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Evolutionary Origin of *Eptesicus lynni*

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Currently, three species of bats of the genus *Eptesicus* (*fuscus*, *guadeloupensis*, and *lynni*) are recognized as occurring on islands in the Antilles. Of these, *E. fuscus* and *E. guadeloupensis* are believed to belong to the *fuscus*-group of the genus (Davis, 1966; Genoways and Baker, 1975). However, the status and relationships of *E. lynni* are unclear. Shamel (1945) described *lynni* as a member of the *brasiliensis*-group. On the other hand, Sanborn (1941) considered three earlier specimens of *lynni* as members of the subspecies *E. fuscus hispaniolae* (we have examined the Sanborn specimens and they are referable to *lynni*). Baker and Genoways (1978) stated that with available data it could not be determined whether *lynni* evolved from a *fuscus* or *brasiliensis* progenitor. The current study was designed to determine the genic similarities of *E. lynni* to *E. fuscus* of the *fuscus*-group and *E. brasiliensis* and *E. diminutus* of the *brasiliensis*-group in an attempt to understand better the origin of this endemic Antillean species.

Materials and methods.—Specimens examined were *E. lynni* (2 ♀♀, 2 ♂♂), Jamaica, St. Ann Parish, Green Grotto; *E. diminutus* (1 ♀, 4 ♂♂), Venezuela, Guarico, 45 km S Calabozo; *E. brasiliensis* (1 ♀), Venezuela, Miranda, Parque Nacional Guatopo, Aqua Blanca; and *E. fuscus* (8 ♀♀, 2 ♂♂), Massachusetts, Middlesex Co., Lexington; (5 ♀♀, 4 ♂♂), Georgia, Clarke Co., Athens. Voucher specimens are deposited as follows: Carnegie Museum of Natural History, *lynni*; The Museum, Texas Tech University, all *fuscus* and two *diminutus*; Division de Fauna, Ministerio del Ambiente y de los Recursos Naturales Renovables, Caracas, Venezuela, three *diminutus* and one *brasiliensis*.

Methods for tissue preparation and starch gel electrophoresis and enzyme designations are similar to those of Selander et al. (1971) as modified by Greenbaum and Baker (1976). Nineteen presumptive loci, consisting of both enzymatic and nonenzymatic proteins, were assayed. Lactate dehydrogenase-1 and -2, Phosphoglucose isomerase-1 and -2, Albumin, Isocitrate dehydrogenase-1 and -2, Malate dehydrogenase-1 and -2, Phosphoglucomutase-1 and -2, 6-Phosphogluconate dehydrogenase, and Peptidase were resolved on a tris citrate pH 6.7 continuous buffer system. The substrate for the Peptidase stain was the dipeptide Glycyl-L-Leucine. α-Glycerophosphate dehydrogenase, Glutamate dehydrogenase, Leucine aminopeptidase, and Glutamate Oxalate transaminase-1 and -2 were resolved using a tris citrate pH 8.0 continuous buffer system. Hemoglobin was resolved on a tris maleate pH 7.4 continuous buffer system.

TABLE 1.—*Allele frequencies for 11 polymorphic loci for five populations of* Eptesicus. *Loci designations are as in text. The most common allele present in the population of* E. fuscus *from Lexington was designated as the 100 allele for each locus. Variant alleles were designated as fractions of the 100 allele.*

Locus	*E. fuscus* (Lexington)				*E. fuscus* (Athens)				*E. diminutus*				*E. lynni*				*E. brasiliensis*			
Phosphoglucomutase-2	100	120			100	120			100	120			100	120			100	120		
	1.0				1.0					1.0			1.0				1.0			
Phosphoglucomutase-1	100	146	55		100	146	55		100	146	55		100	146	55		100	146	55	
	0.95	0.05			0.89	0.055	0.055		1.0				1.0				1.0			
Albumin	100	96	88	109	100	96	88	109	100	96	88	109	100	96	88	109	100	96	88	109
	1.0				1.0					1.0					1.0					1.0
Lactate dehydrogenase-1	100	108			100	108			100	108			100	108			100	108		
	0.99	0.01			1.0				1.0				1.0				1.0			
Malate dehydrogenase-1	100	150			100	150			100	150			100	150			100	150		
	1.0				1.0				1.0					1.0			1.0			
Isocitrate dehydrogenase-1	100	113	174		100	113	174		100	113	174		100	113	174		100	113	174	
	0.95	0.05			0.94	0.06					1.0		1.0						1.0	
α-Glycerophosphate dehydrogenase	100	167			100	167			100	167			100	167			100	167		
	1.0				1.0				1.0					1.0			1.0			
Peptidase	100	88			100	88			100	88			100	88			100	88		
	1.0				1.0					1.0			1.0					1.0		
6-Phosphogluconate dehydrogenase	100	107	150	123	100	107	150	123	100	107	150	123	100	107	150	123	100	107	150	123
	1.0				1.0						1.0		0.25	0.75						1.0
Glutamate dehydrogenase	100	119			100	119			100	119			100	119			100	119		
	1.0				1.0					1.0			1.0				1.0			
Glutamate oxalate transminase-1	100	167			100	167			100	167			100	167			100	167		
	1.0				1.0					1.0			1.0					1.0		

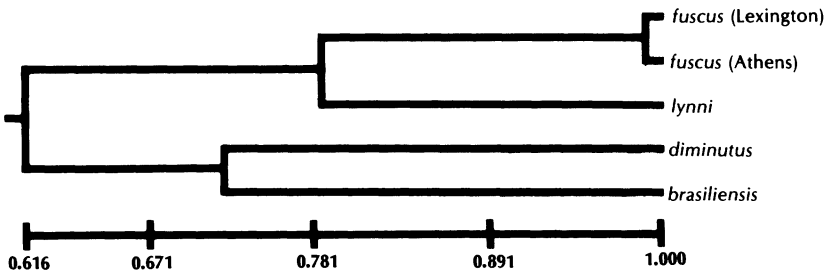

FIG. 1.—Genic similarities for four species of *Eptesicus*.

Electromorph (allele) frequencies (eight loci were monomorphic for all four taxa and the frequency of the other 11 loci are given in Table 1) calculated directly from banding patterns present on the electrophoretic gels were used to generate Rogers' similarity (Rogers, 1972) values, which were utilized to produce a phenogram of genetic similarities (Fig. 1). The generation of the phenogram was based on the UPGMA option given by Rohlf and Kishpaugh (1972).

Results and discussion.—As indicated by Fig. 1, two species clusters are formed on the basis of genic similarity coefficients. The upper species group includes the two populations of *E. fuscus*, which are genically very similar ($\bar{S}$ = .993), and the population of *E. lynni*, which shares approximately 80% of its alleles ($\bar{S}$ = .794) with the *fuscus* samples. At an average similarity value of .616 the populations of *E. diminutus* and *E. brasiliensis* separate from the other two species. The *diminutus* and *brasiliensis* samples share an $\bar{S}$ value of .737. These genic coefficients generally agree with the currently accepted taxonomic relationships of these species (Williams, 1978). Our sample indicates much lower amounts of genic similarity between *lynni* and either *brasiliensis* or *diminutus* than is found between *lynni* and *fuscus*.

The range of coefficients found in our study is in concordance with previously reported intra- and interspecific values in the bat families Vespertilionidae (Straney et al., 1976) and Phyllostomatidae (Straney et al., 1979). In addition, comparisons of other vertebrate populations have yielded similar values (Avise, 1974). Based upon findings in recent studies (Sarich, 1977; Gorman and Renzi, 1979), no significant changes in $\bar{S}$-values would be expected if the population sample sizes were increased.

In conclusion, genic data indicate the most likley origin of *E. lynni* is from the *E. fuscus* complex. Intraspecific populations generally differ at an average of 15% or less of their electrophoretically detectable loci (Avise, 1974). *Eptesicus lynni* is divergent from *E. fuscus* at approximately 20% of the loci examined, which does not lend support to the conclusion that *lynni* is conspecific with *fuscus*. Before final conclusions are reached on this matter, a genic comparison between *E. f. hispaniolae* and *E. lynni* is needed.

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