Abstract

Introduction. The status of msp1, msp2 and glurp allele frequency and the diversity of Plasmodium falciparum in Northwestern Colombia before the implementation of an artemisinin-based combined therapy have been explored only by a few authors and in a relatively small number of samples from this highly endemic region. Objective. To evaluate the frequency of msp1, msp2, and glurp alleles and the diversity of P. falciparum in two Colombian regions before the use of an artemisinin-combined therapy. Methods. This study was part of a major anti-malarial efficacy trial designed as a random, clinically-controlled study for which 224 subjects were recruited. Region 2 of msp1 and msp2 (central region) were amplified by a nested PCR; glurp (region R2) was amplified by a seminested PCR. Results. For msp1, five genotypes were observed, representing the K1, MAD20, and RO33 allelic families. All samples corresponded to a MAD20 150 bp allele. For msp2 (IC family), two alleles were detected and for glurp, eight were observed. A total 33 haplotypes were detected. Conclusions. Analysis of glurp can be used to successfully genotype parasite populations in the new studies in Colombia aimed at exploring Plasmodium spp. population dynamics. In addition, analysis of msp1 and msp2 can also be of value for comparisons with past studies, but not when the objective is to study parasites obtained from the same patient in a reduced period of time; for instance, during treatment efficacy studies.

Keywords
Plasmodium falciparum, malaria, msp1, msp2, glurp, Colombia.