



# Bacterial Microbiome in Wild-Caught *Anopheles* Mosquitoes in Western Thailand

Krajana Tainchum<sup>1,2†</sup>, Chloé Dupont<sup>3,4†</sup>, Theeraphap Chareonviriyaphap<sup>2</sup>, Estelle Jumas-Bilak<sup>3,4</sup>, Michael J. Bangs<sup>2,5</sup> and Sylvie Manguin<sup>3\*</sup>

<sup>1</sup> Agricultural Innovation and Management Division, Faculty of Natural Resources, Prince of Songkla University, Songkhla, Thailand, <sup>2</sup> Center for Advanced Studies for Agriculture and Food, KU Institute for Advanced Studies, Kasetsart University, Bangkok, Thailand, <sup>3</sup> HydroSciences Montpellier, Institut de Recherche pour le Développement, CNRS, Université Montpellier, Montpellier, France, <sup>4</sup> Centre Hospitalier Universitaire, Laboratoire d'Hygiène Hospitalière, Montpellier, France, <sup>5</sup> Public Health & Malaria Control, PT Freeport Indonesia/International SOS, Kuala Kencana, Indonesia

## OPEN ACCESS

### Edited by:

Josué Martínez-de la Puente,  
Consejo Superior de Investigaciones  
Científicas (CSIC), Spain

### Reviewed by:

Guido Favia,  
University of Camerino, Italy  
Rajnikant Dixit,  
National Institute of Malaria Research,  
India

### \*Correspondence:

Sylvie Manguin  
sylvie.manguin@ird.fr

†These authors have contributed  
equally to this work

### Specialty section:

This article was submitted to  
Infectious Diseases,  
a section of the journal  
Frontiers in Microbiology

Received: 20 December 2019

Accepted: 22 April 2020

Published: 21 May 2020

### Citation:

Tainchum K, Dupont C,  
Chareonviriyaphap T, Jumas-Bilak E,  
Bangs MJ and Manguin S (2020)  
Bacterial Microbiome in Wild-Caught  
*Anopheles* Mosquitoes in Western  
Thailand. *Front. Microbiol.* 11:965.  
doi: 10.3389/fmicb.2020.00965

Among the complex microbial community living in the mosquito midgut, some bacteria (e.g., *Enterobacter* spp.) can deliver effector molecules with anti-*Plasmodium* effects suppressing the development of malaria parasites (*Plasmodium falciparum*) before the ookinete can penetrate the mosquito midgut epithelium. Despite knowledge of this phenomenon, only a few studies have defined the diversity of microbiota in wild-caught adult *Anopheles* species. The objective of this study was to analyze and compare the bacterial microbiota in different *Anopheles* species, including representatives of the primary malaria vectors in western Thailand. Wild female *Anopheles* species were sampled from malaria-endemic areas in Tak and Mae Hong Son provinces near the Thai-Myanmar border. Midgut/abdominal bacterial diversity was assessed by examining the 16S rRNA gene, V3 hypervariable region, using PCR-Temporal Temperature Gel Electrophoresis (PCR-TTGE) profiling and sequence analysis. A total of 24 bacterial genera were identified from eight *Anopheles* species. Five bacterial genera were newly reported in *Anopheles* mosquitoes (*Ferrimonas*, *Megasphaera*, *Pectobacterium*, *Shimwellia*, and *Trabulsiella*). Five genera, including *Megasphaera*, were detected exclusively in a single-malaria (*Plasmodium vivax*) infected *Anopheles minimus* and not observed in other non-infected mosquitoes. The use of PCR-TTGE provides the first characterization of the midgut bacterial microbiome present in wild adult *Anopheles* in Thailand. Evidence that microbiota might impact pathogen development (suppression) in *Anopheles* and thereby reduce the risk of pathogen transmission deserves more studies to describe the presence and better understand the biological role of bacteria in natural mosquito populations.

**Keywords:** *Anopheles* mosquitoes, malaria, bacterial microbiota, biodiversity, Thailand

## INTRODUCTION

Despite significant progress in the control of malaria throughout the country, Thailand remains malaria-endemic, particularly along the international borders with Cambodia, Lao PDR, Malaysia, and Myanmar (DDC, 2018). The vast majority of recorded malaria cases, primarily *Plasmodium vivax* (73%) and *Plasmodium falciparum* (18%), occur along the Thai-Myanmar border (70–80%), especially in Tak and Mae Hong Son provinces (DDC, 2018). Of the 79 recognized *Anopheles* species