



Studies on *Plasmodium Falciparum* Drug Resistance in Endemic Regions of India

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ABSTRACT: Drug resistance in *Plasmodium falciparum* parasite has increased tremendously in the past few years against the conventional antimalarial drugs. In India alone, *P. falciparum* accounts for more than 50% of all confirmed malaria cases at present. The most commonly used antimalarial drugs; viz. chloroquine (CQ) and sulphadoxine-pyrimethamine (SP) have been rendered ineffective and are replaced by the artesunate-based combination therapy (ACT) in most part of world including India. The rapid spread of anti-malarial drug resistance over the past few decades has necessitated intensive monitoring of drug resistance which is essential for an effective malaria control strategy. This prompted us to monitor the drug resistance status of India by identifying single nucleotide polymorphism in the molecular markers *crt*, *dhps* and *dhfr* genes. Previous studies revealed that isolates from India contains mutations in the *dhfr* gene at codon positions 51(N51I), 59(C59R), 108(S108N/T) and 164(I164L). In case of *dhps* gene mutations occur at five codon positions 436(S436F/A), 437(A437G), 540(K540E), 581(A581G) and 613(A613S/T). Considering these mutations the *P. falciparum* population from endemic states of India i.e. Jharkhand, Odisha, Andhra Pradesh and Uttar Pradesh are screened to find out the present status of drug resistance in these areas by using DNA-Sequencing method. Investigation carried out on Jharkhand, Odisha and Andhra Pradesh samples showed higher number of two locus mutations in *dhfr* and *dhps* genes. These results indicate that the drug pressure is high in these endemic states. This study would provide valuable information of drug resistance status and help in formulating National Antimalarial Drug Policy. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.

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