ABSTRACT

PENDAHULUAN. Malaria masih menjadi permasalahan kesehatan di Indonesia saat ini. *P. falciparum* merupakan salah satu spesies dari *Plasmododium* parasit malaria yang menimbulkan gejala berat pada penderita. Upaya pengendalian dan pencegahan terhadap malaria terhambat oleh resistensi terhadap obat anti malaria dan insektisida sehingga vaksin malaria sangat dibutuhkan. *Merozoit surface protein-1* (msp-1), *merozoit surface protein-2* (msp-2) dan *glutamate rich protein* (glurp) adalah antigen merupakan kandidat vaksin malaria tahap darah yang potensial. Namun variasi genetik ini menghambat pengembangan vaksin yang evektif. Selain itu, variasi genetik pada populasi merupakan salah satu indikator penting untuk mengetahui intensitas penularan malaria di suatu lokasi penelitian. Penelitian ini bertujuan untuk mengidentifikasi variasi genetik pada gen msp-1, msp-2 dan glurp dari isolat *P. falciparum* di Kabupaten Merauke Provinsi Papua.
METODE. Isolasi DNA dari *dried blood spoot* (DBS) pada pasien yang terinfeksi *P. falciparum* yang diambil di RSUD Merauke Provinsi Papua selama bulan Mei 2019 – Juli 2019. Isolat DNA tersebut kemudian diamplifikasi untuk *Nested Polymerase Chain Reaction* (PCR) menggunakan primer spesifik.
HASIL. Genotyping berdasarkan PCR menghasilkan 51 sampel DBS yang terinfeksi *P. falciparum* dapat diidentifikasi mengandung gen msp-1, msp-2 dan glurp. Ditemukan 39 varian alel gen msp-1, 36 gen alel msp-2 dan 18 alel gen glurp. Sebanyak 98,04% dari isolate *P. falciparum* merukan infeksi multigenotype, rata-rata *multiplicity of infection* (MOI) adalah 2,65.
KESIMPULAN. Terdapat variasi genetik yang tinggi dari *P. falciparum* msp1, msp-2 dan glurp dari penderita malaria di Kabupaten Merauke Provinsi Papua. Tingginya infeksi multigenotype dan besarnya MOI menunjukkan tingginya penularan malaria pada lokasi penelitian tersebut.

Kata Kunci: *Plasmodium falciparum*, msp-1, msp-2, glurp, genotyping, PCR

ABSTRACT

BACKGROUND. Malaria is still a leading health concern in Indonesia until now. *P. falciparum* is one of species from malaria parasite *Plasmodium* that causes severe symptoms in patients. Control and prevention of malaria is limited because of resistance that is developed towards anti-malarial and insecticide drugs, therefore malarial vaccine is crucially needed. Merozoite surface protein-1 (msp-1), merozoit surface protein-2 (msp-2) and glutamate rich protein (glurp) are potential antigens for malarial vaccine, mainly for parasites in the blood. However, genetic variation limits an effective vaccine development. Furthermore, genetic variation in a population is one of important indicators to determine malaria transmission intensity at a research site. This research aimed to identify genetic variation on msp-1, msp-2 and glurp genes from *P. falciparum* isolate in Merauke, Papua Province.

METHODS. Dried blood spot (DBS) of *P. falciparum*-infected patients were collected at Merauke General Hospital, Papua Province from May 2019-July 2019. DNA isolates were then amplified for Nested Polymerase Chain Reaction (PCR) using specific primer for Pfmsp-1, Pf-msp-2 and glurp of gene loci.

RESULTS. PCR-based genotyping resulted in 51 DBS of *P. falciparum*-infected samples contained 39 msp-1, 26 msp-2, and 18 glurp variants of gene alleles. All *P. falciparum* isolates, 98.04% were multigenotype infection, mean of multiplicity of infection (MOI) was 2.65.

CONCLUSION. A high genetic variant of msp1, msp-2 and glurp of *P. falciparum* from malaria patients in Merauke, Papua Province indicated a high rate of multigenotype infection and MOI suggested a high malaria transmission at this research site.

Keywords: *Plasmodium falciparum*, msp-1, msp-2, glurp, genotyping, PCR