

Title: Plasmodium Falciparum Chloroquine Resistance (Pfcrt) Mechanisms: An Intra-Erythrocytic Developmental Stage.

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Abstract: Chloroquine (CQ), cheap and long history antimalaria has failed in the treatment of malaria. This work therefore, sought to expose the resistance mechanism(s) of *Plasmodium falciparum* (*Pf*) at the Intra-erythrocytic developmental stage. By considering the activity involved at this stage and reviewing polymorphism within the food vacuolar membrane protein Pfcrt, chloroquine resistance polymorphism at that level will be determined. The biochemical network of *P.f* and the gene expression data were downloaded from the genebank, NCBI, EMBL, plasmDB and geneDB. The data were performed as confirmed by the Blast and ClustalX programme using NCBI blast against the biochemical network of *Pf*, and mapped onto the enzymatic reaction nodes of the metabolic network. The result shows that there was a variation in the targeted metabolic pathways of the erythrocytic cycle, likewise the genes that codes for the enzymes of the metabolic pathways. These methods give a better understanding of how resistance process occurs, as well as the important mechanisms that *P.f* deplores for resisting these anti-malaria drugs. The knowledge therefore, facilitates the rationale to design new, effective and well tolerated antimalaria drugs.