

# **Proposed technical consultation on the role of parasite genetics in malaria surveillance to optimize response by national programmes**

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October 2018, Geneva, Switzerland

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## **Introduction**

An important role of the WHO Global Malaria Programme (GMP) is the identification of priority policy-relevant research questions and the development of normative guidance in the areas of epidemiological, entomological, insecticide and drug resistance surveillance (1-3). Increasingly, molecular epidemiology has become an important source of information on drug and insecticide resistance. With advances in parasite and mosquito genotyping methods, research into the use of parasite and mosquito genetics in understanding malaria transmission has also increased. Emerging evidence shows that mosquito genotyping can improve the understanding of mechanisms of speciation and the processes that influence the ability of mosquitoes to transmit malaria parasites to humans, leading to a better understanding of vectorial capacity and consequently better targeting of interventions (4-6). Research in parasite genotyping also indicates potential applications in the understanding of parasite gene flow, including drug resistant genes, the quantification of malaria importation risks, stratification and the description of changing transmission intensity (7-8). However, most of the work conducted in malaria genetic epidemiology remains within the realm of research and is not guided by clearly defined policy-relevant questions, with few examples of its role in improving operational decisions made by national malaria programmes.

For these reasons, GMP proposes to convene a technical consultation on the role of genetic epidemiology in our understanding of drug resistance gene flow, malaria transmission intensity and elimination surveillance. The focus of this consultation will be on parasite genetics because of the potential complexity of convening a single consultation that will be effective in discussing the priority research areas, policy and operational implications of both mosquito and parasite genetic epidemiology and surveillance.

## **Objectives**

1. Review the evidence of the role of parasite genetic epidemiology in our understanding of drug resistance gene flow, malaria transmission intensity and elimination surveillance.
2. Identify key research questions relevant to policy and operational national programme activities.
3. Discuss standards for study designs and access to data.

## Process

The technical consultation will be jointly convened by the GMP units responsible for Surveillance, Monitoring and Evaluation; Drug efficacy and Resistance; and Elimination. The Surveillance, Monitoring and Evaluation unit will provide administrative support. The technical consultation will involve up to 30 participants. It is expected that at least two representatives from MPAC will participate. Three main sessions are proposed: drug resistance gene flow (facilitated by Dr Pascal Ringwald); transmission intensity (Dr Abdisalan Noor); elimination (Dr Kimberly Lindblade). The conclusions and draft recommendations will be shared with MPAC by the first meeting of 2019.

## Timelines

It is proposed that the technical consultation is convened late January or early February 2019.

## References

1. Methods for surveillance of antimalarial drug efficacy. Geneva: World Health Organization; 2009. <http://www.who.int/malaria/publications/atoz/9789241597531/en/>
2. Global plan for insecticide resistance management in malaria vectors. Geneva: World Health Organization; 2012. <http://www.who.int/malaria/publications/atoz/gpirm/en/>
3. Malaria surveillance, monitoring & evaluation: a reference manual. Geneva: World Health Organization; 2018. <http://www.who.int/malaria/publications/atoz/9789241565578/en/>
4. Neafsey DE *et al.* Mosquito genomics. Highly evolvable malaria vectors: the genomes of 16 *Anopheles* mosquitoes. *Science*. 2015;347(6217):1258522. doi: 10.1126/science.1258522.
5. Neafsey DE, Volkman SK. Malaria Genomics in the Era of Eradication. *Cold Spring Harb Perspect Med*. 2017;doi: 10.1101/cshperspect.a025544. Review.
6. *Anopheles gambiae* 1000 Genomes Consortium *et al.* Genetic diversity of the African malaria vector *Anopheles gambiae*. *Nature*. 2017;552(7683):96-100. doi: 10.1038/nature24995
7. Bei AK *et al.* Dramatic Changes in Malaria Population Genetic Complexity in Dielmo and Ndiop, Senegal, Revealed Using Genomic Surveillance. *J Infect Dis*. 2018;217(4):622-627. doi: 10.1093/infdis/jix580.
8. Wong W *et al.* Genetic relatedness analysis reveals the cotransmission of genetically related *Plasmodium falciparum* parasites in Thiès, Senegal. *Genome Med*. 2017;24;9(1):5. doi: 10.1186/s13073-017-0398-0.
9. Rice BL *et al.* Genetic evidence that the Makira region in northeastern Madagascar is a hotspot of malaria transmission. *Malar J*. 2016;Dec 20;15(1):596. doi: 10.1186/s12936-016-1644-4.
10. Daniels RF *et al.* Modeling malaria genomics reveals transmission decline and rebound in Senegal. *Proc Natl Acad Sci USA*. 2015;112(22):7067-72. doi: 10.1073/pnas.1505691112.