Alaska Department of Fish and Game
Wildlife Restoration Grant

Grant Number: AKW-20

Project Title: Using genomics to identify population structure and inform models of Southeast Alaskan wolves

Project Duration: 1 July 2016–30 June 2019

Report Due Date: 1 September 2017

PRINCIPAL INVESTIGATOR: Gretchen Roffler

COOPERATORS: Dr. Michael Schwartz, Katherine Zarn, and Kristine Pilgrim at the National Genomics Center for Wildlife and Fish Conservation, Rocky Mountain Research Station, USFS, Missoula, MT.

WORK LOCATION: Game Management Units 1-5, Region I, Southeast Alaska

I.   PROGRESS ON PROJECT OBJECTIVES DURING LAST SEGMENT

OBJECTIVE 1: COLLECT SAMPLES FOR DNA ANALYSIS

During the reporting period we collected biological samples from wolves for DNA extraction and genotyping. Thus far, we have made progress on achieving a valid sample size (n ≥ 20) for each GMU (1–5). We have also been able to collect samples from geographical areas widely-distributed throughout each GMU in Region I for use in our landscape genomics analyses. Finally, we have collected wolf samples from outside Region I for comparison of genetic differentiation among coastal and interior wolves.

OBJECTIVE 2: GENOTYPE WOLF SAMPLES

During the reporting period, DNA has been extracted from wolf samples and prepared for genotyping (to be conducted in FY 2018) at the US Forest Service National Genomics Center for Wildlife and Fish Conservation (NGCWFC). In coordination with our collaborators at the NGCWFC, we selected an approach to develop an assay of single nucleotide polymorphisms (SNPs) that will best meet the project objectives. The method selection criteria included adequate whole genomic coverage (e.g., 50,000 – 70,000 SNPs), inclusion of SNPs variable in Southeast Alaskan wolves, the ability to reliably genotype low-quality biological samples, and lack of ascertainment bias. These data will be used to inform genetic structure and other questions about wolves throughout Southeast Alaska.

OBJECTIVE 3: DATA ANALYSIS

No data analysis was completed during the reporting period, as genomic data will not be available until FY 2018.

OBJECTIVE 4: DATA SYNTHESIS AND PREPARATION OF PUBLICATIONS

No data synthesis or publication preparation was completed during the reporting period.

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

JOB/ACTIVITY 1A: We will collect hair and muscle tissue samples from harvested wolves from throughout Southeast Alaska and neighboring portions of British Columbia and the Yukon.

Accomplishments: We coordinated with area biologists, trappers, sealers, and other ADF&G staff to obtain wolf muscle and skin tissue samples from across Region I for wolf genomics analyses. We collected and prepared wolf samples from the 2016–2017 harvest season resulting in additional 115 samples from GMUs in Region I (GMU 1A: n = 6, GMU 1B: n = 21, GMU 1C: n = 22, GMU 1D: n = 12, GMU 2: n = 13, GMU 3: n = 39, GMU 4: n = 2). In addition, we conducted targeted collections in geographical areas of interest (e.g., Snow Pass, Prince of Wales Island) of non-invasive samples (hair and scat) for testing the SNP assay on lower-quality samples.

JOB/ACTIVITY 2A: We will collaborate with the National Genomics Center for Wildlife and Fish Conservation in Missoula, Montana to obtain genotypes of wolves region-wide.

Accomplishments: DNA was extracted and archived from 213 wolf tissue (muscle, bone, and skin) samples collected in GMUs1, 2, 3, 4, and 5. Samples from 70 harvested wolves (blood, muscle, and skin) collected in the Yukon Territory have also been prepared for DNA extractions.

We have conducted research to select the most appropriate method to develop a SNP assay to sequence Southeast Alaskan wolves. We have determined that the best approach will be to perform low-coverage pooled whole genome sequencing (pool-seq) on a subset of samples (n≈50) selected to represent multiple putative wolf populations that are geographically widely-distributed across Region I. Using the SNPs identified in the pool-seq experiment, we will generate a custom targeted capture to sequence SNPs in additional samples.

JOB/ACTIVITY 3A: We will use spatially-explicit, individual-based models to assess patterns of gene flow at the regional scale.

Accomplishments: No work was completed on this job during the reporting period.

JOB/ACTIVITY 3B: We will test the relative influence of landscape features, habitat types, and geographic distance on patterns of genetic relatedness**.**

Accomplishments: No work was completed on this job during the reporting period.

JOB/ACTIVITY 3C: We will use population assignment tests to identify recent immigrants from different regions**.**

Accomplishments: No work was completed on this job during the reporting period.

JOB/ACTIVITY 3D: We will characterize fine-scale genetic structure of wolves within GMUs (presence of multiple populations).

Accomplishments: No work was completed on this job during the reporting period.

JOB/ACTIVITY 3E: We will use parentage approaches to identify wolf packs and disperser vs. resident wolves.

Accomplishments: No work was completed on this job during the reporting period.

JOB/ACTIVITY 4: We will synthesize and compare data sets from wolves throughout the region and beyond. We will prepare annual progress reports and a final report. We will strive to produce several peer-reviewed publications from this project. We will share our findings with the public as needed.

Accomplishments: This progress report was prepared. No other work was completed on this job during the reporting period.

III.   SIGNIFICANT DEVIATIONS AND/OR ADDITIONAL FEDERAL AID-FUNDED WORK NOT DESCRIBED ABOVE THAT WAS ACCOMPLISHED ON THIS PROJECT DURING THIS SEGMENT PERIOD
    None.

IV.   PUBLICATIONS Prepared by: Gretchen Roffler, Wildlife Biologist III

Submitted by: Susannah Woodruff, Research Coordinator

Date: 9/1/2017