Project Title: Spatial Population Genetic Structure Of White-Winged Scoters (*Melanitta fusca*)

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Partners: USFWS Migratory Bird Management, SDJV; USGS

Project Description: Like other sea duck species in Alaska, white-winged scoters are experiencing a long-term decline. This makes understanding of population dynamics, including structuring of populations and migratory connectivity, especially important. Conventional and satellite telemetry studies offer the potential for discovery of migration pathways, staging and wintering habitats of breeding birds, but costs are prohibitive due to the large number of experimental birds required and the remote and expansive geographic areas to be evaluated. We are augmenting these approaches by using molecular genetic techniques to identify populations. We are gathering information from the maternally-inherited mitochondrial DNA and from bi-parentally-inherited and sex-linked nuclear microsatellite loci, to characterize breeding and wintering populations of white-winged scoters in Alaska.

Objectives: The general objectives of this study are to use molecular genetic markers to characterize the breeding populations of white-winged scoters across their range in Alaska and Canada, and to address hypotheses regarding genetic relationships of birds from these areas. The first steps in such an effort are to sample white-winged scoters from several nesting areas to evaluate population relationships based on molecular genetic markers, and to explore the feasibility of using molecular genetic markers to evaluate the composition of non-breeding populations. To meet these objectives, we have screened and developed, then tested a variety of genetic markers for feasibility in use for characterizing population genetics parameters. These markers are currently being used to assess genetic characteristics of two breeding populations and 5 spring or wintering populations.

Preliminary Results: We have developed and/or screened and tested five classes of molecular markers for white-winged scoters. Among the 75 specific loci screened, appropriately variable and informative markers include:

1. 24 autosomal (nuclear) microsatellite markers
2. Two sex-linked (z-specific) nuclear microsatellite markers
3. Primers that preferentially amplify the domain I portion of the maternally-inherited mtDNA control region and cytochrome b gene
4. Primers that preferentially amplify nuclear sequences of mitochondrial origin (numt) for the control region pseudogene, and
5. The Chromo-Helicase-DNA binding genes for determining gender.

Many of the same markers are variable in surf and black scoters as well, and will thus provide valuable comparative data.

Project Status: Based on preliminary analyses of a single population, using microsatellite markers, and several individuals from different populations, using mtDNA markers (Table 1), we have determined these markers can be used to gather phylogeographic and population-level genetic data of appropriate quality to answer the main objectives of this study. These objectives include characterization of breeding populations of white-winged scoters across their range in Alaska and Canada, and addressing hypotheses regarding the relationships of birds from populations in these areas relative to wintering and spring aggregations. However, without samples from additional breeding populations, we cannot determine whether sufficient differentiation exists among specific breeding populations to allow assignment of individuals within admixed groups to breeding origin. We are therefore continuing our effort to obtain samples from additional breeding areas while collecting additional data from samples currently archived at the Molecular Ecology Laboratory (USGS/ASC) in Anchorage. Specifically, we have again augmented the number of microsatellite markers variable in this species, and currently have a suite of over 20 variable microsatellite loci for this species. In addition, we have begun investigating variation within the species at a suite of 5 nuclear markers, including βFIB-7, OD-7, LaminA, *c-mos* and RAG-1. All of these markers are known to be variable within species for a number of avian species, including waterfowl (Talbot, unpublished data). We have also recently received over 100 blood samples collected from over 100 white-winged scoters breeding in the Northwest Territories (Stewart Slattery, DU, *pers. comm.*). DNA is currently being extracted from each of these samples, and data from this population will be compared to those from the population breeding on Yukon Flats, Alaska.

Table 1. Frequencies and distribution of 7 mtDNA cytochrome b haplotypes found among 44 white-winged scoters sampled from spring and wintering populations. CRD = Cordova; ALEU = Dutch Harbor; KOD = Kodiak; ALX = Alexander Archipelago; PWS = Prince William Sound.

	n per locality						Sequence Position
							00111234
							00077550
Haplotype	CRD	ALEU	KOD	ALX	PWS	TOTAL	38847815
A	2	11	2	9	10	34	TGGAGAAA
B	-	1	-	-	1	2	..A.....
C	-	1	-	2	-	3	......G.
D	-	1	-	-	-	1	C.......
E	-	-	-	2	-	2	...GAG..
F	-	-	-	-	1	1	.......G
G	-	-	-	-	1	1	.A....G.
Haplotypes/population	2	14	2	13	13		

Project Funding Sources (US$)

SDJV (USFWS) Contribution	Other U. S. Federal Contributions	U. S. Non-federal Contributions	Canadian Non-Federal Contributions	Source of Funding (agency or organization
	$15,000.00			USFWS
	$ 2,000.00[1]			USGS

Total Expenditures by Category (US$)

Activity	Breeding	Molting	Migration	Wintering	TOTAL
Banding					
Surveys					
Research	$15,000.00			$2,000.00	$17,000.00
Communication					
Coordination					

[1] Monetary value of in-kind contributions