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Genetic structure in a wintering population of American Coots.—American Coots (*Fulica americana*) wintering on the Savannah River Site (SRS), near Aiken, South Carolina, arrive in stages and exhibit temporally stable patterns of site fidelity. Site fidelity in color-marked coots was observed both throughout the winter and across years (Potter 1987) on various portions of Par Pond reservoir on the SRS. In addition, Brisbin et al. (1973) and Potter (1987) found that cesium-137 body burdens of coots differed significantly between

birds from different sites on this reservoir and varied in accordance with the levels of contamination in those sites. These data led us to ask whether the birds from these sites represented distinct and stable population-specific or demographic cohorts which arrived at the reservoir in the same temporal sequence each year and, therefore, were structured on the reservoir with regard to population of origin.

If genetically differentiated breeding populations of coots occupy different sites within a given wintering area, then genetic analyses of the birds on the wintering area should elucidate this structure. Likewise, specific sex and/or age classes of birds from genetically differentiated breeding populations could be detected within a given wintering area. If such populations or sex/age cohorts of coots are mixed on Par Pond, the data should reflect this in two ways. First, there should be a heterozygote deficiency in the overall sample of coots from the reservoir; this is known as the Wahlund (1928) effect. Second, when groups of birds from different breeding areas are categorized correctly on the wintering area, such as site-specific aggregations of birds or sex/age classes, *F*-statistics should indicate that a substantial amount of the total genetic variance is partitioned among these groups within the wintering population. Our objectives were to survey genetic variability in the Par Pond wintering population of American Coots and to use genetic techniques to assess spatial and demographic subsets of these wintering coots in an effort to understand the migratory behavior of this species.

Study area and methods.—Coots were collected from Par Pond, an 1130-ha reservoir on the U.S. Dept. of Energy's Savannah River Site located in Aiken, Allendale, and Barnwell Counties, South Carolina. The reservoir consists of three main extensions which were formed in 1958 by damming the confluence of three adjoining stream systems (Parker et al. 1973). These are referred to as the hot, north, and west arms of Par Pond. A total of 77 birds, 24–27 from each of these arms, were shot on 23 January 1990. Sex was determined by dissection and examination of the gonads and age (1st year, 2nd year, or ≥3rd year birds) was determined from tarsal color (Gullion 1952, Crawford 1978) and/or by examination of the bursa (Eddleman and Knopf 1985). All birds collected showed full tarsal coloration, with no evidence of any of the fading that Crawford (1978) suggested might occur outside of the breeding season. Samples of liver and muscle tissue were removed for electrophoretic analysis and stored at −70°C.

Allozyme electrophoresis was used to estimate genetic variation of each individual. Tissues were thawed and ground with an equal portion of buffer (0.60 gm Tris, 42.8 gm sucrose, 0.45 gm dithiothreitol, and water to equal 500 ml) and centrifuged for approximately 30 sec. The resulting supernatant was screened for variation at 23 presumptive loci, with polymorphisms being consistently resolvable for two loci: PEP-la-1 and PGM (Table 1). Loci were considered variable if the frequency of the most common allele was ≤95%. Each individual was scored for all loci. Buffers and stains are described in Selander et al. (1971), Clayton and Tretiak (1972), and Harris and Hopkinson (1976). Loci were designated numerically beginning with the most anodal. Alleles were designated based on their anodal or cathodal position relative to the most common allele observed. Single and multiple locus heterozygosity, measures of allozyme diversity, were estimated using the computer program BIOSYS-1 (Swofford and Selander 1981). This program was also used to evaluate fit of the data to Hardy-Weinberg expectations and to calculate *F*-statistics (F_{ST}, F_{IS}, and F_{IT}; Nei 1977) for comparisons among birds in the three arms of Par Pond as well as for comparisons between sexes, among ages, and among sex and age classes of coots present in the reservoir. F_{ST} measures the extent to which subpopulations show genetic heterogeneity or more specifically, it indicates the proportion of genetic variation in the total population that is accounted for by the subpopulations. F_{ST} can range from 0 (no differentiation among subpopulations) to 1 (complete differentiation or fixation of alternate alleles). F_{IS} and F_{IT} measure

TABLE 1

PROTEIN ABBREVIATION, LOCUS NAME, ENZYME COMMISSION (E. C.) NUMBER, BUFFER, TISSUE, NUMBER OF ALLELES, AND AVERAGE HETEROZYGOSITY (H) FOR LOCI SURVEYED IN AMERICAN COOTS WINTERING ON THE PAR POND RESERVOIR IN SOUTH CAROLINA

Abbreviations	Locus name	E. C. number	Buffer[a]/tissue[b]	Alleles	h
AAT-1	Aspartate aminotransferase-1	2.6.1.1	AC/M	1	0.00
AAT-2	Aspartate aminotransferase-2	2.6.1.1	AC/M	3	0.03
AH	Aconitate hydratase	4.2.1.3	AC/M	1	0.00
ACP	Acid phosphatase	3.1.3.2	AC/L	1	0.00
ADA	Adenosine deaminase	3.5.4.4	TC8.0/M	2	0.03
FH	Fumarate hydratase	4.2.1.2	AC/L	1	0.00
GPI-1	Glucose-6-phosphate isomerase-1	5.3.1.9	AC/L	1	0.00
GPI-2	Glucose-6-phosphate isomerase-2	5.3.1.9	AC-L	1	0.00
IDH-2	Isocitrate dehydrogenase-2	1.1.1.42	TC8.0/M	2	0.01
LDH-1	Lactate dehydrogenase-1	1.1.1.27	AC/L	2	0.01
LDH-2	Lactate dehydrogenase-2	1.1.1.27	AC/L	1	0.00
LAP	Leucine aminopeptidase	3.4.–.–	AC/L	1	0.00
MDH-1	Malate dehydrogenase-1	1.1.1.37	AC/M	1	0.00
MDH-2	Malate dehydrogenase-2	1.1.1.37	AC/M	1	0.00
ME-1	Malic enzyme-1	1.1.1.38	AC/M	2	0.01
ME-2	Malic enzyme-2	1.1.1.38	AC/M	3	0.08
MPI-1	Mannose-6-phosphate isomerase-1	5.3.1.8	TC8.0/L	3	0.04
MPI-2	Mannose-6-phosphate isomerase-2	5.3.1.8	TC8.0/L	1	0.00
PEP-la-1	Peptidase-leucyl alanine-1	3.4.–.–	AC/L	4	0.10
PEP-la-2	Peptidase-leucyl alanine-2	3.4 –.–	TC8.0/L	1	0.00
PGM	Phosphoglucomutase	5.4.2.2	AC/L	5	0.20
6PGD	6-phosphogluconate	1.1.1.44	AC/L	1	0.00
SORDH	Sorbitol (=L-iditol) dehydrogenase	1.1.1.14	TC8.0/L	1	0.00

[a] Buffers: AC = Amine-citrate pH 6.1; TC 8.0 = Tris-citrate pH 8.0.
[b] Tissues: L = liver; M = muscle.

the heterozygote deficiency or excess relative to the expected heterozygosity within subpopulations (F_{IS}) and the total population (F_{IT}), respectively, and range from −1 to 1. Positive numbers indicate heterozygote deficiency and negative numbers indicate heterozygote excess.

Results.—The mean multilocus heterozygosity of 23 loci for all individuals sampled was 0.021 ± 0.010 (1 SE) and was similar among birds from the three arms of Par Pond. Single locus heterozygosity for all individuals sampled ranged from 0.00 to 0.195 (Table 1). The mean F_{ST} for the comparison of coots among the three arms of Par Pond was 0.01 with only 1% of the genetic variation being partitioned among birds from different portions of the reservoir. A 10–11% heterozygote deficiency was observed within the groups of birds sampled in different portions of the reservoir and for all birds combined (Table 2).

F-statistics calculated for comparisons between sexes and among ages of coots on the reservoir were quite similar to those calculated from analyses of the birds in the three sampling sites. Comparison between sexes indicated that little of the total genetic variation was partitioned between males and females present in the reservoir. Comparison among age

TABLE 2

MEAN F_{IS}, F_{IT}, AND F_{ST} VALUES (NEI 1977) FROM GENETIC ANALYSES OF AMERICAN COOTS COLLECTED FROM THE SAVANNAH RIVER SITE ON 23 JANUARY 1990

Grouping[e]	F_{IS}	F_{IT}	F_{ST}
Capture site[a]	0.097	0.107	0.011
Age[b]	0.075	0.096	0.022
Sex[c]	0.114	0.117	0.003
Sex/age class[d]	0.000	0.065	0.064

[a] Sample sizes for capture sites are 25, 27, and 27 for the Hot, North, and West arms.
[b] Sample sizes for the three age classes are 26, 31, and 22 for year classes 1–≥3.
[c] Sample sizes for the sexes are 47 and 32 for males and females.
[d] Sample sizes for sex/age classes are 14, 14, and 4 for females year 1–≥3 and 12, 17, and 18 males year 1–≥3.
[e] *F*-statistics were calculated for comparisons of all birds among three capture sites, among three age classes (Crawford 1978), between sexes, and among sex and age classes of birds.

classes of coots also indicated that little of the total genetic variation was partitioned among birds in year classes 1, 2, and 3. There were again large heterozygote deficiencies within males, females, and each age class (Table 2). F_{IT} values from the analyses performed between sexes and among ages were also large and indicated heterozygote deficiencies in the total reservoir population. However, when the *F*-statistics were calculated for comparisons among the six sex/age classes (i.e., year 1 males, year 1 females, year 2 males, etc.) there were no heterozygote deficiencies within these groups, but a significant amount (6.5%) of the total genetic variation was partitioned among these groups. The F_{IT} value from this analysis (0.065) was almost identical to the F_{ST} (0.064) as would be expected in an analysis of spatially subdivided randomly mating subpopulations.

Discussion.—The mean heterozygosity of coots on Par Pond (2.1%) was lower than the mean of 6.5% (range 0–30.7%) for 79 other species of birds (Evans 1987) but was similar to that of King Rails (*Rallus elegans*) and Clapper Rails (*R. longirostris*; 3% and 4%, respectively; Avise and Zink 1988). The small F_{ST} (0.011) calculated for the birds from the three sampling locations indicated that very little of the genetic variation was partitioned among the birds located in the Par Pond sampling sites. The F_{IS} and F_{IT} (0.097 and 0.107, respectively) values indicated an overall deficiency of heterozygotes (Wahlund effect) in the samples within each site and for the overall sample. These data suggest that birds from each arm of the reservoir are a mixture of birds from genetically differentiated breeding populations and do not represent specific cohorts from distinct breeding populations.

Data from both sexes and each age class of birds exhibited heterozygote deficiencies and little of the total genetic variance was partitioned among these groups. Although there is evidence for some waterfowl species such as Mallards (*Anas platyrhynchos*) that birds of different ages may winter in different locations (Nichols and Hines 1987:50), our data suggest that the wintering population of coots on Par Pond may be composed of a mixture of sex/age classes from genetically differentiated breeding populations.

A combination of site fidelity and sex/age stratified wintering behavior in American Coots may be responsible for the patterns of genetic structure observed on Par Pond. Site fidelity to wintering grounds is not unique to coots; it has previously been described in Sanderlings (*Calidris alba*; Myers et al. 1979), and Red Knots (*Calidris canutus*; Harrington et al. 1988). Studies by Potter (1987) found that during fall migration coots returned to the three arms of Par Pond sequentially, with numbers peaking first in the west arm, followed by the hot and north arms. Sightings of coots color-marked by Potter (1987) also indicated site fidelity

of individual coots to specific arms of Par Pond across years, with only 2% of 272 sightings of 85 individual coots being outside of the reservoir arm where they had been initially captured during January–February of the same year. During the following winter, only three of 30 sightings of these same coots were not in the same arm where they had been captured originally, and one year later (2 years after initial capture), a single sighting of a marked coot was again in the same reservoir arm where it had been originally captured.

The results of the present study suggest that, rather than population-specific cohorts arriving differentially at Par Pond, there are more likely demographic cohorts such as sex/age classes from different breeding populations that mix randomly across the reservoir. The temporal site fidelity of coots on Par Pond observed by Potter (1987) may reflect the site fidelity of such specific sex/age classes of coots as they return year after year. Sightings of two neck-collared coots, one wintering on Par Pond and another spending two consecutive winters at the same location on another reservoir located approximately 167 km to the north of the Savannah River Site, indicate that at least some of these birds represent a population that breeds in the Horicon March, Wisconsin (D. Rusch, pers. comm.).

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Birds breeding in or beneath Osprey nests in the Great Lakes basin.—Ospreys (*Pandion haliaetus*) build large stick nests, most commonly at the top of dead trees close to, or standing in, water. Material is added to nests each year, and if the supporting branches are strong enough, a nest may reach up to 3 m deep (Bent 1937, pers. obs.). There are scattered reports in the literature of other bird species breeding within occupied Osprey nests or immediately below them (e.g., Bent 1937, Reese 1977, Terres 1991), but many reviews of Osprey ecology do not mention this habit (e.g., Cramp 1980, Henny 1986, Poole 1989). In addition, a variety of open-nesting bird species will breed in unoccupied Osprey nests (e.g., Yocom 1952, Wetmore and Gillespie 1976, Poole 1989). During the course of eco-toxicological work on Ospreys in the Great Lakes basin in 1991 and 1992 (PJE), and during long-term studies of population biology and general ecology of Ospreys in central Michigan since the early 1960s (SP), we recorded a variety of bird species nesting either in Osprey nests or in the supporting structure. In this paper, we present details of these observations, as well as some recent incidental records, and provide a review of the scattered literature relating to this intriguing phenomenon.

Observations during the 1991 and 1992 breeding seasons (mid-April to early August) were made at intervals of 2–4 weeks, while we checked nests in four study areas in Ontario and Michigan. At Ogoki Reservoir (51°N, 88°W), north of Lake Nipigon, all nests were in dead conifer snags in deep water. In the St. Marys River (46°N, 84°W), in NW Lake Huron,