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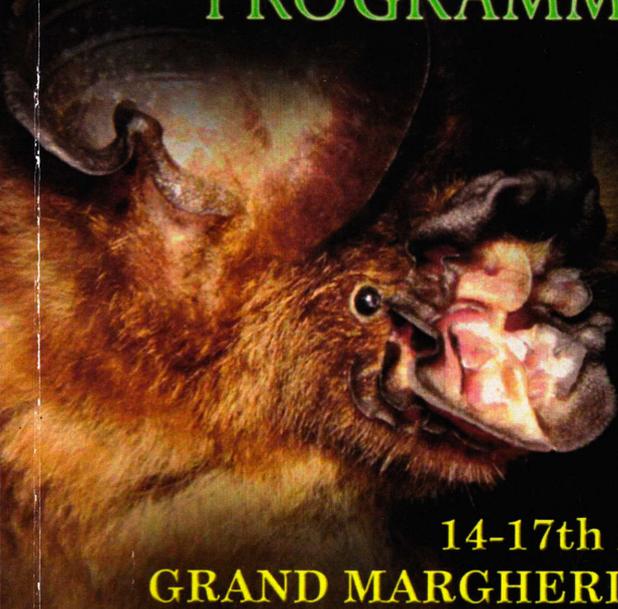


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Mitochondrial DNA Structure of Lyles's Flying Fox *Pteropus lylei*

Thongchai Ngamprasertwong^{1*}, Vibol Hul², Julien Cappelle^{3,4}, & Somsak Panha¹

¹Department of Biology, Faculty of Science, Chulalongkorn University, Bangkok, Thailand; ²Institut Pasteur du Cambodge, Virology Unit, Phnom Penh, Cambodia; ³CIRAD, AGIRs, Montpellier, F-34398, France; ⁴Institut Pasteur du Cambodge, Epidemiology and Public Health Unit, Phnom Penh, Cambodia; *Corresponding author: thongchai.n@chula.ac.th

Lyle's flying fox *Pteropus lylei* is one of the major reservoirs for Nipah virus in Southeast Asia. Several outbreaks of this virus occurred in many areas of South East Asian and South Asia in the last decade. More than 200 people in those areas have died due to this viral infection since 1998. An accurate understanding of the potential for epidemiology spread and disease risk requires an understanding of population ecology and population genetic structure of the primary host. This study investigated the spatial distribution of mitochondrial DNA diversity among Lyle's flying fox populations in order to clarify their population genetic structure and characterize the potential epidemiology spread of Nipah virus among bat populations. The current mitochondrial DNA survey suggested the genetic homogeneity of mtDNA among Lyle's flying fox populations in Thailand and Cambodia.

Values of Forest Patches in Conserving Bat Diversity on Penang Island, Malaysia

Nur Izzati Abdullah¹, Joe Chun-Chia Huang², Faisal Ali Anwarali Khan³, Mohd Abdul Muin Md Akil⁴, Shahrul Anuar Mohd Sah⁴, & Lee-Sim Lim^{1*}

¹School of Distance Education, Universiti Sains Malaysia, 11800, Penang, Malaysia; ²Department of Biological Sciences, Texas Tech University, Lubbock, Texas, USA; ³Department of Zoology, Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Kota Samarahan, Sarawak, Malaysia; ⁴School of Biological Sciences, Universiti Sains Malaysia, 11800, Penang, Malaysia; *Corresponding author: leesim.lim@usm.my

The natural habitats on Penang Island has been largely transformed for urban and industry developments over the past century. Only few relative large forests are remained as reserves and the other forest patches are usually small and discontinuously distributed within agricultural and urban landscapes. The values of these forest patches and forest-like habitats (e.g. orchard) in conserving the island's bat diversity are understudied. We surveyed bat diversity with harp traps and mist nets at five forest sites and two orchard sites in continuous forest, agriculture, and urban landscapes from November 2014 to May 2015. A total of 398 individuals from 22 bat species of six families were recorded. *Cynopterus brachyotis* was the most abundant species across sites, followed by *Rhinolophus affinis*. The two sites in agriculture landscapes, regardless habitat types, had higher values of Simpson Index (0.16 for the forest site and 0.37 for the orchard site) than sites in forest landscapes (0.41-0.46, n = 3) and urban landscapes (0.46 and 0.50, n = 2). The results suggest that species compositions in agriculture landscapes were more even than other landscapes. With an estimate of over 60 species, we suggest that the small sample size in our study may underestimate the overall species diversity for Penang Island. We will include more sample sites to justify the patterns reported here and more comparisons of bat assemblage structure in forest patches among the three study landscapes. The values of forest patches within each landscape on conserving Penang's forest bats will be discussed.