ADVANCES IN PARASITOLOGY

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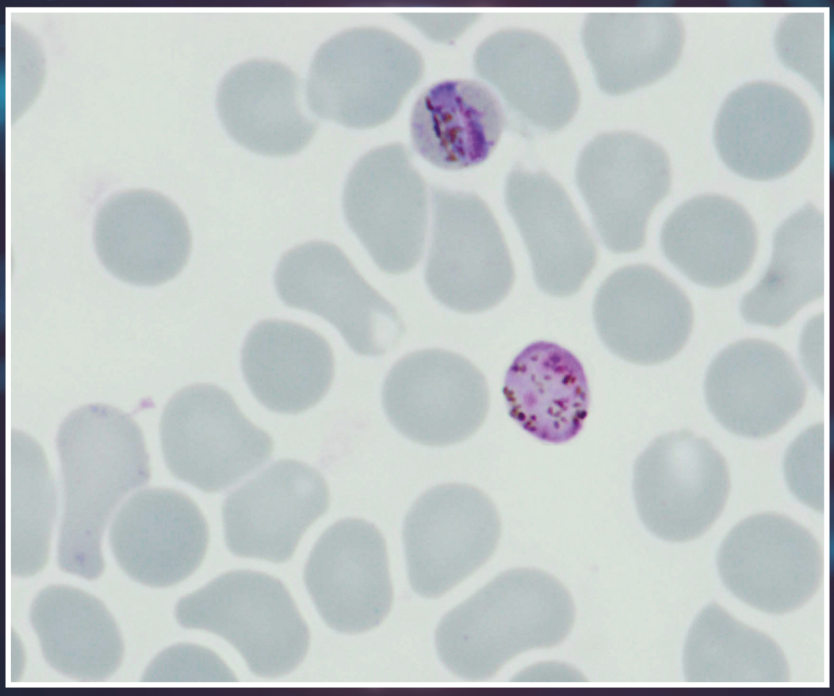

CURRENT RESEARCH ON NATURALLY TRANSMITTED *PLASMODIUM KNOWLESI*

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Cover image: Microscopy image of Giemsa stained thin film from a *P. knowlesi* infected patient in Sarawak, Malaysia - image courtesy of Paul Divis

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CHAPTER FIVE

Molecular epidemiology and population genomics of *Plasmodium knowlesi*

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Abstract

Molecular epidemiology has been central to uncovering *P. knowlesi* as an important cause of human malaria in Southeast Asia, and to understanding the complex nature of this zoonosis. Species-specific parasite detection and characterization of sequences were vital to show that *P. knowlesi* was distinct from the human parasite species that had been presumed to cause all malaria. With established sensitive and specific molecular detection tools, surveys subsequently indicated the distribution of *P. knowlesi* infections in humans, wild primate reservoir host species, and mosquito vector species. The importance of studying *P. knowlesi* genetic polymorphism was indicated initially by analysing a few nuclear gene loci as well as the mitochondrial genome, and subsequently by multi-locus microsatellite analyses and whole-genome sequencing. Different human infections generally have unrelated *P. knowlesi* genotypes, acquired from the diverse

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