

Preface

After the rediscovery of Mendel's research at the dawn of the 20th century, maize became the model genetic organism in the plant kingdom because of the simplicity of its analysis, particularly the ease of outcrossing and phenotyping. These facile technologies, rapidly joined by unmatched cytogenetics and mutagenesis, allowed the initiation of study into what has turned out to be a very complex genome. Although maize nuclear DNA content is less than half that of the average flowering plant, it is the most complicated genome in any species to be currently slated for full genome sequence analysis. Most of the maize genome, and most of the plant DNA on this planet, is comprised of transposable elements (TEs). Although first discovered in maize, TEs have been found to be ubiquitous across all the kingdoms of life and are the major motive force in the evolution of plant genome structure. Most of these TEs are kept silent, most of the time, by epigenetic regulation that itself may have arisen primarily as a mechanism to minimize the damage induced by parasite-like TEs and true parasites such as viruses. Perhaps the abundance of TEs in maize, and their close association with the great majority of genes, partly explains why the discovery that epigenetic phenomena existed and could regulate genes was also first made in maize.

In Volume II of *The Maize Handbook: Genetics and Genomics*, we have recruited chapters that describe part of the rich history of maize genetics, the history and modern practice of maize improvement, the nature and dynamics of the maize genome, the ever-strengthening toolkit of maize genetic technologies, the genetics of some important maize gene families, and a vision for the future of maize genetics. These chapters were provided by the leaders in their disciplines, both in maize and in the wider field of genetics, and they present state-of-the-art descriptions of the key areas in plant genetics and genomics.

The first two chapters describe the origins of maize genetics, featuring the exceptional contributions of East, Emerson and McClintock. Chapter 3 provides a very personal view, from Schwartz and Hannah, of the role of maize in the origin of the field called plant molecular biology. The development of one of the great glories of maize research, its outstanding collection of mutations with dramatic phenotypes, is described in Chapter 4. Chapters 5–7 describe modern maize improvement, from its US origins in the 19th Century, including its demonstration

of the commercial value of hybrid vigor, through the focus on maize as a biotech target, to the current practice of maize breeding in the public and private sectors. Chapters 8–24 provide the most comprehensive description of the nature, biology and evolution of any plant genome yet published, with particular emphases on the great wealth of knowledge that continues to be amplified from TE studies. Chapters 8–11 emphasize maize genome structure and evolution, while chapter 12 by Dawe describes our current understanding of maize centromere structure and origin. Chapters 20–22 feature epigenetic characterization of maize, a field that is certain to continue to rocket towards insights of exceptional importance for understanding the evolution of complex regulatory circuits. Chapter 24 provides a comprehensive analysis of the organellar genomes in maize.

Chapters 25–34 supply a sampling of the major genetic and genomic technologies that are now in place in maize study, and indications of how these technologies are likely to improve in the foreseeable future. Chapter 28 on transposon tagging from McCarty and Meeley and Chapter 31 on transformation from Wang and co-workers describe components of vital reverse genetic tools that will soon lead maize into an era of unprecedented genetic study. Chapters 35–38 discuss some of the most important sets of genes in the maize genome, from regulatory loci to the genes responsible for cell wall synthesis (and for the possible future role of maize as a lignocellulosic source of liquid biofuels). Chapter 39 describes one person's prediction of the future of maize genetics, and its possible contributions to food, feed, energy and high-value industrial products.

In sum, Volume II of *The Maize Handbook: Genetics and Genomics* provides the most comprehensive analysis available of modern maize genetics and genomics, set in the historical context of how this important field of research arose. The visionaries who provided the chapters in *The Maize Handbook* also indicate where they see their disciplines headed, and how maize will contribute to this future. Maize has generated nearly a century of exceptional genetic discovery, and the rate of novel observations that this organism provides shows a continuation of its decades-long upward trajectory. We hope Volume II, and *The Maize Handbook* in its entirety, provides a valuable tool for understanding and further characterization of maize, other plants, eukaryotes, and the full spectrum of life on earth.

Handbook of Maize

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