

**Sea Duck Joint Venture  
Annual Project Summary  
FY 2016 – (October 1, 2015 to Sept 30, 2016)**

**Project Title (including SDJV project tracking #):** SDJV Project # 142: Delineating Pacific Barrow's Goldeneye populations: A multi-techniques 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):**

Christy Haughey, USGS Alaska Science Center  
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**Project Description (issue being addressed, location, general methodology):**

Our ability to manage North American sea ducks is largely dependent on appropriate delineation of demographically or spatially independent sub-units. Population delineation is a necessary precursor for interpreting other management-relevant information, including monitoring, population dynamics, disease, and harvest. Available satellite telemetry data show that Barrow's Goldeneyes wintering in south-central Alaska, southeast Alaska, and southern British Columbia occupy discrete areas throughout the annual cycle suggesting existence of population structuring at these scales (Figure 1). Genetic signatures, in contrast, reflect both contemporary and historical dispersal patterns, which will provide insight on the levels of natal dispersal (i.e. gene flow) and connectivity among breeding areas. Therefore, it is valuable to employ a multi-technique approach to population delineation studies to generate a more comprehensive view of movement and dispersal of individuals; satellite telemetry data reveal current patterns of breeding and non-breeding site fidelity, whereas genetic markers reveal past and current patterns of natal and breeding dispersal (Chabot et al. 2012).

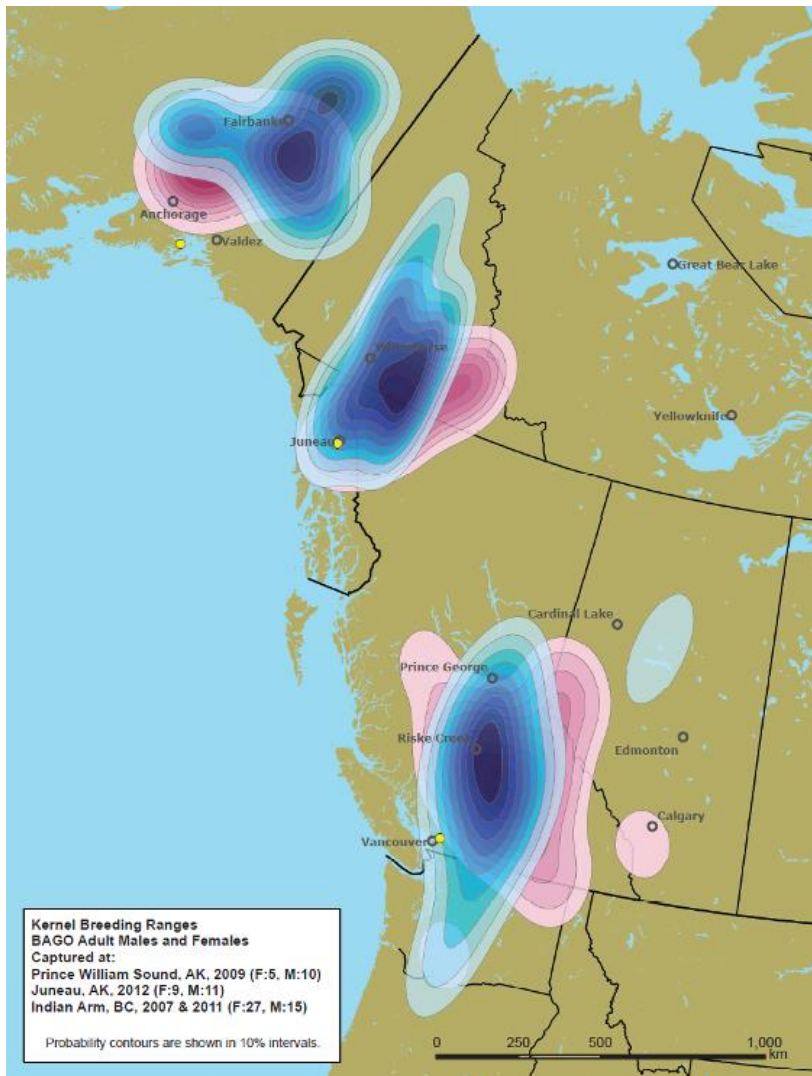


Figure 1. Breeding distributions of male (blue) and female (pink) Barrow's goldeneyes captured and marked with satellite transmitters (PTTs) at 3 wintering areas (yellow dots).

### *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 connectivity among breeding locales (e.g. Sonsthagen *et al.* 2009, 2011). Genetic data are being collected following 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, AK (n = 46), Kodiak, AK (n = 22), Prince William Sound, AK (n = 40), Juneau, AK (n = 35), Indian Arm, BC (n = 28), and Kitimat, BC (n = 40). Initially, we screened 31 microsatellite loci for variability. Genotype data were collected at 9 loci that were variable within Barrow's goldeneye. One locus did not conform to Hardy-Weinberg expectation (HWE) and was removed from subsequent analyses. Once that locus was removed, all populations and loci conformed to HWE and loci were in linkage equilibrium.

Genetic structure among sampled locations was estimated using two methods: standard  $F_{ST}$  (frequency based) and a Bayesian approach which assigns individuals into groups based on HWE. No genetic structure was detected among sampled areas ( $F_{ST} = 0.001$ ,  $P = 0.296$ ); however, the Bayesian approach (STRUCTURE) did uncover two clusters. An individual from Kitimat had an intermediate phenotype and was identified in the field as a suspected hybrid. This individual's membership coefficient is split between the two clusters (60/40). These findings suggest that the observed structure is likely attributable to common goldeneye introgression and not structuring within Barrow's goldeneyes among locales.

**Project Status (e.g., did you accomplish objectives, encounter any obstacles, what are your plans for the future?)**

We have completed data collection for the 9 microsatellite loci including quality control procedures. Sequence information from mtDNA control region uncovered a nuclear pseudogene. We are pursuing other maternally inherited markers for inclusion in this study to assess sex-biases in gene flow. Additional analyses (and comparisons with other data types, such as PTT data and morphology) are needed to make final conclusions.

This information is preliminary or provisional and is subject to revision. It is being provided to meet the need for timely best science. The information has not received final approval by the U.S. Geological Survey (USGS) and is provided on the condition that neither the USGS nor the U.S. Government shall be held liable for any damages resulting from the authorized or unauthorized use of the information.

**References**

- Chabot, A.A., K.A. Hobson, S.L. Van Wilgenburg, G. McQuat, and S.C. Loughheed. (2012). Advances in linking wintering migrant birds to their breeding-ground origins using combined analyses of genetic and stable isotope markers. *PLoS ONE* 7(8): e43627. doi:10.1371/journal.pone.0043627.
- Pritchard, J.K., M. Stephens, and P. Donnelly. 2000. Inference of population structure from multilocus genotype data. *Genetics*, 155, 945–959.
- Schnieder, S., D. Roessli, and L. Excoffier. 2000. ARLEQUIN, version 2.0: A software for population genetic analysis. Genetics and Biometry Laboratory, University of Geneva, Geneva, Switzerland.
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- Sonsthagen, S. A., S. L. Talbot, K. T. Scribner, and K. G. McCracken. 2011. Multilocus phylogeography of Common Eiders (*Somateria mollissima*) breeding in North America and Scandinavia. *Journal of Biogeography*, 38, 1368–1380.

