

Proposal for Research to the
North American Sea Duck Joint Venture (SDJV):

**Factors Involved in Population Dynamics
and Delineation of North American Mergansers**

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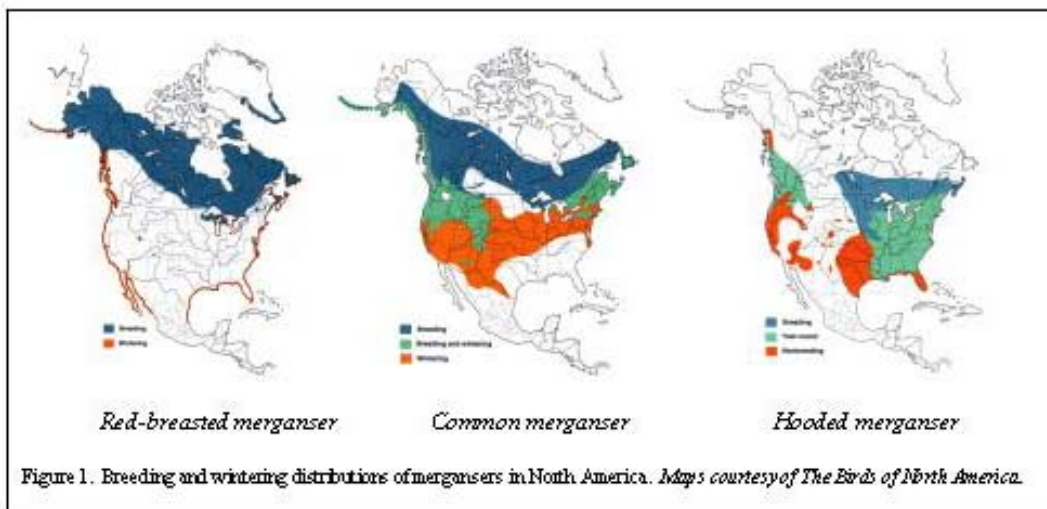
Key words: common merganser, red-breasted merganser, hooded merganser, population delineation, population dynamics, genetic structure, nesting ecology

Problem/Issue Statement: Aspects of breeding biology, population dynamics and delineation are lacking for all 3 merganser species in North America. This proposal addresses these information needs as identified by the Sea Duck Joint Venture (SDJV) Management Board (2001) through a combination of field marking (banding and telemetry) and genetic analysis.

SDJV Populations Targeted: Populations in Alaska, Canada, and the contiguous U.S.

Justification: As with North American eider and scoter populations 10 years ago, little is known about the habits and ecology of common, red-breasted, and hooded mergansers. While trend data suggests that all species are stable, if not increasing in North America, our understanding of population status and trends of these species is limited (Dugger et al. 1994, Titman 1999, Mallory and Metz 1999). Aerial surveys flown throughout North America are not designed to sample large sections of river and coastal areas commonly used by mergansers. When encountered, mergansers are not differentiated to species, but lumped into a single “merganser” category. As a result, surveys detect variable numbers of birds each year, poorly describe the distribution of mergansers, and leave large portions of the distribution of these species unsurveyed (e.g., Hodges et al. 1996). On the Kodiak National Wildlife Refuge of Alaska, changes in the abundance of common and red-breasted mergansers have been noted over the past 20 years (D. Zwiefelhofer, pers. comm.) with red-breasted mergansers becoming less abundant in some areas. Factors responsible for such shifts in distribution are poorly understood as are those that influence overall population dynamics and genetic structure (Dugger et al. 1994, Titman 1999, Mallory and Metz 1999). All mergansers occupy portions of the boreal forest in Alaska and Canada and this ecozone is experiencing rapid conversion to agriculture in Canada, declining by as much as 89% per year since 1974 in some areas (Hobson et al. 2002). The lack of basic biological information for mergansers has prompted the SDJV Management Board (2001) to list “Population Dynamics” as the highest priority and most urgent information need for the management of common and red-breasted mergansers and “Population Delineation” as the highest priority for hooded mergansers.

The distributions of all 3 species of merganser differ markedly across North America (Fig. 1), likely because of species-specific nesting habits, rates of dispersal, and responses to the retreat of glaciers 20,000 years ago (Hewitt 2000). As a result, populations may differ demographically and genetically. The hooded merganser is restricted to temperate forested areas of North America with a disjunct population, divided between the east and west coast. The common and red-breasted mergansers are Holarctic, but largely segregated by breeding at different latitudes and by



occupying interior vs. coastal habitat in winter. The designation of separate subspecies of common mergansers in North America and Eurasia on the basis of plumage differences (Johnsgard 1979), suggests limited dispersal of these two species across and potentially within continents. The high latitude distribution of the red-breasted merganser suggests a strong dispersal tendency that may result in a lack of genetic structure among areas. However, this species does nest colonially and is prone to creching, a behavior hypothesized to occur among related individuals that could lead to local areas of genetic similarity and thus, differences among populations.

This project proposes to investigate factors involved in population dynamics of common and red-breasted mergansers, such as aspects of nesting ecology and annual fidelity to breeding areas. This study will also establish a marked population for documenting annual movements and estimating survival and recruitment. Nesting and demographic data will be collected on the Kenai National Wildlife Refuge (NWR) of Alaska, an area that contains several river drainages and numerous individuals of both common and red-breasted merganser. Since field-based estimates of fidelity may not be representative of larger regions, DNA samples will be collected from across North America with the help of numerous collaborators (Appendix 1). DNA sampling will be stratified according to past vegetation and glaciation history (e.g., Fig. 2) because recent studies of arctic species have found strong links between patterns of genetic variation and past geographic events (Hewitt 2000).

The linkage of multiple markers, such as banding and genetic data, is important because both historical and contemporary factors influence the distribution and genetic differentiation of populations. For example, Pearce et al. (2003a) observed nearly identical genetic traits among widely distributed populations of king eiders, suggesting historical range expansion and/or widespread gene flow. Results from a concurrent study involving stable isotope ratios of nesting females (Mehl et al. 2003) indicated that eastern and western arctic king eiders behave as one population, as opposed to the two distinct populations suggested from banding data. Thus, the combination of these different markers allowed more confident conclusions about the location of population mixing and a possible mechanism for genetic similarity across the arctic. Since many arctic dwelling species have only recently colonized deglaciated areas, genetic similarity could mean that fidelity takes place, but is not manifested in genetic data. Therefore, direct estimates from banding and telemetry data are crucial to fully understand population movements in relation to genetic patterns.

Mergansers remain the last group of sea ducks to be studied in Alaska. Previous and current studies in Alaska on eiders (Scribner et al. 2001, Petersen and Flint 2002, Pearce et al. 2003a, b), scoters (Pearce et al. 2002, Schamber et al. 2002), long-tailed ducks (Pierson et al. 2002), goldeneyes (Esler et al. 2000), and harlequin ducks (Lanctot et al. 1999, Esler 2000) have

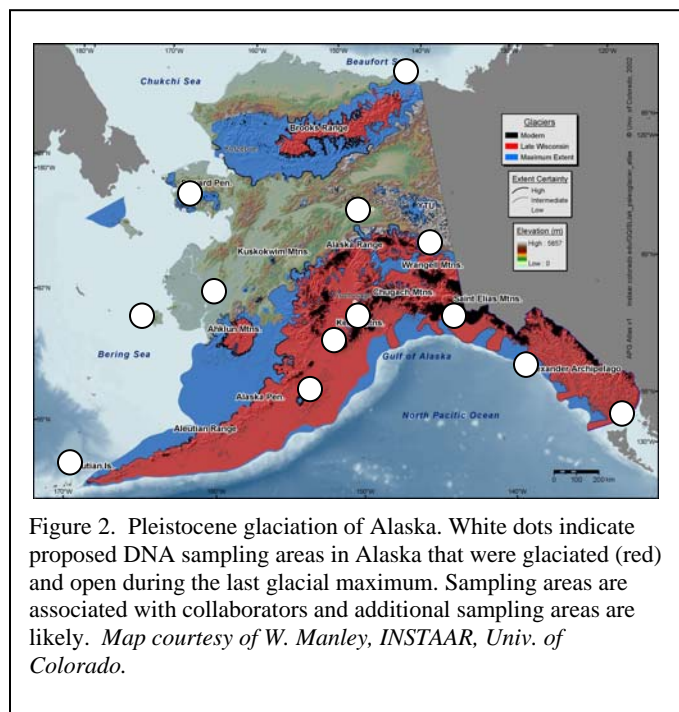


Figure 2. Pleistocene glaciation of Alaska. White dots indicate proposed DNA sampling areas in Alaska that were glaciated (red) and open during the last glacial maximum. Sampling areas are associated with collaborators and additional sampling areas are likely. Map courtesy of W. Manley, INSTAAR, Univ. of Colorado.

identified a wide spectrum traits that influence population dynamics and genetic differentiation. This spectrum will be further defined by examining the basic life-history traits and genetic structure of mergansers. This project will also obtain information on the timing and movements of mergansers that will be important for developing appropriate survey methods to enumerate and monitor populations.

Objectives:

- 1. Document general nesting ecology, estimate levels of fidelity, and examine how these influence population dynamics and structure of common and red-breasted mergansers in Alaska.** Specifically, use banding data and radio telemetry document nesting ecology, movement patterns, estimate levels of fidelity, and establish a marked population for subsequent estimates of survival and recruitment.
- 2. Assess population genetic structure of common and red-breasted mergansers in Alaska.** Specifically, use nuclear and mtDNA data to estimate genetic relatedness among nesting females on the Kenai NWR and infer levels of fidelity by quantifying population differentiation across Alaska.
- 3. Assess phylogeography of all three merganser species across North America.** Specifically, examine mtDNA from samples obtained across North America for insights into how current demographic and historical events shape the breeding distributions of mergansers (phylogeography). Population level data obtained in Objectives #1 and 2 will strengthen conclusions about continent-wide patterns.

Scope and Location: Objective #1 will be addressed through fieldwork on the Kenai NWR where at least two major river drainages and numerous (> 20 per drainage) common and red-breasted mergansers can be captured annually. The nearby road access throughout much of the Kenai watershed will eliminate the need for a major field camp. Fieldwork will be conducted via road access and by boat with occasional spike camp. Field crews will work in coordination with the Kenai NWR, which is currently conducting river-based harlequin duck captures and surveys. Since field-based estimates of population dynamics and nesting ecology from the Kenai NWR may not be representative of larger regions, Objectives #2 and 3 will broaden the scope of the project by collecting DNA from across Alaska and North America (Figs. 1 and 2). Estimates of fidelity and gene flow among these larger areas can then be assessed via genetic analyses and compared to estimates derived from banding and telemetry (Objective #1).

Experimental Design:

Objective#1: In 2004, initiate capture and marking of common and red-breasted mergansers on the Kenai NWR with leg bands and conventional temporary radio transmitters (20 per species) to: (1) test the assumption that mist-netted females captured in spring are breeding locally, and (2) follow marked females to nests, examine the feasibility of characterizing nest sites and estimating nesting success and productivity. Standard mist nets and other capture methods will be used. Mist nets yielded four unintentional captures of red-breasted merganser on the Kenai NWR during harlequin field work in 2003, suggesting that mist nets are one possible capture method. In mid-summer, up

to 10 brood rearing female common and red-breasted mergansers found on rivers will be captured and receive implanted conventional transmitters with 15-month batteries. Previous studies found that approximately 75% of radios using 15-month batteries lasted through to the subsequent nesting season (J. Hupp, pers. comm.). Trapping of females and broods was investigated in 2003 and results lead us to conclude that various methods of capture will prove successful. Radios will be used primarily to help document fidelity of females in 2005, but will also be monitored periodically during the winter to determine if locally breeding females remain on or nearby the study area. Banding data outside of Alaska suggests that coastal populations are essentially non-migratory (Erskine 1972, U.S.G.S. Bird Banding Laboratory). The methodology for transmitter implant and monitoring is well established for breeding waterfowl in Alaska (Hupp et al. 2003). Recaptures of banded individuals in 2005 – 07 will also provide information on rates of fidelity. We plan to estimate fidelity to the entire Kenai study area rather than to a specific section of river or nest site, but depending upon capture and recapture success, finer scale models may be explored at a later date using Program MARK. Banding on the Kenai NWR will establish a marked population that can eventually be used to estimate annual survival and recruitment.

Objective #2. DNA will be collected on the Kenai NWR from all captured individuals and from nest materials (Pearce et al. 1997). Samples from across Alaska will be obtained with the assistance of various collaborators (Appendix 1). All captured birds will be banded. For common mergansers, methods are in place to allow high throughput of samples using cytochrome *b* and control region mtDNA sequencing primers and eleven nuclear microsatellite markers recently developed in Europe (B. Gautshci, pers. comm.). An additional 45 microsatellite and numerous mtDNA primers are in use at the Molecular Ecology Laboratory and are informative for several sea duck species (S. Talbot, pers. comm.). Thus, suitable primers are likely also available for red-breasted and hooded mergansers. Inferences about population genetic and phylogeographic patterns will follow previous studies conducted by the Alaska Science Center's Molecular Ecology Laboratory (Scribner and Pearce 2000, Pearce et al. 2000, Pearce et al. 2003a, b). Microsatellite loci and mtDNA data will be used for inferring rates of fidelity, gene flow among river drainages and state-wide sampling locales, and for estimating among individual relatedness. MtDNA data will also be used to examine phylogeographic patterns within Alaska.

Objective #3. Numerous individuals from across North America have already contributed samples or plan to obtain additional samples (Appendix 1). Samples are being sought from the Canadian Wildlife Service's Specimen Bank, hunter harvest Wing Bee's in both Canada and the United States, and individuals with nest box programs that encounter hooded and common mergansers. We plan to obtain 10 – 20 samples per locale, which is an average sample size for mtDNA phylogeographic analyses.

Anticipated Output: Annual progress reports to the SDJV, U.S. Fish and Wildlife Service, Project Personnel, and all other interested parties will be provided at the end of each field season. These progress reports can also be converted to links for the SDJV web site. Results will be presented at local and national meetings as they are scheduled. Final results will be summarized and presented in peer-reviewed scientific journals. Possible manuscripts include the following: (1) Nesting ecology of common and red-breasted mergansers, (2) Genetic relatedness among nesting common and red-breasted mergansers on the Kenai NWR, (3) Population genetic structure and

phylogeography of common and red-breasted mergansers in Alaska, (4) Phylogeography of North American mergansers.

Management Implications: Research proposed here addresses priorities of the North American SDJV and U.S. Fish and Wildlife Service. The limited information on status and biology of these species prompted the SDJV Management Board (2001) to identify “Population Dynamics” as the highest and most immediate information need for management of common and red-breasted mergansers. “Population Delineation” was listed as the highest priority for hooded mergansers (SDJV 2001). This project will address both of these high priority information needs. This project will also obtain information on the timing and movements of mergansers that will be important for developing appropriate survey methods for enumerating and monitoring merganser populations.

Relationship to Other Projects: Since proposed DNA sampling across North America will be conducted in collaboration with existing field operations in many areas (Appendix 1), this project relates to the activities of numerous projects. For National Wildlife Refuges in Alaska and elsewhere, information on the population genetics and status of local birds will be informative for Refuge management plans. Genetic data will be directly comparable to previous and current studies of sea duck populations, providing a more complete picture of species-specific traits within the sea duck tribe.

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Personnel: Numerous collaborators (Appendix 1) have offered assistance with DNA sampling across North America. Field and laboratory work will be conducted by the following principal investigators:

John M. Pearce, M.Sc. John Pearce is a Research Wildlife Geneticist with the U. S. Geological Survey, Alaska Science Center in Anchorage. Proposed responsibilities for this project include study design, oversight and leadership of field data collection, DNA sample analysis, data summary and presentation of results. His current research focuses on the application of genetic and demographic data to migratory waterfowl, especially to those species that are of current management concern and for those that are remain poorly studied. He has been involved in numerous genetic studies of waterfowl in Alaska and elsewhere, including sea ducks. Specifically, he has been involved with projects investigating population structure and phylogeography of Spectacled, King and Steller’s eiders, Black and White-winged scoters, Harlequin ducks, and Canada geese. He has authored or co-authored 15 peer-reviewed journal papers since completion of his M.Sc. from the University of Idaho in 1996.

Sandra L. Talbot, Ph.D. Sandra Talbot is a Research Wildlife Geneticist with the U. S. Geological Survey, Alaska Science Center in Anchorage and is the director of the Center’s Molecular Ecology Laboratory. Proposed responsibilities for this project include providing assistance with genetic analysis, data summary, and interpretation of results. She has been involved in numerous genetic studies of waterfowl in Alaska and elsewhere, including sea ducks. Specifically, she has been involved with projects investigating population structure and phylogeography of Spectacled, Common, King and Steller’s Eiders, Long-tailed Ducks, Harlequin Ducks and White-winged Scoters. She has authored or co-authored over 30 peer-reviewed journal papers. Talbot attended Brigham Young University and earned a B. S. in Wildlife and Range Management, and a M. S. in

Zoology (Terrestrial Ecology). Her Ph. D. dissertation research at in Biology from the University of Alaska Fairbanks involved investigation into the population genetics and phylogeography of brown bears of Alaska.

Paul L. Flint, Ph.D. Paul Flint is a Research Wildlife Biologist with the U.S. Geological Survey, Alaska Science Center in Anchorage. Proposed responsibilities for this project include assistance with project design, data analysis, and summary of results. He has been involved in numerous studies of waterfowl in Alaska, particularly sea ducks, since 1985. He has studied various aspects of sea duck ecology of Spectacled Eiders, Steller's Eiders, Black Scoters, Common Eiders, Long-tailed Ducks, and Harlequin Ducks. Specifically, he has been involved with projects estimating annual survival of Spectacled Eiders, Common Eiders Steller's Eiders and Long-tailed Ducks. He has authored or co-authored over 40 peer-reviewed journal papers. Dr. Flint has a BS and a PhD in Biology from the University of Alaska Fairbanks.

Dirk V. Derksen, Ph.D. Dirk Derksen is Chief of the Wetlands and Estuarine Ecology Branch of the U.S. Geological Surveys' Alaska Science Center. Proposed responsibilities for this project include assistance with project design and support. He has conducted or supervised numerous studies of waterfowl in Alaska since 1976. He has authored or co-authored over 20 peer-reviewed journal papers. Dr. Derksen has a B.A. and M.A. from the University of Minnesota and a Ph.D. in Biology from Iowa State University.

John M. Morton, Ph.D. John M. Morton is the Supervisory Fish & Wildlife Biologist at the Kenai National Wildlife Refuge, U.S. Fish and Wildlife Service. Proposed responsibilities for this project include providing assistance with project design and logistical support. Previously, he was the Supervisory Biologist at the Blackwater NWR, Maryland, and Project Leader for population studies of endangered Mariana crows and Vanikoro swiftlets in the Mariana Islands. He has authored or co-authored 20 peer-reviewed journal papers. Morton has a B.S in Wildlife Ecology from the University of Wisconsin-Madison, and M.S. and Ph.D. in Wildlife Science from Virginia Polytechnic Institute & State University. His masters thesis was a study of the wintering ecology of American black ducks at Chincoteague NWR. His doctoral research was a study of the effects of human disturbance on the behavior and energetics of nonbreeding sanderling.

Logistical Requirements: Nesting biology fieldwork will be based largely at the Kenai NWR. No field camps are proposed. Use of boats and survey aircraft will be coordinated with the Kenai NWR or a local air charter company. DNA sampling statewide and across North America will be based in Anchorage at the Alaska Science Center. Every effort will be made to reduce travel costs by asking proposed collaborators to assist with DNA sampling when convenient. Travel funds will be used to obtain samples in areas where no cooperative efforts are possible.

Schedule: DNA sampling and preliminary fieldwork will begin in 2004, with focused work to be conducted in 2005–06. Genetic analysis will be conducted each winter as samples become available. Annual progress reports will be made available at then end of each field season (October 1). Final analysis and results should be available by 2007.

Appendix 1. List of proposed collaborators with existing DNA samples or those that can assist with collection of additional samples. Additional collaborators are likely.

First name	Last name	Agency
Birgit	Braune	Canadian Wildlife Service, National Wildlife Research Centre
Jenny	Bryant	Koyukuk/Nowitna National Wildlife Refuge, Alaska
Vern	Byrd	Alaska Maritime National Wildlife Refuge
Jeff	DiMatteo	Minnesota Department of Natural Resources
Steve	DuBois	Alaska Department of Fish and Game
Bruce	Dugger	Oregon State University
Dan	Esler	Simon Fraser University, Vancouver, British Columbia
David	Evers	BioDiversity Research Institute, Portland, Maine
Carol	Fugagli	The Nature Conservancy, Gila River Preserve, New Mexico
Barbara	Gautschi	University of Uppsala, Sweden
Dan	Gibson	University of Alaska Fairbanks
Scott	Gilliland	Canadian Wildlife Service, Newfoundland
Jean-Francois	Gobeil	Canadian Wildlife Service, National Wildlife Research Centre
Alan	Hanson	Canadian Wildlife Service, New Brunswick
Mike	Hoy	USDA/APHIS/Wildlife Services, Arkansas
Steve	Kendall	Arctic National Wildlife Refuge, Alaska
Gilles	Lupien	Société de la faune et des parc du Québec
Charles	Maisonneuve	Société de la faune et des parcs du Québec
Mark	Mallory	Canadian Wildlife Service, Nunavut
Brian	McCaffery	Yukon Delta National Wildlife Refuge, Alaska
Kevin	McCracken	University of Alaska Fairbanks
Rob	McDonald	Togiak National Wildlife Refuge, Alaska
Katherine	Mehl	Ducks Unlimited Canada, Nova Scotia
Matt	Moran	US Forest Service, Chugach National Forest, Alaska
Chris	Nicolai	University of Nevada
Pau	Padding	USGS, Patuxent Research Center, Maryland
Matt	Perry	USGS, Patuxent Research Center, Maryland
Michel	Robert	Canadian Wildlife Service, Quebec
Chris	Thompson	Washington Department of Fish and Wildlife
Roger	Titman	McGill University, Quebec
Denny	Zwiefelhofer	Kodiak National Wildlife Refuge, Alaska