

# Genome of yellow fever/dengue fever mosquito sequenced

May 17 2007

---

Developing new strategies to prevent and control yellow fever and dengue fever has become more possible with the completion of the first draft of the genome sequence of *Aedes aegypti* mosquito by scientists led by Vishvanath Nene at The Institute for Genomic Research (TIGR) and David Severson at the University of Notre Dame. The genome is the complete set of genetic material including genes and other segments of DNA in an organism.

The research appears in the May 18, 2007 *Science Express*, in the article, "Genome Sequence of *Aedes aegypti*, A Major Arbovirus Vector." Researchers at 24 universities and other institutions worldwide contributed to the effort.

Among the co-authors are members of the Vector-Borne Infectious Disease Research Group at Virginia Tech, Zhijian (Jake) Tu, associate professor in the Department of Biochemistry; James K Biedler, biochemistry postdoctoral associate; Song Li, research specialist senior in biochemistry; and Monique Royer Coy, biochemistry graduate student; and Chunhong Mao, senior project associate with the Virginia Bioinformatics Institute at Virginia Tech.

Tu coordinated efforts with TIGR and five research laboratories in the United States, Spain, and France to annotate transposable elements (TEs) in the *Ae. aegypti* genome. TEs are segments of nucleic acids, or genetic material, that move around the genome and have a significant impact on its structure and size.

Also, Jinsong Zhu, assistant professor of biochemistry at Virginia Tech, who was a senior researcher at the University of California, Riverside, is involved in this process that has so far validated about 80 percent of the 15,419 predicted protein coding genes in *Ae. aegypti*. He explains, "An important part of this project is gene annotation which predicts numbers and locations of mosquito genes in the genome. In parallel to sequencing DNA in chromosomes, scientists have also sequenced large amounts of messenger RNAs collected from different mosquito tissues at distinct developmental stages. Matching a messenger RNA to a predicted gene will validate authenticity of this gene."

The TE team, lead by the Tu laboratory, uncovered and described more than 1,000 transposable elements, which occupy approximately 50 percent of the entire *Ae. aegypti* genome. For example, a transposable element named Feilai has more than 50,000 copies interspersed in the genome. By comparison, *Anopheles gambiae*, the malaria mosquito genome is probably less than 25 percent TEs. The *Ae. aegypti* genome is five times the size of the malaria mosquito genome.

"Although the majority of protein coding TE copies in *Ae. aegypti* appear to be degenerate, a significant number of elements have potentially active TE copies, indicating that they may be developed as tools for genetic studies of mosquitoes," Tu said.

"If you look at the genome as an ecological system, TEs are different lineages that co-evolve with the rest of the genome" said Tu. "They evolve different relationships with the genome. Some are genetic parasites; they appear to do nothing except replicate within the genome. Others are used by the host -- the individual organism's genetic machinery --to perform biological functions."

TEs may be developed as genetic tools to study the interaction between mosquitoes and pathogens, and thus may lead to controls of transmission

of disease, Tu said. Control might take the form of a genetic control, such as using TEs to carry a gene into the genome that would make the mosquito resistant to the virus and stop its role as a vector for disease. Although that scenario is challenging, the payoff is potentially great, Tu said.

"By introducing TEs in a more or less random way to see what happens to the laboratory mosquitoes, the TEs become a tool to study the genetic mechanism of mosquito-virus interaction, to help us understand mosquito biology and reveal new ways to interfere with disease transmission," Tu said.

According to the article in *Science Express*, the general failure to date of conventional disease prevention strategies for most mosquito-borne pathogens provides a strong incentive to explore and develop novel control strategies that efficiently disrupt the transmission cycle or enhance existing strategies. The *Ae. aegypti* genome sequence is expected to stimulate efforts to elucidate interactions at the molecular level between mosquitoes and the pathogens they transmit to humans.

Source: Virginia Tech

Citation: Genome of yellow fever/dengue fever mosquito sequenced (2007, May 17) retrieved 1 May 2024 from <https://phys.org/news/2007-05-genome-yellow-feverdengue-fever-mosquito.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--