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SHORT REPORT

First Gut Microbiome Profiling of the Critically Endangered Tricolour Langur (*Presbytis chrysomelas cruciger*) and Vulnerable Silvery Langur (*Trachypithecus cristatus*) in Sarawak, Malaysia

Roberta Chaya Tawie Tingga[1,2] | Ahmad Ampeng[3] | Jack Liam[1,3] | Bilhan Deli[3] | Mohd Luqman Anuar[3] | Dayang Nuriza Abang-Abdillah[1,3] | Noraini Johari[3] | Abd Rahman Mohd-Ridwan[2] | Badrul Munir Md-Zain[1]

[1]Department of Biological Sciences and Biotechnology, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, Bangi, Selangor, Malaysia | [2]Centre for Pre-University Studies, Universiti Malaysia Sarawak, Kota Samarahan, Sarawak, Malaysia | [3]Forest Department Sarawak, Bangunan Baitul Makmur II, Medan Raya, Kuching, Sarawak, Malaysia

Correspondence: Badrul Munir Md-Zain (abgbadd1966@yahoo.com)

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ABSTRACT

DNA metabarcoding is used to explore the gut microbiome of *Presbytis chrysomelas cruciger* and *Trachypithecus cristatus* from the Jemoreng Protected Forest. Phylum Firmicutes, family Lachnospiraceae, and genus *Shuttleworthia* are suggested as the key microbiome components for both species. The microbiome was primarily composed of beneficial bacteria essential for food digestion.

1 | Introduction

DNA metabarcoding has emerged as a viable option for large-scale research sampling in environments where species identification through conventional morphological methods is logistically or financially challenging [1]. This approach has been adopted in various mammalian microbiome studies [2–5], and findings from these studies have contributed to local conservation strategies and captive management.

In this study, we explored the composition of the gut microbiome of *Presbytis chrysomelas cruciger* and *Trachypithecus cristatus*, which were recently discovered in the Jemoreng Protected Forest, Mukah, Malaysia. Little is known about the microbiome composition of both primates. *P. c. cruciger* is a transboundary primate that classified as critically endangered species in Sarawak and Kalimantan [6, 7], while *T. cristatus* is classified as vulnerable under the IUCN Red List category. Investigating the gut microbiome of wild primates is of particular interest as this is underexplored in Malaysia, especially *P. c. cruciger*. Moreover, wild primates serve as bioindicators for assessing changes in their natural environment that may affect their gut health. As gut microbiome diversity is associated with a primate's overall health [4, 8, 9], the outcome of this research is essential for the conservation strategy focusing on *P. c. cruciger* and *T. cristatus* in their natural habitat.

2 | Materials and Methods

Fecal samples from a single individual of *P. c. cruciger* (AAPCQ922; Accession number: SRR31067676) and *T. cristatus* (AATCQ920; Accession number: SRR31049265) were obtained from the Jemoreng Protected Forest (JPF), Sarawak (2°42′00″ N, 111°39′00″ E) during scientific surveys conducted by the Forest Department Sarawak [6]. Genomic DNA was extracted from the samples using the QIAamp PowerFecal Pro DNA Kit according to the manufacturer's protocol. The quality and quantity