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Factors allowing the development of a pathogen to reach the infecting stage in a mosquito are poorly known. On the nearly 500 species of mosquitoes recorded within the *Anopheles* genus, only 60-70 are able to transmit parasites responsible for malaria. In vector-parasite interactions, the vector gut represents the first point of contact between parasites ingested and the vector epithelial surfaces. In the midgut, the parasites have the opportunity to undergo their life cycle, but of the tens of thousands *Plasmodium* gametocytes ingested by mosquitoes, less than five oocysts might be produced. The factors responsible for this drastic reduction are poorly understood. Recent studies showed that one of these factors concerns the primordial role played by the bacteria naturally present in mosquito midgut. However, studies on bacterial diversity are still rare and their objective is mainly based on the identification of bacteria to be used for biological control of malaria following genetic changes. Insects with a diverse microbiota flora seem more resistant to infections. In *Anopheles albimanus*, co-infections with the bacteria, *Serratia marcescens*, and *Plasmodium vivax* resulted in only 1% of mosquitoes being infected with oocysts, compared with 71% infection for control mosquitoes without bacteria. Bacteria present in *Anopheles* populations have a great influence on parasite transmission, it is therefore crucial to analyze its biodiversity for a better understanding of variation phenomenon of the vectorial capacity observed in time and space, as well as from one species to the other. Estimation of the bacterial biodiversity in the midgut of *Anopheles* mosquitoes, vectors of human parasites in Thailand and Vietnam was analyzed and will be discussed. The microbiota of seven different *Anopheles* species in Vietnam and Thailand was analyzed among which three and seven species are respectively malaria vectors. Three species being malaria vectors were common to both countries, *An. dirus*, *An. maculatus* and *An. sawadwongporni*, the latter two belonging to the Maculatus group. The microbiota counted 21 genera in Vietnam and 17 in Thailand. When the Enterobacteriaceae are removed the number of genera changes to 20 and 9 respectively, showing the higher bacterial biodiversity found in the *Anopheles* from Vietnam.

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