MAMMALIA 40(2):344-347. 1976

BIOCHEMICAL GENETICS OF *Myotis californicus* AND *Pipistrellus hesperus* FROM SOUTHERN NEVADA

Availability of electrophoretic techniques capable of resolving allelic differences in enzymes and other proteins has resulted in a gowing literature on the genetic composition of wild populations of mammals (Selander and Johnson, 1973 ; Nevo *et al.*, 1974) and other organisms (Selander and Kaufman, 1973). Estimates for mammals of the mean proportion of loci in heterozygous state per individual *(H)* range from 0. 0. in *Geomys tropicalis* (Selander *et al.*, 1974) to 0.163 for *Myotis velifer* (Straney *et al.*, 1976). To date, only two representatives of the order Chiroptera have been studied (Straney *et al.*, 1976). We report here the results of a study of 21 proteins coded by 22 gene loci in *Myotis californicus* and *Pipistrellus hesperus*. Thirty-two individuals of each species were assayed, all collected on 25 June, 1974 in mist nets at White Spot Spring, Desert National Widlife Range, Clark Co., Nevada.

Procedures for starch gel electrophoresis, buffer systems, enzyme assays, and banding patterns are similar to those described by Selander *et al.*, 1971. Specific modifications for bats are reported elsewhere (Straney *et al.*, 1976) except that, in the present study, phosphoglucomutase was assayed on tris-maleate gels from kidney samples. The lactate dehydrogenase-2 homotetramere banded faintly in *Pipistrellus*. Esterase phenotypes of *P. hesperus* differ from those we have observed in other species of bats. Two zones of activity are apparent, one (*ES*-A) slightly slower in mobility than *ES*-1 in *Myotis*, the other (not scored) a diffuse band in the region of "*ES*-3" of *Myotis* (Straney *et al.*, 1976). Attempts at differential staining using various esterase substrates and inhibitors were unsuccessful and we do not know the homologies of esterase loci between the two species. We assume a monomeric structure for *ES*-1 and *ES*-A. Hemoglobin was scored as a single monomeric locus.

Table 1 summarized allele frequencies and heterozygosity at each locus studied. Allele frequencies at no locus deviated significantly from Hardy-Weinberg expectations. Three loci contribute most of variability in *Myotis californicus*, esterase-1, 6-phosphogluconate dehydrogenase, and hemoglobin. The only loci polymorphic in *Pipistrellus* are two of these, hemoglobin and esterase-A.

The differences in heterozygosity between these species is striking considering the similarities in their biology. Both are small insectivorous bats of the Southwestern desert which roost solitarily in rock crevices or abandoned or little used human constructions (Barbour and Davis, 1969). *Myotis californicus*, however, does occur in clusters of individuals and makes more extensive use of caves, mines and buildings than does *Pipistrellus*. They are only locally abundant, but both were present in large numbers at our collecting site. Both species are heterothermic and are active throughout fall and winter, temporarily reviving from torpor to seek water at ambient temperatures as low as —5° to —8 °C (O'Farrell and Bradley, 1970).

Selander and Kaufman (1973) have explained the difference in hererozygosity between vertebrates and invertebrates in terms of the grain size (Levins, 1968) to which each group is exposed. *Myotis californicus* and *Pipis-*

Loci	*Myotis californicus*	h	*Pipistrellus hesperus*	h
Albumin	a(1.00)	0	a(1.00)	0
Alcohol dehydrogenase	a(.97) b(.03)	0	c(1.00)	0
Esterase-A	Absent		a(.47) b(.30) c(.23)	.438
Esterase-1	a(.70) b(.21) c(.09)	.531	Absent	
Esterase-4	a(1.00)	0	Absent	
General protein-1	a(1.00)	0	b(1.00)	0
Glutamic oxalacetic transaminase-1	a(.97) b(.03)	.063	a(1.00)	0
Glutamic oxalacetic transaminase-2	a(1.00)	0	b(1.00)	0
αGlycerophosphate dehydrogenase	a(.81) b(.19)	.313	a(1.00)	0
Hemoglobin	a(.55) b(.45)	.656	c(.94) d(.06)	.063
Indolophenol oxidase-1	a(1.00)	0	b(1.00)	0
Indolophenol oxidase-2	a(1.00)	0	b(1.00)	0
Isocitrate dehydrogenase-1	a(1.00)	0	b(1.00)	0
Isocitrate dehydrogenase-2	a(1.00)	0	a(1.00)	0
Lactate dehydrogenase-1	a(1.00)	0	b(1.00)	0
Lactate dehydrogenase-2	a(1.00)	0	a(1.00)	0
Malate dehydrogenase-1	a(1.00)	0	a(1.00)	0
Malate dehydrogenase-2	a(.97) b(.03	.063	c(1.00)	0
Phosphoglucomutase	a(.98) b(.02)	.031	a(1.00)	0
6-Phosphogluconate dehydrogenase	a(.58) b(.42)	.656	c(1.00)	0
Phosphoglucose isomerase	a(1.00)	0	b(1.00)	0
Sorbitol dehydrogenase	a(.61) b(.39)	.344	c(1.00)	0
		$\bar{H}$ = 0.126		$\bar{H}$ = 0.026

TABLE 1. — Alleles and frequencies (in parentheses) at 22 enzymatic and protein loci in *Myotis californicus* and *Pipistrellus hesperus* from *Clark County, Nevada*. *h* is the proportion of individuals heterozygous at a given locus. *H* is the proportion of loci in heterozygous state per individual. *NS* indicates the locus was not scorable. Where alleles are shared between species, the same letter is used to designate the allele.

trellus hesperus most likely experience their environments as similar in grain size and intensity. Under this view, it could be expected that the two species should show similar levels of heterozygosity. That we do not observe this similarity in heterozygosity should not be taken as a disproof of Selander and Kaufman's (1973) hypothesis.

Selander and Kaufman have attempted to explain the broad patterns that have emerged from studies of genetic variability in a variety of species. Much current theory supports the view that grain size and intensity do contribute to the maintenance of heterozygosity (Levene, 1953 ; Levins, 1968 ; Templeton and Rothman, 1974). There are, however, a number of factors which can reduce variability independant of environmental heterogeneity. Historical factors, such as bottlenecks in population size and concomitant drift, could be very powerful in reducing variability in this way. Only rarely have historical elements been known well enough to estimate their genetic importance (*Bonnell* and Selander, 1974 ; Selander *et al.*, 1974). We feel that the differences between the species reported here may be best explained in terms of historical differences in the populations. Ecological differences between the populations are not large enough to explain the magnitude of the difference in heterozygosities. We expect that *Pipistrellus* populations show marked fluctuations in numbers, resulting in bottlenecks where gene frequencies drift to fixation over time and successive bottlenecks. *Myotis californicus* should show more constant and larger population size than does *Pipistrellus*, either in terms of population numbers or gene flow. Data on population dynamics in these and other bat species are badly needed.

Estimates of genetic similarity (Rogers's S ; Rogers, 1972) between *Myotis californicus* and *Pipistrellus hesperus* are higher than expected for an intergeneric comparison (S = 0.55). Smith, Selander and Johnson (1973) estimated the similarity between subgenera of *Peromyscus* to be S = 0.30 while Johnson and Selander (1971) provide as estimate of S = 0.17 for a comparison between subfamilies of heteromyid rodents. Data available for other organisms also suggest that intergeneric genetic similarities should be at least below 0.4 (Avise, 1975). Webster, Selander and Yang (1973) have reported similarity values between *Anolis* species in the range of 0.1-0.2. These very low values as well as our high estimated suggest that genetic similarity may not be well correlated with a rank across widely diverse groups. Genetic similarity alone will probably be rarely useful in assigning higher taxonomic rank without fairly intensive studies of the group involved at lower taxonomic levels.

This work was supported by Contract AT (38-1)-819 between the U. S. Energy Research and Development Administration and the University of Georgia.

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