

Preface

Grasses dominate many natural ecosystems and produce most of the calories consumed by humans either directly in the form of grains or indirectly through forage/grain fed animals. In addition, grasses grown as biomass crops are poised to become a significant source of renewable energy. Thus, the enormous economic and environmental importance of grasses is undeniable. Despite this, research into grass biology has been hampered by the lack of a truly tractable experimental model system. While much valuable research has been conducted in crops like maize, rice, wheat, and barley, none of these grasses possess the full suite of traits necessary for a truly tractable model system (e.g., small size, rapid generation time, small diploid genome, self-fertile, simple growth requirements, and easily transformed). The power of applying a model system approach to plant biology has been amply demonstrated by the tremendous advances achieved using *Arabidopsis thaliana* as a model organism. Unfortunately, *A. thaliana* is a eudicot and about 150–200 million years of evolution separates it from the grasses. Thus, there are many biological traits unique to the grasses for which *A. thaliana* is an unsuitable model. Furthermore, even for shared traits the specific genes and regulatory networks often differ considerable between *A. thaliana* and the grasses. Thus, there is a pressing need for a grass model system. Over the past decade, *Brachypodium distachyon* has emerged to fill this void.

This book describes the current state of *B. distachyon* research tools and how they have been applied to a wide range of topics. Specific chapters describe the development of key resources and techniques including a high-quality reference genome sequence, the development of high-efficiency transformation methods, the creation of a large collection of insertional mutants, the assembly of extensive germplasm collections, genome sequencing of natural accessions, the optimization of efficient crossing techniques, and the creation of recombinant inbred lines. Chapters focused on the application of these tools cover a wide range of topics including cell wall biosynthesis, seed development including starch and storage protein biosynthesis, microRNA and small RNA biology, cytogenetics, adaptation to local environments, abiotic stress, plant–pathogen interactions, root biology, and

flowering time. In addition, recent advances using closely related *Brachypodium* species as models for perenniality and polyploidy are described.

That the current state of *Brachypodium* research can fill a book is a testament to the maturity of the system. Additional evidence in this regard includes the enormous number of seed orders distributed and the rapidly rising number of publications using *B. distachyon* as an experimental model. In comparison to other model systems, this maturity has come at an exceptional pace. In a little over a decade *B. distachyon* has gone from a curiosity to a full-blown model organism used by over 350 laboratories around the world. This explosive growth followed a new paradigm in which a genome sequencing project was initiated early on in the development of a model system. The genome project catalyzed both the rapid development of experimental tools and the adoption of the system by many researchers. While this “sequence it and they will come” strategy helps explain the rapid rise of *B. distachyon* as a model for the grasses, another crucial factor was the conscious effort by a handful of early *B. distachyon* researchers to freely share material and information long before publication. This fostered the development of a collaborative and open community ethos that is the fertile ground necessary to grow a model system. As *B. distachyon* emerges from adolescence, its future is indeed bright.

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