

## SHORT NOTES

### Cryptic sympatric diversity in *Emballonura alecto*: further bat species?

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#### INTRODUCTION

The problem of cryptic diversity has grown into a hot topic in bat taxonomy during recent years. This is especially so for the region of western Palearctic. The list of bat fauna has expanded from 31 to 46 species due to discoveries of cryptic species alone (cf. e.g., Corbet, 1978 or Horáček *et al.*, 2000 versus Mayer and Helversen, 2001; Helversen *et al.*, 2001; Kiefer *et al.*, 2002; Spitzenberger *et al.*, 2001; Mucedda *et al.*, 2002; Hulva *et al.*, 2004; Simmons, 2005 and/or Spitzenberger *et al.*, 2006) since the first cases of sympatric sibling species were reported there in sixties and seventies. Most of these discoveries appeared recently through the application of molecular methods. Although a significant degree of population substructures was not expected in volant mammals, molecular tools revealed a surprising amount of phylogenetic gaps in a variety of phylogeographic patterns. This calls not only for rearrangements in taxonomy of the respective clades but also for reconsideration of the speciation mechanisms producing the cryptic species diversity.

The discovery of these cryptic species questioned the universality of a standard model of allopatric speciation explaining the sympatric situations by secondary range extension of the respective allopatric species. This resulted in a lively discussion on speciation under parapatric or sympatric conditions and on the ecological and behavioral mechanisms that may affect it (see e.g., Losos and Glor, 2003 for a review). A detailed model of sympatric speciation in bats was first proposed by Jones (1997) and Barratt *et al.* (1997) who stressed the possible role of divergence in echolocation call frequency for niche partitioning and social recognition in the speciation process of the western Palearctic cryptic species group, *Pipistrellus pipistrellus*. An example of such a model of speciation has recently been provided in the case of the SE Asiatic large-eared horseshoe bats (*Rhinolophus philippinensis*) where switching of frequencies to different harmonics of the same fundamental frequency was shown to be major factor that promoted reproductive isolation of three sympatric size morphs of this bat (Kingston and Rossiter, 2004). Correspondingly, multiple

divergences in foraging strategies were proposed as a mechanism of sympatric speciation within *Scotophilus dinganii* complex (Jacobs *et al.*, 2004).

Although bats are volant and this is presumed to enhance migratory capability, common geographical barriers can limit gene flow considerably. For example, Castella *et al.* (2000) showed that the 14 km narrow Gibraltar Strait has completely isolated population of *Myotis myotis* for at least several million years. In cave dwelling bats, the spatial dislocation of carstic areas and the social system, especially a rigid roost philopatry and pronounced tradition in dislocation of home ranges can effectively suppress gene flow between moderately distant populations and cause an allopatric speciation without apparent geographic barriers. Such microallopatric diversification was described even in a migratory species *Miniopterus schreibersii* in South Africa (Miller-Butterworth *et al.*, 2003). All such events can be further combined with the mechanisms by which the traditional model explains the sympatric situations, i.e. secondary range admixture while retaining established genetic isolation. Hulva *et al.* (2004) demonstrated possible validity of such a model for *Pipistrellus pipistrellus* complex and discussed the proposed scenario of the speciation history in terms of the paleobiographic events in the distributional range. It should be stressed that there are many occasions in the near past in the temperate zone of Western Palearctic, e.g., its vigorous landscape history and extensive climatic oscillations (tectonics, glaciation, sea level oscillation, aridization etc.), that could produce effective barriers and consequent vicariant events. The question is, however, whether and to what degree any of these processes appeared also in climatically stable (see e.g., Bradley, 1999) tropics and whether even there a corresponding amount of cryptic variation can be

expected. The few pilot studies on genetic diversity in tropic bats do not provide much support for it. Bradley and Baker (2001) screened intrapopulation cytochrome *b* variability in 24 populations belonging to 11 species of phyllostomatid bats by examining Kimura 2-parameter corrected genetic distances in 24 populations in Barro Colorado. Values of genetic distances ranged from 0.00 to 3.83% with average 1.28% and do not suggest cryptic variation reaching the species level.

However, in spite of the fact that a vast majority of chiropteran diversity occurs in the tropics, the actual cryptic variation in tropical bats is nearly unknown. For this reason and because of the significance of each case of sympatric cryptic diversity to a better understanding of the factors contributing to biodiversity of that group, any case of cryptic diversity in tropic bats is worthy of particular attention and should be immediately reported. Here we report such a case for the E-Oriental emballonurid *Emballonura alecto* (Eydoux and Gervais, 1836).

## MATERIALS AND METHODS

We discovered a colony of several bat species, including ca. 50 individuals of *E. alecto*, in a cave situated in primary forest ca. 1 km NEE of a small village Lingup, NE Kalimantan, Borneo ( $03^{\circ}12'N$ ,  $116^{\circ}35'E$ ) and sampled it by netting on 21st and 22nd June 2001. Seven individuals of *E. alecto* were netted, all nearly identical in external characters (forearm length 44–46 mm) and four of these were taken as voucher specimens. The genetic analysis of the sample was performed by sequencing 402 bp of cytochrome *b* gene (see Hulva *et al.*, 2004 for protocols). Three specimens (2♂, 1♀) were genetically identical (GenBank Access No. AY426101) but one male (AY057946) belonged to a distinct haplotype. The simple p-distance between these two haplotypes was 4.23%. Corrected distance was not computed due to the absence of suitable sample size of relative sequences useful for assessing the substitution model. For a sequence divergence of about 4%, the degree of mutational saturation is expected to be low (e.g., Page and Holmes, 2000) and the values of corrected

distances (useful for comparing with results of other datasets) will be identical or slightly higher. All measurements were supplemented with aid of mechanical caliper or with ocular micrometer ZEISS SMXX (dental measurements — see Benda *et al.*, 2004).

#### SPECIES COMPARISON

*Emballonura alecto*, which is distributed on Philipines, Sulawesi and Molucas, represents a sibling species of the W-Indonesian *E. monticola* Temminck, 1838 the range of which is centered in Malaysia, Sumatra and Java (Simmons, 2005). Both species are reported to share complete sympatry in Borneo (Corbet and Hill, 1992; Payne and Francis, 1998). The former species is clearly larger (particularly in cranial and dental measurements with almost no overlap: condylocanine length 12.7–13.8 versus 11.8–12.8) and differs from the latter also in a diastema between the upper anterior and posterior premolars. With respect to these discriminating characters all four specimens in our study (condylocanine length

12.92–13.80) fall within the variation range of *E. alecto* (cf. Appendix and Fig. 1). They exhibit an indistinct variation in some fine dental characters such as in size of mesial cingular cusp of C<sup>1</sup> and P<sup>4</sup> or in a diastema vs contact between C<sup>1</sup> and P<sup>3</sup> or in shape of C<sub>1</sub>. However, the male with the distant haplotype shows no extreme position in these characters. It is slightly larger (condylocanine length 13.8) and differs from other specimens in a narrow diastema (0.12 mm) between lower premolars (P<sub>3</sub> and P<sub>4</sub>). In all cranial characters both haplotypes seem to fall in variation range observed in a small topotypic series of *E. alecto* (Jagor collection, Luzon, Philippines) deposited in Museum für Naturkunde Berlin (cf. Appendix and Fig. 2).

#### DISCUSSION

We neither compared our material directly to types of both *alecto* and *monticola*, nor examined patterns of geographic variation in the respective species and actual

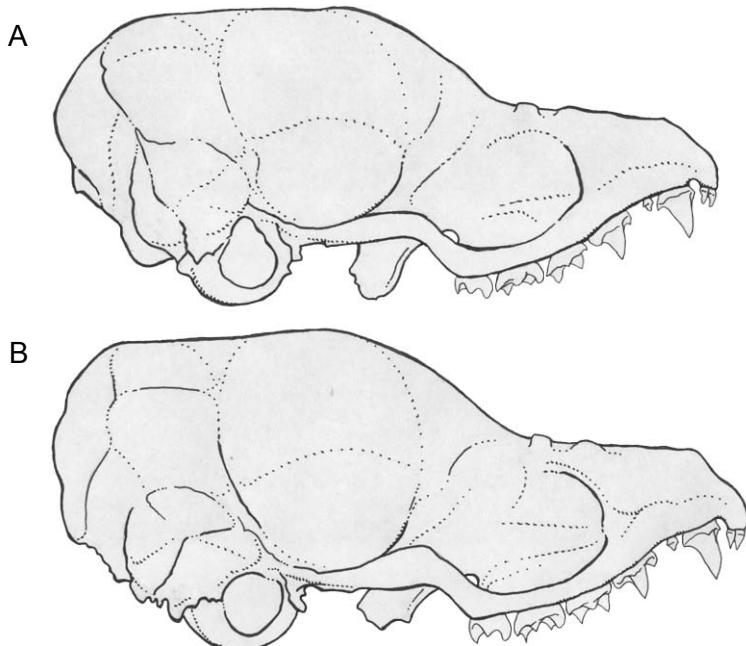


FIG. 1. A lateral view of skull in *E. alecto* haplotype A (specimen No. BOR 56) and haplotype B (BOR 58)

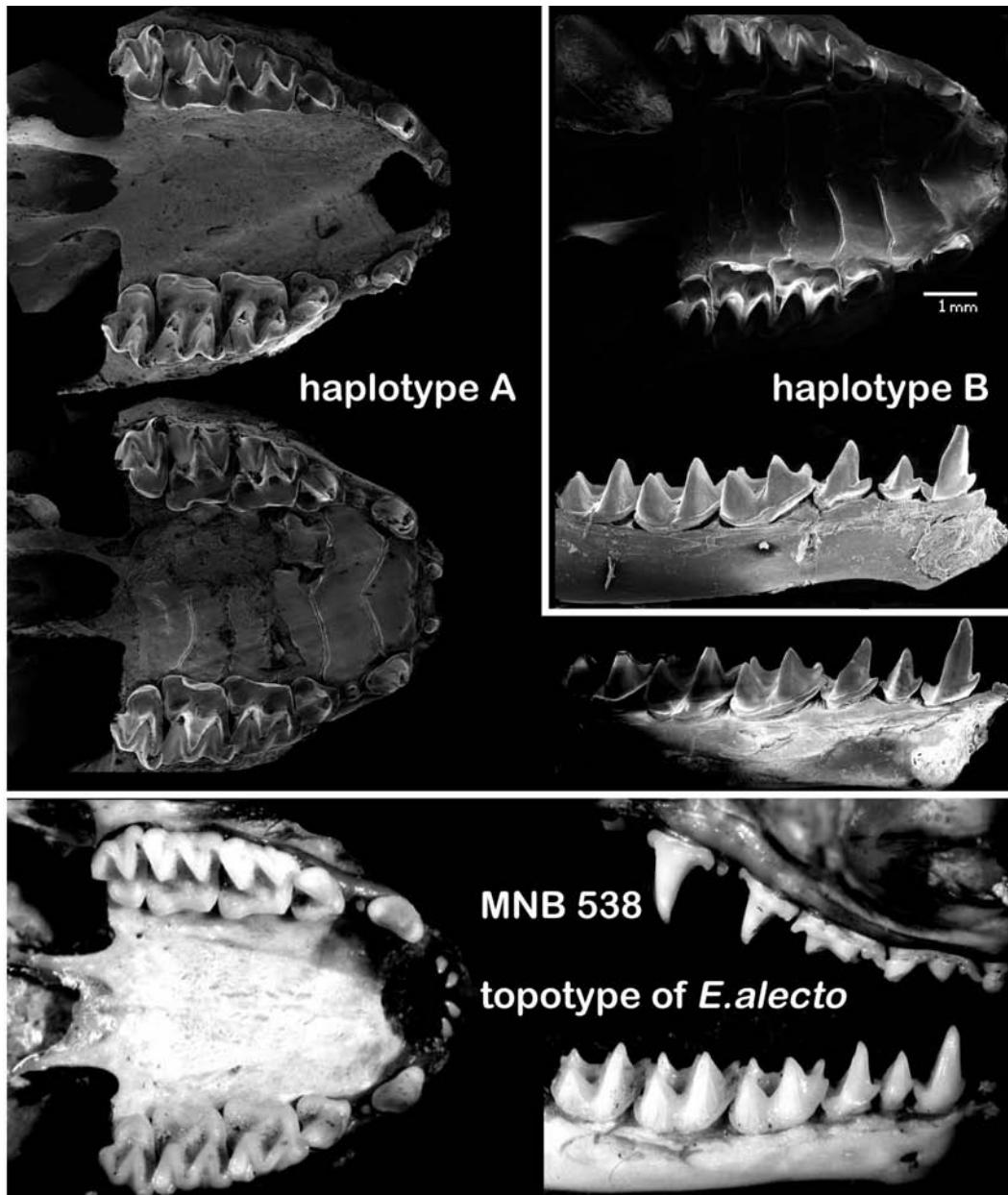


FIG. 2. Maxillary and mandibular dentition in the specimens of haplotype A (BOR 56, BOR 59) and haplotype B (BOR 58) and the same situation in a topotypic specimen of *E. alecto* (MNB 538: Luzon, Phillipines)

relevance of the discrimination characters suggested in the literature. Hence, it would be premature to discuss more about definite taxonomic allocation of the samples. Nevertheless, here we simply intended to report an evident fact of sympatric appearance of two divergent haplotypes separated

with considerable genotypic distance but indistinct in respect to morphological characters, regardless to nomenclatorial assignment of the respective forms. Compared to other data on sympatric cryptic variation in tropical bats (e.g., Bradley and Baker, 2001), with  $p = 4.23\%$  (corrected distance

identical or slightly higher), the present case exhibits exceptional degree of sympatric diversification corresponding to a distinctness at the level of separate species. The case of *E. alecto* suggests that the phenomenon of sympatric cryptic variation may be pertinent for tropical bats too, and that the topic of cryptic variation in tropical bats would be undoubtedly worth of a particular attention. The reliable data on that subject are urgently needed as a source of the comparative information for estimating the actual role of sympatric speciation as a possible factor of chiropteran diversity (Jones 1997).

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## APPENDIX

Measurements (in mm) of four specimens representing two haplotypes of *E. alecto* from Borneo compared to those in a small topotypic series from Luzon, Phillipines (MN Berlin: 1st — 538, 2nd — 538.2, 3rd — A625.1, 4th — A625.2)

Character	Haplotype A		Haplotype B		Topotypes MNB			
	♂	♂	♀	♂	1	2	3	4
Head-and-body length	45.5	48.0	50.0	49.0	—	—	—	—
Tail length	19.5	16.5	17.0	15.5	—	—	—	—
Forearm length	44.5	45.0	44.0	45.0	—	—	—	—
Ear length	13.5	14.5	14.0	12.0	—	—	—	—
Tail length	5.5	5.0	5.5	4.7	—	—	—	—
Hind foot length	7.8	7.8	8.0	7.5	—	—	—	—
Tibia length	17.8	17.0	16.5	18.5	—	—	—	—
Greatest length of skull	15.7	—	15.1	15.2	15.16	15.45	14.89	14.72
Condylar basal length	14.0	—	13.5	14.2	13.69	14.06	13.42	13.45
Condylar canine length	13.1	13.2	12.9	13.8	—	—	—	—
Zygomatic breadth	9.2	—	9.1	9.3	—	10.05	8.65	8.93
Braincase breadth	7.3	—	7.3	7.5	7.18	7.10	6.98	6.96
Mastoid breadth	7.8	—	7.7	8.0	7.64	7.71	7.47	7.56
I <sup>1</sup> M <sup>3</sup>	6.3	—	6.2	6.6	6.58	6.69	6.04	6.16
C <sup>1</sup> M <sup>3</sup>	5.6	—	5.5	5.9	5.65	5.62	5.02	5.38
P <sup>4</sup> M <sup>3</sup>	4.1	—	4.1	4.3	—	—	—	—
M <sup>1</sup> M <sup>3</sup>	—	3.4	3.4	—	—	—	—	—
C <sup>1</sup> C <sup>1</sup>	3.4	—	3.5	3.9	3.61	3.40	3.24	3.50
P <sup>4</sup> P <sup>4</sup>	4.7	—	4.8	5.0	—	—	—	—
M <sup>3</sup> M <sup>3</sup>	—	6.2	6.4	—	6.20	5.75	6.22	—
Mandibular length	10.5	—	10.4	11.0	10.13	10.00	10.16	9.90
IM <sub>3</sub>	—	—	6.7	7.2	6.39	6.60	5.95	6.00
CM <sub>3</sub>	6.0	—	5.6	6.6	5.74	5.58	5.29	5.43
P <sub>4</sub> M <sup>3</sup>	4.1	—	4.3	4.6	—	—	—	—
M <sub>1</sub> M <sub>3</sub>	—	3.6	3.8	—	—	—	—	—