Genetic Diversity of *Plasmodium falciparum* in Zimbabwe

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ABSTRACT

The genetic diversity of *Plasmodium falciparum* in Zimbabwe was studied by molecular characterisation of deoxyribonucleic acid (DNA) extracted from dried blood spots (day 0) samples of patients with symptomatic, rapid diagnostic test and microscopy confirmed *P. falciparum* monoinfections attending any one of the eight therapeutic efficacy sentinel site clinics around Zimbabwe. The products of nested polymerase chain reaction (PCR) with the highly polymorphic genetic markers glutamate rich protein (*glurp*), merozoite surface protein 1 (*msp1*) and merozoite surface protein 2 (*msp2*) including their respective allelic families K1, MAD20, RO33, FC27 and 3D7/IC were analysed for genetic diversity by length polymorphism following gel electrophoresis. A total of 38 out of 100 (38%) of samples showed a PCR positive outcome in at least one genetic marker. The PCR negative samples were excluded from analysis. The majority of the samples had monoclonal infections with only 4/38 (11%) of the samples carrying multiple *P. falciparum* genotypes for both *msp1* and *msp2*. The total number of genotypes was 12 for *msp1* (7 K1; 4 MAD20; 1 RO33), 7 for *msp2* (3 FC27; 4 3D7/IC) and 16 for *glurp*. The estimated expected heterozygosity was highest for *msp1* (0.7676) and lowest for *msp2* (0.5715). Both allelic distribution and genetic diversity found in the study were similar to previous reports and the malaria transmission intensity of the areas being reflected by the high multiplicity of infection and expected heterozygosity values.