

Partner studies: GenRe manuscript

1125-PF-TH-NOSTEN

Investigating artemisinin resistance emergence on Thai-Burmese border

P. falciparum resistance to artemisinin derivatives emerged on the Thai Myanmar border between 2000 and 2010. The Shoklo Malaria Research Unit (SMRU) has collected phenotypic data on more than 3,000 patients with uncomplicated hyperparasitaemia and stored packed red blood cells for over 600 at the time of admission. This constitutes a unique collection of samples available for genomic analysis to determine changes in the parasite population structures and to identify potential molecular markers associated with resistance to artesunate.

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1148-PF-BD-MAUDE

Assessing the contribution of migration to the emergence and spread of antimalarial drug resistance in Southeast Bangladesh

This study measured population movement by travel surveys and mobile phone call record data and combined these with parasite genotype data and malaria incidence to examine the role of population movement on the spread of malaria and antimalarial drug resistance.

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1172-PF-KH-FAIRHURST-SM

Resistance to artemisinin and ACT partner drugs in Cambodia

Investigating clinical and molecular aspects of resistance to artemisinin and ACT partner drugs, in particular piperaquine.

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1179-PF-KH-TME-VONSEIDLEIN

Targeted Chemo-elimination (TCE) of Malaria (TME)

Targeted Malaria Elimination (TME) studies took place in western Myanmar, Vietnam, Cambodia, and Laos during 2013-17, led by the Mahidol-Oxford Tropical Medicine Research Unit. This project consisted of 2 stages. Firstly, multiple malaria prevalence surveys and collection of treatment records to define the epidemiology of the asymptomatic reservoir, infection risk factors, prevalence of simian malarias, and spatio-temporal mapping. Secondly, a controlled clinical trial of mass drug administration which successfully interrupted falciparum transmission. MORU's project was funded by the Wellcome Trust and the Bill and Melinda Gates Foundation.

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1180-PF-TRAC2-DONDORP

Tracking Artemisinin Resistance Collaboration (TRAC II)

A multi-centre, open-label randomized trial to assess the efficacy, safety and tolerability of Triple Artemisinin-based Combination Therapies (TACTs) compared to Artemisinin-based Combination Therapies (ACTs) in uncomplicated falciparum malaria and to map the geographical spread of artemisinin and partner drug resistance.

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1181-PF-VN-THUYNHIEN

Monitoring the susceptibility of *P. falciparum* to antimalarial drugs in malaria endemic areas in southern Vietnam

Routine monitoring of the efficacy of anti-malarial drugs used is necessary for effective case management, early detection of drug resistance and to provide background information for the development and evaluation of drug policies. In parallel with yearly clinical monitoring the susceptibility of *P. falciparum* to current ACT used in Vietnam, the study aims to investigate the molecular markers (to artemisinin and partner drugs) and using them to support the early detection of drug resistance - one of actions required in dealing with the emergence and possible spread of *P. falciparum* resistance.

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1198-PF-METF-NOSTEN

Malaria Elimination Task Force

The objectives of this programme were to scale-up the targeted mass drug administration strategy regionally, and measure its effect on the incidence of clinical malaria in eastern Karen/Kayin state, Myanmar, a difficult-to-access hilly and forested area with complex political and geographical landscapes, where malaria transmission is seasonal and where artemisinin resistant *P. falciparum* is prevalent.

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1207-PF-KH-CNM-GENRE

Integrating genetic epidemiology as an intensified surveillance tool into the National Center for Parasitology Entomology and Malaria Control of Cambodia

Genetic surveillance project conducted by the National Malaria Control Programme in partnership with GenRe-Mekong in endemic regions of Cambodia. This is part of a large project of genetic surveillance of malaria in the Greater Mekong Subregion, funded by the Bill and Melinda Gates Foundation. Dried blood spot (DBS) samples are to be collected along with short surveys on patient demographics and population movement from every confirmed case of *P. falciparum* and/or *P. vivax* malaria presenting at public health facilities. The aim is to determine the prevalence and geographic distribution of antimalarial drug resistance-linked genetic mutations, as well as the genetic structure of the parasite population, likely routes of gene flow between populations, and geographic origins of parasites.

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1208-PF-LA-CMPE-GENRE

Genetic epidemiology of *P. falciparum* malaria and associated antimalarial drug resistance in Lao PDR

Genetic surveillance project conducted by the National Malaria Control Programme in partnership with GenRe-Mekong in endemic region of the Lao PDR. This is part of a large project of genetic surveillance of malaria in the Greater Mekong Subregion, funded by the Bill and Melinda Gates Foundation. Dried blood spot (DBS) samples are to be collected along with short surveys on patient demographics and population movement from every confirmed case of *P. falciparum* and/or *P. vivax* malaria presenting at public health facilities. The aim is to determine the prevalence and geographic distribution of antimalarial drug resistance-linked genetic mutations, as well as the genetic structure of the parasite population, likely routes of gene flow between populations, and geographic origins of parasites.

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1209-PF-VN-IMPEQN-GENRE

Genetic epidemiology of *P. falciparum* malaria and associated antimalarial drug resistance in Central Vietnam

Genetic surveillance project conducted by the National Malaria Control Programme in partnership with GenRe-Mekong in endemic region of Vietnam. This is part of a large project of genetic surveillance of malaria in the Greater Mekong Subregion, funded by the Bill and Melinda Gates Foundation. Dried blood spot (DBS) samples are to be collected along with short surveys on patient demographics and population movement from every confirmed case of *P. falciparum* and/or *P. vivax* malaria presenting at public health facilities. The aim is to determine the prevalence and geographic distribution of antimalarial drug resistance-linked genetic mutations, as well as the genetic structure of the parasite population, likely routes of gene flow between populations, and geographic origins of parasites.

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1210-PF-TH-MAUDE

Epidemiology of malaria in northeast Thailand: a case-control study

This study aimed to determine risk factors for catching malaria in northeast Thailand, including travel, to identify where people were likely being infected and determine how much antimalarial drug resistance there is.

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1238-PF-VN-NIMPE-GENRE

Research on malaria molecular and genomic epidemiology in all drug-resistance regions of Vietnam: case-control research on the risk factors

Genetic surveillance project conducted by the National Malaria Control Programme in partnership with GenRe-Mekong in endemic regions of Vietnam. The study aimed to determine risk factors for catching malaria in high endemic areas of Viet Nam, including travel, to identify where people were likely being infected and determine how much antimalarial drug resistance there is. Dried blood spot (DBS) samples were collected along with surveys on potential risk factors from every confirmed case of *P. falciparum* and/or *P. vivax* malaria presenting at public health facilities. The aims of the genetic analysis were to determine the prevalence and geographic distribution of antimalarial drug resistance-linked genetic mutations, as well as the genetic structure of the parasite population, likely routes of gene flow between populations, and geographic origins of parasites.

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