

Largest genetic study of mosquitoes reveals spread of insecticide resistance across Africa

November 29 2017



Mosquito that causes malaria, *Anopheles gambiae*. Credit: NIAID, CC BY

The largest ever genetic study of mosquitoes reveals the movement of insecticide resistance between different regions of Africa and finds several rapidly evolving insecticide resistance genes. Reported today (29 November) in *Nature*, this genetic resource will be used to develop new tools for monitoring resistance and managing insecticide use, and for

designing novel control methods.

Malaria is transmitted by [mosquitoes](#) and rising resistance to insecticides is hampering efforts to control the disease. The study by researchers from the Wellcome Trust Sanger Institute and their collaborators also discovered that wild mosquitoes collected in Africa were genetically far more diverse than had been thought. This helps to explain how mosquitoes evolve insecticide resistance so quickly.

More than 200 million people are infected with the [malaria](#) parasite worldwide each year, which is transmitted by blood-sucking Anopheles mosquitoes. Malaria caused the deaths of around 429,000 people in 2015 with the majority of cases in sub-Saharan Africa.

Public health measures in Africa such as insecticide-treated bed nets and insecticide-spraying have helped reduce the numbers of malaria cases since 2000, but many mosquitoes have evolved resistance to insecticides. This is now threatening to derail [malaria control](#) in Africa.

To understand how mosquitoes are evolving, researchers working with the Anopheles gambiae 1000 genomes project sequenced the DNA of 765 wild Anopheles mosquitoes. These were taken from 15 locations across eight African countries, creating the largest data resource on natural genetic variation for any species of insect. They then examined each of the mosquito genomes.

The researchers revealed that the Anopheles gambiae mosquitoes are extremely genetically diverse compared with most other animal species. High genetic diversity enables rapid evolution and the study found 52 million small differences amongst the mosquito genomes.

Dr Mara Lawniczak, a corresponding author on the paper and Faculty at the Wellcome Trust Sanger Institute, said: "The diversity of mosquito

genomes was far greater than we expected. Such high levels of genetic variation poise mosquito populations to rapidly evolve in response to our efforts to control them whether that be with insecticides or any other control measure, including [gene drive](#)."

New strategies to control mosquitoes are being developed that use 'gene drive'- using the latest Crispr/Cas 9 genetic tools to make mosquitoes infertile or unable to carry the malaria parasite. However, this technology requires an exact match with any targeted gene. The researchers found that gene drive is unlikely to work for most mosquito [genes](#) because they are too variable in nature, however they also used the data to highlight less variable targets that are potentially more suitable for gene drive based methods to control mosquitoes.

The mosquito genomes also revealed rapid evolution of several genes that had previously been implicated in insecticide resistance. Unexpectedly, the researchers discovered many previously-unknown genetic variants within those genes that could be causing insecticide resistance. Worryingly, they showed that these genetic variants for insecticide resistance were not only emerging independently in different parts of Africa, but were also being spread across the continent by mosquito migration.

Professor Martin Donnelly, a corresponding author from the Liverpool School of Tropical Medicine and Honorary Faculty at the Wellcome Trust Sanger Institute, said: "We know that mosquito populations are rapidly evolving resistance to insecticides, which is a serious threat to the future of malaria control in Africa. We have been able to see that a diverse array of genes linked to insecticide resistance are under very strong selection, confirming that they are playing an important role in the evolution of [insecticide resistance](#) in natural mosquito populations. Our study highlights the severe challenges facing public efforts to control mosquitoes and to manage and limit [insecticide resistance](#)."

Alistair Miles, lead author from the University of Oxford and the Wellcome Trust Sanger Institute, said: "The data we have generated are a unique resource for studying how mosquito populations are responding to our current control efforts, and for designing better technologies and strategies for mosquito control in the future. More data will be needed to fill in the geographical gaps and study how mosquito populations change over time and in response to specific [control](#) interventions. However, this study demonstrates a clear path towards building a new and much-needed source of intelligence to support the campaign to eradicate malaria in Africa."

More information: Alistair Miles et al, Genetic diversity of the African malaria vector *Anopheles gambiae*, *Nature* (2017). [DOI: 10.1038/nature24995](#)

Provided by Wellcome Trust Sanger Institute

Citation: Largest genetic study of mosquitoes reveals spread of insecticide resistance across Africa (2017, November 29) retrieved 3 May 2024 from <https://phys.org/news/2017-11-largest-genetic-mosquitoes-reveals-insecticide.html>

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