

MEDIA RELEASE

Thursday 26 January 2017

Scientists complete the genome sequences of malaria parasites

An international team of scientists has sequenced the genomes of the final two species of malaria parasites. The findings have important implications for malaria eradication worldwide and will help researchers to develop new drugs and a vaccine.

The results of the study have been published today in the highly prestigious journal *Nature*.

The research was led by a team from the Wellcome Trust Sanger Institute in the United Kingdom and involved collaborators from QIMR Berghofer Medical Research Institute, and the Menzies School of Health Research.

Malaria is caused by one of five different species of *Plasmodium* parasites, which are spread to humans by the female *Anopheles* mosquito. The genomes of three of the species are relatively well studied, especially *Plasmodium falciparum*, the most common malaria parasite.

However, very little was known about *Plasmodium malariae* and *Plasmodium ovale*, which are believed to cause up to five per cent of malaria cases, or an estimated 10 million cases, worldwide each year. These species can remain dormant in humans for years.

By comparing these new genomes with those of the three malaria parasites already sequenced, the researchers identified genes that could be involved in human infection and in adapting to the human host. They found that up to 40 per cent of the *Plasmodium malariae* and *Plasmodium ovale* genomes contained genes that probably allowed the parasites to evade the human immune system.

Professor James McCarthy from QIMR Berghofer said the findings would enable better surveillance and diagnosis of malaria.

“Although these two species of parasites are rarer and less lethal than *Plasmodium falciparum*, they are likely to be much more difficult to eliminate,” Professor McCarthy said.

“It’s crucial that we develop better tools to diagnose these parasites, as well as drugs and vaccines to control them.

“Having these genomes sequenced should help with the development of a vaccine and improved diagnostic tools, and should also help to ensure that drugs work against the parasites.”

Professor Ric Price from the Menzies School of Health Research said the study had significantly added to the available body of knowledge on malaria.

“It is very difficult to study these parasites because they can’t be grown in the lab,” Professor Price said.

“In this study we isolated the parasites from blood samples directly from malaria patients and determined these final *Plasmodium* genome sequences,” Professor Price said.

“This will help us understand the evolution of the *Plasmodium* species, and how these parasites can survive undetected in patients’ blood for long periods of time.”

P. ovale actually consists of two distinct species, *Plasmodium ovale wallikeri* and *Plasmodium ovale curtisi*. The authors showed that the split between these species was ancient and occurred long before the much more virulent *P. falciparum* emerged.

The researchers also sequenced *Plasmodium* parasites taken from chimpanzees living in a sanctuary in Gabon. They compared these to the human samples, and to existing data from other *Plasmodium* parasite infections in chimpanzees, which offered insights into how malaria parasites have adapted to different host species.

The study’s lead author, Dr Thomas Dan Otto from the Sanger Institute, said the study provided long-awaited reference genomes for the malaria research community.

“The parasites are present in malaria zones worldwide yet researchers have limited knowledge about their biology,” Dr Otto said.

“The genomes of these more neglected species will enable the development of tools to study malaria transmission and spread, which will be essential to achieve the goal of complete malaria eradication.”

Read the paper in [Nature](#).

- ENDS -

Media contacts:

Menzies School of Health Research

Paul Dale	Claire Addinsall
Senior communications officer	Communications manager
(08) 8946 8658	(08) 8946 8680 / 0448 512 576
communications@menzies.edu.au	

QIMR Berghofer

Siobhan Barry
media@qimrberghofer.edu.au
(07) 3845 3919

Menzies School of Health Research

Menzies School of Health Research is one of Australia’s leading medical research institutes dedicated to improving Indigenous, global and tropical health. Menzies has a history of over 30 years of scientific discovery and public health achievement. Menzies works at the frontline, joining with partners across the Asia-Pacific as well as Indigenous communities across northern and central Australia. Menzies collaborates to create new knowledge, grow local skills and find enduring solutions to problems that matter.

Menzies’ work in tropical health is funded by the National Health Medical Research Council and Department of Foreign Affairs and Trade, building translational research capacity in the north of Australia and with collaborative partners across the Asia-Pacific.

QIMR Berghofer

QIMR Berghofer is a world-leading medical research institute in Brisbane, Australia. It has established an international reputation for research excellence and consistently rates in Australia's top two medical research institutes. QIMR Berghofer's research is focused on cancer, infectious diseases, mental health and chronic disorders. The institute is conducting clinical trials of promising malaria drugs using funding from Medicines for Malaria Venture (MMV).

The Wellcome Trust Sanger Institute

The Wellcome Trust Sanger Institute is one of the world's leading genome centres. Through its ability to conduct research at scale, it is able to engage in bold and long-term exploratory projects that are designed to influence and empower medical science globally. Institute research findings, generated through its own research programmes and through its leading role in international consortia, are being used to develop new diagnostics and treatments for human disease. <http://www.sanger.ac.uk>