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High prevalence of PfCRT K76T mutation in *Plasmodium falciparum* isolates in Ghana

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Background: Plasmodium falciparum has successfully developed resistance to almost all currently used antimalarials. A single nucleotide polymorphism in the P. falciparum chloroquine resistance transporter (Pfcrt) gene at position 76 resulting in a change in coding from lysine to threonine (K76T) has been implicated to be the corner stone of chloroquine resistance. Widespread resistance to chloroquine in endemic regions led to its replacement with other antimalarials. In some areas this replacement resulted in a reversion of the mutant T76 allele to the wild-type K76 allele. This study was conducted to determine the prevalence of the K76T mutation of the Pfcrt gene eight years after the ban on chloroquine sales and use.

Methods & Materials: A cross-sectional study was conducted in 6 regional hospitals in Ghana. PCR-RFLP was used to analyze samples collected to determine the prevalence of Pfcrt K76T mutation.

Results: Of the 1,318 participants recruited for this study, 246 were found to harbour the P. falciparum parasites, of which 60.98% (150/246) showed symptoms for malaria. The prevalence of the Pfcrt T76 mutant allele was 58.54% (144/246) and that of the K76 wild-type allele was 41.46% (102/246). No difference of statistical significance was observed in the distribution of the alleles in the symptomatic and asymptomatic participants (P = 0.632). No significant association was, again, observed between the alleles and parasite density (P = 0.314), as well as between the alleles and Hb levels of the participants (P = 0.254). The 58.54% prevalence of the Pfcrt T76 mutation recorded in this study is considered very high after eight years of the abolishment of chloroquine usage in Ghana.

Conclusion: This is in sharp contrast to findings from other endemic areas where the mutant allele significantly reduced in the population after a reduction chloroquine use.

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Schistosoma PCR among high school girls in South Africa as a complimentary diagnostic tool for Female Genital Schistosomiasis (FGS)

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Background: Millions of women and girls in developing countries are at risk of Schistosomiasis. In sub-Saharan Africa *Schistosoma haematobium* is the predominant species which affects both the urinary and genital tracts. Early diagnosis and treatment among girls may prevent or reduce Female Genital Schistosomiasis (FGS). In this study we explore the use of *Schistosoma* PCR in urine and vaginal lavage samples as a diagnostic tool.

Methods & Materials: Urines, vaginal lavage and cytology Pap smears were collected from 400 young women aged 16-21 years from rural high schools in KwaZulu Natal, South Africa. Vaginal lavage was performed by spraying 10 ml saline four times on the cervico-vaginal mucosal surfaces. Urines (20 mL) and Pap smears were examined microscopically for the presence of ova of *S. haematobium*. Quantification of *Schistosoma*-specific DNA by an ITS-based real-time PCR was performed on 200 μL aliquots of urine and vaginal lavage samples using an automated DNA isolation and PCR set-up.

Results: Schistosoma-specific DNA was found in 83 (20.8%) of the urines and 35 (8.8%) of vaginal lavages. In 8 (2%) of the participants Schistosoma DNA was positive in lavage but negative in urine. Ova were detected in the Pap smears of 6 (1.5%) of the women, all showed detectable *Schistosoma* DNA in their lavage. *S. haematobium* eggs were seen in 71 (17.8%) of the urines examined microscopically.

Conclusion: The intravaginal lavage PCR detected almost six times more positive cases than Pap smears. The PCR results from urine samples and those of lavage samples compare well and suggest that genital schistosomiasis does exist in this young population. Lavage PCR may be a useful indicator of FGS but should be explored alongside clinical findings.

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