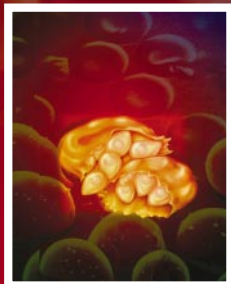


Good 'omics' for the poor?



Cover illustration
Infected red blood cells liberating *P. falciparum* merozoite parasites. (Image credit: Debbie Maizels.)

This week marks a milestone in malaria research, with the publication of complete genome sequences for the human parasite, the apicomplexan *Plasmodium falciparum* (this issue of *Nature*), and its vector, the mosquito *Anopheles gambiae* (*Science*, 4 October). Some may warn against excessive optimism, because the global problems caused by malaria are daunting (see Malaria Insight, *Nature* 415, 669–715, 2002; News and Views, this issue, pp. 493–497; News Features, pp. 426–430). As an antidote to pessimism, let us celebrate the science you will find in this section, which will without doubt aid researchers in the fight against malaria.

Plasmodium falciparum is the first eukaryotic parasite for which we have a complete genome (pp. 498, 527, 531 & 534). The large proportion (70%) of predicted genes already validated experimentally allow firm conclusions to be drawn about the evolution of metabolic pathways. Comparison with the human genome also reveals some pathways that are specific to the pathogen or its peculiar organelles; these will usher in the development of specific drugs with lesser side effects. Completion of a second full genome, that of the model rodent malaria parasite *P. yoelii yoelii*, allows, for the first time, the comparison of two eukaryotic species within a single genus: *Plasmodium* (page 512). Despite their evolutionary similarity, these pathogens exhibit striking differences in their immune evasion strategies. The immediate availability of two state-of-the-art proteomics studies provides stimulating new insights for the development of both drugs and vaccines (pp. 520, 537). Newly discovered patterns of gene expression during the *Plasmodium* life cycle will lead to strategies for targeting several parasitic stages at once.

The fruits of applying this knowledge may take years to materialize, so could this be just another end of a beginning? We believe not. This major achievement will maintain the momentum in the scientific community worldwide. Researchers have already used the freely available PlasmoDB database (p. 490) to identify new potential antimalarial drugs (*Nature Medicine* 7, 167; 2001). In the same spirit, all of this section's contents, along with seminal malaria research, news and features articles previously published in *Nature*, are available free online (www.nature.com/nature/malaria). A CD-ROM containing similar items, plus an interactive GenePlot from PlasmoDB, will be distributed with a future issue of *Nature*, bringing this wealth of information to researchers in countries with limited Internet access. That high-tech genomics and proteomics are being mobilized against the emblem disease of poverty is a good omen indeed.

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