified from hair samples, and the 5 suspected dogs. Based on microsatellites, the putative dogs clustered together and apart from the known wolf samples (as well as the wolves identified from hair samples). This analysis along with our evidence from the photos suggests these five individuals are dogs and not wolves. Thus, we dropped the putative dogs from the rest of the analysis.

We analyzed DNA samples (blood and hair) from 7 live-captured wolves tagged on the study area and 41 harvested wolves from POW. Of these 41 harvested wolves, 13 wolves were harvested from or close to our study area.

During the mark-recapture sessions (1 November-8 December), we caught 9 individual wolves in the hair traps. We had 4 total recaptures of these wolves that occurred in different sessions for 13 capture events. Four wolves were recaptured only once and 4 wolves were recaptured twice. In addition, we had 7 radiocollared wolves in the study area at the same time. We didn't catch any collared wolves in the hair traps. Because we didn't find some hair boards until February, we identified 2 more wolves later in the winter. Thus, we identified 11 wolves from the hair traps.

Five of these wolves marked during the hair trapping were eventually harvested during the trapping season (2012–2013). In addition, we had at least 2 of our radiocollared wolves taken by trappers. Therefore, we had 7 marked wolves killed from the 13 wolves harvested and sampled on our study area. We had evidence of 2 more wolves that were known to be killed, but they were not sealed (no samples were collected).

JOB/ACTIVITY 3: Analysis and population estimation

Using only the DNA results, we counted a minimum of 21 wolves in our study during 2012–2013. We recorded 13 harvested wolves that included 5 wolves captured in the hair traps. Six more wolves were identified from the hair traps. Two wolves were known to be killed, but not sealed (no DNA samples), bringing the total to 21 wolves.

In addition, 7 wolves were live-captured and radiocollared during autumn 2012. Two of these 7 wolves were recorded in the 13 harvested wolves. Thus, the minimum population size was 26 wolves. At least 15 wolves were taken by humans (58%) during 2012–2013.

No additional analysis was done this report period.

JOB/ACTIVITY 4: Publication and report writing

We completed this annual progress report. No other publications were completed during this reporting period.

III. Not applicable.

IV. SIGNIFICANT DEVIATIONS AND/OR ADDITIONAL FEDERAL AID-FUNDED WORK NOT DESCRIBED ABOVE THAT WAS ACCOMPLISHED ON THIS PROJECT DURING THIS SEGMENT PERIOD

None.

V. PUBLICATIONS RECOMMENDATIONS FOR THIS PROJECT This project was redesigned and is beginning of a new phase of sample collections and analyses. The work will occur in conjunction with a separate wolf radio-collaring effort that will compliment the DNA analyses with respect to providing an independent means of estimating wolf abundance for the study area.

Literature Cited

14.26 Estimating wolf populations in Southeast Alaska using noninvasive DNA sampling
FY13 Annual Research Performance Report

Ausband, D. E. 2011. Hair of the dog: obtaining samples from coyotes and wolves noninvasively. *Wildlife Society Bulletin* 35:105–111.

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