

Researchers uncover global, evolving, and historic make-up of malaria species

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Credit: CDC

A team of scientists has uncovered the global, evolving, and historic make-up of *Plasmodium vivax*, one of the five species of malaria that infect humans. The research, which links the spread of the parasite back to colonial seafaring, among other phenomena, underscores the challenges health experts face in controlling the parasite.

"*Plasmodium vivax* is going to be the last [malaria](#) parasite standing," observes Jane Carlton, a professor in New York University's Department of Biology, who led the study. "Our findings show it is evolving in response to anti-malarial drugs and adapting to regional differences, indicating a wide range of approaches will likely be necessary to eliminate it globally."

"The DNA data show that *P. vivax* has clearly had a different history of association with global human populations than other malaria parasites, indicating that unique aspects of its biology may have influenced the ways in which it spread around the world," adds Daniel Neafsey, associate director of the Genomic Center for Infectious Disease at the Broad Institute, who generated the data and co-led the analysis.

P. vivax causes an estimated 15.8 million clinical malaria cases each year. However, it remains understudied because it is both less lethal than other species and because it has historically been difficult to analyze since it cannot be grown in the laboratory. Another challenge is separating the parasite's DNA from human DNA.

In their study, which appears in the journal *Nature Genetics*, the research team sequenced approximately 200 DNA samples of *P. vivax* collected from patients—the largest number of *P. vivax* genomes sequenced to date—in 11 countries, including Brazil, Colombia, India, Mexico, Myanmar, Papua New Guinea, Peru, and Thailand. The scientists were able to separate *P. vivax* DNA from its human host by using a set of unique 'sticky baits' that captured the parasite DNA, enabling the human DNA to be washed away.

The researchers collected patient samples through the International Centers of Excellence for Malaria Research, a global network of independent research centers in malaria-endemic settings that provide knowledge, tools, and evidence-based strategies to support in-country

researchers working in a variety of settings, especially within governments and healthcare institutions.

The sequencing of the parasite's genome offered an array of new insights into the nature of *P. vivax* as it exists today and also served as a "genetic history book" of the studied regions:

- Central and South American *P. vivax* populations are very genetically diverse and distinct from all other contemporary *P. vivax* populations, suggesting that New World parasites may have been introduced by colonial seafarers and represent a now-eliminated European parasite population.
- Contemporary African and South Asian *P. vivax* populations are genetically similar, suggesting that South Asian *P. vivax* populations may have genetically mingled with European lineages during the colonial era—or, alternatively, reflect ancient connections between human populations in the Eastern Mediterranean, Middle East, and Indian subcontinent.
- The relatively homogeneous genetic makeup of *P. vivax* in Mexico reflects a steady decline of the disease in this country over the last decade, falling to under 10,000 cases.
- By contrast, the Papua New Guinea (PNG) population of *P. vivax* is very diverse relative to other *P. vivax* populations, with implications for developing different methods of control in this region of the world.
- *P. vivax* is significantly more genetically diverse than the more widely studied and deadlier malaria species *P. falciparum*, which may make it more elusive to methods of control and thus more difficult to eliminate.
- Resistant forms of two genes associated with antimalarial drug resistance have swept through the global population.
- Several genes were identified as adapting to regional differences in the human host and mosquito vector—for example, a gene

involved in evasion of the mosquito immune response that enabled the species to successfully adapt to development and transmission in New World mosquito species.

More information: Population genomics studies identify signatures of global dispersal and drug resistance in *Plasmodium vivax*, *Nature Genetics*, [DOI: 10.1038/ng.3588](https://doi.org/10.1038/ng.3588)

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