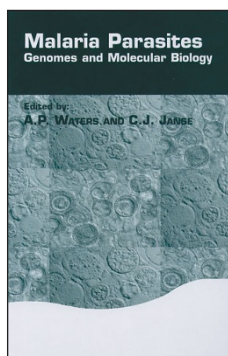


Postgenomic Plasmodium



Malaria Parasites: Genomes and Molecular Biology

Edited by Andy Waters & Chris Janse

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Reviewed by Mike Dyer

I was pleased to be given this copy of *Malaria Parasites: Genomes and Molecular Biology*, edited by one of the most respected teams in parasitology: Andy Waters and Chris Janse of the Leiden University Medical Centre, The Netherlands. Its depth and coverage are second to none.

At this price, the volume unfortunately will not adorn the bookshelves of every student parasitologist. It most certainly will be found, however, in every research group working on any aspect of any species of malaria parasite, the library of every college and university that teaches parasitology and in the collections of many other individuals interested in the biology of the Apicomplexa.

The release of this book could not be more timely, coming swiftly on the heels of the sequencing of the three genomes: those of the human host, *Plasmodium falciparum* parasite and *Anopheles gambiae* vector. It offers a comprehensive and highly readable account of the international collaborative effort to overcome the technical obstacles of sequencing the *P. falciparum* genome, one of the most AT-rich on record. It also brings together in a series of fully referenced review chapters by leaders in their fields the current state of knowledge of malaria parasite biology, including the findings from the genome and subsequent global expression analyses. Although each chapter provides independent, up-to-date coverage of a particular aspect of malaria research, the impact of the *P. falciparum* genome sequence and the application of the postgenomic technologies stitches it together into an exhibition-like whole. The book is themed around this pivotal period in biological research in which single (often *in silico*) experiments can release a previously unthinkable quantity of meaningful data. (Meaningful, that is, if only we can extract answers to appropriate questions by application of the correct analysis.) One chapter, called “Getting the most out of bioinformatics resources”, catalogs the tools now available to do just this—to help design new experimental approaches and include the appropriate controls. The chapter is a fine bioinformatics primer

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designed specifically for malaria researchers and avoids getting bogged down in the inner workings of many of the common tools. Plenty of references are provided alongside a compendium of online resources. It sets out how the data are generated, stored in relational databases, and analyzed by a series of queries. It makes excellent use of screen views from PlasmodB for illustration and the reader is guided step-by-step through the application of a series of database queries intended to elucidate candidate vaccine antigens. The approach's power becomes apparent but it is balanced with an honest explanation of the main pitfalls. This chapter (chapter 3) would have been more logically placed immediately after chapter 1, “The genome of *Plasmodium falciparum*”, but because it is unlikely that many people will read the entire 546-page book straight through, the ordering of chapters is not of paramount importance. (I surprised myself by completing it in just three mammoth, and I must say rather pleasant, reading sessions.)

The big step from gene sequence and expression data to biological function is addressed directly in the chapter titled “Manipulating the genome”. A historical account of the development of the current *Plasmodium* genetic toolbox is given, emphasizing the need for development of systems for conditional mutagenesis and random integration for the generation of functional mutants. To offset the tone of doom and gloom, the recent developments in gene targeting studies are celebrated and areas of investigation from which these developments may arise are explored. The value of the rodent malaria models for functional characterization of genes is well-presented, and using the virtually complete genome sequence of the rodent model malaria parasite *P. yoelii yoelii*, the usefulness of comparative analyses of multiple genomes in identifying genes as well as in determining *Plasmodium* evolutionary history and processes is illustrated. As sequencing of other genomes, such as avian and primate model malaria parasites, human field isolates and other Apicomplexa, are in various stages of progress, the call for improvement in computational and experimental methods to keep pace with the availability of whole-genome data is made loud and clear.

Other chapters (there are 16 in total) are dedicated to different aspects of the malaria parasite biology (chromosome structure, control of gene expression, developmental changes in ribosomal RNA gene expression, cell cycle control, the apicoplast, chloroquine resistance) or particular life cycle stages (the invasive merozoite, proteins found on the surface of the infected erythrocyte, sexual development, the ookinete), with an outlier charting the complementary advantages of using two Apicomplexan parasite models, *Plasmodium* and *Toxoplasma*. Each chapter deserves its own review.

My dislikes? Number one has to be the tedious list of individual merozoite antigens, each given meticulous coverage, which makes this the longest chapter at a yawn-worthy 80 pages.

The book is complete, with down-to-earth assessment of where the genome may lead in terms of malaria control through both drug and vaccine development. Full of conundrums and surprises, the parasitic biology of *Plasmodium* is revealed in all its molecular glory as never before.

Buy it. ■