

Repetitive sequences upstream of the pfg27/25 gene determine polymorphism in laboratory and natural lines of Plasmodium falciparum.

Abstract:

The structure of the genomic region located upstream of the gametocyte-specific gene pfg27/25 of *Plasmodium falciparum* was analysed in laboratory lines and field isolates of the parasite. The gene is located in a subtelomeric region of chromosome 13 in parasite clones 3D7 and HB3. Analysis of laboratory lines and field isolates of *P. falciparum* indicated that polymorphism upstream of pfg27/25 is mainly due to the structure of a repetitive DNA region located at about half a kilobase from the pfg27/25 coding sequence. Different types of repetitive sequences are present in this region, whose copy number is variable in different parasite lines. In addition a GC-rich sequence element contained in this region, which is proposed to be the startpoint of pfg27/25 mRNA, presents either a direct or a reverse orientation in different parasite lines. Genomic deletions upstream of the pfg27/25 gene are also described in two laboratory lines of the parasite, which eliminate two newly identified malaria genes, orf P and orf Gap, from the genome of these parasites. One of them, orf Gap, deleted from the reference parasite clone 3D7, is abundantly expressed as mature mRNA in asexual parasites. PCR analysis on 64 field isolates of *P. falciparum* indicated that orf P and orf Gap sequences are present in all tested samples of naturally propagating parasites.