

FUNDING PROGRAM FOR NEXT GENERATION WORLD-LEADING RESEARCHERS

Project Title: Development of new method for identification of drug resistance genes from malaria parasites

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1. Background of research

Malaria is caused by infection with the parasitic protozoan, *Plasmodium spp*, and is a major public health problem that contributes significantly to global mortality. At this point, no effective vaccines are available to prevent this infectious disease and management therefore relies on drug treatment. However parasite resistance to most drugs has increased globally, rendering these drugs useless in most malaria-endemic areas. Therefore, the prevention of the spread of drug resistant parasite is important issue in malaria control.

2. Research objectives

Mutation in particular genes confer the resistance to the parasites. If the genes responsible for the resistance could be identified, it will be possible to diagnose the patient based on their sequence information and then treat each of them with suitable drugs. But there have been no effective methods to identify them yet. In this project, we aim to develop the robust method for the identification of the resistance genes by using the Plasmodium artificial chromosome. We further plan to identify them from the field-isolated parasites in Thailand by using this developed method.

3. Research characteristics (incl. originality and creativity)

The artificial chromosome, which consists of three essential elements, the centromere, the telomere and the replication origin, is an attractive genetic tool for the molecular biology-based study of eukaryotes. The Plasmodium artificial chromosome is first developed by Mie University research group and is new genetic tool for the malaria research. The identification of drug resistance genes by using the artificial chromosome technology is an innovative attempt with no precedent.

4. Anticipated effects and future applications of research

The success of our project will promote the identification of novel drug resistance genes. These resistance genes could be utilized as molecular markers for the development of an accurate and rapid diagnostic method, which could be used to select the appropriate drugs for an individual patient and produce more effective treatments. Furthermore, functional analysis of the product of drug resistance genes will reveal the resistant mechanism, leading to the development of new antimalarial drugs.