

where mongooses do not occur (Swedberg, 1967). The West Indian Whistling-Duck (*Dendrocygna arborea* Linnaeus) has suffered losses in the West Indies due to mongoose predation (Kear and Williams, 1978). As suggested by Phillips (1923), we suspect that the White-cheeked Pintail in the West Indies is also threatened by the mongoose. The high concentration of White-cheeked Pintails on Green Cay, where the mongoose does not occur, may imply that pintail nesting success is greater on islands where the mongoose is absent.

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Geographic Protein Variation in the Jamaican Blind Snake, *Typhlops jamaicensis* (Serpentes: Typhlopidae)

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The blind snakes of the family Typhlopidae are pantropical in distribution and relatively uniform in morphology. Nearly all species are cylindrical in shape, have smooth scales, and are similar in coloration. Species often are distinguished by minor differences in scalation. Eighteen species are recognized in the West Indies (Thomas, 1989).

Recently, several cryptic species of *Typhlops* from the Puerto Rican Bank were detected by electrophoresis (Hedges and Thomas, unpubl.). Those results raised the possibility that cryptic species of *Typhlops* might exist on other Antillean islands. With that in mind, geographic protein variation was examined in the Jamaican blind snake, *T. jamaicensis* Shaw.

Specimens of *Typhlops jamaicensis* were collected during seven trips to Jamaica during the period 1981-1988. Animals were either returned to the laboratory alive or processed in the field, in which case tissue samples were transported to the laboratory in a liquid nitrogen tank. Snakes were killed in ice water, after which blood was obtained for albumin immunological studies, and viscera (excluding gut contents) and skeletal muscle were removed for electrophoresis. The

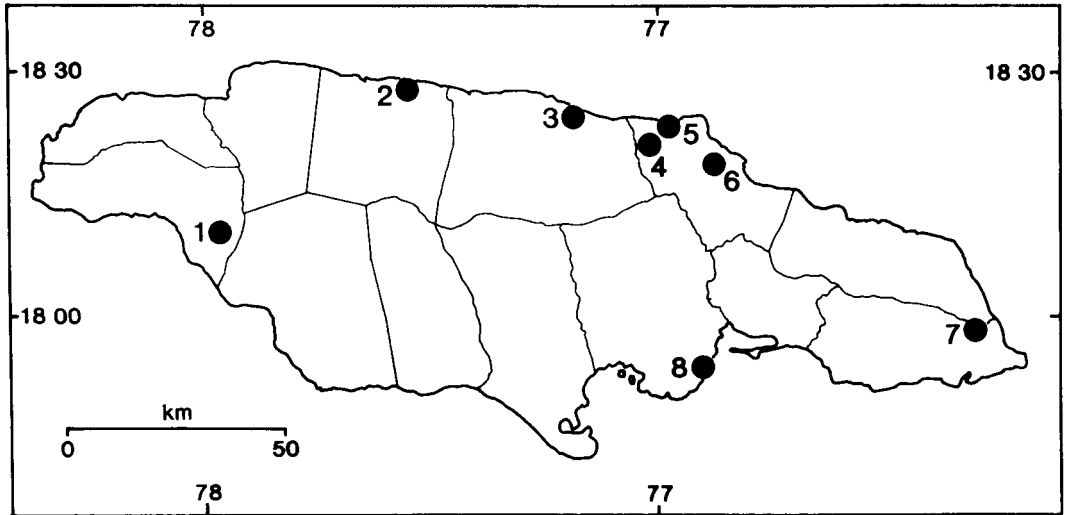


FIG. 1. Populations of *Typhlops jamaicensis* samples for electrophoresis.

remaining carcass was then preserved in 10% formalin (transferred later to 70% ethanol) and deposited in the United States National Museum of Natural History.

Thirteen snakes from eight widely-distributed lo-

calities were obtained (Fig. 1): (1) Westmoreland Parish, 6.1 km NW Newmarket ($n = 1$); (2) Trelawny, 0.3 km W Duncans ($n = 2$); (3) St. Arms, 2.1 km E St. Arms Bay ($n = 1$); (4) St. Mary, 1.6 km S Retreat ($n = 1$); (5) St. Mary, 6.2 km W Oracabessa ($n = 5$); (6) St. Mary,

TABLE 1. Allelic variation in *Typhlops jamaicensis* (eight populations) and *T. richardi* (one population) at 15 polymorphic loci.

Locus	Population								<i>richardi</i>	
	1	2	3	4	5	6	7	8		
<i>Ak</i>	b	b	b	b	b	b	b	b	b	a
<i>Aat-1</i>	a	a	a	a	a	a	a	a	a	b
<i>Ck-1</i>	b	b	b	b	b	b	b	b	b	a
<i>Gpi</i>	a	a	a	a	a (0.9) b (0.1)	a	a	a	a	c
<i>Icd-1</i>	b	b	b	b	b	b	b	b	b	a
<i>Ldh-1</i>	a	a	a	a	a	a (0.5) c (0.5)	a	a	a	b
<i>Lgl</i>	a	a	a	a	a	a	a	a	a	b
<i>Mdh-2</i>	b	b	a (0.5) b (0.5)	b	a (0.1) b (0.9)	b	a	b	b	b
<i>Mpi</i>	a	a	a	a	a	a	a	a	a	b
<i>Pep-1</i>	a	a	a	a	a	a	a	a	a	b
<i>Pep-2</i>	c (0.5) d (0.5)	c	c (0.5) d (0.5)	c	c (0.8) d (0.1) e (0.1)	c	c	c (0.5) d (0.5)	c (0.5) d (0.5)	a (0.5) b (0.5)
<i>Pgd</i>	a	a	a	a	a (0.9) b (0.1)	a	a	a	a	a
<i>Pt-5</i>	b	b	b	b	b	b (0.5) c (0.5)	b	a (0.5) b (0.5)	a (0.5) b (0.5)	b
<i>Pk</i>	b	b	b	b	b	b	b	b	b	a
<i>Sod</i>	a	a	a	a	a	a	a	a	a	b
<i>N</i>	1	2	1	1	5	1	1	1	1	1

TABLE 2. Genetic distances (Nei, 1978) among eight populations of *Typhlops jamaicensis* and one population of *T. richardi*. Mean heterozygosities are listed on diagonal (in parentheses).

Population	1	2	3	4	5	6	7	8	<i>richardi</i>
1	(0.045)	0.011	0.012	0.011	0.005	0.036	0.059	0.012	0.762
2		(0.000)	0.023	0.000	0.000	0.023	0.047	0.023	0.773
3			(0.091)	0.023	0.013	0.049	0.023	0.024	0.801
4				(0.000)	0.000	0.023	0.047	0.023	0.773
5					(0.045)	0.025	0.038	0.017	0.771
6						(0.091)	0.072	0.036	0.801
7							(0.000)	0.072	0.878
8								(0.091)	0.801
<i>richardi</i>									(0.045)

6.4 km S Port Maria ($n = 1$); (7) St. Thomas, 7.7 km N Hordley ($n = 1$); and (8) St. Catherine, Hellshire Beach ($n = 1$). A species from the Virgin Islands, *T. richardi* Duméril and Bibron (St. Thomas, Dorothea; $n = 1$) was included for comparative purposes. Both *T. jamaicensis* and *T. richardi* are believed to be members of the same large group of West Indian *Typhlops*, the "major Antillean radiation" (Thomas, 1989).

Sample preparation and electrophoretic methodology followed procedures described elsewhere (Hedges, 1986). The following 22 loci were examined: acid phosphatase (*Acp*), aconitate hydratase (*Acon-2*), adenylate kinase (*Ak*), aspartate aminotransferase (*Aat-1*), creatine kinase (*Ck*), glucose-6-phosphate isomerase (*Gpi*), isocitrate dehydrogenase (*Icd-1* and *Icd-2*), L-lactate dehydrogenase (*Ldh-1* and *Ldh-2*), lactoyl-glutathione lyase (*Lgl*), malate dehydrogenase (*Mdh-1* and *Mdh-2*), mannose-6-phosphate isomerase (*Mpi*), peptidase (*Pep-1* and *Pep-2*), phosphoglucomutase (*Pgm*), phosphogluconate dehydrogenase (*Pgd*), general protein (*Pt-2* and *Pt-5*), pyruvate kinase (*Pk*), and superoxide dismutase (*Sod*).

Genetic distances (Nei, 1978) were used to construct a UPGMA phenogram of the relationships. This distance was used so that the taxonomic status of the populations could be assessed by comparison with other studies (Thorpe, 1983). Confidence estimates of the clusters defined in the phenogram were obtained

by bootstrapping (Felsenstein, 1985). A modified version of BIOSYS-1 (Swofford and Selander, 1981) was used in the distance analysis and generation of 100 bootstrapped trees.

Allelic variation among the eight populations of *T. jamaicensis* and one population of *T. richardi* is presented in Table 1. Seven loci (*Acp*, *Acon-2*, *Icd*, *Icd-2*, *Mdh-1*, *Pgm*, and *Pt-2*) were monomorphic. Genetic distances (Nei, 1978) and average heterozygosities are given in Table 2.

No evidence for the existence of cryptic species was found among the eight populations of *Typhlops jamaicensis*. A phylogenetic tree produced by phenetic clustering of Nei's genetic distances (Fig. 2) shows very little differentiation among the populations, with population 7 being the most divergent at a D of only 0.05. All eight populations clustered in 100% of the bootstrapped trees and seven of those populations (all except population 7) clustered in 64% of the bootstrapped trees. All other clusters were defined in less than 50% of the bootstrapped trees.

Electrophoretic studies of natural populations have shown that genetic distance can be a useful indicator of taxonomic status (Avice, 1975). Less than 1% of interspecific genetic distances (Nei, 1972, 1978) fall below 0.10 (Thorpe, 1983). The low level of genetic differentiation found among populations in this study, with genetic distances between 0.00 and 0.07 (Table

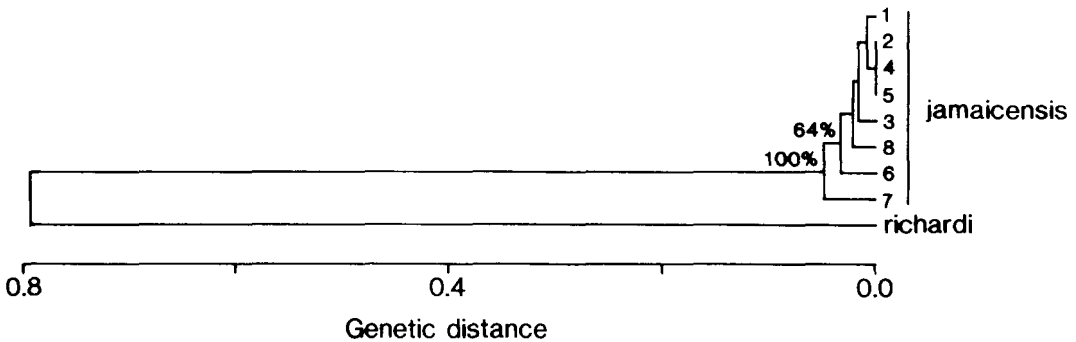


FIG. 2. Phylogenetic tree of eight populations of *Typhlops jamaicensis* and one population of *T. richardi* constructed by UPGMA clustering of Nei's (1978) unbiased genetic distances. Numbers on tree are bootstrapped confidence estimates for clusters (values $\leq 50\%$ not shown). Goodness-of-fit values: 0.998 (cophenetic correlation coefficient) and 5.70 (Prager and Wilson's [1976] F -value).

2), suggests that there are no cryptic species within these samples of *Typhlops jamaicensis*. This contrasts with a recent study of Puerto Rican Bank *Typhlops* (Hedges and Thomas, unpubl.), and preliminary data on variation in Hispaniolan *Typhlops*, where cryptic species were detected.

In studies of intraspecific variation, it is desirable to have sufficient sample sizes in order to obtain accurate estimates of allele frequencies. Most of the sample sizes used in this study are too low for that purpose, but are a reflection of the difficulty in collecting *Typhlops* on Jamaica.

Morphological variation in *T. jamaicensis* was examined by Thomas (1976). Although he found substantial intrapopulation variation in some scale counts, not unusual in *Typhlops*, no geographic patterns were discernible. Thus, he found no morphological evidence for more than one species of Jamaican *Typhlops*.

Although only eight populations of *Typhlops jamaicensis* were examined, they are from widely distributed localities. One locality (7) is within the John Crow Mountains, a region of local differentiation for other species of reptiles and amphibians (Underwood and Williams, 1959; Schwartz and Fowler, 1973). Another locality (8) is in a relatively isolated xeric habitat in southern Jamaica, the Hellshire Hills, which may have been a separate island in the past. However, snakes from both localities show very little electrophoretic differentiation (Fig. 2). Two other areas of regional endemism in Jamaica, the Cockpits and the Portland Ridge peninsula, were not sampled in this study but are worthy of future investigation.

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Notas sobre *Sminthillus limbatus* (Cope)

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Sminthillus limbatus (Cope) es sin duda una de las formas más interesantes de la batracofauna cubana, ya que exhibe un conjunto de adaptaciones que dificultan su catalogación sistemática. Desde su descripción en 1863 la especie ha sido asignada a diferentes taxones, pero recientemente, un número considerable de herpetólogos ha favorecido su inclusión dentro de la familia Leptodactylidae, y más precisamente, dentro de la sección *planirostris* del multiespecífico género *Eleutherodactylus* (Vease a Bogart, 1981).

No obstante los profundos estudios osteológicos y cariológicos realizados con esta especie, muy poco es lo que se ha escrito con relación a su coloración e historia natural, lo que tal vez se deba a su pequeño tamaño y a lo difícil que se hace observarlo en su medio natural. Estas notas aportan algunas observaciones acumuladas durante varios años de intensa colecta herpetológica a través del territorio cubano.