

PREFACE

A bittersweet truth in our fast-paced genetic world is that an organism-specific book on genetics and genomics is outdated by the time it goes to print. This is especially true for the burgeoning field of Oomycete genetics and genomics where the foundations for genetic discovery have only recently been laid. Ten years ago who would have thought there would be genome sequences for multiple *Phytophthora* species, a *Hyaloperonospora*, and soon, a *Pythium*? Strangely enough, these reference genomes may themselves soon be viewed as archaic. Although only touched on in the chapter on genome sequencing, the ongoing quest to develop faster and less costly genetic sequencing has led to sequencing platforms that make it feasible to discover *all* of the changes between multiple whole genomes or transcriptomes — without the need for a reference genome. With so much forward momentum, there is *never* a good time to stop and take stock of where we've been. Our goal is to provide a useful overview of this fascinating group: a resource that can be handed to an incoming graduate student, a new colleague or a potential collaborator.

The book begins by presenting an overview of the evolutionary relationships within the Oomycetes. The diversity of life forms is astounding, and it is clear that additional taxa and sequences will continue to clarify this important area of research. The white blister rusts provide a good example of how genetic data can resolve relationships among morphologically similar yet evolutionarily distinct taxa — an important challenge in an age of costly quarantines and worldwide movement of pathogens. Interesting possibilities spring from the phylogenetic perspective, including the idea that terrestrial plant pathogens may have hitched an evolutionary ride from the open sea via nematodes and switched hosts to plant roots — on more than one occasion. For those

interested in discovering whole new worlds of diversity, a plethora of lower oomycetes are waiting, particularly in the Tropics and Polar regions. A question lingering throughout is whether the parasitic lifestyle is derived from a saprophytic lifestyle or vice versa.

After the introductory chapters is an overview of asexual and sexual reproduction. This provides a useful framework for the next sections, which explore the population structure of representative species in natural populations, and the interactions with plant and animal hosts. These chapters range from overviews of the entrenched pathogen of potato, *Phytophthora infestans*, a staple crop and staple research area since the dawn of micro-organism research, to newly emerging invasive species such as the Sudden Oak Death pathogen, *Phytophthora ramorum*. For investigators familiar with the impact of Oomycetes on sessile organisms, the chapters on Oomycetes that attack fish, crustaceans, and humans should be particularly interesting. And finally, there are specific chapters describing the application and development of molecular tools to better understand these notoriously intractable organisms.

The response by the authors to contribute their work and perspective was overwhelmingly positive, and we are hopeful that this snapshot will stimulate new relationships and research.