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The *Plasmodium falciparum*genome

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In the October 3 Nature, a collaborative team of researchers from The Institute for Genomic Research, The Wellcome Trust Sanger Institute and the Stanford Genome Technology Center reports the genome sequence of the malaria parasite *Plasmodium falciparum* (*Nature*, **419:**498-511, October 3, 2002).

Malaria kills over one million people a year and some estimates predict that the number of cases may double in the next two decades. *P. falciparum* is the most lethal of the human *Plasmodium* species and an international effort to sequence its genome began six years ago.

Gardner *et al.* carried out whole chromosome shotgun sequencing of *P. falciparum* clone 3D7 and observed that the genome is 22.8 Mb long, organized into 14 chromosomes and has an unusually high A+T composition (averaging 80.6% and rising to 90% in introns and intergenic regions). They predict that there are around 5,300 protein-coding genes, half of which contain introns. About half of the predicted genes match with results from proteomic and EST analyses. The *P. falciparum*genome exhibits minimal redundancy of tRNAs, lacks long tandem repeats of rRNA genes and has a complex subtelomeric repeat structure.

Unsurprisingly the *P. falciparum* genome contains large numbers of genes implicated in cell adhesion and evasion of the host immune system, but a relative dearth of genes encoding enzymes and transporters, and around 60% of the predicted genes could not be assigned a function - more than found in other eukaryotes. The malaria parasite harbors an 'apicoplast' (an organelle thought to be plant derived) that is necessary for survival, and which has a 35 kb genome that encodes about 30 proteins that may be supplemented by as many as 551 nuclear-encoded proteins. Perhaps as a consequence of this, the *P. falciparum* genome is more similar to that of *Arabidopsis* than to any other sequenced eukaryotic genome.

The authors report extensive analysis of genes involved in metabolism, membrane transport, DNA metabolism, secretory pathways and immune evasion. They expect the genome sequence to stimulate the identification of potential antigens for vaccine development programmes and the design of high-throughput immunological assay systems.

The availability of parasite, vector and host genomes offers a unique opportunity to understand the complex interactions underlying malaria and could spur the development of new strategies to combat the disease.

References

1. Gardner MJ, Hall N, Fung E, White O, Berrimsn M, Hyman RW, Carlton JM, Pain A, Nelson KE, Bowman S, *et al.*: Genome sequence of the human malaria parasite *Plasmodium falciparum Nature*, 419:498-511, October 3, 2002., [http://www.nature.com/]

2. The Institute for Genomic Research, [http://www.tigr.org]

3. The Wellcome Trust Sanger Institute, [http://www.sanger.ac.uk/Projects/Protozoa]

4. Stanford Genome Technology Center, [http://www-sequence.stanford.edu/group/malaria]

5. Plasmo Db, [http://plasmodb.org]