



## Gut Bacterial Diversity in *Plasmodium*-infected and *Plasmodium*-uninfected *Anopheles minimus*

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### ABSTRACT

*Anopheles minimus* is one of the main malaria vectors in Thailand. *Plasmodium* transmission depends primarily on the success of the parasite survival in the mosquito's gut. Several factors affect the development of *Plasmodium* in the mosquito, including the gut microbiota. Here, we used culture-independent method to identify microbiota and compared the bacterial communities in the gut of *Plasmodium*-infected and *Plasmodium*-uninfected mosquitoes. Fifty-three genera within four phyla were detected and 14 of them were discovered in malaria vectors for the first time. In addition, we found that the bacterial diversity and the profile of the gut bacterial communities between the *Plasmodium*-infected and those of the uninfected mosquitoes were quite different. The result showed that the bacterial diversity in the gut of the uninfected mosquitoes was also much higher than that of the infected counterpart. Gammaproteobacteria were prevalent in the infected *An. minimus* while betaproteobacteria were the most abundant in the uninfected mosquitoes. Three genera, *Acinetobacter* in gammaproteobacteria, *Alcaligenes* and *Burkholderia* in betaproteobacteria were the core set of bacteria found in the gut of the malaria vector.

**Keywords:** *Anopheles minimus*, gut microbiome, 454 sequencing, malaria vector, *Plasmodium*

### 1. INTRODUCTION

Malaria is one of the serious public health concerns in several countries. Approximately 3.4 billion people worldwide are at risk of being infected with malaria [1]. In 2012, there were estimated 207 million cases of malaria

and 627,000 deaths [1]. Although the disease can be cured by anti-malarial drugs, the resistance of *Plasmodium* to the medicines has been found worldwide, especially in Asia [2,3]. Even though using of bed net and indoor