

## Expansion of the wild\_type pfcr<sub>t</sub> 76K allele in Plasmodium falciparum populations in Mbita, Kenya

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### SUMMARY

**Background and Methodology:** Chloroquine resistance in *P. falciparum* is conferred by mutations in the pfcr<sub>t</sub> gene with K76T mutation being definitive in as far as chloroquine resistance is concerned. The prevalence of point mutations at codons 74, 75 and 76 of *P. falciparum* of the pfcr<sub>t</sub> gene was determined by dot\_blot/probe hybridization analysis in 121 samples collected in May 2009 twelve years after chloroquine cessation in Kenya.

**Results:** We found out that 80.17% of the field isolates from Mbita harbor the T76 mutation while 19.83% have the wild type allele K76 [ T test, P= 0.108 (2005 versus 2009)]. Majority of the isolates had MNT haplotype at codons 74, 75 and 76.

**Conclusion:** The study showed a significant expansion of the pfcr<sub>t</sub> 76K allele and thus expansion of parasite populations that are sensitive to chloroquine.

**Key words:** Plasmodium falciparum; Dot1blot/probe hybridization; Chloroquine resistance.

[*Afr J Health Sci.* 2012; 22:176-187]