Abstract

A quantitative nucleic acid sequence-based amplification (QT-NASBA) assay was employed to predict retrospectively the outcome of sulfadoxine-pyrimethamine (SP) treatment of uncomplicated malaria in children aged <6 years in an endemic region. Blood samples were collected at initial diagnosis and during follow-up. Mutation-specific nested PCR methods to analyse DHFR (Arg-59) and DHPS (Glu-540) mutations that are associated with SP drug resistance were applied. Parasite genotyping was performed to distinguish between re-infection and recrudescence. Eighty-six patients were recruited of which 66 were available for follow-up. Nine children were classified as early treatment failure, 13 cases were classified as late clinical failure, 32 as late parasitological failure, and only 12 children had an adequate clinical and parasitological response. DHFR and DHPS mutations conferring SP resistance were abundant in the Plasmodium population. Blood samples obtained 7 days after treatment were used to predict retrospectively the outcome of SP treatment. QT-NASBA was able to give a correct prediction of treatment outcome in 85.7% of the cases. Positive predictive value (PPV) of QT-NASBA case was 95% (95% confidence interval = 88.3-100) and negative predictive value (NPV) was 63% (95% CI = 39.5-86.5). In contrast, microscopy correctly predicted outcome in only 37.5% of the cases. PPV of microscopy was 100% (95% CI = 73.9-100) and the NPV was 25.5% (95% CI = 13.0-38.0). The analysis of a day 7 blood sample with QT-NASBA allows for the prediction of late clinical or parasitological treatment failure in the majority of the cases analysed in the present study.