
Preface

Parasitic diseases caused by both protozoal and helminth pathogens afflict hundreds of millions of people across the globe and are a significant cause of morbidity and mortality. While the main burden of disease occurs in the tropical and subtropical regions of the world, they have a significant impact in all societies. Unlike other infectious agents, there is a total lack of vaccines and chemotherapy options are often limited or have to be carefully managed to minimize toxicity to the patient. Many of these diseases, in particular those caused by vector borne parasites restricted to tropical regions of the world, lack investment in drug development such that frontline treatments utilize medicines developed many decades ago. The advent of whole genome sequencing of larger organisms such as parasites has led to renewed impetus in identifying druggable targets for future development. This together with increasing funding from philanthropic and not for profit organizations has led to new investment in targeting these neglected diseases.

The advent of affordable next generation sequencing has had a dramatic effect on the methodologies employed to research almost all areas of human health. The declining cost and increasing availability of sequencing has led to an era of massive data generation and provision of publically available annotated genomes. This has provided the platform for the generation of new large-scale methodologies that go beyond the static genome allowing for renewed insight into the structure, function, and adaptability of these pathogens. Although the size and complexity of parasite genomes has resulted in this field not benefiting from this technology as rapidly as other fields in infectious disease research, we are now in an era where large-scale genomic, transcriptomic, proteomic, and metabolomic data are being made readily available via public data repositories. Utilizing this data from these “omics” studies is the challenge faced by researchers with access to such huge data resources. *Parasite Genomics Protocols, Second Edition* is designed to detail the methodologies that have been adapted to research these unique organisms in the postgenomic era. While the parasites investigated in these studies represent the most significant of the protozoan and helminth pathogens involved in human disease, these methods are equally relevant to other related organisms of either veterinary or ecological importance.

One of the most important resources available to the researcher is the public databases and repositories that house genomic and postgenomic data. These have evolved from static data repositories used predominantly by a select few to complex relational databases accessible by anyone with an Internet browser that can be comprehensively interrogated by users with minimal training or bioinformatics skills. As well as the ability to construct complex queries, users can also download selected data to their computer for separate analysis and publication. Cooperation between research centers has also led to the linking up of databases providing a one-stop solution to users accessing a platform they are familiar with. The first chapter of *Parasite Genomics Protocols, Second Edition* details the methods used to use and query EuPathDB the largest of the parasite-specific data resources that is made up of a family of genus-specific datasets all linked together and utilize the same format such that a single set of instructions can be applied to all databases either singularly or collectively.



<http://www.springer.com/978-1-4939-1437-1>

Parasite Genomics Protocols

Peacock, C. (Ed.)

2015, XII, 367 p. 49 illus., 34 illus. in color. With online files/update., Hardcover

ISBN: 978-1-4939-1437-1

A product of Humana Press