MEASURING ALLELIC HETEROGENEITY IN *PLASMODIUM FALCIPARUM* BY A HETERODUPLEX TRACKING ASSAY

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Abstract

We developed a novel *Plasmodium falciparum* genotyping strategy based on the heteroduplex tracking assay (HTA) method commonly used to genotype viruses. Because it can detect both sequence and size polymorphisms, we hypothesized that HTA is more sensitive than current methods. To test this hypothesis, we compared the ability of HTA and a nested polymerase chain reaction (PCR) to detect genetic diversity in 17 Thai samples. The HTA detected more MSP1 sequence variants in eight isolates (47%), less sequence variants in three isolates (18%), and an equal number of sequence variants in six isolates (35%), suggesting that HTA is equal to or more sensitive than the nested PCR. This study is a proof of concept that HTA is a sensitive allelic discrimination method able to determine genetic diversity in *P. falciparum* and warrants its use in studies of antimalarial drug efficacy.