
Preface

The first genome of a plant pathogen (*Xylella fastidiosa* that causes citrus variegated chlorosis) was published in 2000. In that same year, the United States Department of Agriculture (USDA) first offered a competitive grants program to support sequencing of agriculturally relevant microorganisms. At that time, only a few microbes of agricultural significance were being sequenced. In 2001, the United States National Science Foundation (NSF) joined USDA, and the jointly-offered program was expanded to support the genomic sequencing of an even broader range of microorganisms. The partnership lasted until 2009, by which time sequencing costs had decreased dramatically and sequencing speed had increased enormously. USDA's support for microbial genomics shifted more towards functional analysis of genome sequences. During the 10 years that the genome sequencing program was offered, the genomes of a large number of agriculturally significant microorganisms were sequenced with support from the USDA, including bacteria, viruses, fungi, oomycetes, and even a nematode. The genomes of microbes relevant to basic science were sequenced with funding from the NSF. Three books are being published to describe the impact of some agriculturally relevant genomes and their analysis. In addition to this volume, two other volumes (edited by Dr. Ralph Dean, Dr. Ann Lichens-Park and Dr. Chittaranjan Kole) describe the genomic analysis of plant-associated fungi and oomycetes. These volumes are entitled "Genomics of Plant-Associated Fungi: Monocot Pathogens" and "Genomics of Plant-Associated Fungi and Oomycetes: Dicot Pathogens." This book describes how the availability of some agriculturally important plant-associated bacterial genomes, many of which were first sequenced with support from the USDA, have revolutionized our understanding of these bacteria and how they can be managed to improve the sustainability of agriculture worldwide.

Bacterial genome data is a launching pad (or scientific springboard) that, with appropriate functional analysis, can lead to greater knowledge of bacterial evolution and diversity, ecological adaptation, and environmental influences on gene expression and phenotype. Because

bacterial genomes are generally much smaller than the genomes of eukaryotic organisms, important insights about how the bacteria function can be obtained from appropriate functional analysis, often in less time than that needed for such analyses employed in higher eukaryotes. At the same time, studies aimed at understanding how bacteria interact with plants can lead to new insights about important plant processes and metabolic pathways, some of which may be exploited by bacterial pathogens to cause diseases. As is explained in the chapter on the genomics of *Xanthomonas oryzae*, the availability of xanthomonad genomic information has led to discoveries of new technologies such as transcription activator-like effector nucleases (TALENs) that facilitate targeted genome editing and will revolutionize approaches to genetic engineering in eukaryotes.

Each chapter in this book describes the genomic analysis of a particular bacterial genus, species or group of related bacteria about which the genome sequence and genomic analysis have led to significant new insights. Some chapters address bacterial pathogens that are readily tractable to genetic analysis and are, therefore, considered to be good model systems. *Pseudomonas syringae*, the subject of two chapters, is an important pathogen and a model system. Other chapters focus on bacterial pathogens that are less tractable genetically, but which are responsible for diseases that can result in devastating economic losses for growers. *Xanthomonas citri* causes citrus canker, a disease that can result in severe losses to citrus crops. One chapter focuses on *Pseudomonas fluorescens*, which is a beneficial bacterial species that can help prevent diseases in plants. The very first plant pathogen, *Erwinia amylovora*, was first described in the 1800's and is the subject of one of the chapters. The fastidious phloem-limited bacteria, exemplified by the phytoplasmas and the liberibacters, were first described in recent years, and are each the subject of one chapter.

Several "themes" run through the chapters in this volume. These include the growing evidence for the importance of horizontal gene transfer or "nature's transgenes" in originating new bacterial strains and species. Advances in transcriptomic analysis are facilitating studies describing complex regulatory networks critical to expression of processes important in plant-microbe interactions. The technology is leading to identification of new bacterial factors or products that mediate communication with and establishment in the plant host. Genomic studies of plant-associated bacteria promise to lead to a better understanding of the natural microbial communities associated with plants (the phytobiome) and to innovative means of controlling diseases caused by plant pathogens.

We wish to express our thanks to the lead authors and co-authors of the chapters in this volume. They have done a marvelous job of

explaining the advances and significance of the new knowledge described in their chapters. We also wish to express our thanks to some special people who are current or former employees of USDA and NSF whose support has been critical to 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, and all of the USDA and NSF Program Officers and staff who worked with Dr. Lichens-Park while the Microbial Genome Sequencing Program was offered. Space limitations prevent us from describing each of the roles played by these individuals but they all have been significant and we are extremely grateful to all of them.

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