Genome sequences of 2 malaria parasites defined

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Professor Alan Cowman, Professor Brendan Crabb, Dr Paul Gilson and Dr Toby Sargeant are WEHI members of international research teams that have made significant discoveries about two deadly malaria parasites, *Plasmodium knowlesi* and *Plasmodium vivax*.

Cowman and Sargeant have contributed to defining the genome sequence of the malaria parasite *P. knowlesi*, which has recently been recognised as a major malaria pathogen of humans. Concurrently, Crabb, Gilson and Sargeant have participated in the genome sequencing of *P. vivax*, a form of malaria that causes a severely debilitating and sometimes fatal form of the disease.

The natural host of *P. knowlesi* is the kra monkey, but it has now been established that the parasite is capable of infecting humans. Evidence from the field suggests that human infections by *P. knowlesi* in South East Asia have been widely misdiagnosed as infections by a comparatively more benign malaria parasite, *P. malariae*. This has led to unsuitable treatments being prescribed for *P. knowlesi* victims.

P. knowlesi is the first monkey malaria parasite to be genetically described. It provides new research opportunities for comparisons with the recently completed *P. vivax* genome and other sequenced *Plasmodium* genomes. Establishing similarities and differences between the parasites' genomes will assist in the selection of genetic targets for vaccine and drug development.

The notorious malaria parasite *P. falciparum* is by far the most lethal strain, causing up to 75% of malaria infections and 90% of malaria's three million annual fatalities. The next most deadly strain is *P. vivax*.

The final three *Plasmodium* strains - *malariae*, *ovale* and *knowlesi* – are certainly dangerous, but considerably less virulent than *falciparum* and *vivax*.

P. vivax is the major cause of malaria outside Africa, being endemic in the wet tropical regions of Asia and Central and South America. The form of malaria caused by *P. vivax* causes recurring bouts of severe and incapacitating illness, sometimes leading to death.

P. vivax can be transmitted during cooler seasons and in more temperate climates not tolerated by *P. falciparum*. This extends the reach of *P. vivax* to half of the world's population. To add to this difficult scenario, drug resistance in *P. vivax* is becoming more widespread, hindering the management of clinical cases.

As with *P. knowlesi*, the definition of the genome of *P. vivax* will enable fresh research into its distinctive biological features, which will in turn help to determine genetic targets for the development of new drugs and vaccines.

The research papers were published in the prestigious international journal *Nature* on 9 October 2008.

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