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SciencePortal ASEAN

January 2026

Translated from Japanese

AI analysis reveals protein interactions in malaria parasites

Researchers at Nanyang Technological University (NTU) in Singapore announced that they have used a new method to comprehensively analyse the interactions of protein complexes in the malaria parasite, revealing numerous previously unknown interactions. The research results were published in the academic journal *Nature Microbiology*.

Malaria remains a global health challenge, claiming the lives of more than 500,000 people each year. The rise of parasites resistant to antimalarial drugs also threatens disease control. The most lethal form of malaria is caused by the parasite *Plasmodium falciparum*. This parasite produces more than 5,200 proteins, and interactions between proteins at each stage of its life cycle are involved in pathogenicity. However, the functions and molecular interactions of approximately half of these proteins remain unknown.

To investigate these interactions, the research team developed a method called "Meltome-Assisted Protein Complex Profiling (MAP-X)" that integrates artificial intelligence (AI). First, they measured protein stability upon heating using thermal proteome profiling (TPP) and noted that interacting proteins exhibit similar behaviour. By analysing the TPP data using AI, they were able to compare and monitor a large number of proteins simultaneously.

MAP-X analysis identified more than 20,000 protein interactions across seven stages of the *P. falciparum* life cycle in human blood. "MAP-X not only confirmed known protein complexes, but also uncovered new parasite-specific protein complexes and biochemical pathway blueprints," said Professor Zbynek Bozdech, the paper's last author. "By characterising protein complexes, we can identify new targets for the treatment of drug-resistant malaria," explained first author Dr. Samuel Pazicky. Professor Tim Gilberger, who co-led the study, also noted that MAP-X can reveal previously undescribed interactions and stage-specific dynamics.

The research team plans to use MAP-X to investigate the effects of antimalarial drugs on the protein complex.

https://spap.jst.go.jp/asean/news/260103/topic_na_03.html