

Combine data to improve malaria tracking, say scientists

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Credit: CDC

Scientists have identified a way to provide more detailed information on malaria transmission both locally and across borders, according to two new papers published today in *eLife*.

The studies, from collaborators in the US, UK, Thailand, Bangladesh, Namibia and Norway, suggest that combining data on parasite genetics

and human movement can provide greater insight on how [malaria](#) spreads among populations. This approach, applied to data from Southern Africa and Bangladesh, could allow malaria control programs to strengthen their local and regional efforts for eliminating the disease.

A global decline of malaria in recent decades has led to a push for complete elimination of malaria [parasites](#) in 21 countries by 2020. But [malaria transmission](#) differs among countries and policy-makers must focus on reducing transmission in locations where the disease remains, while protecting areas where it has been controlled from imported infections that threaten to reintroduce parasites. This is a particular concern for countries that share an international border with those that have high-transmission rates.

"Countries and regional blocs are working to identify where parasite importations are common and to pinpoint the sources of imported cases to develop more effective and targeted malaria interventions," explains Sofonias Tessema, a postdoctoral scholar at University of California, San Francisco, US, and co-first author of the Southern Africa study. "But routinely collected data, such as malaria case counts obtained from [health facilities](#), may not provide much information on importations. Malaria cases are often classified as either having been infected locally or imported based on the patient's self-report of recent travel. With only travel history data, it can be difficult to assess accurately whether malaria parasites were acquired locally or during travel."

To address this, the team used parasite [genetic data](#) to estimate the contribution of importation and compared it with human-mobility data to identify relevant sources of malaria parasites in Southern Africa.

"We found that parasites from cases near to each other were much more likely to be closely related genetically, providing evidence that the majority of malaria cases were from local transmission," says co-first

author Amy Wesolowski, Assistant Professor at Johns Hopkins Bloomberg School of Public Health, Baltimore, US.

Using genetic data from malaria parasites, the team also identified more detailed evidence of parasite connectivity over hundreds of kilometers than the other data sources, within Namibia and across the Angolan and Zambian borders. While these data are not yet routinely collected, they suggest the need to strengthen local interventions and regional coordination to successfully eliminate malaria from a critical region of Southern Africa.

Meanwhile, for the second study, researchers measured the spatial spread of malaria parasites in southeast Bangladesh. To do this, they analysed epidemiological surveillance data, travel surveys, parasite genetic data and anonymised, aggregated mobile data from their collaboration partners at Telenor Research and Grameenphone, both part of Telenor Group, Norway. "Our combined method gave us detailed insight into the direction and intensity of parasite flow between locations," explains co-first author Hsiao-Han Chang, Research Associate at Harvard T.H. Chan School of Public Health, Boston, US.

Contrary to current beliefs, the team found that frequent mixing occurs in low-transmission areas in the southwest of the Chittagong Hill Tracts region, and elimination will require interventions in addition to reducing imported infections from forested regions. "Unlike risk maps generated from clinical case counts alone, our method also distinguished areas of frequent importation as well as high transmission," adds Richard Maude, Head of Epidemiology at Mahidol-Oxford Tropical Medicine Research Unit (MORU), and a co-senior author of this study.

Altogether, the findings suggest that the ability to gather useful information from genetic data, using new methods, provides a strong case for the coordinated collection of regional [data](#) on parasite genomics

in areas where importation of malaria is a potential concern, and where efforts are being focused to eliminate the disease.

Provided by eLife

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