
Preface

Parasitic diseases remain a major health problem throughout the world, for both humans and animals. For many of us, our technologically advanced lifestyle has decreased the prevalence and transmission of parasitic diseases, but for the majority of the world's population, they are ever present in homes, domestic animals, food, or the environment. The study of parasites and parasitic disease has a long and distinguished history. In some cases, it has been driven by the great importance of the presence of the parasite to the community, for example, those that affect our livestock. In other cases, it is clear that applied research has suffered for lack of funding because the parasite affects people with few resources, such as the rural poor in resource-poor countries. These instances include the so-called "neglected diseases," as defined by the World Health Organization (WHO).

Parasites have complicated life cycles, and a thorough understanding of the unique characteristics of a particular parasite species is vital in attempts to avoid, prevent, or cure infection or to alleviate symptoms. Of course, the biological characteristics that each parasite has developed to aid survival and transmission, to avoid destruction by the immune system, and to adapt to a changing environment are of lasting fascination to basic biologists as well. The elegance of these biological systems has ensured that the study of protozoan and metazoan parasites also remains an active field of research in countries where the diseases are not a threat to the population.

Over the last decade, we have seen the increasing application of genomics technology to the study of parasites and parasitic disease. Malaria genomics was first, and we can thank the timely intervention of the World Bank/United Nations Development Program/WHO Special Program in Tropical Diseases Research for the fact that several parasites causing neglected diseases also entered the genome sequencing programs at a relatively early stage. The nuclear genomes of the protozoan parasites malaria, African and South American trypanosomes, and *Leishmania* are complete or close to completion. Comparative genomics programs involving shotgun sequencing of genomes of related species are already underway. Several other organisms have benefited from substantial expressed sequence tag programs, such as the protozoans *Toxoplasma* and *Eimeria* and the metazoan parasites *Schistosoma* and *Filaria*, prior to entering a genome-sequencing program.

However, relatively few of the world's parasites will have the luxury of a genome sequencing program. Also, the field of parasitology encompasses a

vast range of organisms, single-celled and multicellular, extracellular and intracellular, that offer different advantages and disadvantages for genome analysis. For this reason, it is not simple to compile a volume of methods that are widely applicable. For example, extraction of DNA or RNA from extracellular parasites that may be cultured *in vitro* or *in vivo* is usually relatively facile, but extraction of pure parasite nucleic acids is more difficult when working with intracellular parasites. Where neither *ex vivo* culture nor *in vivo* growth in laboratory rodents is possible, the use of many of the techniques described in *Parasite Genomics Protocols* is severely limited. Many of the protozoan parasites have no or few introns, such that genome sequencing is particularly efficient for gene discovery. However, the very high (80%) adenine-thymine content of the *Plasmodium falciparum* genome and the astonishing polymorphism of the *Trypanosoma cruzi* genome both required the development of new methods for sequencing and algorithms for analysis. Transformation of organisms with foreign DNA is considered a vital part of efficient functional genomic analysis, yet this is only possible in few species.

Parasite Genomics Protocols begins with three reviews from two major sequencing centers to set in context the genome data that are available. Different sequencing approaches result in different types of datasets that can be confusing for the user. Annotation is an often misunderstood area, and it is vital to understand its strengths and its limitations to avoid over- or underinterpretation of the data presented. The multiplicity of databases can also prove frustrating if the user is not able to appreciate the basis of the different decisions taken by developers. Chapters 1–3 aim to help researchers avoid the obvious pitfalls and to gain access to these resources with minimum frustration.

The remaining chapters describe methods that may be loosely grouped under one or more umbrellas headed genomics, functional genomics, or postgenomics. Some of these protocols have been enabled or facilitated by the availability of DNA sequence and/or by the biological resources created by the sequencing programs, such as microarray analysis. Some techniques were developed without regard to the availability of whole-genome sequence data, but are now seen as major players in the functional analysis of novel genes identified in sequencing programs, such as RNA interference, gene knockout, mutagenesis, and others. Included are protocols that are also applicable to organisms for which limited sequence data are available, such as rapid amplification of cDNA ends (RACE), subtraction libraries, amplified fragment length polymorphism (AFLP) analysis and others. We can see from the various methods presented that genome sequencing, annotation, and the development of user-friendly databases are essentially enabling technologies, allowing

researchers to progress more rapidly in their genetic research while opening new avenues for global analysis.

I would like to thank all the authors of *Parasite Genomics Protocols* for the care they took in preparing their detailed protocols and for their suggestions of additional chapters. I would also like to thank John Walker, the series editor, for his help with editing. I especially thank Vanessa Toone for her time and care during the critical phase of preparation for publishing. I am very aware that this is but a snapshot of the relevant research being carried out in laboratories across the world and, indeed, that new applications are already on the horizon. However, we have aimed to provide sufficient details and tips to allow interested researchers to assess which of these techniques may be applied and developed for the study of their parasite of interest.

The full scientific potential of the availability of genome sequence and associated resources is not yet realized, neither in actuality nor in our imagination. For those of us who will remember the before and after, it will be exciting to reflect in years to come on their contribution to rapid progress in the study of the molecular biology and biochemistry of these fascinating organisms in the 21st century.

Sara Melville



<http://www.springer.com/978-1-58829-062-5>

Parasite Genomics Protocols

Melville, S.E. (Ed.)

2004, XVI, 452 p., Hardcover

ISBN: 978-1-58829-062-5

A product of Humana Press