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Makokha, Francis W
Mount Kenya University

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Prevalence of *Plasmodium falciparum* chloroquine resistant gene markers, *pfcrt*-76 and *pfmdr1*-86, eight years after cessation of chloroquine use in Mwea, Kenya

Sabah Ahmed Omar,1 Francis W. Makokha,2,3 Fat’hia Abdo Mohammed,1 Francis T. Kimani,1 Gabriel Magoma3

1Kenya Medical Research Institute, Centre for Biotechnology Research and Development (KEMRI, CB RD.), P.O. Box 54840-00200 Nairobi, Kenya; 2Institute of Tropical Medicine and Infectious Diseases (ITROMID), P.O. Box 54840-00200 Nairobi, Kenya; 3Jomo Kenyatta University of Agriculture and Technology (J KUAT), Biochemistry Department, P.O. Box 62000-00200, Nairobi, Kenya.

Abstract

Background and Methodology: The prevalence of T76 and Y86 *Plasmodium falciparum* molecular markers for chloroquine (CQ) resistance in the *Pfcrt* and *Pfmdr1* genes were investigated by PCR-RFLP and dot blot analysis in samples (50 for *Pfcrt* and 51 for *Pfmdr1*) collected in May 2005, eight years after chloroquine (CQ) cessation.

Results: Our findings show that 94% of field isolates from this site still harbor T76 mutation in *Pfcrt* while 6% have the wild type allele K76 [T test, P=0.04058 (1997 versus 2005)]. Dot blot analysis revealed that most of the isolates had MET polymorphism at position 74, 75 and 76 wild type allele of the *Pfcrt* gene. When *Pfmdr1*-86 was analyzed by dot blot, 6% of the isolates had wild type allele N86, 73% had mutant allele Y86, and 21% had both N and Y [T test, P=0.04058 (1997 versus 2005)].

Conclusions: Dot blot hybridization was found to be more sensitive and specific than PCR-RFLP. The study showed a moderate reversal to sensitivity by the *P. falciparum* population in the study site compared to the situation before CQ cessation.

Key Words: *Plasmodium falciparum*, Chloroquine resistance, PCR-RFLP, Dot blot.


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