New method for researching understudied malaria-spreading mosquitoes

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Researchers at the Johns Hopkins Malaria Research Institute have developed a new method for studying the complex molecular workings of *Anopheles albimanus*, an important but less studied spreader of human malaria. *An. albimanus* carries *Plasmodium vivax*, the primary cause of malaria in humans in South America and regions outside of Africa. Unlike *Anopheles gambiae*, the genome of the *An. albimanus* mosquito has not been sequenced and since these two species are evolutionarily divergent, the genome sequence of *An. gambiae* cannot serve as an appropriate reference. The researcher's findings were published online in the journal *Molecular & Cellular Proteomics*.

"Technologies and platforms are needed to bridge the scientific gaps that could eventually spur the development of novel interventions to combat all human malarias," said study author, Rhoel Dinglasan, PhD, MPH, an assistant professor with the W. Harry Feinstone Department of Molecular Microbiology and Immunology at the Johns Hopkins Bloomberg School of Public Health. "To our knowledge, no approaches have been published that address this issue."

For the study, Dinglasan and his colleagues developed a method to compare proteins of the midgut of *An. albimanus* and *An. gambiae*. The mosquito midgut is a critical stage in the lifecycle of the malaria parasite and in the transmission of malaria to people. For *An. albimanus*, the researchers developed a seamless, integrated transcriptomic-to-proteomic approach involving assembly of the *An. albimanus* midgut transcriptome followed by acquisition of the luminal midgut microvilli

proteome.

Dinglasan added, "This comparative proteomic analysis of the midgut brush borders of two important malaria vectors, *An. gambiae* and *An. albimanus*, which we envision will be one of many comparative studies, will help researchers develop new mosquito-based targets for drugs, vaccines or other interventions that would theoretically work in blocking both *P. falciparum* and *P. vivax*."

Malaria sickens more than 250 million people worldwide resulting in over 800,000 deaths, mostly African children.

More information: "A Bioinformatics Approach for Integrated Transcriptomic and Proteomic Comparative Analyses of Model and Non-sequenced Anopheline Vectors of Human Malaria Parasites" *Molecular & Cellular Proteomics*, 2013.

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