

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

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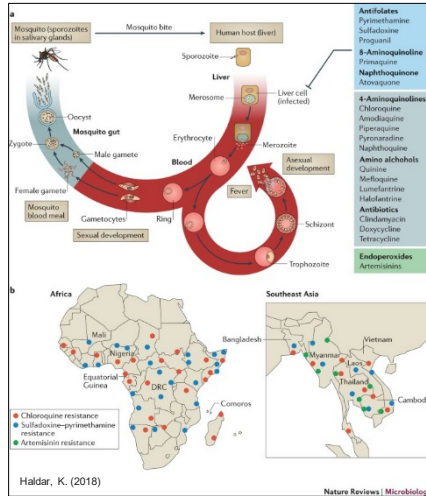
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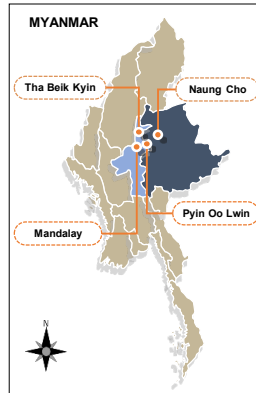
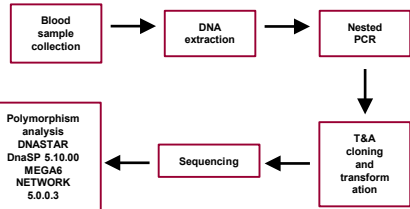
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INTRODUCTION

- 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



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.

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

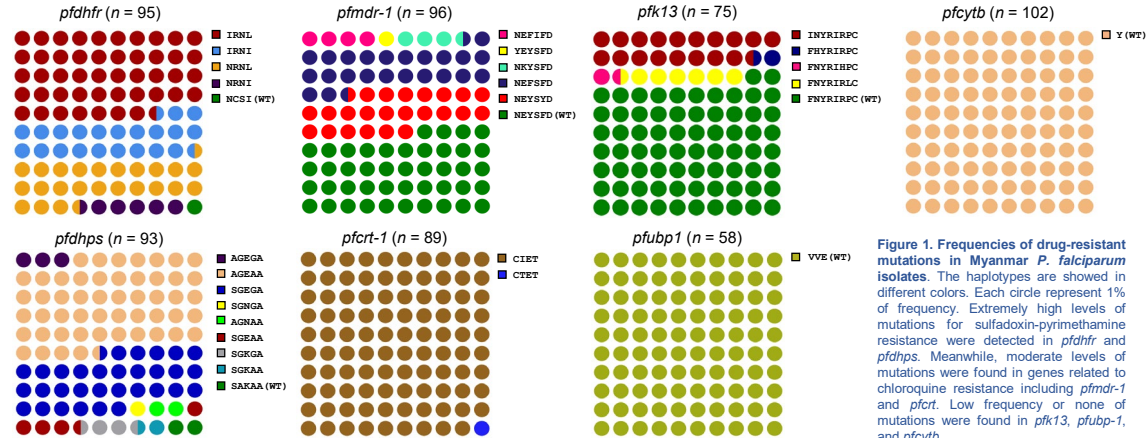


Figure 1. Frequencies of drug-resistant mutations in Myanmar *P. falciparum* isolates. The haplotypes are showed in different colors. Each circle represent 1% of frequency. Extremely high levels of mutations for sulfadoxin-pyrimethamine resistance were detected in *pfdhfr* and *pfdhps*. Meanwhile, moderate levels of mutations were found in genes related to chloroquine resistance including *pfmdr-1* and *pfcr1-1*. Low frequency or none of mutations were found in *pfk13*, *pfubp-1*, 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 |
| <i>pfdhps</i> (n = 93) | I164L | 71.6 |
| | S436A | 57.0 |
| | A437G | 97.8 |
| | K540E | 90.3 |
| | K540N | 3.2 |
| <i>pfmdr-1</i> (n = 96) | A581G | 38.7 |
| | A613S | 0.0 |
| | N86Y | 1.0 |
| | E130K | 3.1 |
| | Y184F | 28.1 |
| <i>pfcr1-1</i> (n = 89) | S1034I | 4.2 |
| | S1034C | 0.0 |
| | N1042D | 0.0 |
| | F1226Y | 24.0 |
| | D1246Y | 0.0 |
| <i>pfk13</i> (n = 75) | C72S | 0.0 |
| | M74I | 98.9 |
| | M74T | 1.1 |
| | N75E | 100.0 |
| | K76T | 100.0 |
| <i>pfcytb</i> (n = 75) | F446I | 17.7 |
| | N458H | 1.3 |
| | R561H | 1.3 |
| | P574L | 6.3 |

RESULTS

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

