

Sequencing of malaria genomes reveals challenges, opportunities in battle against parasite

August 5 2012

Genetic variability revealed in malaria genomes newly sequenced by two multi-national research teams points to new challenges in efforts to eradicate the parasite, but also offers a clearer and more detailed picture of its genetic composition, providing an initial roadmap in the development of pharmaceuticals and vaccines to combat malaria.

The research appears in two studies published in the latest issue of the journal *Nature Genetics*. They focus on *Plasmodium vivax* (*P. vivax*), a species of malaria that afflicts humans and the most prevalent human malaria parasite outside Africa, and *Plasmodium cynomolgi* (*P. cynomolgi*), a close relative that infects Asian Old World monkeys.

"The bad news is there is significantly more [genetic variation](#) in *P. vivax* than we'd thought, which could make it quite adept at evading whatever arsenal of drugs and vaccines we throw at it," said Professor Jane Carlton, senior author on both studies and part of New York University's Center for Genomics and [Systems Biology](#). "However, now that we have a better understanding of the challenges we face, we can move forward with a deeper analysis of its genomic variation in pursuing more effective remedies."

In one study, the researchers examined *P. vivax* strains from different geographic locations in [West Africa](#), South America, and Asia, providing the researchers with the first [genome](#)-wide perspective of

global variability within this species. Their analysis showed that *P. vivax* has twice as much [genetic diversity](#) as the world-wide Plasmodium falciparum (*P. falciparum*) strains, revealing an unexpected ability to evolve and, therefore, presenting new challenges in the search for treatments.

The second study, performed jointly with Professor Kazuyuki Tanabe at Osaka University, Japan, sequenced three genomes of *P. cynomolgi*. The researchers compared its genetic make-up to *P. vivax* and to Plasmodium knowlesi (*P. knowlesi*), a previously sequenced malaria parasite that affects both monkeys and humans in parts of Southeast Asia.

Their work marked the first time *P. cynomolgi* genomes have been sequenced, allowing researchers to identify genetic diversity in this parasite. Its similarity to *P. vivax* means that their results will also benefit future efforts to understand and fight against forms of malaria that afflict humans.

"We have generated a genetic map of *P. cynomolgi*, the sister species to *P. vivax*, so we can now push forward in creating a robust model system to study *P. vivax*," explained Tanabe. "This is important because we can't grow *P. vivax* in the lab, and researchers desperately need a model system to circumvent this."

More information: DOI: 10.1038/ng.2373 , DOI: 10.1038/ng.2375

Provided by New York University

Citation: Sequencing of malaria genomes reveals challenges, opportunities in battle against parasite (2012, August 5) retrieved 26 April 2024 from <https://medicalxpress.com/news/2012-08-sequencing-malaria-genomes-reveals->

[opportunities.html](#)

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.