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## Preface

Ever since Darwin, biologists have been interested in understanding the intricacies of natural variation patterns and the evolutionary forces that shape this diversity. Although these dual objectives have long been central goals in evolutionary biology, they recently have assumed a new prominence arising from the development of breathtaking new genomic technologies and their application to natural systems. These technological leaps have invigorated the already thriving discipline variously referred to as *molecular evolution*, or *genome evolution*, or sometimes *evolutionary genomics*, empowering it with a vastly expanded insight into the diversity of genomes and their evolutionary dynamics. As a result, excitement in the discipline has never been higher. Notwithstanding this vibrancy and the attendant meteoric rise in the number of published papers and professional journals devoted to molecular evolution, remarkably few books on the topic are available. To be sure, there are a number of classic texts, written more than a decade ago, just as the genomics revolution was ramping up, and a larger suite of hybrid books variously combining aspects of bioinformatics, genome evolution, population genetics, and methods of phylogenetic inference. To date, however, there exists no single modern treatment of what we have learned about the diversity and evolution of plant genomes and their various genomic residents.

It was to fill this void that the present project was initiated. Inspired by the seemingly ever-expanding pace of insights into the evolution of plant genomes, and motivated by the desire to provide for students and researchers a single point of entry into a burgeoning literature, we invited leading authorities in plant molecular evolution to participate in a project aimed at providing a comprehensive (but not encyclopedic) yet accessible introduction to the current state of the art in the field. This is accomplished here in a total of 16 chapters that collectively cover the discipline. Although these are arranged in a logical progression and are interconnected, each chapter also serves as a stand-alone introduction and review, thus providing a text that may flexibly be used by advanced undergraduate students, graduate students, and professionals in many fields in the plant sciences and beyond.

The volume appropriately begins (Flagel and Blackman, Chap. 1) with a review of the immense insights that have been gleaned from plant genome sequencing projects, as well as a prospective view of both the promises and challenges that lie ahead. This is followed by two complementary chapters on the primary constituents of plant genomes, namely, transposable elements (TEs); the first of these (Kejnovsky et al., Chap. 2) focuses on the diversity of TEs, their genomic ecology, and their role in genome size evolution, whereas the second (Slotkin et al., Chap. 3) reviews the remarkable role TEs play in genetic and epigenetic regulation, and as evolutionary fodder for the origin of novel genes and for chromosomal evolution. Perhaps the most obvious features of chromosomes are centromeres and telomeres, for which our knowledge regarding structure and evolution have been dramatically increased by genomic technologies, as reviewed by Hirsch and Jiang (centromeres, Chap. 4) and Siomos and Riha (telomeres, Chap. 5).

Having described the major structural features and organization of plant genomes, we turn our attention to smaller genomic residents, including small RNAs, for which Lee et al. (Chap. 6) present a synopsis of the diversity, regulatory roles, and evolution of the different classes of small RNAs. This is followed by a chapter on genic evolution, with a special focus on rate variation within and among lineages and the utility of this information for timing divergence events (Burleigh, Chap. 7), and on the detection and significance of conserved non-coding DNA (Subramaniam and Freeling, Chap. 8). Mowers et al. (Chap. 9) and Wolf (Chap. 10) offer timely reviews of the structure and evolutionary dynamics of plant mitochondrial and plastid genomes, respectively.

One of the key emergent realizations of the genomics era has been that plant genomes are replete with evidence of historical and ongoing duplications, large and small. Barker et al. (Chap. 11) review the processes that generate duplications as well as their longer term evolutionary outcomes, whereas Nieto-Feliner and Rossello (Chap. 12) present an update on a curious non-Mendelian consequence of sequence multiplicity, namely, sequence homogenization via one or more means of “concerted evolution”. Paterson et al. (Chap. 13) further describe the consequences of genome duplication and divergence on longer-term colinearity and syntenic relationships among divergent lineages. A final consequence of genome divergence, variation in base composition, is considered by Šmarda and Bureš (Chap. 14), who provide an overview of the phenomenon and its possible causative forces. We close with two chapters devoted to the vibrant new frontier of plant epigenomics, one (Zhang, Chap. 15) describing the epigenetic landscape in plants and the various forms of chromatin modification, and the second (Richards et al., Chap. 16) devoted to the evolutionary signification of epigenetic variation.

We are living in a tremendously exciting time to be a biologist, perhaps one that in the future will be thought of as having been a “golden era”, replete with technological and conceptual breakthroughs. We hope that you find this volume evocative in this sense, as stimulating to read as it was to produce, and inspiring in the promise of its content.

Of course there are many people to thank for bringing this project to fruition. First and foremost are the many authors, who are experts in their field and hence are very busy people. Yet they willingly and generously set aside the time to imagine and create their contributions. To them I offer my sincere appreciation. I also offer thanks to many of my professional colleagues, who reviewed drafts of the manuscripts and offered numerous insights and suggestions for improvement. It should go without saying that this book would not have been possible without the vision of the publisher, Springer-Verlag, who recognized that this volume would fill an important and presently largely vacant niche, and for moving the project along expeditiously toward completion. Finally, I need to express my delighted gratitude to my co-editors of this soon-to-be two volume set, Ilia Leitch, Jaroslav Doležal, and especially Editor-in-Chief Johann Greilhuber, for their many modes of assistance throughout project conception and execution.

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