

## Article

# Cryptic Diversity and Demographic Expansion of *Plasmodium knowlesi* Malaria Vectors in Malaysia

Sandhya Pramasivan<sup>1</sup>, Van Lun Low<sup>2,\*</sup> , Nantha Kumar Jeyaprakasam<sup>3</sup> , Jonathan Wee Kent Liew<sup>4</sup>, Romano Ngui<sup>1,5</sup> and Indra Vythilingam<sup>1,\*</sup> 

- <sup>1</sup> Department of Parasitology, Faculty of Medicine, Universiti Malaya, Kuala Lumpur 50603, Malaysia; sandhya96@gmail.com (S.P.); nromano@unimas.my (R.N.)
- <sup>2</sup> Tropical Infectious Diseases Research & Education Centre (TIDREC), Universiti Malaya, Kuala Lumpur 50603, Malaysia
- <sup>3</sup> Biomedical Science Program, Center for Toxicology and Health Risk Studies, Faculty of Health Sciences, Universiti Kebangsaan Malaysia, Kuala Lumpur 50300, Malaysia; nanthakumar@ukm.edu.my
- <sup>4</sup> Environmental Health Institute, National Environment Agency, Singapore 569874, Singapore; jonathan\_liew@nea.gov.sg
- <sup>5</sup> Malaria Research Centre, Faculty of Medicine and Health Sciences, Universiti Malaysia Sarawak (UNIMAS), Kota Samarahan 94300, Sarawak, Malaysia
- \* Correspondence: vanlun\_low@um.edu.my (V.L.L.); indrav@um.edu.my (I.V.)

**Abstract:** Although Malaysia is considered free of human malaria, there has been a growing number of *Plasmodium knowlesi* cases. This alarming trend highlighted the need for our understanding of this parasite and its associated vectors, especially considering the role of genetic diversity in the adaptation and evolution among vectors in endemic areas, which is currently a significant knowledge gap in their fundamental biology. Thus, this study aimed to investigate the genetic diversity of *Anopheles balabacensis*, *Anopheles cracens*, *Anopheles introlatus*, and *Anopheles latens*—the vectors for *P. knowlesi* malaria in Malaysia. Based on cytochrome c oxidase 1 (*CO1*) and internal transcribed spacer 2 (*ITS2*) markers, the genealogic networks of *An. latens* showed a separation of the haplotypes between Peninsular Malaysia and Malaysia Borneo, forming two distinct clusters. Additionally, the genetic distances between these clusters were high (2.3–5.2% for *CO1*) and (2.3–4.7% for *ITS2*), indicating the likely presence of two distinct species or cryptic species within *An. latens*. In contrast, no distinct clusters were observed in *An. cracens*, *An. balabacensis*, or *An. introlatus*, implying a lack of pronounced genetic differentiation among their populations. It is worth noting that there were varying levels of polymorphism observed across the different subpopulations, highlighting some levels of genetic variation within these mosquito species. Nevertheless, further analyses revealed that all four species have undergone demographic expansion, suggesting population growth and potential range expansion for these vectors in this region.

**Keywords:** *Plasmodium knowlesi*; Malaysia; *Anopheles*; mosquitoes; genetic diversity



**Citation:** Pramasivan, S.; Low, V.L.; Jeyaprakasam, N.K.; Liew, J.W.K.; Ngui, R.; Vythilingam, I. Cryptic Diversity and Demographic Expansion of *Plasmodium knowlesi* Malaria Vectors in Malaysia. *Genes* **2023**, *14*, 1369. <https://doi.org/10.3390/genes14071369>

Academic Editor: Maria Anice Mureb Sallum

Received: 30 May 2023

Revised: 26 June 2023

Accepted: 27 June 2023

Published: 28 June 2023



**Copyright:** © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

## 1. Introduction

Malaria remains a persistent global public health challenge, and countries in Southeast Asia have been assigned the goal of malaria elimination by 2030. This ambitious target highlights the urgency and importance of concerted efforts to combat malaria and reduce its burden in the region. Malaysia has been free of human malaria since 2018 [1], but *P. knowlesi*, a simian malaria parasite, is the predominant species currently occurring in the country [2]. All countries in SEA have reported the occurrence of *P. knowlesi*, with the exception of Timor-Leste [3]. It is crucial to consider the WHO [4] recommendation to postpone the certification of a malaria-free status for countries reporting significant *P. knowlesi* cases in the region. This highlights the importance of ongoing surveillance, monitoring, and control efforts to effectively address the persistence of malaria and prevent the potential reintroduction of human malaria in Malaysia and neighboring countries.