Changes in Genotypes of Plasmodium Falciparum Human Malaria Parasite Following Withdrawal of Chloroquine in Tiwi, Kenya. (2012).

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Abstract

Chloroquine (CQ) drug was withdrawn in 1998 as a first-line treatment of uncomplicated malaria in Kenya. This was in response to resistance to the drug in Plasmodium falciparum malaria parasite. Investigations were conducted to determine prevalence of CQ resistance genotypes in the parasites in Tiwi, a malaria endemic town in Kenya, before and about a decade after the withdrawal of the drug. Blood samples were collected and spotted on filter papers in 1999 and 2008 from 75 and 77 out-patients respectively with uncomplicated malaria. The sampling was conducted using finger pricking technique. DNA was extracted from individual spots in the papers and screened for the presence of P. falciparum chloroquine resistance transporter (Pfcrt) and multi drug resistance (Pfmdr-1) markers using nested PCR. Nature of mutations (haplotypes) in the Pfcrt and Pfmdr-1 markers in the samples were confirmed using dot blot hybridization technique. Changes in pattern of CQ resistance in the parasite samples in 1999 and 2008 were assessed by Chi Square test. There was a significant ($P < 0.05$) reduction in CQ resistant genotypes of the parasite between 1999 and 2008. Pfmdr and Pfcrt CQ resistant genotypes in 2008 reduced to 54.10 and 63.64% respectively, from 75.39 and 88.0% respectively in 1999. This reduction was accompanied by emergence of Pfcrt specific CQ sensitive (IEK) and intermediate/partially CQ resistant (MET) haplotypes. Results suggest significant reversal of the phenotype of the parasite from chloroquine resistant to wild/sensitive type. The novel haplotypes indicates transitional phase of the parasite to the wild type. Current prevalence of chloroquine resistant genotype is definitely above the threshold for efficacious re-introduction of chloroquine for treatment of malaria in Tiwi.

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