Preface

The ability to cost-effectively and rapidly sequence genomes, advances in computational biology and development of high-throughput technologies that facilitate dissection of the ever-expanding list of "omics" has revolutionized research approaches within the biological sciences. For example, the concept of reverse vaccinology has brought antigen identification into the genomics era, and bioinformatics tools can now be used to select and prioritize a list of candidate vaccine antigens from predicted pathogen proteomes for further testing. In addition, the ability to infer metabolic capacity based on pathogen genome sequences has resulted in the identification of several targets for chemogenomics, a discipline that may lead to the generation of novel chemotherapeutics. These two tangible outputs, candidate vaccine antigens and drug targets, have energized efforts in developing improved methods of pathogen control. In addition, development of genome-wide molecular diagnostic tools provides an opportunity to study pathogen genotypes and population dynamics, and should allow those all-important correlates with phenotype to be made. Thus, genomics technologies are now being used to develop a holistic approach to study the genetics of host and pathogen populations and their molecular responses to each other at a level of detail not previously possible. Application of genomics technologies to study the process of infection, disease, vaccination, and interventions leading to immunity is likely to result in building databases, which will help realize the holy grail of developing rational approaches for pathogen and disease control.

The scope for a book on genome mapping and genomics of animal-associated microbes is too huge. We decided to exclude viruses and nonpathogenic microbial associations and chose livestock as the target animals. We concentrated on selecting bacterial or protozoan pathogens of global and developing country significance. We also picked pathogens whose genome sequence has been available for a few years so that the impact of genomics in driving research would be more apparent to the reader. Of the six pathogens chosen, most affect ruminants, and three are vector-transmitted, increasing the complexity of their "animal" associations but providing another target for potential intervention.

We are grateful to the senior authors and co-authors of the chapters presented in this volume, as they have done a marvelous job in summarizing complex topics. They have provided excellent overviews of their pet pathogens as well as comparative aspects with related pathogens. Remarkable progress has been made in studying the organisms reported on here and the next few years promise exciting scientific breakthroughs in both basic and applied pathogen biology.

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