

Scientists assemble new reference genomes of mosquitoes to fight malaria

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A research team from Virginia Polytechnic Institute and State University (Virginia Tech), George Washington University and ITMO University has presented new data for studying the behavior and physiology of two types of malaria mosquitoes. This information will help find regions of

the genome that are responsible for connection with the pathogen and for their feeding behavior. Research was published in *GigaScience* .

A total of 400 types of insects are considered to be [malaria mosquitoes](#); 30 of them are the major vectors of the disease. Malaria is caused by the parasite Plasmodium that mosquitoes transmit to humans when they bite them. In order to fight this disease, it's important to understand how the feeding behavior of dangerous and "regular" mosquitoes differ genetically. This information would help find a way to change the "diet" of particular species so that they would either stop feeding on human blood or stop transmitting parasites. Previously, scientists only had a reference [genome](#) of *Anopheles gambiae*, but now, there are also genomes of two more species—African malaria mosquitoes *Anopheles coluzzii* and *Anopheles arabiensis*.

The process of connecting multiple short zones of DNA into one long sequence is called sequence assembly. The best assemblies of a specific species are called reference genomes. It means that those are "average" genomes of an organism. With their help, scientists can determine how individuals or entire populations differ from each other.

"Assembling a mosquito's genome is a moderately difficult task. On the one hand, its genome is quite large: There are about 300 million base pairs, which is only 10 times smaller than what humans have. On the other hand, mosquitoes only have three pairs of chromosomes, whereas humans have 23. Due to the fact that one mosquito provides us with little genetic material, we used material taken from the entire colony, which means that DNA from multiple individuals was put into the sequencing machine at the same time. As a result, we can see individual features of mosquitoes that need to be neutralized in order to create a reference genome," explains Anton Zamyatin, a researcher at ITMO University's [Laboratory of Genomic Diversity](#).

Research started in 2018. Genome extraction and sequencing took place at Virginia Polytechnic Institute and State University, where the scientists have colonies of insects separated by species for experimental needs. Then, specialists from ITMO University started to assemble the genome. They also plan to work on new projects related to the sequence assembly of reference genomes for other types of [malaria mosquitoes](#).

More information: Anton Zamyatin et al. Chromosome-level genome assemblies of the malaria vectors *Anopheles coluzzii* and *Anopheles arabiensis*, *GigaScience* (2021). [DOI: 10.1093/gigascience/giab017](https://doi.org/10.1093/gigascience/giab017)

Provided by ITMO University

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