

Publication

A comparison of methods to detect and quantify the markers of antimalarial drug resistance

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Author(s) Hastings, Ian M; Nsanzabana, Christian; Smith, Tom A

Author(s) at UniBasel [Smith, Thomas A.](#) ;

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We compare, contrast, and evaluate methods to quantify genetic markers of antimalarial drug resistance. Frequency estimates should be reported along with crude prevalence. There are four main potential methods to estimate frequencies in blood samples: simple counting of single nucleotide polymorphisms (SNPs) and haplotypes in samples with multiplicity of infection (MOI) = 1; SNP counting in samples with MOI ≤ 2 ; SNP and haplotypes counting in samples with unambiguous genotypes; statistical inference using SNP and MOI data from all samples. Large differences between the methods became apparent when analyzing field data with high MOI. Simple counting dramatically reduced sample size and estimate precision, and we show that analysis of unambiguous samples is biased, leaving maximum likelihood or similar statistical inference as the only practical option. It is essential to account for genotyping missing minor clones; ignoring this phenomenon resulted in a 2-fold underestimation of SNPs and haplotypes present at low frequencies

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