polymorphisms in the pfcrt and pfmdr1 genes in plasmodium falciparum isolates from south sumatera, indonesia

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Over the past decade, antimalarial drug resistance has rapidly become a major public health problem in South East Asia region including South Sumatra. This study aimed to determine the extent of gene polymorphisms associated with chloroquine resistance (CQR) in P. falciparum isolates from Lahat, Sekayu, Baturaja and Palembang district.

Methods: A molecular study was conducted to identify the mutant alleles of the genes associated with the resistance to chloroquine among the isolates of Plasmodium falciparum from South Sumatera. Blood from 25 patients was collected, DNA was isolated, and the sequences of two different genes (Plasmodium falciparum chloroquine resistance transporter/pfcrt and Plasmodium falciparum multidrug resistance/pfmdr1) were analyzed using polymerase chain reaction (PCR) and restriction fragment length polymorphism (RFLP).

Results: This study identified polymorphism in the pfcrt 76-Thr in all isolates and pfmdr1 86-Tyr. These findings may reflect the failure of treatment with the standard dose of chloroquine within the last few years in South Sumatera.

Conclusion: PCR-RFLP technique provide a simple and rapid method of detecting polymorphisms in genes that may predict chloroquine resistance (CQR). Although the identification of the polymorphism in the pfcrt and pfmdr1 genes provides a significant indicator of CQR, further studies are needed to determine the role of these polymorphisms in the in vivo and in vitro responses to drug treatment.