

Preface

Among flowering plants, several “warm-season” grasses are the most efficient at fixing atmospheric carbon, thanks to “C4” photosynthesis, a complex combination of biochemical and morphological specializations discovered in sugarcane that increase net carbon assimilation at high temperature. The Saccharinae clade of grasses is of singular importance, including one cereal that is fifth in importance among the world’s grain crops, as well as three leading biofuel crops, and several of the world’s most noxious weeds.

Sorghum bicolor L. Moench. is a leading cereal, fifth in importance among the world’s grain crops. Introduced into the USA about 200 years ago, sorghum is grown on 8–10 million acres and has a farm-gate value of ~\$1 billion/yr. *Sorghum* is unusually tolerant of drought, a feature essential in the US Southern Plains that often receive too little rain for other grains. In arid countries of northeast Africa, sorghum contributes 26–39% of calories in the human diet. Increased demand for limited fresh water, along with rising global temperature and aridity, suggest that sorghum will be of growing importance.

Expansion of agriculture to provide plant biomass for production of fuels and/or feedstocks will require additions to our present repertoire of crops. The Saccharinae clade of grasses shows singular promise, including three leading biofuel crops, *Saccharum* (sugarcane, the world’s #1 fuel ethanol crop), *Sorghum* (currently the #2 source of seed-based fuel ethanol in the USA, and a promising potential source of cellulosic ethanol), and *Miscanthus*, a promising potential cellulosic ethanol crop with much higher yield than another leading candidate, switchgrass, in the US Midwest. Its adaptability to continental Europe shows the feasibility of producing *Miscanthus* in temperate latitudes.

The *Sorghum* genus also includes one of the world’s worst weeds “Johnsongrass” (*S. halepense*), a naturally occurring polyploid hybrid that reduces yields of many crops by up to 45 %. The first federal appropriation for weed control research targeted Johnsongrass. Functional genomic data may lead to new strategies for environmentally benign plant growth regulation, suppressing weed dispersal. Better understanding of reproductive barriers in sorghum may lead to strategies to reduce risk that transgenic *S. bicolor* outcrosses with *S. halepense*.

An important breeding line of *Sorghum bicolor* recently became only the second monocot to have its genome essentially fully sequenced, providing an important complement to the previously sequenced genome of rice and opening new doors into the study and improvement of members of the clade. As a model for the tropical grasses, sorghum is a logical complement to *Oryza* (rice). Sorghum is representative of warm-season grasses in that it has “C4” photosynthesis, while rice is more representative of temperate grasses, using “C3” photosynthesis. The ~740 megabase sorghum genome, with ~90 % of DNA and ~98 % of genes placed in their chromosomal context, is a logical bridge to the ~2,500 megabase maize genome that is also being sequenced, and the ~4,000 megabase genome of sugarcane, the world’s leading biomass/biofuels crop. Sorghum shared common ancestry with maize (12–15 million years ago, mya) and sugarcane (5–9 mya) much more recently than rice (42–47 mya). The most recent genome duplication in sorghum appears to be ~70 mya versus ~12 mya in maize and <5–9 mya in sugarcane with lower genetic redundancy promising a higher success rate in relating sorghum genes to phenotypes.

For a multitude of reasons—invigorated interest in biofuels, concerns about a looming worldwide water crisis, the need for more precise and more environmentally benign methods of weed control—the Saccharinae clade has seen a resurgence of interest in the past few years. The Saccharinae have an important role to play in a more bio-based economy and a more sustainable agroecosystem. Sequencing of additional members of the clade has begun, building on their rich histories of conventional breeding and genetics research, but constrained by the challenges of their large and complex genomes. In this book, we seek to share with you, the reader, our enthusiasm about the advances in genetics and genomics of the Saccharinae of the past few years and those that loom on the horizon.

In closing, a clarification of nomenclature is important. As described in detail in Chap. 1, the taxonomic nomenclature of the species that are the focus of this book remains unclear. For the purposes of this book, the authors have been encouraged to adopt the view expressed and explained in Chap. 1, that it appears appropriate that subtribe Sorghine (presently including sorghum) should be merged into subtribe Saccharinae (including *Saccharum* and *Miscanthus*). Accordingly, the chapter authors have been encouraged to refer to the Saccharinae as inclusive of all three taxa.

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