

Scientists complete the world's first in-depth study of the malaria parasite genome

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Groundbreaking research done at Singapore's Nanyang Technological University's (NTU) School of Biological Sciences (SBS) could lead to the development of more potent drugs or a vaccine for malaria, which is transmitted to humans by infected mosquitoes and kills up to three million people each year.

Assistant Professor Zbynek Bozdech and his team of researchers, including graduate students and post-doctorals from SBS' Division of Genomics & Genetics, have scored a world first in successfully using transcriptional profiling to uncover hitherto unknown gene expression (activity) patterns in [malaria](#).

The research team's breakthrough made the January 2010 edition of the top-ranked journal, *Nature Biotechnology*, which is a satellite publication of *Nature*, the world's leading peer-reviewed journal.

Transcriptional profiling is the measurement of the activity of thousands of genes at once, to create a global picture of cellular function. These profiles can, for example, distinguish between cells that are actively dividing, or show how the cells react to a particular treatment.

This outcome in infectious disease pathology could potentially be the decade's big breakthrough as it has yielded critical information about how the [malaria parasite](#) *Plasmodium falciparum* - the most deadly form of malaria - responds to existing compounds with curative potential.

The genome or the complete DNA content of the *Plasmodium falciparum* has about 5,300 genes. Up till now, scientists have a good understanding of the gene functions for only about half of the more than 5,000 genes. Using transcriptional profiling, Asst Prof Zbynek Bozdech's team has successfully uncovered the gene functions for almost the entire genome, with more than 90 percent of the [gene functions](#) from the previously unknown half now better understood.

"Drawing on our findings, pharmaceutical companies could explore ways to design a drug that targets the weakest link," said Asst Prof Bozdech of his research which was supported with S\$900,000 in grants from Singapore's Ministry of Education and the National Medical Research Council. "We have predicted all the genes that could be used for a vaccine as well," he said.

Researchers at Germany's renowned institute for tropical diseases, the Bernhard Nocht Institute for Tropical Medicine, have validated the research findings, which are expected to provide exciting new insights into parasite biology.

"The successful NTU-BNI joint project has led to the creation of the world's first database to predict the functions of more than 2,500 genes of the malaria parasite previously unknown. The database would be useful to scientists around the world who are developing new vaccines and drugs," says Dr. Tim Gilberger, Head, Malaria Research at BNI.

Preventing malaria infection is important because resistance to anti-malarial drugs is a growing problem worldwide. There is currently no vaccine for malaria, which is widespread in poorer countries where it remains a hindrance to economic development. Also of growing concern to scientists is the confirmation of the first signs of resistance to the only affordable treatment left in the global medicine cabinet for malaria: Artemisinin.

In successfully using transcriptional profiling to study the behavior of the malaria parasite, NTU's researchers have ventured into the unknown and paved the way for future breakthroughs in healthcare.

"The wealth of new information arising from our extensive four-year study is a major contribution to the worldwide effort to better understand and treat malaria," said Prof Peter Rainer Preiser, Deputy Director of NTU's BioSciences Research Centre and a member of the NTU research team.

Provided by Nanyang Technological University

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