

Sequence diversity and molecular evolution of the merozoite surface antigen 2 of *plasmodium falciparum*

[Ingrid Felger](#), [Vikki M. Marshal](#), [John C. Reeder](#), [John A. Hunt](#), [Charles S. Mgone](#) & [Hans-Peter Beck](#)

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Abstract

Eleven new alleles of the *Plasmodium falciparum* merozoite surface antigen 2 (*MSA2*) from Papua New Guinea were analyzed by direct sequencing of polymerase chain reaction (PCR) products. We have used the sequence information to trace the molecular evolution of *MSA2*. The repeats of ten alleles belonging to the *3D7* allelic family differed considerably in size, nucleotide sequence, and repeat copy number. In the repeat region of these new alleles, codon usage was extremely biased with an exclusive use of NNT codons. Another new allele sequenced belonged to the *FC27* family and confirmed the family-specific conserved structure of 96 and 36 bp repeats. In order to assess sequence microheterogeneity within samples defined as the same genotype by restriction fragment length polymorphism (RFLP), we have analyzed single-strand conformation polymorphism (SSCP) of different samples of the most frequent allele (*D10* of the *FC27* family) in the study population. No sequence heterogeneity could be detected within the repeat region. Based on analysis of the repeat regions in both allelic families, we discuss the hypothesis of a different evolutionary strategy being represented by each of the allelic families.