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Exploring Parasite Genomes

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Preface

Information concerning parasite genomes will be fundamental to the future directions of parasitology research in the new millennium. Already the complete sequences of numerous pathogenic bacteria are available to the scientific community. These sequences contain essential information and clues on drug targets and vaccine candidates and will eventually help to unravel the mechanisms whereby pathogens succeed in their often complex and intricate life cycles. The void between a complete genome sequence of a pathogenic organism and the tools for its control might be truly enormous but the sequence provides the essential foundation for future study. Considerable progress has been made over the last five years to transfer genome technologies to eukaryotic pathogens and it was timely for the British Society for Parasitology to consider parasite genome research at the Autumn Symposium in September 1998. The meeting provided the opportunity to consider the rapid progress being made in various parasite genome projects, bioinformatics of genome analysis (including availability and access) and the exciting possibilities for research in the post-genomic era.

Parasite genome research is neither easy nor straightforward. Parasite genomes vary widely in size and ease of analysis. Some parasite genomes such as those of *Schistosoma* (170 MB) are far too large to contemplate complete genome sequencing at present, others such as *Trypanosoma* show surprising plasticity in relation to their chromosomes, whereas the AT-rich genome of *Plasmodium* means that large fragments are generally unstable in *E. coli*. In addition, the complex life styles of parasites often restrict the availability of experimental material but pose interesting questions in relation to development and gene expression. In 1995 the World Health Organization launched genome projects for three protozoa and two helminth parasites which formed a useful addition to the ongoing work on *Plasmodium falciparum*. This provided the necessary seed money and impetus to form international collaborations to commence the immense tasks of gene discovery and physical mapping. The chapters in this volume arising from the meeting provide a clear statement of the current state of parasite genome analysis. We were particularly fortunate to have Derek Hood and Elizabeth Winzler (the Wellcome Trust Lecturer), who provided information on bacterial and yeast systems respectively, which allowed intriguing insights into the remarkable research possibilities that open up once complete genome sequences are established. Current state of progress was reviewed for Protozoa by Chris Newbold and Jennie Blackwell and for Helminths by Steve Williams (The Pfizer lecturer) and David Johnston. Analysis of genome data presents many new challenges, Dan Lawson and Mark Blaxter together with Martin Aslett presented papers concerned with the use of genome data-bases and showed how to maximise the potential value of the available information. Much interest lies in the function of newly discovered genes and in the manipulation of parasite and host populations. The potential for manipulation of parasite genomes was highlighted by talks from Dominique Soldati on *Toxoplasma* and Catherine Lilley on plant parasitic nematodes.

This volume marks a step along the way to a more complete understanding of parasite genomes. Many new genes have been discovered and many now await more detailed characterization. As new technologies and funding become available the speed of data acquisition will increase enormously. There can be little doubt that the generation and efficient handling of genome data will significantly enhance our ability to understand and control parasitic diseases.

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