

**Sea Duck Joint Venture
Annual Project Summary for Endorsed Projects
FY06 – (October 1, 2005 to September 28, 2006)**

Project Title: (SDJV #43) Factors involved in population dynamics and delineation of North American mergansers

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Project Description: A three-year project (2004 – 2006) examining general ecology and population genetics of hooded, common, and red-breasted mergansers across North America.

Revised objectives for FY 2006:

- I. Assess population genetic structure of Common and Red-breasted mergansers in Alaska.**
- II. Assess phylogeography of all three merganser species across North America.**

Preliminary Results (ordered by objectives listed above):

Objectives I & II. In 2006, we conducted four sampling trips in Alaska and received numerous contributed samples from collaborators across North America and Europe. Samples from common and red-breasted merganser come from across the state of Alaska and include all areas that were initially proposed except the Seward Peninsula, which we plan to visit in May of 2007. A total of 1,176 DNA samples (594 Common, 321 Red-breasted, and 530 Hooded) are now archived at the Alaska Science Center, Molecular Ecology Laboratory.

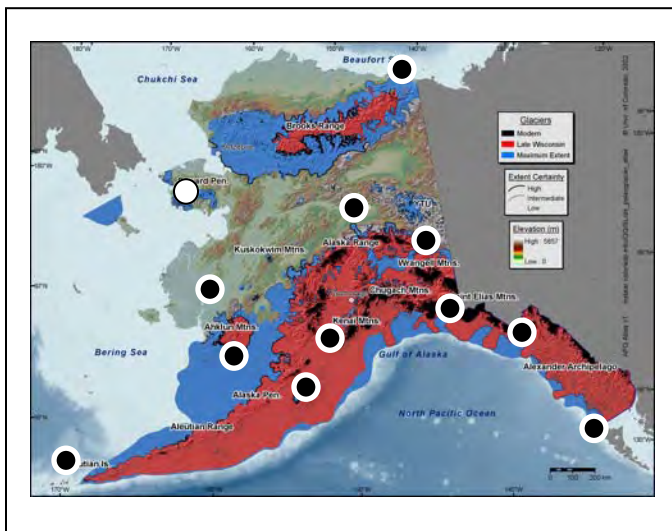


Figure 1. Late Wisconsinian glaciation of Alaska (10,000–35,000 years before present). Areas in Alaska that were glaciated during the last glacial maximum are shown in red and blue. Other areas were open habitat. Black dots indicate areas in Alaska that were sampled for common and red-breasted merganser DNA during 2004–2006. *Map courtesy of W. Manley, INSTAAR, Univ. of Colorado.*

Laboratory processing of hooded merganser samples from six breeding areas across North America (Pacific coast US, Minnesota, Missouri, Louisiana, Ontario and Northeastern US) for both nuclear and mitochondrial (mt) DNA is complete and write-up of analyses for a peer-reviewed journal article is underway. This manuscript will also include an analysis of annual survival and fidelity based on a 13-year mark-recapture study conducted by Peter Blums in southern Missouri. This combination of data types will permit more robust conclusions about rates of dispersal by both juvenile and adult hooded merganser females and the implication of these dispersal events on the population genetic characteristics of the species across its breeding range in North America.

On-going analysis of common merganser DNA samples has revealed additional genetic divisions within this species since the 2005 annual report to the Sea Duck Joint Venture (Fig. 2). Based on approximately 450 base pairs of the mtDNA control region, we observed substantial differentiation between Alaska and more southerly locales of North America. There are additional divisions within these two clades, suggesting that Washington common merganser samples are derived from samples collected in Vermont, US and New Brunswick, Canada. Samples from Scotland represent the nominate race (*M. m. merganser*), whereas all other samples are from *M. m. americanus*. Additional samples are also being sought from the Russian Far East to better understand the association of these populations to those in Alaska.

While the lack of association between Alaska and lower-48 samples may bolster previous conclusions that common mergansers are essentially non-migratory in some areas (Erskine 1972, Mallory & Metz 1999, Pearce et al. 2005), an initial analysis of samples collected from molting common mergansers at Kodiak Island, Alaska suggest that male common mergansers molting at Kodiak Island originate from areas across Alaska and throughout the Pacific coast of North America, as far away as Vancouver, British Columbia and Washington state (data not shown). Additional research is being proposed for funding by the Sea Duck Joint Venture to further quantify breeding area origins of common mergansers that molt at Kodiak Island and use this migration information as an individual covariate in the mark-recapture study initiated by the Kodiak National Wildlife Refuge. Additional breeding samples collected as part of this initial study will continue to be added to this analysis. Laboratory genetic work on red-breasted DNA samples will commence during the winter of 2006–2007.

Figure 2. Tree diagram of mtDNA sequences from breeding samples of common mergansers. The dashed line represents the genetic division between samples from Alaska and more southerly areas of North America. Numbers along the tree indicate bootstrap support for a particular node. Values > 70% indicate high support for a particular grouping. Values < 70% are not shown.

