

## **Fighting mosquito resistance to insecticides**

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This tropical mosquito is the vector of numerous human diseases such as yellow fever, dengue and Chikungunya. Credit: Institut de Recherche pour le Développement (IRD), N. Rahola.

Controlling mosquitoes that carry human diseases is a global health challenge as their ability to resist insecticides now threatens efforts to prevent epidemics. Scientists from the CNRS, IRD, Université Claude Bernard Lyon 1, Université Joseph Fourier in Grenoble and Institut Pasteur in French Guiana have identified new genetic markers for mosquito resistance to insecticides, which could improve its detection in the field. This work was published in *Genome Research* on 23 July 2015.

The ability of mosquitoes to resist <u>insecticides</u> represents a serious threat to the prevention of diseases such as malaria, dengue and Chikungunya.



The detection and monitoring of the resistances developed by natural mosquito populations will be essential to enabling their management in the field for as long as there are no alternatives to the use of insecticides.

Some of these resistance mechanisms remain little known. For example, genetic factors for the metabolic resistance of mosquitoes, linked to the biodegradation of insecticides by detoxification enzymes, are still poorly understood. The scientists used a novel approach involving massive DNA sequencing in order to identify the genetic bases for this resistance in the Aedes aegypti mosquito, a close cousin of the Asian tiger mosquito and the vector of dengue fever and Chikungunya in tropical regions. Indeed, rather than sequencing the entire genome of the mosquito-a costly and laborious process-the scientists used bioinformatic techniques to target more than 760 genes potentially involved in insecticide resistance. After analyzing these genes by very high-throughput sequencing, the team determined that an increase in the activity of detoxification enzymes in resistant mosquitoes was often triggered by a rise in the number of copies of genes coding for these enzymes. They were also able to demonstrate that mutations affecting these enzymes could increase the biodegradation of insecticides in resistant mosquitoes.

The researchers also observed that the biomarkers of resistance appeared to be little conserved in some continents. These findings suggest that among the large panel of detoxification enzymes acquired by mosquitoes during their evolution (sometimes more than 200 genes), some are reused by these insects to resist chemical insecticides, depending on gene flow between populations, their evolutionary history, the appearance of mutations, as well as environmental changes, such as the use of pesticides in agriculture.

These findings represent a major step forward in our understanding of the genetic mechanisms developed by <u>mosquitoes</u> to adapt to



insecticides, and provide new opportunities to detect them at an early stage (for example, using molecular tests). This will improve their control in the field, and make it possible to adapt treatments to different resistance phenomena.

This work also allowed the scientists to initiate a consortium involving more than 40 countries and ten institutions, with a view to compiling the first global map of mosquito <u>resistance mechanisms</u> to insecticides . This key initiative has already received the support of the World Health Organization (WHO).

Provided by Cold Spring Harbor Laboratory

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