

**Determination of the systematic status  
of the genus *Cynopterus* (Chiroptera: Pteropodidae)  
(short-nosed fruit bats) in Sri Lanka  
based on  
conventional morphology, multivariate morphometrics  
and mitochondrial DNA sequence analysis**

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## ABSTRACT

The systematic status of the genus *Cynopterus*, especially with regard to the status of *C. sphinx* and *C. brachyotis*, is still much in debate. The aim of this study was to conduct a comprehensive systematic study to resolve the taxonomic ambiguity of the *Cynopterus* species complex in Sri Lanka.

The aim was achieved by using suite of taxonomic methods including conventional taxonomy, phenetics and molecular systematics. Conventional taxonomic methods were first employed to investigate the morphological and morphometric variation within a sample of 614 specimens (including adults, sub adults and juveniles) of the *Cynopterus* collected from all regions of the island except the north and north-east. Morphometric data of multiple character systems including external, wing and cranio-dental, comprising 47 measurements from 391 adult specimens, were subjected to phenetic analyses of principal component, canonical variate and UPGMA. Twenty three specimens were examined for mitochondrial DNA (mtDNA) sequence divergence in a 425 bp region of the Cytochrome b gene.

Two distinct morphotypes of *Cynopterus* (designated as large and small morphotypes) were identified using conventional taxonomy. The shape of the baculum and the ear were identified as two new diagnostic characters to distinguish between the two morphotypes. The large morphotype had affinities to *C. sphinx* and the small morphotype had affinities to *C. brachyotis*. The two morphotypes were identified as two distinct taxonomic groups by the three phenetic methods. Within each taxonomic group geographic sub populations were also identified. The mtDNA sequence data revealed the presence of only two major phylogenetic groups with a sequence divergence of 9.2%, indicating that the species complex comprised two distinct genetic species. This permitted the assignment of the large morphotype to the nominate species *C. sphinx* Vahl, 1797 and the small morphotype to the nominate species *C. brachyotis* (Müller, 1838). *C. sphinx* was the more commoner species and was found both in the secondary forest areas and in disturbed areas. *C. brachyotis* was rare and found only in the primary or secondary forest areas or in forest borders and was absent in altitudes below 30m where only *C. sphinx* was found.

A total of seven mtDNA haplotypes were found in the *Cynopterus* species complex, five belonging to *C. brachyotis* and two belonging to *C. sphinx*. The sequence data did not provide evidence for the existence of genetically distinct geographical sub populations of *C. sphinx* but supported the existence of eco-morphotypes of *C. sphinx*. The study reveal that the other species of genus *Cynopterus*, *C. horsfieldii*, *C. musatenggara*, and *C. titthaecheilus* are absent in the island.

In conclusion, the study resolved the taxonomic ambiguity of the *Cynopterus* species complex and identified two different species of *Cynopterus* in Sri Lanka: *C. sphinx* and *C. brachyotis*. The study enabled the revision of the current classification and the establishment of a key to each species. This is the first global report of a mtDNA sequence based study performed on the genus *Cynopterus* to resolved its taxonomy and the sequence data of part of the cytochrome b gene of *C. sphinx* and *C. brachyotis* are reported first in this thesis.