

## FOR IMMEDIATE RELEASE

### Press release

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# Study of wild type mosquitoes in Burkina Faso discovers new signs of insecticide resistance

## Summary

- Researchers from Target Malaria have published new data on the genomics of wild-type malaria mosquitoes in Burkina Faso on Malaria Journal: "[Whole-genome sequencing of major malaria vectors reveals the evolution of new insecticide resistance variants in a longitudinal study in Burkina Faso](#)".
- One of the main findings was the discovery of emerging new variants in genes associated with insecticide resistance, particularly in genes which are key targets for insecticides used in long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS).
- *Anopheles coluzzii* was found to be the most predominant species in the sampled villages in Burkina Faso, accounting for 53% of samples, followed by *Anopheles gambiae sensu stricto (s.s.)* with 39%, while *An. arabiensis* only comprised 8% of samples collected.

**OUAGADOUGOU, Burkina Faso, 17 October 2024** – A new scientific paper authored by a team of researchers led by Dr. Mahamadi Kientega, a medical entomologist at the Institut de Recherche en Sciences de la Santé (IRSS) in Burkina Faso, was published in Malaria Journal. Titled "[Whole-genome sequencing of major malaria vectors reveals the evolution of new insecticide resistance variants in a longitudinal study in Burkina Faso](#)", the publication is the result of a collaborative study by the Institut de Recherche en Sciences de la Santé-IRSS (Institute of Research in Health Sciences) in Bobo-Dioulasso, MalariaGEN Vector Observatory and Target Malaria. Between 2012 and 2017, mosquito samples were collected in three villages of Burkina Faso: Bana, Souroukoudinga and Pala. They sequenced the genome of these mosquitoes to study the evolution of variants associated with resistance to insecticides.

One of the main discoveries of the study is the identification of new variants in genes associated with insecticide resistance in *Anopheles* mosquitoes, the primary vectors of malaria in West Africa, and potential novel resistance mechanisms, emphasizing the importance of genomic surveillance. Variations were observed in the voltage-gated sodium channel (VGSC) and acetylcholinesterase (ACE1) genes, which are key targets for insecticides used in long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS). Signal of positive selection were identified in those genes suggesting a potential role in mosquito adaptation to vector control tools. Insecticide resistance is a major threat to the development of solutions to eliminate malaria because resistance reduces the efficacy of two of the main vector control measures that have been key to reducing malaria incidence in endemic countries: bed nets and spraying.

“Today more than ever, it is crucial to understand the genomics of mosquitoes to monitor and understand how this champion of biological evolution continues to evade vector control strategies. In response to the high coverage of insecticidal nets, mosquitoes’ biting behavior have changed in several areas in Africa and we need to start considering efficient and sustainable new vector control tools,” says Dr. Mahamadi Kientega, researcher at Institut de Recherche en Sciences de la Santé (IRSS), Burkina Faso.

### **The central role of genomic surveillance**

Long-lasting insecticidal nets (LLINs) and indoor residual spraying (IRS) are a cornerstone of current malaria interventions. **In 2023, the [Global Fund](#) distributed 227 million mosquito nets to families and covered 7.9 million households with spraying to prevent malaria cases.** Globally, an estimated 2.1 billion malaria cases and 11.7 million malaria deaths were averted in the period 2000–2022 according [World Malaria Report](#).

However, progress in reducing malaria mortality and morbidity has stalled, and the world is off track to meet the [2030 targets](#) for malaria morbidity and mortality. Intensive deployment of insecticide-based malaria vector control tools has been effective although it is resulting in the rapid evolution of phenotypes resistant to insecticides like organophosphate or pyrethroids.

This collective study on mosquito genomics involving several research partners underscores the **importance of molecular surveillance of existing insecticide resistance variants, new variants and understanding evolutionary processes underlying their emergence.**

“Detecting insecticide resistance will enable us to adapt our strategy for the fight against malaria, anticipate the loss of steam of conventional vector control

interventions and boost sustainable and innovative alternatives, such as genetically modified mosquitoes, natural symbionts and insecticidal compounds,” adds Kientega.

### **A better understanding of malaria vector population dynamics**

As part of [The \*Anopheles gambiae\* 1000 genomes project \(Ag1000G\)](#), the genome of the samples comprised of 1409 *Anopheles gambiae sensu lato* (s.l.) mosquitoes (978 females and 431 males) were sequenced. The findings provide a comprehensive analysis of genetic diversity in *Anopheles gambiae* complex species, with a particular focus on *An. gambiae s.s.*, *An. coluzzii*, and *An. arabiensis*. The results of the study uncover distinct population structures across different regions, which is important for understanding how resistance spreads and evolves geographically.

*Anopheles coluzzii* was the most predominant species found in the three villages where mosquitoes were collected. *An. coluzzii* accounts for 53% of samples, followed by *An. gambiae s.s.* with 39%, while *An. arabiensis* only comprised 8% of samples collected. *An. coluzzii* remains the most predominant species in Bana (84%) and Souroukoudinga (61%) while *An. gambiae s.s.* is prevalent in Pala (71%). Two hybrids of *An. gambiae s.s.* and *An. coluzzii* were also identified.

Analyses of the genetic diversity in *An. gambiae s.s.* and *An. coluzzii* seem to indicate low genetic differentiations and ongoing gene flow, meaning that those two species are strictly related and often mate to each other, with genes easily flowing between the two (including insecticide resistance). On the contrary, *An. arabiensis* displayed higher genetic differentiation from the other species, suggesting limited gene flow.

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### **About Target Malaria:**

Target Malaria is a not-for-profit research consortium that aims to develop and share new, cost-effective and sustainable genetic technologies to modify mosquitoes and reduce malaria transmission. Our vision is to contribute to a world free of malaria. We aim to achieve excellence in all areas of our work, creating a path for responsible research and development of genetic technologies, such as gene drive.  
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