Search of *Plasmodium falciparum* artemisinin resistance candidate mutations in Brazilian isolates

**Objective**

This study was performed to better understand the genetic diversity of described polymorphisms in *pfatpase6* and *pfmdr1* genes before the introduction of ACT in Brazil, in order to get a genotypic snapshot of *Plasmodium falciparum* parasites that may be used as baseline reference for future studies.

**Methods**

Parasites from *P. falciparum* samples collected at 2002, 2004 and 2006-2007 were genotyped using PCR and DNA sequencing at codons 86, 130, 184, 1034, 1042, 1109 and 1246Y for *pfmdr1* gene, and 243, 263, 402, 431, 623, 630, 639, 683, 716, 776, 769 and 771 for *pfatpase6* gene.

**Results**

A *pfmdr1* haplotype NEF/CDVY was found in 97% of the samples. In the case of *pfatpase6*, four haplotypes, wild-type (37%), 630S (35%), 402V (5%) and double-mutant 630S + 402V (23%), were detected.

**Conclusion**

Although some polymorphism in *pfmdr1* and *pfatpase6* were verified, no reported haplotypes in both genes that may mediate altered response to ACT was detected before the introduction of this therapy in Brazil. Thus, the haplotypes herein described can be very useful as a baseline reference of *P. falciparum* populations without ACT drug pressure.