Abstract

Introduction. Studies on the molecular epidemiology of antimalarial resistance constitute a useful tool to understand the events underlying treatment failure and resistance in falciparum malaria in Colombia. Several authors have reported on the efficacy of some molecular markers to predict drug resistance in Plasmodium falciparum and the P. falciparum pfcrt gene has been widely characterized in this context. Objective. To study the frequency of pfcrt gene mutations in P. falciparum and their association with treatment failure to the antimalarials chloroquine, mefloquine, amodiaquine and sulfadoxine/pyrimethamine in two highly malaria endemic regions, the Turbo and Bajo Cauca, regions of northwestern Colombia. Materials and methods. A representative sample of patients with non-complicated falciparum malaria was selected from each region for assessment of the treatment response together with the status of codons 72, 74, 75 and 76 in the pfcrt gene using a PCR-RFLP approach. Results. A high frequency of treatment failure to chloroquine (82%) and to amodiaquine (29%) was confirmed while mefloquine and combined therapy remained effective in clearing the infection. The presence of the T76 mutation in pfcrt was confirmed in all 172 samples; the most common haplotype was CMNT (67%). Conclusions. No significant association could be confirmed between a particular haplotype and the treatment response in any of the treatment groups. Herein, we report, for the first time in Colombia, presence of two haplotypes, SMET and SMNT; mixed mutant and wild-type alleles were found in 12% of the samples.

Keywords
Plasmodium falciparum, malaria, antimalarials, chloroquine, mutation, Colombia.