

Application of a novel SNP (single-nucleotide polymorphism) biomarker-approach for distinguishing between new infections and recrudescence.

The significance of malaria as a health problem is increasing in many parts of the world. The absence of adequate health services frequently results in recourse to self-administration of drugs, often with incomplete treatment. This is a major factor in the increase in resistance of malaria parasites to previously effective drugs¹. The control of malaria requires an understanding of the different selection pressures on the malaria parasite population. Genotyping methods can be used to track both directional (drug resistance) as well as frequency dependant balancing (immune response) selection pressures².

A number of single nucleotide polymorphisms (SNPs) have been validated as drug-resistance markers. We are evaluating the application of these and other SNPs as a tool to identify delayed recrudescence of parasites after apparently successful treatment of a primary infection or cause the shift of drug sensitivity to drug resistance. In order to achieve this, we are designing and evaluating a highly sensitive and accurate SNP assay for discrimination between recrudescence and reinfection. Further outputs envisaged will include the establishment of a database linking SNP's in the malaria genome with phenotypic traits or specific genes in the malaria parasite.

Principal Investigator: Mr J de Ridder
Department of Biochemistry
University of Pretoria

¹ World Health Organisation *World malaria situation in 1994*. *WER* 1997 **36**, 269-274.

² Polley SD, Chokejindachai W & Conway DJ *Allele frequency-based analyses robustly map sequence sites under balancing selection in a malaria vaccine candidate antigen*. *Genetics* 2003 165:555-61.