Project Title:

Genetic and genomic epidemiology of malaria: dissecting patterns of *Plasmodium vivax* transmission and adaptation

Project Summary:

Once considered a benign infection, *Plasmodium vivax* is now acknowledged to be an important public health threat capable of causing severe and life-threatening disease. Chloroquine remains the mainstay for treating vivax malaria in most regions, but evidence of declining efficacy underpins the urgency to contain this species. *P. vivax* is challenging to control owing to the species' ability to form dormant liver stages that can relapse weeks to months after initial infection, and pre-symptomatic development of transmissible blood stages. *P. vivax* also exhibits extensive genetic diversity. These properties enhance the parasite's ability to survive and adapt to antimalarial drugs, mosquito vectors, host immunity, and other selective pressures. Successful interruption of *P. vivax* transmission will, therefore, require a better understanding of local transmission patterns, infection spread, reservoirs of infection, drug resistance, and other forms of adaptation. This project aims to address these knowledge gaps using genetic and genomic approaches to dissect the epidemiology of *P. vivax*. The successful applicant will use a unique biobank of *P. vivax* samples collected within the framework of longitudinal cohorts and cross-sectional studies in Asia and the horn of Africa to explore the following research areas:

- Genomic analysis to identify genes under strong positive selection. We have previously used this approach in Thailand, Cambodia and Indonesia, confirming known drug resistance determinants and identifying new candidates. The project will extend this work to additional populations.

- Characterise the spatial patterns of *P. vivax* diversity to inform on local patterns of transmission and spread. The project will use amplicon-based sequencing to genotype infections from densely sampled regions of Southeast Asia and Africa, applying population genetic measures to elucidate local transmission networks.

- Characterise the genetic patterns of recurrent infections in patients recruited into longitudinal cohorts. Amplicon-based sequencing data will be used to characterise the temporal dynamics of individual infections.

Supervision contact:

Primary: 1) Sarah Auburn

Associate: 2) Ric Price

3) Jutta Marfurt

Location of the project: Menzies School of Health Research, Darwin (with potential opportunities for study visits to collaborating sites)

Outreach work?

N	☒	
Y	☐	
If Y,	Interstate	☐
	Remote	☐
	International	☐

Type of project:

MPH thesis [max **6 months** 1 FTE]	☐
Hons [max **9 months** 1 FTE]	☐
MSc by research [max **2 years** 1 FTE]	☒
PhD [max **3-4 years** 1 FTE]	☒

Skill base:

Essential:	Moderate bioinformatics skills (comfortable using R or a similar programming language)
Desirable:	Basic knowledge in statistics

Additional comments: The project will suit a student interested in bioinformatics, with opportunities to also perform some complementary wet-lab research. You will be supported by a multi-disciplinary team of clinicians and scientists with expertise in clinical studies, pathophysiology, and genetic and genomic epidemiology of malaria. The team has well established programs in antimalarial drug resistance and has built a strong collaborative network for clinical and molecular epidemiology studies of *P. vivax*. There will be an opportunity to learn and develop skills in laboratory-based molecular biology techniques, clinical epidemiology, population genetics and genomics.