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## EVOLUTIONARY ORIGIN OF *EPTESICUS LYNNI*

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, Phosphoglucumutase-1 and -2, 6-Phosphoglucuronate 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.  $\alpha$ -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	<i>E. fuscus</i> (Lexington)		<i>E. fuscus</i> (Athens)		<i>E. diminutus</i>		<i>E. lynni</i>		<i>E. brasiliensis</i>	
	100	120	100	120	100	120	100	120	100	120
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	100	146	100	146	100	146	100	146
	0.95	0.05	0.89	0.055	1.0	0.055	1.0	0.055	1.0	0.055
Albumin	100	96	100	96	100	96	100	96	100	96
	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	100	113	100	113	100	113	100	113
	0.95	0.05	0.94	0.06	1.0	0.06	1.0	0.06	1.0	0.06
$\alpha$ -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	100	107	100	107	100	107	100	107
	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 transaminase-1	100	167	100	167	100	167	100	167	100	167
	1.0		1.0		1.0		1.0		1.0	

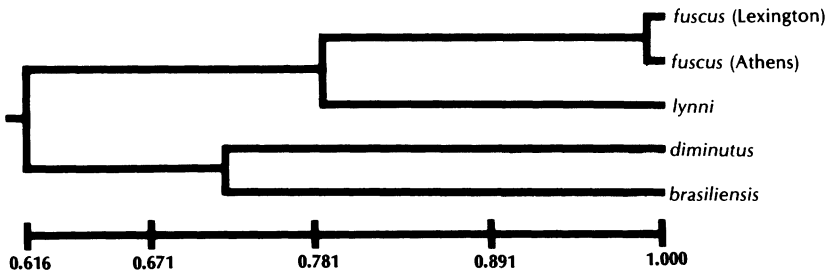


FIG. 1.—Genic similarities for four species of *Eptesicus*.

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 (Avice, 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 likely 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 (Avice, 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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## KARYOTYPE OF *MYSTACINA TUBERCULATA* (CHIROPTERA: MYSTACINIDAE)

Karyological data are now available for species from most bat families (Baker, 1970, 1979; Bickham, 1979; Capanna and Civitelli, 1970; Matthey, 1973). Herein we report the karyotype of *Mystacina tuberculata* Gray, 1843, the only species of the endemic New Zealand family Mystacinidae.

An adult female was mist-netted at the colony of short-tailed bats reported by Daniel (1976) in Omahuta Kauri Sanctuary, Northland, New Zealand. The specimen, referable to *M. t. tuberculata*, is preserved as specimen number M-77-1 in the bat collection of Ecology Division, New Zealand Department of Scientific and Industrial Research. A fibroblast culture was established from a biopsy of the external ear and grown in Ham's F-10 medium fortified with 20% fetal calf serum. Chromosomal preparations were made using 0.05% colchicine as the mitotic inhibitor, medium diluted 1:2 with distilled water as the hypotonic solution, and 3 parts methanol to 1 part acetic acid as the fixative. The cells were stained with giemsa.

The karyotype of *M. tuberculata* ( $2n = 36$ ; FN = 60) (Fig. 1) is composed of six pairs of large, six pairs of medium-sized, and two pairs of small biarmed chromosomes. There are four pairs of small acrocentric chromosomes. The morphology of the X-chromosome was not determined but is assumed to be a medium-sized biarmed pair as it is in most bat species.

The diploid number of *M. tuberculata* ( $2n = 36$ ) is within the range of variation of the Vespertilionidae, Molossidae, Natalidae, Phyllostomatidae, Rhinolophidae (inclusive of the Hipposideridae), Rhinopomatidae, and Emballonuridae. The fundamental number (FN = 60) is found also in species of Molossidae, Phyllostomatidae, Mormoopidae, Rhinolophidae, and Emballonuridae (see Baker, 1970, 1979; Capanna and Civitelli, 1970; Matthey, 1973; Pathak, 1967). Species of the mormoopid genus *Pteronotus* have  $2n = 38$ , FN = 60 (Baker, 1970), the molossid *Molossops greenhalli* has  $2n = 34$ , FN = 60 (Baker, 1970), and three species of the phyllostom-