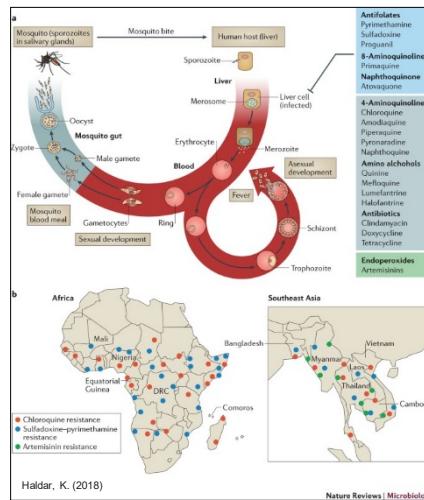
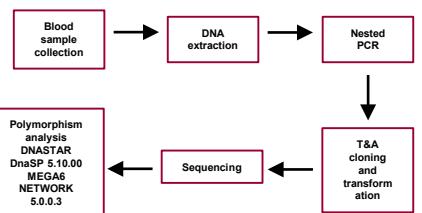


INTRODUCTION

- Emergence and spreading of antimalarial drug-resistant malaria parasites are a great hurdle to combat malaria
- The Great Mekong Sub-region (GMS) has been recognized as breeding hubs of antimalarial drug resistance malaria parasites
- Analyses of molecular markers associated with antimalarial drug resistance provide valuable molecular information for mapping drug resistance status



METHODS



RESULTS



CONCLUSIONS

Overall patterns for antimalarial drug resistance genes in *P. falciparum* of Mandalay region suggest that the parasite population in the region showed lower levels of antimalarial drug resistances compared to those from border areas and Northern parts of Myanmar. Continuous monitoring of antimalarial drug resistance is necessary to plan a proper antimalarial drug regime to control and eliminate malaria in Myanmar.

MOLECULAR PROFILES OF MULTIPLE ANTIMALARIAL DRUG RESISTANCE GENES IN *PLASMODIUM FALCIPARUM* IN THE MANDALAY REGION, MYANMAR

Hương Giang Lê^{1,2}, Haung Naw^{1,2}, Jung-Mi Kang^{1,2}, Tuấn Cường Võ^{1,2}, Moe Kyaw Myint³, Zaw Than Htun³, Won Gi Yoo^{1,2}, Byoung-Kuk Na^{1,2}

¹Department of Parasitology and Tropical Medicine, and Institute of Health Sciences, Gyeongsang National University College of Medicine, Republic of Korea

²Department of Convergence Medical Science, Gyeongsang National University, Republic of Korea

³Department of Medical Research Pyin Oo Lwin Branch, Pyin Oo Lwin, Myanmar

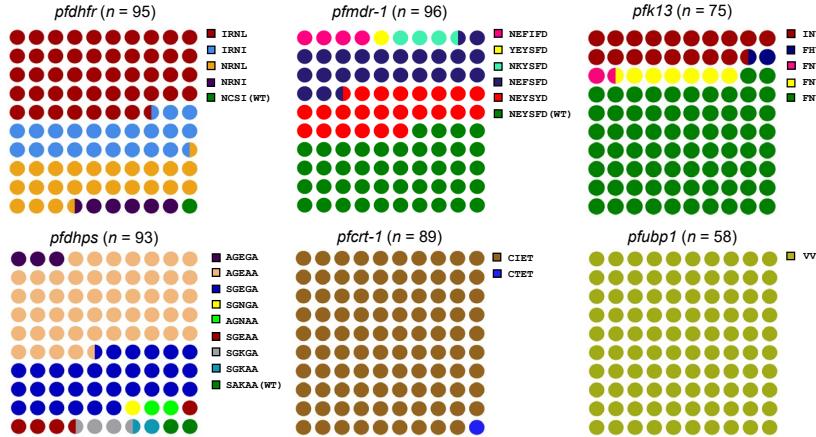
Substantial levels of mutations in antimalarial drug resistance genes were detected in Myanmar *P. falciparum* isolates

Figure 1. Frequencies of drug-resistant mutations in Myanmar *P. falciparum* isolates. The haplotypes are showed in different colors. Each circle represent 1% of frequency. Extreme high levels of mutations for sulfadoxine-pyrimethamine resistance were detected in *pfdhfr* and *pfdhps*. Meanwhile, moderate levels of mutations were found in genes related to chloroquine resistance including *pfrndr-1* and *pfcrt*. Low frequency or none of mutations were found in *pfk13*, *pfbp1*, and *pfcytb*.

Gene	Mutation	Frequency (%)
<i>pfdhfr</i> (n=95)	A16V	0.0
	N51I	69.5
	C59R	98.9
	S108N	98.9
	S108T	0.0
	I164L	71.6
	S436A	57.0
	A437G	97.8
	K540E	90.3
	K540N	3.2
	A581G	38.7
	A613S	0.0
<i>pfdhps</i> (n=93)	N86Y	1.0
	E130K	3.1
	Y184F	28.1
	S1034I	4.2
	S1034C	0.0
	N1042D	0.0
	F1226Y	24.0
	D1246Y	0.0
<i>pfrndr-1</i> (n=96)	C72S	0.0
	M74I	98.9
	M74T	1.1
	N75E	100.0
	K76T	100.0
<i>pfcrt</i> (n=89)	F446I	17.7
	N458H	1.3
	R561H	1.3
	P574L	6.3
<i>pfk13</i> (n=75)	Y (WT)	100.0
<i>pfbp1</i> (n=58)	Y (WT)	100.0
<i>pfcytb</i> (n=55)	Y (WT)	100.0

Frequencies of haplotypes in antimalarial drug resistance genes were varied in Myanmar *P. falciparum* isolates