

University of Nebraska - Lincoln

DigitalCommons@University of Nebraska - Lincoln

Mammalogy Papers: University of Nebraska
State Museum

Museum, University of Nebraska State

5-1-1980

Evolutionary Origin of *Eptesicus lynnii*

Michael L. Arnold

Texas Tech University, Lubbock, TX

Robert J. Baker

Texas Tech University, rjbaker@ttu.edu

Hugh H. Genoways

University of Nebraska - Lincoln, h.h.genoways@gmail.com

Follow this and additional works at: <https://digitalcommons.unl.edu/museummammalogy>



Part of the [Biodiversity Commons](#), [Other Ecology and Evolutionary Biology Commons](#), and the [Zoology Commons](#)

Arnold, Michael L.; Baker, Robert J.; and Genoways, Hugh H., "Evolutionary Origin of *Eptesicus lynnii*" (1980). *Mammalogy Papers: University of Nebraska State Museum*. 67.
<https://digitalcommons.unl.edu/museummammalogy/67>

This Article is brought to you for free and open access by the Museum, University of Nebraska State at DigitalCommons@University of Nebraska - Lincoln. It has been accepted for inclusion in Mammalogy Papers: University of Nebraska State Museum by an authorized administrator of DigitalCommons@University of Nebraska - Lincoln.

- cific variation in the kangaroo rats *Dipodomys spectabilis* Merriam and *Dipodomys deserti* Stephens. Unpubl. Ph.D. dissert., Univ. Illinois, Urbana, 221 pp.
- NIE, N. H., ET AL. 1975. SPSS: statistical package for the social sciences. McGraw-Hill, Inc., New York, 675 pp.
- ROHLF, F. J., J. KISHPAUGH, AND R. BARTCHER. 1969. Numerical taxonomy system of multivariate statistical programs. State Univ. New York, Stonybrook.
- SCHMIDLY, D. J. 1971. Population variation in *Dipodomys ordii* from western Texas. J. Mamm., 52:108-120.
- SCHMIDLY, D. J., AND F. S. HENDRICKS. 1976. Systematics of the southern races of *Dipodomys ordii*. Bull. So. California Acad. Sci., 75:225-237.
- SETZER, H. W. 1949. Subspeciation in the kangaroo rat, *Dipodomys ordii*. Univ. Kansas Publ., Mus. Nat. Hist., 1:473-573.
- SHAVER, W. M. 1973. Skeletal morphology as an index of variation among selected subspecies of Ord's kangaroo rats, *Dipodomys ordii* (Rodentia: Heteromyidae). Unpubl. M.S. thesis, Univ. Mississippi, Oxford, 47 pp.
- SNEATH, P. H. A., AND R. R. SOKAL. 1973. Numerical taxonomy. W. H. Freeman and Co., San Francisco, 573 pp.
- TROWBRIDGE, A. H., AND H. L. WHITAKER. 1940. A new kangaroo rat from Oklahoma. J. Mamm., 21:343-345.

MICHAEL L. KENNEDY¹, MELVIN L. BECK¹, AND TROY L. BEST², ¹*Ecological Research Center, Department of Biology, Memphis State University, Memphis, TN 38152, and* ²*Llano Estacado Center for Advanced Professional Studies and Research, Eastern New Mexico University, Portales, NM 88130. Submitted 28 March 1979. Accepted 26 July 1979.*

J. Mamm., 61(2):311-319, 1980

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, Agua 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. 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	<i>E. fuscus</i> (Lexington)		<i>E. fuscus</i> (Athens)		<i>E. diminutus</i>		<i>E. lynni</i>		<i>E. brasiliensis</i>	
Phosphoglucumutase-2	100 1.0	120	100 1.0	120	100 1.0	120	100 1.0	120	100 1.0	120
Phosphoglucumutase-1	100 0.95	146 0.05	55 0.89	55 0.055	100 1.0	146 0.055	55 1.0	100 1.0	146 1.0	55
Albumin	100 1.0	96 1.0	88 1.0	88 1.0	100 1.0	96 1.0	88 1.0	100 1.0	96 1.0	88 1.0
Lactate dehydrogenase-1	100 0.99	108 0.01	100 1.0	108 1.0	100 1.0	108 1.0	100 1.0	100 1.0	108 1.0	108
Malate dehydrogenase-1	100 1.0	150 1.0	100 1.0	150 1.0	100 1.0	150 1.0	100 1.0	100 1.0	150 1.0	150
Isocitrate dehydrogenase-1	100 0.95	113 0.05	174 0.94	174 0.06	100 1.0	113 1.0	174 1.0	100 1.0	113 1.0	174 1.0
α -Glycerophosphate dehydrogenase	100 1.0	167 1.0	100 1.0	167 1.0	100 1.0	167 1.0	100 1.0	100 1.0	167 1.0	167
Peptidase	100 1.0	88 1.0	100 1.0	88 1.0	100 1.0	88 1.0	100 1.0	100 1.0	88 1.0	88
6-Phosphogluconate dehydrogenase	100 1.0	107 1.0	150 1.0	123 1.0	100 1.0	107 1.0	150 0.25	123 0.75	100 1.0	107 1.0
Glutamate dehydrogenase	100 1.0	119 1.0	100 1.0	119 1.0	100 1.0	119 1.0	100 1.0	100 1.0	119 1.0	119
Glutamate oxalate transaminase-1	100 1.0	167 1.0	100 1.0	167 1.0	100 1.0	167 1.0	100 1.0	100 1.0	167 1.0	167 1.0

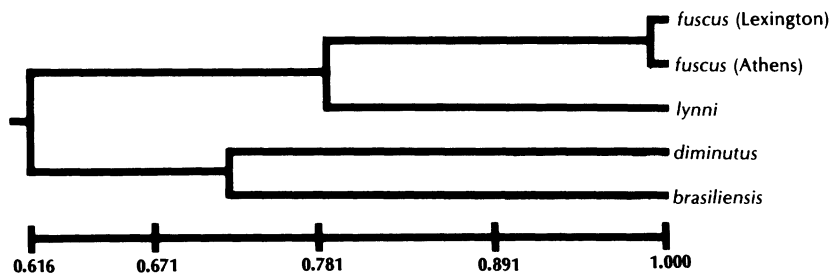


FIG. 1.—Genic similarities for four species of *Eptesicus*.

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 (Avisé, 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 (Avisé, 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.

Acknowledgments.—For assistance in collecting, we thank J. W. Bickham, P. V. August, L. August, J. C. Patton, and C. Burnett. For logistical support in Venezuela, we thank Dr. R. Orta and Sr. T. Blohm. M. Bogan critically evaluated the manuscript. D. F. Williams assisted in identification of specimens. This study was supported by National Science Foundation grant number DEB 76-20580, and the Institute of Museum Research. The Jamaican field work was supported by M. Graham Netting Research Fund, Carnegie Museum of Natural History, through a grant from the Cordelia Scaife May Charitable Trust. Venezuelan field work was supported by an International Environmental Sciences Program awarded to J. Eisenberg.

LITERATURE CITED

- AVISE, J. C. 1974. Systematic value of electrophoretic data. *Syst. Zool.*, 23:465-481.
- BAKER, R. J., AND H. H. GENOWAYS. 1978. Zoogeography of Antillean bats. Pp. 53-97, in *Zoogeography in the Caribbean* (F. B. Gill, ed.). Spec. Publ. Philadelphia Acad. Sci., 13:1-128.
- DAVIS, W. B. 1966. Review of South American bats of the genus *Eptesicus*. *Southwestern Nat.*, 11:245-274.
- GENOWAYS, H. H., AND R. J. BAKER. 1975. A new species of *Eptesicus* from Guadeloupe, Lesser Antilles (Chiroptera: Vespertilionidae). *Occas. Papers Mus., Texas Tech Univ.*, 34:1-7.
- GORMAN, G. C., AND J. RENZI, JR. 1979. Ge-

- netic distance and heterozygosity estimates in electrophoretic studies: effects of sample size. *Copeia*, 1979:242-249.
- GREENBAUM, I. F., AND R. J. BAKER. 1976. Evolutionary relationships in *Macrotus* (Mammalia: Chiroptera); biochemical variation and karyology. *Syst. Zool.*, 25:15-25.
- ROGERS, J. S. 1972. Measure of genetic similarity and genetic distance. *Univ. Texas Publ.*, 7213:145-153.
- ROHLF, F. J., AND J. KISHPAUGH. 1972. Numerical taxonomy system of multivariate statistical programs. The State Univ. of New York at Stony Brook, Stony Brook, New York, 87 pp.
- SANBORN, C. C. 1941. Descriptions and records of Neotropical bats. *Field Mus. Nat. Hist., Zool. Ser.*, 27:371-387.
- SARICH, V. M. 1977. Rates, sample size and the neutrality hypothesis for electrophoresis in evolutionary studies. *Nature*, 265:24-28.
- SELANDER, R. K., ET AL. 1971. Biochemical polymorphism and systematics in the genus *Peromyscus*. I. Variation in the old-field mouse (*Peromyscus polionotus*). *Studies Genetics VI*, Univ. Texas Publ., 7103:49-90.
- SHAMEL, H. H. 1945. A new *Eptesicus* from Jamaica. *Proc. Biol. Soc. Washington*, 58:107-110.
- STRANEY, D. O., M. H. SMITH, R. J. BAKER, AND I. F. GREENBAUM. 1976. Biochemical variation and genic similarity of *Myotis velifer* and *Macrotus californicus*. *Comp. Biochem. Physiol.*, 54B:243-248.
- STRANEY, D. O., M. H. SMITH, I. F. GREENBAUM, AND R. J. BAKER. 1979. Biochemical genetics. Pp. 157-176, in *Biology of bats of the New World family Phyllostomatidae*, Part III (R. J. Baker, J. K. Jones, Jr., and D. C. Carter, eds.). *Spec. Publ. Mus., Texas Tech Univ.*, 16:1-441.
- WILLIAMS, D. F. 1978. Taxonomic and karyological comments on small brown bats, genus *Eptesicus*, from South America. *Ann. Carnegie Mus.*, 16:361-383.

MICHAEL L. ARNOLD¹, R. J. BAKER¹, AND H. H. GENOWAYS², ¹*Department of Biological Sciences and The Museum, Texas Tech University, Lubbock, TX 79409*, and ²*Section of Mammals, Carnegie Museum of Natural History, 4400 Forbes Ave., Pittsburgh, PA 15213*. Submitted 2 April 1979. Accepted 15 November 1979.

J. Mamm., 61(2):319-322, 1980

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-