PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Malaria's many guises

ArticleInfo		
ArticleID	:	4534
ArticleDOI	:	10.1186/gb-spotlight-20020719-01
ArticleCitationID	:	spotlight-20020719-01
ArticleSequenceNumber	:	200
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2002–7–19 OnlineDate : 2002–7–19
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

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Understanding the genetic variation of the malarial parasite, *Plasmodium falciparum*, is of enormous importance in the continued fight against this public health scourge, but the degree of genetic diversity of *Plasmodium* has been unclear. Two papers in the 18 July Nature, show that *P. falciparum* is a genetically diverse and complex organism with mechanisms to evade both host immunity and other pharmaceutical antimalarial efforts.

John Wootton and colleagues at the US National Institutes of Health (NIH), Bethesda, Maryland, examined microsatellite markers covering the 14 haploid chromosomes of *P. falciparum*. They observed that the level of genetic diversity varies substantially among different regions of the parasite genome, revealing extensive linkage disequilibrium surrounding the key chloroquine resistance gene (CQR) *pfcrt*, and at least four CQR founder events (*Nature* 2002, **418:**320-323).

In the second paper, Jianbing Mu and colleagues, also at NIH, analyzed single nucleotide polymorphisms (SNPs) from 204 genes on chromosome 3 of *P. falciparum*. They identified 403 polymorphic sites, including 238 SNPs and 165 microsatellites, from five parasite clones, establishing chromosome-wide haplotypes and a dense map with one polymorphic marker per ~2.3 kilobases. In addition, they estimate the time to the most recent common ancestor to be ~100,000-180,000 years which coincides with the beginning of the human population expansion (*Nature* 2002, **418:**323-326).

"In principle, *P. falciparum* might rapidly develop resistance to multiple drugs. The genes also seem to have moved across continents with frightening speed, implying that there would be little time to contain the spread of new resistance genes," comments Andrew Clark of Cornell University in an accompanying News and Views article.

References

1. Wootton JC, Feng J, Ferdig MT, Cooper RA, Mu J,Baruch DI, Magill AJ, Su XZ: Genetic diversity and chloroquine selective sweeps in *Plasmodium falciparum*. *Nature* 2002, 418:320-323., [http://www.nature.com]

2. US National Institutes of Health, [http://www.nih.gov/]

3. Mu J, Duan J, Makova KD, Joy DA, Huynh CQ, Branch OH, Li WH, Su XZ:.Chromosome-wide SNPs reveal an ancient origin for *Plasmodium falciparum*. *Nature* 2002, 418:323-326., [http://www.nature.com]

4. Cornell University, [http://www.cornell.edu/]

5. Clark AG: Malaria variorum. *Nature* 2002, 418:283-285., [http://www.nature.com]