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Expansion of the wild_type pfcrt 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 pfcrt 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 pfcrt 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 pfcrt 76K allele and thus expansion of parasite populations that are sensitive to chloroquine.

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