Sea Duck Joint Venture
Annual Project Summary
FY 2015 – (October 1, 2014 to Sept 30, 2015)

SDJV Project #142: **Delineating Pacific Barrow's Goldeneye populations: A multi-technique approach (genetic markers and satellite telemetry).**

Principal Investigator(s) ***(name, affiliation, mailing and email address):***
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Partners (*anyone else providing some kind of support)*:
Tim Bowman, USFWS

Project Description (*issue being addressed, location, general methodology)*:
Our ability to conserve North American sea ducks is largely dependent on being able to delineate demographically or spatially independent sub-units. Population delineation is a necessary precursor for most other management information needs, including monitoring, population dynamics, disease, and harvest. Available satellite telemetry data show that Barrow's Goldeneyes residing in Alaska and southern British Columbia occupy discrete areas throughout the annual cycle suggesting that these birds comprise at least two subpopulations. Satellite telemetry movement data were largely collected from adult birds because hatch year birds typically exhibit higher mortality rates. Therefore, inferences made regarding movement patterns are largely restricted to breeding, molting, and wintering site fidelity among adult birds. Because Barrow's Goldeneyes exhibit delayed breeding, it is not possible (or extremely rare) to observe the first breeding attempt of hatch year birds to describe natal dispersal. Genetic signatures, in contrast, reflect past dispersal patterns, which will provide insight on the level of natal dispersal (i.e. gene flow) and connectivity among areas. Therefore, it is valuable to employ a multi-technique approach in population delineation studies to generate a more comprehensive view of movement and dispersal of individuals; satellite telemetry data reveal current patterns on breeding and non-breeding site fidelity, whereas genetic markers reveal past and current patterns of natal and breeding dispersal (Chabot et al. 2012).

Genetic Data Analysis
The presence of genetic subdivision among locales is dependent on the frequency of successful dispersal events (i.e. gene flow) among areas and therefore can be used to delimit breeding population boundaries. Further, genetic data collected from both the nuclear and mitochondrial genomes can be used to provide insight into sex biases in dispersal to gain additional understanding of the connectivity among breeding locales (e.g. Sonsthagen *et al*. 2009, 2011).

DNA from all samples have been extracted and are currently being genotyped at 9 microsatellite loci, and sequenced at mitochondrial DNA control region using standard protocols at the USGS Alaska Science Center, Molecular Ecology Laboratory. Levels of genetic structure among sampled breeding locales will be determined in Arlequin (Schneider et al. 2000) and among all locales in Structure (Pritchard et al. 2000).

Objectives *(should identify how the project addresses SDJV priorities*):
Population delineation is identified as a high priority for future work in the SDJV Implementation Plan. In particular, population delineation of BAGO is identified as "high urgency to inform survey development or harvest interpretation."

The objective of the proposed research is to complement current satellite telemetry data with molecular data to increase our understanding of dispersal and movement patterns of Barrow's Goldeneyes that will aid in the delineation of populations.

Preliminary Results *(include maps, photos, figures/tables as appropriate):*
We have Barrow's Goldeneye samples from six locales; Kachemack Bay (n = 46), Kodiak (n = 22), Prince William Sound (n = 40), Juneau (n = 35), Indian Arm (n = 28), and Kitimat (n = 40). Initially we screened 31 microsatellite loci for variability and selected 9 loci that were polymorphic for Barrow's Goldeneyes. The number of alleles per locus ranges from 2 to 25 with an average of 8.9 alleles per locus.

Project Status *(e.g., did you accomplish objectives, encounter any obstacles, what are your plans for the future?)*
We are currently collecting genotype data at 9 microsatellite loci and sequence information from the mtDNA control region. In the upcoming year, we plan to finish data collection and quality control and commence with data analysis.