

Preface

Polyploidy (whole-genome duplication; WGD) is common in plants and has long been considered as both an important speciation mechanism and a crucial component of plant genome structure. Analyses of chromosome numbers and hypothesized breaks between diploid and polyploid base numbers have suggested anywhere from 30 to 80 % of all angiosperms are polyploid. While recent polyploids may be easily detected through comparison of chromosome numbers, various processes of diploidization or fractionation may substantially alter chromosome numbers and structure, ultimately masking the evolutionary history of duplication events. In contrast, other footprints of ancient WGD may remain in the genome, even when chromosome numbers no longer carry the signature of past WGDs. Genome sequences and other sources of genomic data tell us that, in fact, all angiosperms, as well as all seed plants, have undergone one or more rounds of polyploidy. Furthermore, ancient WGD characterizes all vertebrates, with subsequent, more recent polyploidization in fishes and amphibians. Ancient WGD is also evident in the genomes of yeast and other fungi. While more common in plants than other major lineages of life, polyploidy is now recognized as a fundamental process in all crown eukaryotes. Polyploidy plays a major role in shaping genome structure and organization and in establishing patterns and mechanisms of gene regulation. In fact, it is now impossible to construct models of genome evolution that do not account for genomic content and genetic interactions contributed by WGD.

It has been over 30 years since the publication of a comprehensive treatment of polyploidy [*Polyploidy: Biological Relevance*, W. H. Lewis (ed.), 1980]. The intervening years have witnessed a technological revolution with a transition from the early days of recombinant DNA to nearly routine genome sequencing of non-model organisms and from limited biological computing to high-performance computing networks for the biological sciences. These transformations in methodology and computation permit fresh perspectives on polyploidy and the ability to ask old questions with new tools.

Over the past decade, it has been a dream of ours to publish a book that synthesizes the rapid progress in understanding the role of polyploidy in genome

evolution, and this book is now a reality. In the current volume, we have compiled the expertise of scientists studying polyploid genome evolution from multiple perspectives in phylogenetically diverse organisms. Topics range from the conceptual and theoretical underpinnings of polyploidy (chapters by McGrath and Lynch, Birchler) to processes at work in polyploid genomes (Zielinski and Mittelsten Scheid, Finigan et al., Evans et al.), to patterns of ancient polyploidy and its detection (Burleigh, Paterson et al.), to a series of case studies that both document attributes of genome evolution in focal species and address general properties of polyploid genomes, from ancient polyploids [maize (Schnable and Freeling), legumes (Doyle), vertebrates (Cañestro), fishes (Braasch and Postlethwait), yeast (Hudson and Conant)] to classic model polyploids [cotton (Wendel et al.), tobacco (Kovarík et al.), wheat (Feldman et al.)] to very recent ones [*Spartina* (Ainouche et al.), *Senecio* (Hegarty et al.), and *Tragopogon* (Soltis et al.)]. The emerging paradigm from these studies is that polyploidy—through alterations in genome structure and gene regulation, some of which occur shortly after polyploid formation—generates genetic and phenotypic novelty that manifests itself at the chromosomal, physiological, and organismal levels, with long-term ecological and evolutionary consequences.

We thank our many colleagues, students, and postdocs for lively and challenging discussions on polyploidy and its many evolutionary consequences. We further acknowledge the support of the U.S. National Science Foundation (Grants 9624643, 0346437, 0614421, 0919254, and 0922003) and thank the National Evolutionary Synthesis Center for its hospitality during the preparation of this book.

Gainesville, April 2012

Pamela S. Soltis
Douglas E. Soltis



<http://www.springer.com/978-3-642-31441-4>

Polyploidy and Genome Evolution

Soltis, P.; Soltis, D.E. (Eds.)

2012, VIII, 420 p., Hardcover

ISBN: 978-3-642-31441-4