

Malarial mosquitoes are evolving into new species, say researchers

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An *Aedes aegypti* mosquito feeding in Dar es Salaam, Tanzania. Image credit: Muhammad Mahdi Karim, GNU FDL.

Two strains of the type of mosquito responsible for the majority of malaria transmission in Africa have evolved such substantial genetic differences that they are becoming different species, according to researchers behind two new studies published today in the journal *Science*.

Over 200 million people globally are infected with malaria, according to the World Health Organisation, and the majority of these people are in Africa. Malaria kills one child every 30 seconds.

Today's international research effort, co-led by scientists from Imperial College London, looks at two strains of the *Anopheles gambiae*

mosquito, the type of mosquito primarily responsible for transmitting malaria in sub-Saharan Africa. These strains, known as M and S, are physically identical. However, the new research shows that their genetic differences are such that they appear to be becoming different species, so efforts to control mosquito populations may be effective against one strain of mosquito but not the other.

The scientists argue that when researchers are developing new ways of controlling malarial mosquitoes, for example by creating new [insecticides](#) or trying to interfere with their ability to reproduce, they need to make sure that they are effective in both strains.

The authors also suggest that mosquitoes are evolving more quickly than previously thought, meaning that researchers need to continue to monitor the [genetic makeup](#) of different strains of mosquitoes very closely, in order to watch for changes that might enable the mosquitoes to evade control measures in the future.

Professor George Christophides, one of the lead researchers behind today's work from the Division of Cell and Molecular Biology at Imperial College London, said: "Malaria is a deadly disease that affects millions of people across the world and amongst children in Africa, it causes one in every five deaths. We know that the best way to reduce the number of people who contract malaria is to control the mosquitoes that carry the disease. Our studies help us to understand the makeup of the mosquitoes that transmit malaria, so that we can find new ways of preventing them from infecting people."

Dr Mara Lawniczak, another lead researcher from the Division of Cell and Molecular Biology at Imperial College London, added: "From our new studies, we can see that mosquitoes are evolving more quickly than we thought and that unfortunately, strategies that might work against one strain of mosquito might not be effective against another. It's important

to identify and monitor these hidden genetic changes in mosquitoes if we are to succeed in bringing malaria under control by targeting mosquitoes."

The researchers reached their conclusions after carrying out the most detailed analysis so far of the genomes of the M and S strains of *Anopheles gambiae* mosquito, over two studies. The first study, which sequenced the genomes of both strains, revealed that M and S are genetically very different and that these [genetic differences](#) are scattered around the entire genome. Previous studies had only detected a few 'hot spots' of divergence between the genomes of the two strains. The work suggested that many of the genetic regions that differ between the M and S genomes are likely to affect mosquito development, feeding behaviour, and reproduction.

In the second study, the researchers looked at many individual mosquitoes from the M and S strains, as well as a strain called Bamako, and compared 400,000 different points in their genomes where genetic variations had been identified, to analyse how these mosquitoes are evolving. This showed that the strains appear to be evolving differently, probably in response to factors in their specific environments - for example, different larval habitats or different pathogens and predators. This study was the first to carry out such detailed genetic analysis of an invertebrate, using a high density genotyping array.

As a next step in their research, the Imperial researchers are now carrying out genome-wide association studies of [mosquitoes](#), using the specially designed genotyping chip that they designed for their second study, to explore which variations in mosquito genes affect their propensity to become infected with malaria and other pathogens.

More information: --DE Neafsey et al. Complex gene-flow boundaries among vector mosquito populations. *Science*. DOI:

10.1126/science.1193036 (2010).

--MKN Lawniczak et al. Widespread divergence between incipient *Anopheles gambiae* species revealed by whole genome sequences.

Science. DOI: 10.1126/science.1195755 (2010).

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