



MARS | Mosquito-based Artemisinin Resistance Surveillance

1. Project data

Project type

interdisciplinary pilot project cross-sector project global health postdoc fellowship

Research areas involved (check all that apply)

Biomedical sciences Public health
 Social sciences and humanities Engineering and other sciences

Project duration

July 2023 – June 2025

Project team

Name	Organization	Discipline(s)
Dr. Welmoed van Loon	Charité-Universitätsmedizin Berlin	Biomedical Sciences, Epidemiology
Dr. Esto Bahizire	Université Catholique de Bukavu, DR Congo	Medicine, Public Health, Epidemiology
Janvier Bandibabone Balikubiri	Centre de Recherche en Sciences Naturelles (CRSN-LWIRO)	Entomology
Dr. Peter Dambach	Heidelberg Institute of Global Health, Universitätsklinikum Heidelberg	Public Health, Geography
Prof. Dr. med. Frank Mockenhaupt	ITMIH, Charité-Universitätsmedizin Berlin	Tropical Medicine, International Health

Case study

Introduction

The recent emergence of artemisinin partial-resistance (AR) in East Africa poses a serious public health threat for the continent. Artemisinin combination therapy (ACT) forms the cornerstone of malaria treatment and control, with no suitable replacement as of today. Fundamental for designing and evaluating AR countermeasures are adequate surveillance systems. These should provide rapid, continuous, and high-resolution data, but today's antimalarial drug surveillance in East Africa has

significant gaps. We propose to exploit blood-fed mosquitoes instead of malaria patient blood for molecular AR surveillance. This may overcome problems in sampling bias, scalability, and logistics.

Summary of the project

Our MARS project aimed to develop, evaluate and implement mosquito-based surveillance (xenomonitoring) of AR in South Kivu, eastern Democratic Republic of the Congo (DRC). The Institute of International Health, Charité Berlin, and the Centre for Tropical medicine and Global Health, Université Catholique de Bukavu, combined their expertise in malaria epidemiology. Partners from the Heidelberg Institute of Global Health (HIGH) and Centre de Recherche en Sciences Naturelles de Lwiro (CRSN-LWIRO) completed the consortium with their contributions in medical entomology, geography for public health and vector control.

The objectives were: 1) to assess how well mosquito-based surveillance of molecular markers of AR corresponds with these in malaria patients in the same region; 2) to assess sensitivity of AR marker screening when pooling the mosquito harvest; 3) to assess the prevalence of AR markers circulating in South Kivu; 4) to identify hotspots of AR and to provide MARS-guided vector control suggestions.

We enrolled 1,000 malaria patients in 13 peripheral health centers, collecting blood samples, alongside clinical and socio-economic data. In parallel, over 7,500 night-active female mosquitoes were sampled from 58 households in geographically matched areas. We developed and tested a molecular analysis method on pooled mosquitoes, analyzed patient data, and mosquito species. Molecular analysis of the mosquitoes is ongoing. We created a comprehensive map of AR markers and mosquito species in South Kivu and laid the foundations of ongoing xenomonitoring in our East African network.



Photo 1: MARS Team distributing mosquito traps © MARS/GLOHRA



Findings

- Pooled, whole mosquitoes can be used for cost-efficient molecular analysis and sensitive detection of major markers for antimalarial drug resistance. This is true for *P. falciparum* infected *Anopheles* mosquitoes as well as for other blood-fed mosquito species. The mosquito pool size should be limited to include maximum one *falciparum*-carrying mosquito. *A priori* estimation of the *falciparum* carriage rate should be done by testing a random sample of individual mosquitoes.
- 16% of *Anopheles* mosquitoes in the Kibali area, DRC, 2023, were infected with *P. falciparum*. Antimalarial drug resistance genes were successfully typed but we did not find AR markers. This analysis served as a proof-of-concept for our molecular pooling methods on field-caught mosquitoes.
- There was strong heterogeneity in odor-bait trap-caught mosquito species between households. 16% of the households accounted for 50% of all *Anopheles* mosquitoes, and 7% of these were blood-fed. Other species included *Culex* (54%) and *Mansonia* (30%). Among blood-fed *Anopheles* mosquitoes, about 20% appear positive for *P. falciparum*, further molecular analysis is ongoing.
- The validated AR marker *PfK13 A675V*, common in Uganda, was sporadically detected among malaria patients presenting at health centers north of Bukavu (<5%). The AR marker *PfK13 R561H*, which is the predominating marker in neighboring Rwanda, remains virtually absent in South Kivu.

Lessons learnt

- a. Community-based mosquito catching is possible and well accepted in the Kivu region. Regular training and evaluation of correct use of mosquito traps is required.
- b. The odor-bait traps appear to rather attract *Anopheles* mosquitoes before their blood-meal instead of after their blood meal. This may limit their usefulness for surveillance.
- c. The Mpox outbreak and conflict in eastern DRC have delayed our activities but also demonstrated how robust and versatile community-driven xenomonitoring can be. Our mosquito catching activities could in most cases continue. Xenomonitoring requires no health staff or handling of infectious blood, which proved especially valuable during the Mpox outbreak.

Materials

- Anvari D, Bandibabone J, Kudom AA, Wieser A, Bahizire E, Mockenhaupt FP, van Loon W. Scalable and cost-effective methods for xenomonitoring of *P. falciparum* and antimalarial drug resistance validated with laboratory and wild-caught mosquitoes. *Sci Rep.* 2025 Sep 23;15(1):32678. doi: 10.1038/s41598-025-20554-0.
- Training material and operating procedures with visual instructions for using odor-bait mosquito traps.
- Biobank of DNA from (unidentified) mosquito species.

Contact

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2. Contact

German Alliance for Global Health Research (GLOHRA)

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