POLYMORPHISMS OF PARTIAL MEROZOITE SURFACE PROTEIN-1 (MSP-1) IN *PLASMODIUM* SPECIES ISOLATED FROM SABAH

GEOFFREY CHUNG WEI JEI

PERPUSTAKAAN
UNIVERSITI MALAYSIA SABAH

BIOTECHNOLOGY RESEARCH INSTITUTE

UNIVERSITI MALAYSIA SABAH

2014

POLYMORPHISMS OF PARTIAL MEROZOITE SURFACE PROTEIN-1 (MSP-1) IN *PLASMODIUM* SPECIES ISOLATED FROM SABAH

GEOFFREY CHUNG WEI JEI

PERPUSTAKAAN
UNIVERSITI MALAYSIA SABAH

DISSERTATION SUBMITTED IN PARTIAL FULFILLMENT FOR THE DEGREE OF MASTER OF SCIENCE

BIOTECHNOLOGY RESEARCH INSTITUTE

UNIVERSITI MALAYSIA SABAH

2014

ABSTRACT

Malaria is a mosquito-borne infectious disease caused by parasitic *Plasmodium* species and resistance to anti-malarial medicines has been documented. Therefore, it is vital to develop malaria vaccine. One of the vaccine candidate antigens is merozoite surface protein-1 (MSP-1). This study was carried out to determine the genetic diversity of *msp-1* gene especially C-terminal region of *Plasmodium falciparum*, *vivax* and *knowlesi* in Sabah. Genomic DNA was extracted from malaria infected blood samples and species-specific nested PCR was carried out to identify *Plasmodium* species. Three independent PCR were used to amplify the *msp-1* gene of the three *Plasmodium* species. Gel purification of PCR product was performed prior to sequencing. Block 2 and C-terminal region of MSP-1 of ten *P. falciparum* isolates were sequenced. Six *P. knowlesi* isolates and three *P. vivax* isolates were sequenced for C-terminal region of MSP-1. Statistical analysis was carried out in C-terminal MSP-1_{19} region for *P. falciparum*, *P. vivax* and *P. knowlesi*. Allelic variation of block 2 of *Pfmsp-1* of Sabah isolates also been characterized and indicated that all *Pfmsp-1* isolates are consists of MAD20-type strain. The allelic variation of *Pfmsp-1* of Sabah isolates were E-TSR-L and Q-KNG-F. By comparing the rate of non-synonymous versus synonymous substitutions, the analytical results showed that MSP-1_{19} of *P. falciparum* and *P. knowlesi* is under positive natural selection while purifying selection is acting on MSP-1_{19} of *P. vivax*. No new allelic variation of *P. falciparum* MSP-1_{19} was observed among the Sabah isolates as the two allelic variants of Sabah isolates were previously reported. In conclusion, these results have provided a general view of polymorphism and allelic variation for *P. falciparum* in Sabah and complement with the existing database on the *Pfmsp-1_{19}*. Further studies are required to determine the allelic variation of *P. vivax* and *P. knowlesi* .

UNIVERSITI MALAYSIA SABAH

ABSTRAK

POLIMORFISME BAGI MEROZOITE SURFACE PROTEIN-1 (MSP-1) SEPARA DI *PLASMODIUM* SPESIS ISOLEK DARI SABAH

Malaria ialah satu penyakit berjangkit bawaan nyamuk dan berpunca daripada spesis parasit *Plasmodium*. Rintangan kepada ubat-ubat antimalaria telah didokumenkan. Oleh itu, penciptaan vaksin malaria sangat penting. Salah satu calon antigen vaksin ialah merozoite surface protein-1. Kajian ini dijalankan unuk menentukan kepelbagaian genetik *msp-1* terutama bahagian C-terminal *Plasmodium falciparum*, *P. vivax* and *P. knowlesi* di Sabah. DNA parasit diekstrak dari malaria sampel and spesis-spesifik PCR dijalankan bagi mengenalpasti spesis *Plasmodium*. Tiga PCR yang berlainan digunakan untuk memperbanyakkan *msp-1* bagi tiga spesis *Plasmodium*. Penulenan gel produk PCR dijalankan. Sepuluh sampel *P. falciparum* dijujukan di blok 2 dan bahagian C-terminal MSP-1. Enam sampel bagi *P. knowlesi* dan tiga sampel bagi *P. vivax* juga di bahagian C-hujung MSP-1. Analisis statistik dijalankan bagi MSP-1_{19} untuk *P. falciparum, P. vivax* dan *P. knowlesi*. Kelainan alel blok 2 menunjukkan semua *Pfmsp-1* sampel dari Sabah terdiri daripada jenis MAD20. Dengan membandingkan kadar bukan sinonim dan penggantian sinonim, keputusan analisis menunjukkan bahawa MSP-1_{19} bagi *P. falciparum* dan *P. knowlesi* di bawah pemilihan semula jadi manakala pemilihan negatif bertindak di MSP-1_{19} bagi *P. vivax*. Pemerhatian menunjukkan tidak ada alel baru bagi *Pfmsp-1_{19}* dari Sabah. Akhir sekali, keputusan kajian ini telah menyediakan maklumat tentang polimorfisme bagi *P. falciparum* di Sabah. Lebih banyak kajian diperlukan bagi menentukan kelainan alel dan polimorfisme bagi *P. vivax* dan *P. knowlesi* .

UNIVERSITI MALAYSIA SABAH