

Hooded Merganser population genetics across North America

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The Hooded Merganser (*Lophodytes cucullatus*) is a small sea duck endemic to North America with a disjunct distribution (Fig. 1). Little is known about the levels of movement and gene flow between the western and eastern portions of North America (Dugger et al. 1994). The disjunct distribution and high levels of female breeding site fidelity (Zicus 1990) leads to a prediction of low levels of gene flow and, as a result, high genetic differentiation between western and eastern populations, provided sufficient time has passed since these two populations became separated.

In a preliminary analysis, 437 base pairs of the mitochondrial (mtDNA) genome (control region domain I) were sequenced. Sixty-two tissue samples were examined from adult female and juvenile Hooded Mergansers harvested between November 2003 and January 2004. Samples came from the U.S. Fish and Wildlife's Parts Collection Survey. No differentiation was observed between Pacific and Atlantic migratory flyways (AMOVA $\Phi_{ST} < 0.01$, $P = 0.82$). A pattern of non-differentiation is also evident in a phylogenetic tree of all mtDNA sequences (Fig. 2). If Pacific and more eastern migratory flyways were genetically distinct, deeper branches would occur between samples and individuals would cluster with respect to geographic area. Summary statistics for the Pacific flyway (Table 1) suggest a colonization event from the east or contemporary female-mediated gene flow between continental populations. The high haplotype and low nucleotide diversity in the Pacific also suggests that this population is expanding relative to other areas.

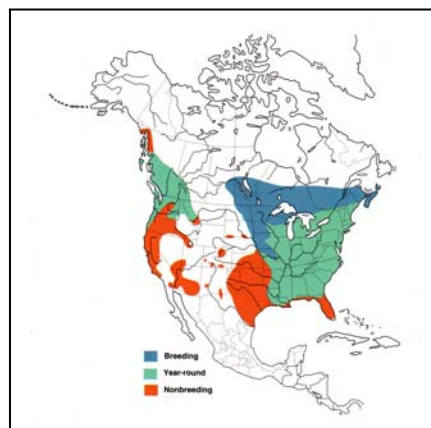
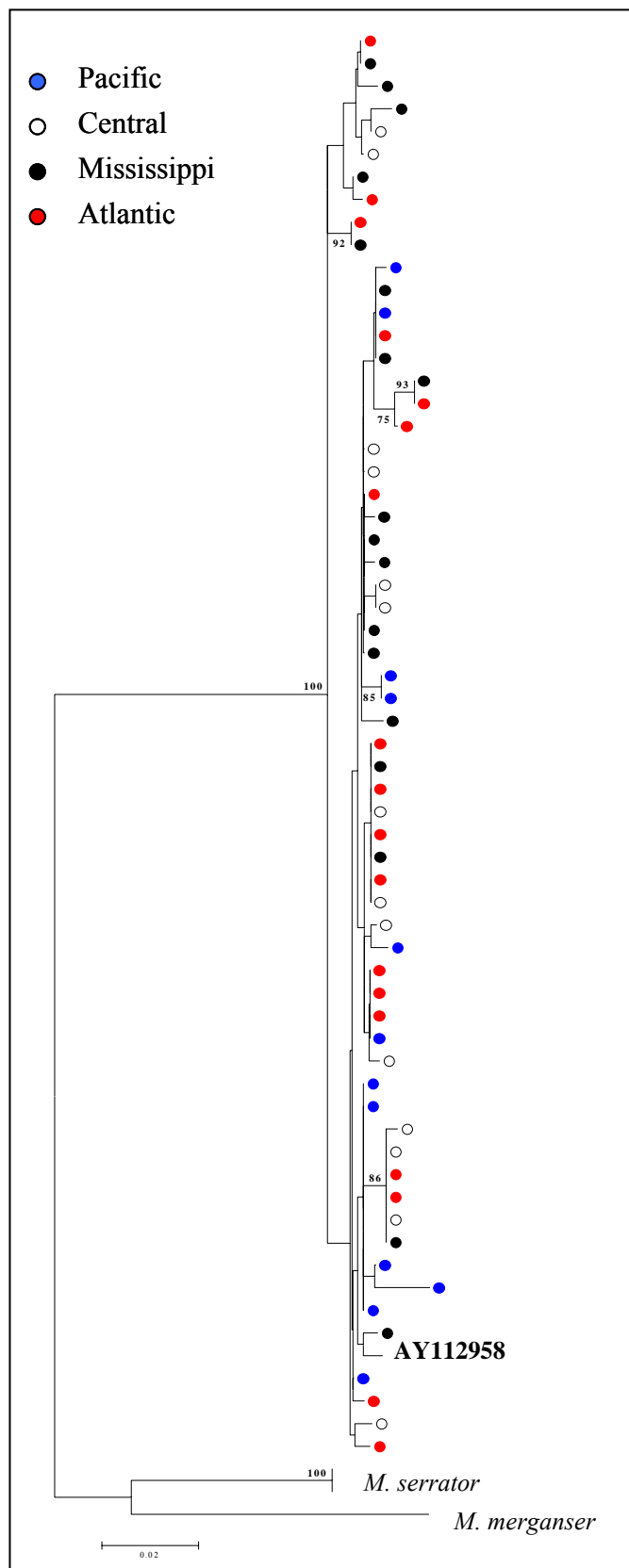


Figure 1. Breeding and wintering distribution of the Hooded Merganser (Dugger et al. 1994). Map courtesy of *The Birds of North America, Inc.*

Table 1. Summary statistics from samples collected during the 2003–2004 U.S. Fish and Wildlife Service Parts Collection Survey.

	Migratory flyway			
	Pacific	Central	Mississippi	Atlantic
Samples available	18	16	68	45
Samples analyzed	12	14	18	18
Haplotypes observed	8	10	14	12
Haplotype diversity (π)	0.89	0.95	0.96	0.93
Nucleotide diversity (h)	0.04	0.15	0.30	0.29
No. pairwise differences	18.1	67.0	134.9	131.0

Future Research Directions: Further work is needed to adequately quantify levels of contemporary movement and gene flow among populations of Hooded Mergansers. Results presented here are based on small sample size, wintering birds, and a single molecular marker (mtDNA), which tends to provide a more historical perspective on demographic patterns of animal populations. If adult female dispersal is limited among breeding areas, increased sampling during the breeding season and additional molecular markers may be more appropriate for quantifying contemporary levels of gene flow.



Request for assistance: To better understand historic and contemporary levels of gene flow, we seek additional Hooded Merganser DNA samples from both breeding and wintering birds. DNA can come from blood, tissue, developing eggs, or nest feathers and egg shell membranes (Pearce et al. 1997) that remain in nest boxes after hatch. State and Federal permits may be required to collect certain materials. Please contact John Pearce at the address above for details and sampling kits.

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Literature Cited

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Figure 1. Phylogenetic tree of 62 wintering Hooded Mergansers from each of the four migratory flyways in North America based on 437 base pairs of control region mtDNA. Hooded Merganser AY112958 is from Donne-Gousse et al. (2002) and is included for comparative purposes. Bootstrap values > 70% are shown and are based on 1,000 permutations. Values < 70% indicate low levels of support for a given branch of the tree. Red-breasted (*M. serrator*) and Common Merganser (*M. merganser*) are shown as outgroups.