Unveiling malaria's 'invisibility cloak'

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The discovery by researchers from the Walter and Eliza Hall Institute of a molecule that is key to malaria's 'invisibility cloak' will help to better understand how the parasite causes disease and escapes from the defenses mounted by the immune system.

The research team, led by Professor Alan Cowman from the institute's Infection and Immunity division, has identified one of the crucial molecules that instructs the parasite to employ its invisibility cloak to hide from the immune system, and helps its offspring to remember how to 'make' the cloak.

In research published today in the journal Cell Host and Microbe, Professor Cowman and colleagues reveal details about the first molecule found to control the genetic expression of PfEMP1 (Plasmodium falciparum erythrocyte membrane protein 1), a protein that is known to be a major cause of disease during malaria infection.

"The molecule that we discovered, named PfSET10, plays an important role in the genetic control of PfEMP1; an essential parasite protein that is used during specific stages of parasite development for its survival," Professor Cowman said.

"This is the first protein that has been found at what we call the 'active' site, where control of the genes that produce PfEMP1 occurs. Knowing the genes involved in the production of PfEMP1 is key to understanding how this parasite escapes the defenses deployed against it by our immune system," he said.

PfEMP1 plays two important roles in malaria infection. It enables the parasite to stick to cells on the internal lining of blood vessels, which prevents the infected cells from being eliminated from the body. It is also responsible for helping the parasite to escape destruction by the immune system, by varying the genetic code of the PfEMP1 protein so that at least some of the parasites will evade detection. This variation lends the parasite the 'cloak of invisibility' which makes it difficult for the immune system to detect parasite-infected cells, and is part of the reason a vaccine has remained elusive.

Professor Cowman said identification of the PfSET10 molecule was the first step towards unveiling the way in which the parasite uses PfEMP1 as an invisibility cloak to hide itself from the immune system. "As we better understand the systems that control how the PfEMP1 protein is encoded and produced by the parasite, including the molecules that are involved in controlling the process, we will be able to produce targeted treatments that would be more effective in preventing malaria infection in the approximately 3 billion people who are at risk of contracting malaria worldwide," he said.

Each year more than 250 million people are infected with malaria and approximately 655,000 people, mostly children, die. Professor Cowman has spent more than 30 years studying Plasmodium falciparum, the most lethal of the four Plasmodium species, with the aim of developing new vaccines and treatments for the disease.

Provided by Walter and Eliza Hall Institute