

Title: Genetic Diversity Of Plasmodium Falciparum Field.

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Abstract: The genetic diversity of Plasmodium falciparum has been extensively studied in various parts of the world. However, limited data are available from Nigeria. In this study, P. falciparum field isolates from Southwestern Nigeria were characterized with two highly polymorphic genetic markers (i.e. the merozoite surface protein 1, msp-1 and merozoite surface protein 2, msp-2 and Glutamic rich protein (Glurp). One hundred blood samples were collected from patients attending state general hospitals in Ogun State. This was done with symptomatic blood-slide which confirmed P. falciparum malaria. The genetic diversity of P. falciparum was analyzed by length polymorphism following gel electrophoresis of DNA products from nested polymerase chain reactions (PCR) targeting block 2 of msp-1 and block 3 of msp-2, including their respective allelic families KI, MAD 20, RO33, and FC27, 3D7 respectively and Glutamate rich protein. A total of 76/100 (76%) patients had positive PCR outcome in at least one genetic marker. Majority of patients had monoclonal infections. Multiplicity of infection for msp-1 and msp-2 were 1.1 and 1.2 respectively. The estimated total number of genotypes was 8 msp-1 (4 KI; 3 MAD; 1 RO33) and 6 msp-2 (3 FC27; 3 3D7). 80% of the isolates harbor the genes that code for Glutamate rich protein with allelic size ranging between 700 and 900bp. There is high genetic diversity and allelic distribution among P. falciparum isolates from Southwestern Nigeria where transmission of malaria is high.