Malaria parasite’s behaviour mapped

The team of researchers from NTU who have mapped the behaviour of the genes of the most deadly malaria parasite comprises (from left) Ms Ramya Ramadoss, Mr Bernardo Feth, Ms Liang Kek Yee, Assistant Professor Zbynek Bozdech, Ms Sachel Mok, Ms Balbir Chhaal, Ms Sabna Cheemadan, Ms Luah Yen Hoon and Ms Liu Bao Shan. ST PHOTO: LAU FOOK KONG

NTU team’s breakthrough will help in drug development for treatment against the disease

By Victoria Vaughan

The secrets of the most deadly malaria parasite have been unravelled by scientists at Nanyang Technological University (NTU), raising hopes that years of stagnation in drug development for the disease can end.

Plasmodium falciparum is one of four malaria parasites in existence, and is responsible for the majority of cases of the disease in Africa, and about half of the cases in the Asia-Pacific.

The team at NTU has mapped the behaviour of the 5,300 genes of the parasite. Previously, only half the genes were understood. The discovery was reported in last month’s edition of the journal Nature Biotechnology.

The lead researcher, Assistant Professor Zbynek Bozdech, originally from the Czech Republic, explained that scientists often do not know how exactly a drug works.

By using a controversial technique called transcriptional profiling, which measures the activity of thousands of genes at once, he and his team have found out how the genes of the parasite react to drugs, which would help pharmaceutical companies in future drug development.

Said Prof Bozdech, 42, who is an expert in the field of transcriptional profiling: “Pretty much the hardest thing was writing my grant proposal, as people didn’t think this technique would work due to negative results in the past. But we didn’t give up. Before this study, we did not know how more than 50 per cent of the genes in the parasite function. Now, by characterising their activity, we can look at possible targets for new drugs.”

The urgency for new drugs to target malaria is growing, due to the rapid spread of resistance to anti-malaria treatment and the lack of vaccines to prevent infection.

“Pharmaceutical companies can also use transcriptional profiling to look at how their drugs work and see if they are effective for malaria treatment and prophylaxis,” added Prof Bozdech.

The work took about four years to complete, and was verified by a laboratory in Germany with expertise in cell biology.

However, Prof Bozdech will continue his work, as he seeks to understand more about the behaviour of the genes. He aims to take his research into the field – Cambodia and Thailand – to look at the disease in patients.

“We have just looked at a small part of the disease’s cycle: when it enters the red blood cells, but there are other stages where it enters the liver and when it is in the mosquito which we want to understand,” he said.

Although his research helps with efforts to find a cure or a vaccine, its impact will be felt only in about 10 years – the average time it takes to develop a drug.

“Development of drugs for malaria hit a wall 10 years ago, and now existing drugs are losing their efficacy. To move forward, we need to understand the biology of the parasite,” Prof Bozdech said.

Mr Thierry Diagana, who heads the malaria programme at the Novartis Institute for Tropical Diseases, said: “This work further advances our understanding of the molecular events within the parasite that are induced by standard drug treatments. In the future, the pathways and genes identified could help design more effective and better drugs.”

Dr Laurent Renia, from the Laboratory of Malaria Immunobiology at the Singapore Immunology Network, said: “This is a very important piece of work. It opens new directions for the development of potent drugs against malaria.”

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