## Alaska Department of Fish and Game Wildlife Restoration Grant

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**Project Title:** Estimating wolf populations in Southeast Alaska using noninvasive DNA sampling

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Report Period: 1 July 2014–30 June 2015

**Report Due Date:** 1 September 2015

**Cooperator:** USFS Tongass National Forest, Rocky Mountain Genetics Laboratory

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Work Location: Prince of Wales Island and Ketchikan, Alaska

#### I. PROBLEM OR NEED THAT PROMPTED THIS RESEARCH

Wolves (Canis lupus) are an important component of southeastern Alaska fauna, and occupy the mainland and most of the islands south of Frederick Sound. They are obligatory predators of ungulates and are mostly dependent on Sitka black-tailed deer (Odocoileus hemionus sitkensis) where the 2 species co-occur. Monitoring wolf populations is merited because wolves are a management indicator species in the Tongass Land Management Plan (USFS 1997, 2008). Additionally, the Center for Biological Diversity and Greenpeace jointly petitioned the U.S. Fish and Wildlife Service (FWS) in 2011 to list Southeast Alaska's Alexander Archipelago wolves (C. l. ligoni) as threatened under the Endangered Species Act (1973), the second attempt in 17 years. This listing petition, together with the regulatory harvest guideline for wolves on Prince of Wales and adjacent islands [Game Management Unit (GMU) 2], established in 1996 by the Alaska Board of Game, makes it imperative that the Alaska Department of Fish and Game (ADF&G) develop a reliable method for estimating and monitoring wolf populations, particularly in GMU 2. Beginning with the 2014–2015 harvest season, the ADF&G reduced wolf harvest in GMU 2 from 30% to 20% of the fall estimated population to address concerns of a declining population. The USDA Forest Service (USFS), because of its land ownership status, shares an interest in wolf management (USFS 1997).

Estimating population abundance of wolves in Southeast Alaska is challenging because the densely forested landscape obscures visibility and lowers success of traditional

methods such as aerial surveys and mark-recapture using radio collars. Moreover, on Prince of Wales Island (POW), which forms the majority of land area in GMU 2, snow cover is often intermittent, prohibiting reliable use of track indices. However, regular population estimates of wolves are necessary for sustainable management, particularly in areas where there is elevated concern for the population's viability. Until this study, the most recent wolf population estimate for GMU 2 was produced for fall 1994 (n = 356, 95% CI = 150–562; Person et al. 1996). Regular population estimates at shorter intervals are required for monitoring and managing sustainable populations of wolves, thus refinement of a cost-effective, reliable method is necessary.

The goal of this research was to develop an integrated strategy for combining multiple measures of abundance, each with its own unique set of strengths and limitations, into a reliable method for estimating wolf populations on POW, GMU 2 and throughout the Southeast region. While the work was conducted on POW, where the need is most immediate and logistics most amenable, the intent is to develop a strategy and methodology that can be applied more broadly throughout the rainforest of Southeast Alaska.

# II. REVIEW OF PRIOR RESEARCH AND STUDIES IN PROGRESS ON THE PROBLEM OR NEED

Person et al. (1996), Kohira and Rexstad (1997), Person (2001), Darimont and Paquet (2002), and Person and Russell (2008, 2009) described the biology and ecology of wolves in the rainforests of southeastern Alaska and coastal British Columbia. Person et al. (1996), Person and Russell (2008, 2009), Person and Logan (2010), and Person and Brinkman (2013) identified major factors influencing wolf population growth in Southeast Alaska. Person et al. (1996) calculated a wolf population estimate for GMU 2 for fall 1994 (n = 356, 95% CI = 150–562).

During 2012–May 2015, ADF&G, in collaboration with the USFS, initiated a project to address the need for timely and accurate wolf population information. This research was the first attempt to compare methods to estimate wolf population abundance in Southeast Alaska and evaluate their effectiveness in terms of cost, effort, and reliability.

#### **III. APPROACHES USED AND FINDINGS RELATED TO THE OBJECTIVES AND TO PROBLEM OR NEEDObjective 1**: To devise a protocol that enables us to estimate wolf numbers in Game Management Unit (GMU) 2.

**Approach:** We applied two methods concurrently within the same northcentral POW study area: 1.) the previously implemented method using radiocollared wolves to produce minimum counts and populations estimates, and 2.) capture-recapture using hair samples to identify individuals genetically (noninvasive sampling). We used foothold traps to capture wolves and instrument them with GPS radio collars. Concurrently, we modified a hair snare method to collect DNA samples to estimate fall density using a spatial capture-recapture approach (SECR; Efford et al. 2004, Efford 2015). We assessed the effectiveness of methods in terms of cost, effort, reliability, and appropriate spatial scale

for application to region-wide monitoring. This research represents the first density estimate of wolves calculated using hair snare and spatial capture-recapture methods.

Wolves were captured in modified foothold traps. Restrained wolves were immobilized and instrumented with a global position system (GPS) radio collar. Capture and handling procedures conformed to guidelines established by the ADF&G Animal Care and Use Committee (ACUC #2012–028 and #2014–15) and the American Society of Mammalogists (Sikes et al. 2011). Radiocollared wolves were aerially tracked approximately every 2 weeks with a fixed-wing airplane (Cessna 185) equipped with receiver antenna and the collar location data was remotely downloaded. Marked wolves, along with their pack members were observed to obtain minimum counts visually. We used radiocollar GPS location data to determine home range size and geographic extent of wolf packs.

We generated a population estimate for our study area using the methods applied by Person et al. (1996) to calculate the 1994 fall population estimate. This method uses the number of known packs, pack size, and home ranges to derive a population estimate (Person et al. 1996) and averages it with the minimum count (the maximum number of wolves observed in the study area) adjusted by 29% to account for the estimated proportion of nonresident wolves in the population.

During fall 2012–2014, we established an array of hair-trap (hereafter hair board) nodes in a grid across the study area to estimate the density of wolves. We increased node density and extent in 2014 with the intention of obtaining more hair samples and improving the precision of our population estimates. The grid size was roughly  $3.9 \pm 1.1$ km during 2012–2013, and  $3.5 \pm 1$  km during 2014. Nodes consisted of 5 hair boards at 100 m spacing intervals. Hair board nodes were deployed 20 October–30 December (2012, n = 37; 2013, n = 36; 2014, n = 72). A discrete analysis grid was defined for the study area by delineating a buffer around the trap array, and then clipping to the POW shoreline. The analysis grid spacing was at 500 m intervals and encompassed an area of 1,684 km<sup>2</sup> in 2012–2013, and 3,393 km<sup>2</sup> in 2014.

We used lured hair boards to collect wolf hair noninvasively, and extract DNA for individual identification through genotyping. Hair board nodes were checked every 10 days in 2012, and in 2013–2014 monitored on a weekly schedule. Uniquely genetically identified wolves were used in SECR models to estimate population density for the study area. We assigned sampling occasions to each capture event and used the individual encounter histories across the sampling period. We evaluated a suite of competing models using information theoretic methods (Burnham and Anderson 1998), and conducted the analyses primarily in the R statistical program (R Development Core Team) using the secr package version 2.9.4 (Efford 2015).

**Findings:** A total of 12 wolves were radiocollared during May 2012–May 2015, including 5 males and 7 females. Of these, 4 were juveniles (<1 years old), 3 were yearlings, and 6 were adults ( $\geq$  2 years old) when captured. We monitored the radiocollared wolves 6 June 2012–30 May 2015, during which time we conducted 58 tracking and download flights, and downloaded ~16,000 GPS locations. Of the 12 radiocollared wolves, 9 died, the fate of 1 is unknown (the radio collar release mechanism detonated as programmed), and 2 are alive. Five wolf mortalities were from harvest (4

wolves were trapped and 1 shot), 3 mortalities were attributed to unreported humancaused mortality, and 1 to intraspecific strife.

Home ranges of wolf packs using minimum convex polygons (MCPs) ranged from 470– 944 km<sup>2</sup> (mean = 707 km<sup>2</sup>, SE = 168 km) and using adaptive kernels ranged from 292– 644 km<sup>2</sup> (mean = 535 km<sup>2</sup>, SE=77). The radiocollared wolves that conformed to a home range represented 2 packs (Honker and Staney) that were largely consistent throughout our study period and 1 additional pack that budded from the Honker wolves (Ratz) and occupied an adjacent territory for 10 months until the representative radiocollared wolf was killed. The 2 radiocollared wolves that are currently alive moved in to this previously used area during spring 2015, and GPS location data suggest they have assumed occupancy of this home range territory.

The 5 packs that occurred in the study area during the reporting period ranged in size from 1–16 wolves, with an annual mean of 6.0 (SE = 0.92). Pack size in the fall (August 15–December 31) ranged from 1–16 (mean = 8, SE = 0.93), and in the spring (March 1–July 1) ranged from 1–15 (mean = 3.9, SE = 0.78). Five of the 12 radiocollared wolves were classified as dispersers or extraterritorials during time they were monitored. Three of the dispersing wolves originated from the Honker pack and dispersed out of the study area, and one wolf dispersed into the study area. The extraterritorial wolf overlapped and remained on the periphery of the Staney pack territory both within and outside of the boundaries of the study area throughout the period of time it was monitored.

The fall minimum count (the maximum number of wolves observed in the study area) based on known wolf packs (3–4 per year) was 19 in 2012, 23 in 2013, and 21 in 2014. Using the method previously implemented by Person et al. (1996), we averaged the fall GMU 2 wolf population estimated from the number of known packs, pack size, and home ranges (n = 240) with the empirical estimate method (minimum counts adjusted upwards by 29% to account for nonresident wolves) to obtain fall population estimates for all study years (2012: n = 192; 2013: n = 207; 2014: n = 200). Due to low samples sizes of radiocollared wolves, we were unable to derive variances of sightability.

Noninvasive sampling in 2012 produced an insufficient number of recaptures (5 wolves redetected once after initial detection) to produce a population density estimate. The 8 recaptured wolves in 2013 consisted of 4 individuals detected twice, and 4 individuals detected 3 times. The 9 recaptured wolves in 2014 included 4 individuals detected twice, 3 individuals detected 3 times, and 2 individuals detected 6 times. The distance between recaptures at hair board nodes in 2013 ranged from 0 (recaptured at same node where originally detected) to 27.7 km (mean distance =  $2.9 \pm 5.9$  km), whereas in 2014 distances moved were larger (range = 0 - 29.6 km; mean distance =  $17.9 \pm 1.6$  km).

The fall 2013 density estimate calculated using the hair snare method was  $24.5 \pm 6.8$  wolves/1,000 km2 (95% CI = 14.4-41.9 wolves/1,000 km<sup>2</sup>). Using the fall 2013 density estimate to predict the population in the majority of GMU 2 resulted in a population estimate of 221 wolves (95% CI = 130-378). The fall 2014 density estimate was significantly lower than the previous year based on bootstrapped 95% confidence intervals. The density estimate from the top-ranked SECR model was  $9.9 \pm 3.0$  wolves/1,000 km<sup>2</sup> (95% CI = 5.5-17.7 wolves /1,000 km<sup>2</sup>), and the predicted number of wolves in GMU 2 was  $89 \pm 27.1$  (95% CI = 49.8-159.4).

## IV. MANAGEMENT IMPLICATIONS

We made efforts throughout the project duration to improve the noninvasive sampling protocol to make it a more effective tool for wolf monitoring. We did not have a sufficient number of recaptures in the fall of 2012 to estimate wolf population density. Beginning in 2013 we reduced the amount of time between hair board checks (from 10 to 7 days), visibly marked the board sites for weekly relocation, and physically secured them so they could not be moved by the wolves. These efforts contributed to obtaining sufficient individual recaptures in 2013 to calculate population density. We also implemented a genotyping screening protocol (analyzing hair samples separately that were suspected to consist of more than one individual) which resulted in increased genotyping success rate from 66% in 2012 to 83% in 2013.

Our efforts in 2014 to improve density estimate precision by increasing the hair sampling intensity and sampling area resulted in more wolf hair samples (n = 108) than in 2012 (n = 74) or 2013 (n = 86), but did not substantially increase the number of wolves detected or redetected (2012 = 6, 2013 = 8, 2014 = 10). Furthermore, trapping success (unique wolf detections/trap/100 days) declined in 2014 (0.84 wolves/100 days) in comparison to 2012 (1.32 wolves/100 days) and 2013 (1.88 wolves/100 days). The increased trapping effort required in 2014 could reflect a variety of conditions, including a reduction in the wolf population in the study area, a redistribution of wolves in the study area leading to fewer recaptures (the Staney home range was not occupied by a wolf pack in 2014), changes in wolf behavior, or other unknown reasons. However, live-trapping and radiocollaring wolves was nearly 12 times more expensive than identifying individual wolves genetically. Additionally, live-trapping required more effort and more of a time commitment.

For application to estimating wolf population density in an area for either a short time period, or over multiple years as part of a monitoring effort, the noninvasive SECR method proved to be more robust, reliable, efficient, and cost-effective than the traditional method. We found that in addition to having higher trapping success and lower costs than the traditional method, the noninvasive method produced a statistically robust population estimate of wolves in the study area with an associated measure of uncertainty, and is therefore preferred for population monitoring.

The noninvasive method has promise for application to wolf monitoring in other regions. The extent of a potential study area is limited mainly by available staffing and access to hair snare locations. Because success of this method is dependent upon obtaining a sufficient number of individual recaptures, we recommend increasing the density of nodes throughout the study area, especially in regions were wolf density is believed to be lower than in our study area.

## V. SUMMARY OF WORK COMPLETED ON JOBS

## FROM PROJECT STATEMENT:

**Objective 1:** To devise a protocol that enables us to estimate wolf numbers in Game Management Unit (GMU) 2.

Job/activity 1: Collection of wolf hair and tissue

Accomplishments: We collected wolf hair samples (2012, n = 74; 2013, n = 86; 2014, n = 108) at the hair board nodes. We also obtained muscle samples and harvest locations taken during annual GMU 2 hunting and trapping seasons (1 December–31 March [State of Alaska regulations; ADF&G 2014]), 1 September–31 March [federal subsistence hunting season], 14 November–31 March [federal subsistence trapping season]), 2012–2014 (n = 40, 49, and 29, respectively). Finally, we collected muscle samples from one road-killed wolf, and one human-caused unreported wolf, in addition to blood samples from 10 of the wolves captured in this project for radiocollaring.

#### Job/activity 2: Extracting DNA from scats and genotyping wolves

**Accomplishments:** Due to difficulties collecting a sample size of wolf feces sufficient to estimate wolf abundance within our study area, we substantially modified this project to obtain unique individual capture histories from hair follicle DNA. Species identification was performed on mtDNA sequences from hair samples, and we used a microsatellite panel to genotype the hair samples identified as canid. During the time period of the hair board sampling (fall 2012–2014), 48 wolves were identified from noninvasively collected hair samples. We also genotyped 93 tissue samples from GMU 2 harvested wolves during the 2012–2013 and 2013–2014 annual hunting and trapping seasons.

Job/activity 3: Analysis and population estimation

## Accomplishments:

The job was completed by 30 June 2015 (see Section III for details).

Job/activity 4: Publication and report writing

Accomplishments: We prepared annual progress reports. A final technical will be prepared later this year.

# VI. PUBLICATIONS

We completed the following publications:

- Division of Wildlife Conservation. 2014. The status and outlook of Southeast Alaska's Unit 2 wolves. Alaska Department of Fish and Game, Wildlife Management report ADF&G/DWC/WMR-2014-2, Juneau.
- Flynn, R. W., G. Roffler and K. Larson. 2014. Estimating wolf populations in Southeast Alaska using noninvasive DNA sampling. Alaska Department of Fish and Game, Division of Wildlife Conservation, Federal Aid Annual Research Performance Report 1 July 2009–30 June 2018, Federal Aid in Wildlife Restoration Project 14.26, Juneau.

Roffler, G. 2014. Wolf population estimation on Prince of Wales Island, Alaska. Alaska Department of Fish and Game, Division of Wildlife Conservation, Federal Aid Annual Performance Report 30 September 2013–30 June 2015, Cooperative Endangered Species Conservation Fund Project E-19-1-1, Juneau.

#### VII. ADDITIONAL FEDERAL AID-FUNDED WORK NOT DESCRIBED ABOVE THAT WAS ACCOMPLISHED ON THIS PROJECT

Not applicable.

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