Mutational analysis of *Plasmodium falciparum* dihydrofolate reductase and dihydropteroate synthase genes in the interior division of Sabah, Malaysia

Abstract

Background

The sulphadoxine/pyrimethamine (SDX/PYR) combination had been chosen to treat uncomplicated falciparum malaria in Malaysia for more than 30 years. Non-silent mutations in dihydrofolate reductase (dhfr) and dihydropteroate synthase (dhps) genes are responsible for the resistance to pyrimethamine and sulphadoxine, respectively. This study reports the mutational analysis of pfdhfr and pfdhps in single Plasmodium falciparum infection isolates from the interior division of Sabah, Malaysian Borneo.

Methods

A total of 22 P. falciparum single infection isolates collected from two districts of the interior division of Sabah from February to November 2010 were recruited for the mutational study of pfdhfr and pfdhps. Both genes were amplified by nested PCR prior to DNA sequencing and mutational analysis.

Results

A total of three pfdhfr and four pfdhps alleles were identified. The most prevalent pfdhfr allele is ANRNL (86%) involving triple mutation at position 108(S to N), 59(C to R) and 164(I to L). In pfdhps, two novel alleles, SGTGA (73%) and AAKAA (5%) were identified. Alleles involving triple mutation in both pfdhfr (ANRNL) and pfdhps (SGTGA), which were absent in Sabah in a study conducted about 15 years ago, are now prevalent.

Conclusions

High prevalence of mutations in SDX/PYR associated drug resistance genes are reported in this study. This mutational study of pfdhps and pfdhfr indicating that SDX/PYR should be discontinued in this region.