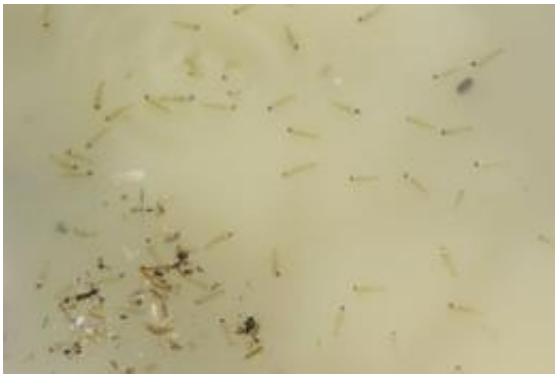


Malaria mosquitoes reveal pathogen defense strategies

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Anopheles gambiae larvae in a puddle at one the research team's field sites in western Sub-Saharan Africa.

(PhysOrg.com) -- In analyzing malaria mosquitoes in sub-Saharan Africa, a Cornell-led team of researchers finds evidence of two very different evolutionary paths in the immune systems of neighboring mosquito groups.

Genes in animal immune systems may evolve in one of two main ways in the constant fight against [pathogens](#): They may evolve diverse forms of [genes](#) (alleles) to fight a wide variety of pathogens, or when only a few pathogens dominate, they may evolve one or a few alleles that specialize against common infections.

The Cornell researchers have found evidence of both these adaptive

strategies occurring in the same immune-defense genes in different subpopulations of the human malaria vector mosquito, *Anopheles gambiae*.

The research, appearing March 8 in the open-access journal [PLoS Biology](#), focused on a cluster of genes called APL1, which are part of the mosquitoes' immune defense against malaria parasites and other pathogens. Malaria infects humans, but it also makes mosquitoes that transmit the disease sick.

"From a purely [evolutionary biology](#) perspective, seeing both of those patterns occur in a single gene is very unusual; it validates both models," said Brian Lazzaro, the study's principal investigator and a Cornell associate professor of evolutionary genetics in the Department of Entomology.

The APL1 genes of one *A. gambiae* subpopulation (the "S" population) carried 10 times more genetic diversity than typical *A. gambiae* genes. Meanwhile, a second mosquito subpopulation (the "M" population) -- which lives in the same geographic area as the "S" population -- showed little genetic diversity among APL1 alleles, indicative of recent, strong natural selection.

"In the 'M' population, we see this recent selection targeting a single or restricted set of pathogens," said Lazzaro.

No difference has been found in transmission of malaria to humans between the two populations, which led the researchers to conclude that a pathogen other than malaria had placed a strong natural selection on the "M" population to specialize its defense system.

"The two populations differ in where they lay their eggs, suggesting that there could be a pathogen in the water that infects the larvae of the 'M'

population," Lazzaro said. "Malaria parasites may be incidental here."

Furthermore, an independently published report found a related immune-defense gene, called Tep1, exhibited the same pattern of high genetic diversity in the "S" population and just a few alleles in the "M" population. Tep1 genes, which reside on a separate chromosome, express proteins that physically bind to APL1 proteins to form a disease-fighting protein complex.

"Finding this same pattern of evolution in different parts of the genome is unusual and suggests that the genes may be evolving in concert," Lazzaro said.

To vector biologists and public health researchers, these genes could be important in fighting [malaria](#).

"It's possible that the differences in genetic diversity could change disease transmission to humans by mosquitoes from these subpopulations, but there is no evidence of this so far. It could also change the susceptibility of these [mosquitoes](#) to other pathogens," Lazzaro added.

Co-authors included researchers from the Institut Pasteur in Paris, University of Minnesota, University of Bamako in Mali and Institut de Recherche pour le Developpement in Cameroon. The study was funded by the National Institutes of Health.

Provided by Cornell University

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