

# “Phylogeography of *Nasalis larvatus* in Malaysian Borneo using mtDNA and Nuclear Gene”

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*Nasalis larvatus* also known as proboscis monkey is an endemic primate to the island of Borneo; categorised under the family Cercopithecidae, subfamily Colobinae. This species depends primarily on mangrove forest, riverine and other swamp habitat. *N. larvatus* is listed as endangered on the IUCN Red List and Appendix I of CITES. Population declining of proboscis monkey had been a major concern under conservation management. However, limited research on the genetics of *N. larvatus* has been carried out in this nation. This study was aimed to determine the genetic variation and genetic structure among proboscis monkey populations throughout Malaysian Borneo by examine D-loop, Cytochrome Oxidase I (COI) and nuclear gene.

The first part of research examined the genetic diversity of *N. larvatus* population based on total 471 base pair of mtDNA D-loop sequences amplified from 70 faecal samples. The result shows that *N. larvatus* in Malaysian Borneo still retained substantial genetic diversity. Population from Bako National Park revealed the highest genetic diversity with low gene flow suggested that this area might be one of the refugium for proboscis monkey in western part of Borneo. Three refugia were discovered which formed from the northeast, west-central and the south-western part of Borneo during the Pleistocene period. The research was followed by exploring highly conserved region of mtDNA, COI gene. Results revealed that proboscis monkey in Malaysian Borneo had been sub-populated into small groups with low gene flow and low genetic variation was detected among the populations. This indicated the clearance of native vegetation had caused population isolation that further leads to break down of migration and dispersal of *N. larvatus* populations. Nevertheless, the analysis of COI gene successfully identified the ancestral population of proboscis monkey was originated from Sabah and subsequently diversified to other parts of Malaysian Borneo. The final part of the research was designed to discover the genetic diversity of *N. larvatus* populations from the recombination of both maternal and paternal lineages by using nuclear gene. Unfortunately, the genetic analyses were unable to proceed due to failed in amplifying nuclear region after many attempts.

Overall, this research had successfully provided important insight on genetic diversity, and population structure of *N. larvatus* in Malaysian Borneo. This genetic information is crucial for better management of this species for a long-term conversation basis.

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