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LOW DEGREE OF GENETIC VARIABILITY
IN THE AMERICAN ALLIGATOR
(Alligator mississippiensis)

for reviews). The apparent lack of genetic variability might reflect a number of genetic conservation mechanisms, directed selection and bottlenecking being among the most appealing. Although a number of persuasive arguments were presented, a more definitive test could come only from analysis of other alligator populations. Thus, an additional collection of 63 animals was made in Canal L67 in Everglades National Park. The size distribution ranged from about 3 ft. to 9 ft. and indicated a number of different year classes. This, coupled with knowledge of alligator mortality and movements in the area, was consistent with the collection not being from a small number of clutches. In all, 44 presumptive protein loci were analyzed by vertical starch gel electrophoresis. Most loci were the same as those examined in the Louisiana study. In the latter case, three proteins were polymorphic (Catalase, Tripeptidase-2 and LDH-2) whereas the Florida population exhibited only one polymorphic locus (LDH-2). The two populations were genetically distinct. The Chi-Square comparing zygotic frequencies of the three polymorphic loci was 98.15 with 8 d.f. Table 1 compares the heterozygosity and polymorphism found in the Fla. population with La. They are essentially the same. Since population size in the Everglades was never as low as that in the Louisiana population, modern bottlenecking is not likely. Although other genetic mechanisms have not been ruled out, the data are consistent with directional selection for physiological plasticity to survive micro heterogeneous environmental components in an otherwise narrow but stable niche.

Gartside et al (1977) recently reported a remarkably low heterozygosity (H) and proportion of polymorphic loci (P) in a Louisiana population of the American Alligator. (Table 1) This was of interest since most terrestrial vertebrates, especially amphibians/and reptiles have been found to be more variable (see Nevo 1978

TABLE 1 - GENETIC VARIABILITY

	# LOCI	P	H	S (H)
LOUISIANA	49	0.06	0.021	±0.012
FLORIDA	44	0.045	0.0086	±0.0082

1. Gartside, D.F., H.C. Dessauer, T. Joanen, (1977) Biochem. Gen. 15:655
2. Nevo, E., (1978) Theoretical Population Biology 13:121

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