

To Eat or Not to Eat? It Never is a Question! Exploring Biodiversity with Single-leech Blood Meals in Peninsular Thailand



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Venue: Auditorium, 1st Floor

Interdisciplinary Research Building

跨領域科技研究大樓1樓演講廳

Host: Dr. Meiyeh Jade Lu 呂美曄研究技師



Abstract

Environmental DNA (eDNA) obtained from blood-feeding invertebrates, i.e. invertebrate-derived DNA (iDNA) from terrestrial leeches, is increasingly recognized as a robust tool for assessing vertebrate diversity in natural habitats. Recent studies further pointed out the possibility of multiple blood meals in the biodiversity hotspot, such as Madagascar, indicating that sequencing of blood meals of individual leeches may be an advantage in monitoring vertebrate in biodiversity-rich forests in Southeast Asia. Therefore, we set the goal to explore the feasibility of establishing a single-leech metabarcoding sequencing workflow using 141 individual leeches to discover vertebrate diversities in Hala-Bala Wildlife Sanctuary, Thailand—one of the world's most biodiverse tropical forests. Using the two mitochondrial markers, mt16S and mt12S), we recovered 133 unique blood meals representing 33 vertebrate taxa including IUCN-listed endangered species such as *Manis javanica* (Sunda Pangolin), *Tapirus indicus* (Malayan Tapir), and *Macaca nemestrina* (Southern Pig-tailed Macaque) and *Manouria emys* (Asian Brown Tortoise). We also detected the flagship species *Neofelis nebulosa* (Clouded Leopard) in the blood meals. Interestingly, we observed of several leeches potentially contained DNA from multiple sympatric hosts, providing a preliminary evidence of hidden feeding complexity that likely reflects high biodiversity in the forests of Peninsular Thailand. However, this assumption may have to be extensively verified in the future. Additionally, the results demonstrated that combining leech iDNA and camera traps may provide a more comprehensive discovery of vertebrate species in a tropical forest, as understory bird species were only detected by camera traps but not in leech iDNA in this study. These findings demonstrated that single-leech sequencing can enhance taxonomic resolution, reveal potential shared microhabitats of elusive species, and provide a powerful, scalable, and adaptable approach that can be extended to other blood-feeding invertebrates and diverse ecosystems for long-term biodiversity monitoring.