

## Prevalence of *Plasmodium falciparum* chloroquine resistant gene markers, *pfcr*-76 and *pfmdr*1-86, eight years after cessation of chloroquine use in Mwea, Kenya

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### Abstract

**Background and Methodology:** The prevalence of T76 and Y86 *Plasmodium falciparum* molecular markers for chloroquine (CQ) resistance in the *Pfcr*t and *Pfmdr*1 genes were investigated by PCR-RFLP and dot blot analysis in samples (50 for *Pfcr*t and 51 for *Pfmdr*1) 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 *Pfcr*t 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 *Pfcr*t gene. When *Pfmdr*1-86 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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