Origin of *Plasmodium falciparum* malaria is traced by mitochondrial DNA

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Abstract

The origin and geographical spread of *Plasmodium falciparum* is here determined by analysis of mitochondrial DNA sequence polymorphism and divergence from its most closely related species *P. reichenowi* (a rare parasite of chimpanzees). The complete 6 kb mitochondrial genome was sequenced from the single known isolate of *P. reichenowi* and from four different cultured isolates of *P. falciparum*, and aligned with the two previously derived *P. falciparum* sequences. The extremely low synonymousnucleotide polymorphism in *P. falciparum* (π=0.0004) contrasts with the divergence at such sites between the two species (K=0.1201), and supports a hypothesis that *P. falciparum* has recently emerged from a single ancestral population. To survey the geographical distribution of mitochondrial haplotypes in *P. falciparum*, 104 isolates from several endemic areas were typed for each of the identified single nucleotide polymorphisms. The haplotypes show a radiation out of Africa, with unique types in Southeast Asia and South America being related to African types by single nucleotide changes. This indicates that *P. falciparum* originated in Africa and colonised Southeast Asia and South America separately.

Keywords: *Plasmodium falciparum*; *Plasmodium reichenowi*; Mitochondrial genome; Genetics; Species; Evolution

Abbreviations: mt, mitochondrial; nt, nucleotide

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