

*Pfdhfr* and *Pfdhps* gene mutations in *Plasmodium falciparum* isolates from Ranong, Thailand

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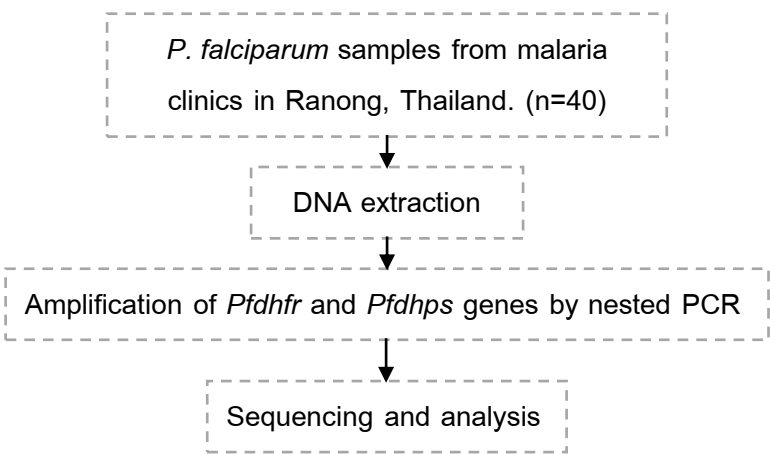
Introduction

Malaria caused by the protozoan parasite, *Plasmodium falciparum*, infection is one of the most important diseases worldwide. *P. falciparum* resistant to antimalarial drugs, Sulfadoxine-pyrimethamine (SP), is the main problem for control and elimination of the diseases. In Thailand, SP resistance have been reported from the Thai-Myanmar border area.

Aim of the study

To detect *Pfdhfr* and *Pfdhps* genes mutation associated with SP resistance in *P. falciparum* isolated from Ranong province, Southern Thailand, by nested PCR and sequencing.

Methods



Results

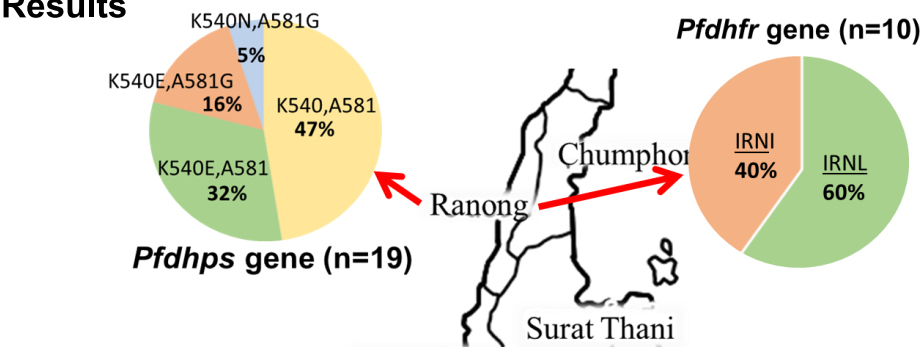


Figure 1: The prevalence of *Pfdhfr* and *Pfdhps* genes detected in *Plasmodium falciparum* from Ranong Province, Thailand

Gene	Category	Haplotype	n(%)
<i>Pfdhfr</i>	Wild type	NCSI	-
	Triple mutant	IRN	10 (100)
	Quadruple	IRNL	6 (60)
<i>Pfdhfr/Pfdhps</i>	Wild type	NCSIK	-
	Quintuple mutant	IRNLE	4(21.05)
		IRNLN	1(5.26)

Table 1 : The prevalence of haplotype and combinations *Pfdhfr-Pfdhps* genes in *Plasmodium falciparum* from Ranong Province, Thailand

Conclusion

This study indicated that SP resistance was occurred in the study area. The surveillance guidelines and policy formulation of the most appropriate malaria treatment strategy in these areas must be implemented.