
Preface

The turn of the century not only ushered in a new millennium, but the age of microbial genomics with the genome sequence of the first plant pathogen *Xylella fastidiosa*, the bacterium that causes citrus variegated chlorosis. At that time, knowledge of genomes of agriculturally significant microbes was extremely limited. In an effort to improve the situation, the United States Department of Agriculture (USDA) offered a competitive grants program in 2000 to support the sequencing of agriculturally relevant microorganisms. In the following year, the United States National Science Foundation (NSF) partnered with USDA to jointly offer a competitive grants program that would support genome sequencing for more diverse microorganisms. The USDA/NSF Microbial Genome Sequencing Program was offered for 10 years. During that time, USDA supported the sequencing of a large number of agriculturally important microbes, including bacteria, viruses, fungi, oomycetes and even a nematode. Some of the most expensive projects were jointly funded by USDA and NSF. Other sequencing projects were completed in collaboration with the United States Department of Energy's (DOE) Joint Genome Institute (JGI). In addition, NSF and DOE supported the genome sequencing of microbes of importance to other areas of science. The last year of the USDA/NSF Microbial Genome Sequencing Program was in 2009, by which time sequencing costs had decreased dramatically and sequencing speed had increased tremendously. USDA's support for microbial genomics had shifted toward functional analysis of the sequenced genomes. This book describes how the availability of the genome sequences of some agriculturally important plant-associated fungi, many of which were first sequenced with support from the USDA, has revolutionized our understanding of these eukaryotic microorganisms. This book also describes how knowledge derived from genomics can be translated into improved ways of managing microbes so as to increase the sustainability of agriculture in the United States and around the world.

Genome sequence information from fungi and oomycetes has laid the foundation for significant increases in knowledge of their lifestyles, their dynamic evolution, and how they interact with plants. New approaches for functional analysis of the genomes are accelerating the progress toward novel understanding and improved management methods.

In this volume on "Genomics of Plant-Associated Fungi: Monocot Pathogens," each chapter describes the genomic analysis of a genus, species

or group of related fungi. Some of these genera contain species that attack dicot hosts, but we include them here because they include important pathogens of cereals and other monocot plants. A companion volume, which we have also edited, is entitled “Genomics of Plant-Associated Fungi and Oomycetes: Dicot Pathogens.” A third volume (edited by Dr. Dennis Gross, Dr. Ann Lichens-Park and Dr. Chittaranjan Kole) describes the genomic analysis of plant-associated bacteria. Taken together, these three volumes illustrate some fundamental discoveries about these microbes with regard to the overall structure of their genomes, their lifestyles, and the molecular mechanisms that form the basis of their interactions with plants. Many of the genomes described exhibit considerable variation in DNA content, even among related species, illustrating selective invasion and expansion of repetitive genetic elements. Some genomes, such as those of *Phytophthora* species, show a large degree of conservation in gene content and colinearity (synteny) among related species. On the other hand, species of *Cochliobolus* and *Mycosphaerella* are more diverged but they exhibit mesosynteny, where gene content is conserved within chromosomes but gene order is not. In other genera, gene conservation is minimal. Some fungal genomes, such as *Pyrenophora tritici-repentis* are unstable and dynamic with large differences in genome size and chromosome number within a population. A number of chapters show that fungal genes, DNA segments (*Verticillium*) and even chromosomes (*Fusarium*, *Alternaria* and *Mycosphaerella*) can move within species, genera, or even across kingdoms. In many instances, these events affect pathogenicity and host range.

Biotrophic fungi feed on living organisms. Genomics has provided new insights about fungal lifestyles, such as obligate biotrophy. Mildews, rusts, and other fungi that are obligate biotrophs have lost many genes involved in primary metabolism (for example, nitrogen, sulfate and amino acid biosynthesis) and also secondary metabolism. Indeed, *Blumaria* and other powdery mildews have only half of the gene content of related fungi. Necrotrophic fungi live on dead plant material. Genome structural and functional analysis has revealed the necrotrophic lifestyle to be more sophisticated than once thought. Necrotrophs possess effectors, typically gene products that affect the development of diseases on host plants. Moreover, necrotrophs do not contain an excess of genes for degradation of plant material. Regulation of these degradative genes, rather than expansion of them, may be the key to the necrotrophic lifestyle.

Genomics has led to practical advances and the understanding needed to implement fair and effective policies. Beginning in 2013, all fungi must have a single name as determined during the Nomenclature Session at the Botanical Congress in Melbourne. It is no longer acceptable to use the anamorph or teleomorph names. Genome sequences, which are the foundation of modern classification, have clarified the species concept in some instances but in other cases the “One Fungus One Name” concept has prompted much debate and controversy among mycologists. A name has important federal and global implications. For example, clear nomenclature is needed for effective quarantine policies.

Fungal diagnostics has been greatly advanced through genomic technologies. The ability to accurately distinguish between closely related pathotypes is another requirement for effective quarantine policies. This can be very important for tracking devastating plant pathogens, such as the Ug99 pathogen that causes wheat stem rust.

Genomic studies of populations enable accurate reconstruction of previous disease epidemics, notably that of *Phytophthora infestans*, the oomycete pathogen that caused the notorious Irish potato famine. Genomic information enables predictions about the spread and evolution of new races. Knowledge about changes in race structure, including fungicide sensitivity, provides insights that influence fungicide use and contribute to improved plant breeding and cultivar release.

We wish to express our thanks to all of the authors and co-authors who contributed to the chapters in this volume. They have done a tremendous job, clearly describing the novel findings and exciting advances enabled by genomics with regard to the microbes addressed in their chapters. We also wish to specifically thank some current and former employees of USDA, NSF and DOE whose support has been invaluable to the success of the microbial genomics program and to the existence of this volume. These people are Dr. Sonny Ramaswamy, Dr. Colien Hefferan, Ms. Betty Lou Gilliland, Ms. Erin Daly, Mr. Edward Nwaba, Dr. Deborah Sheely, Ms. Cynthia Montgomery, Dr. Michael Fitzner, Dr. Daniel Jones, Ms. Pushpa Kathir, Dr. Anna Palmisano, Dr. Mark Poth, Dr. Maryanna Henkart, Dr. Daniel Drell, and all of the USDA and NSF Program Officers and Staff who worked with Dr. Ann Lichens-Park while the Microbial Genome Sequencing Program was offered. Space limitations prevent us from describing the roles played by each of these individuals but their contributions were significant and we are immensely grateful to all of them.

Dr. Ralph A. Dean
Department of Plant Pathology
Center for Integrated Fungal Research
North Carolina State University
Raleigh, NC, USA

Dr. Ann Lichens-Park
United States Department of Agriculture
National Institute of Food and Agriculture
Washington, DC, USA

Prof. Chittaranjan Kole
Bidhan Chandra Krishi Viswavidyalaya
Mohanpur, West Bengal, India

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Dean, R.A.; Lichens-Park, A.; Kole, C. (Eds.)

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