

MAPPING OF THE EVOLUTIONARY PATH OF THE BAT NYCTERIS JAVANICA (CHIROPTERA: NYCTERIDAE) BASED ON DNA BARCODING (MTDNA D-LOOP GENE)

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ABSTRACT

Nycteris javanica is an insectivore bat with excellent echolocation ability and plays a role in controlling pest populations of agricultural crops. This species is an endemic species in Java and Bali which mostly uses caves as its roosting habitat. *N. javanica* is currently under threat of extinction. Endemic status and habitat conditions that are under threat from human activities, especially mining, make the population trend decrease. Extinction becomes inevitable if this downward trend continues. This will certainly be very detrimental both in terms of science and practical benefits for society. On the other hand, not much detailed knowledge both in terms of systematics, ecology, distribution, and other roles of this species has been revealed. This study aims to map the evolutionary path of *Nycteris javanica* based on genetic variation of the D-Loop MtDNA gene. This research will be carried out from March to October 2023. Field sampling sites in Landak and Cekelan caves in Gunung Sewu Karst Area. D-Loop isolation of mitochondrial DNA at IDB Molecular Laboratory, Department of Biology Education, FMIPA UNY, and DNA sequencing at LPPT UGM Laboratory. This research consists of the stages of taking field data for morphometric identification and organ sampling to be used as molecular analysis material. The next stage is the molecular analysis stage, which in the case of the target gene is the D-Loop (Region Control) which is mitochondrial DNA. After molecular analysis, the phylogenetic tree was reconstructed with genomic data from the National Center for Biotechnology Information (NCBI). The data from both forward and reverse sequencing results were aligned using Molecular Evolutionary Genetics Analysis (MEGA) software version 7.0. D-loop DNA from three species has been successfully isolated and sequenced (*M. pusillus*, *M. australis*, and *R. affinis*). D-loop mtDNA sequences, the three species collected from cave habitats in Gunung Sewu form one clade, overlap between habitats, and are genetically close. This species in Java Island also has a high diversity of haplotypes. In addition, haplotypes shared among habitats were also found in this study. The results of this study produced data on D-loop mitochondrial DNA sequences of three species from Indonesia.

Kata Kunci: *evolution, DNA barcode, D-loop, bat*