Preface

The biggest challenge facing agricultural scientists is to feed an ever-increasing human population, which is expected to reach 9.1 billion by 2050. The demand for cereals, for both food and animal feed uses, is projected to reach around 3 billion tons by 2050 from 2.1 billion tons today. This gap is to be filled in spite of decreasing availability of arable land, deteriorating soil fertility, and increased incidences of climatic extremes. Under that context, agriculturists need to make the agricultural practices more climate resilient. Sorghum is the fifth most important cereal crop after rice, wheat, maize, and barley, and is extensively grown in the semi-arid tropics of the world thanks to its inherent ability to tolerate harsh environments. Thus, this is a model crop among grass species to study stress response and ensuring food security for millions of poor masses living in the most impoverished drought-prone regions of the world. Sorghum not only provides food and feed but also serves as an important source of fodder for large cattle with its dry stover. Green plants are also a source of forage for cattle. In recent years, sweet sorghum has turned out to be a source of ethanol production and second-generation lignocellulose-based biofuels. Thus, sorghum has the potential to provide food, feed, fodder, and fuel.

Unlike other cereals such as rice, wheat, and maize, sorghum received lesser attention with regard to genetic and genomics studies in the past. The lesser economic importance of sorghum is the principal reason behind this. However, over the last two and a half decades much progress has been made in this area. After publication of the rice genome sequence, sorghum turned out to be a natural complement to rice in understanding the complexity of the genomes of this most important group of crop plants, that is, the grass family. With its proximity not only to cereal crops but also to commercial crops including sugarcane, sorghum has turned out to be a model crop to initiate genomics research through syntenic studies. With publication of the sorghum genome sequence in 2009, the scenario was revolutionized and this neglected crop started receiving prominence in genomics studies. Stress tolerance of the crop proved to be an added advantage for its popularity.

Over the period of a few decades many reports on sorghum genomics as well as transgenic research have come into the public domain, which deals with almost all traits related to the crop. These studies have exhibited promise to improve the crop further in terms of stress tolerance and yielding ability.
This has also opened up opportunity to improve other related crops as well, using the genomics information generated in sorghum.

The current volume, Compendium of Plant Genomes: The Sorghum Genome, comprises 15 chapters. Chapter 1 deals with the global status of the crop and its economic importance. It has been observed that sorghum yield levels have increased in almost all the sorghum-growing regions except Africa, and this has been achieved both due to genetic gains in the released cultivars and better crop management. Consumption of sorghum as food is declining because of changes in food habits and consumer preference. However, use for animal feed and other industrial purposes is increasing. The world sorghum trade is mainly linked to demand for livestock products. Chapter 2 is devoted to the botany, floral biology, and classification of sorghum and their implications for the breeding methods to be used. It highlights how understanding of botany and taxonomy could be effectively used for improving sorghum yield and nutritional quality.

Genomic studies of a crop are partially dependent on availability of cytogenetic information on it. Due to inherent small sizes of sorghum chromosomes such studies are scanty. Chapter 3 details the progress in molecular cytogenetics that has paved the way for genome sequencing of the crop and for understanding its genetic architecture. Furthermore, sorghum germplasm is best characterized among crop plants, which have been grouped into core and mini-core collections and a genotyping-based reference set. These have been characterized systematically to identify sources of resistance against various stresses and quality traits. All these developments are narrated in Chap. 4.

Completion of sorghum genome sequencing after that of Arabidopsis and rice is a big step leading to widespread genomics applications. Chapter 5 elaborates international private and public efforts leading to sorghum genome sequencing. The chapter also discusses a postgenomic scenario in the context of next-generation sequencing and beyond. Progress in sorghum genomics leading to elaborate syntenic studies with allied and model genomes as well as the computation needs and implications have been described in Chap. 6. Progress in crop genomics has forged a new path of gene mapping in the form of association mapping, paving the way for genomic selection. As compared to fine cereals and maize, progress in this regard in sorghum is meager. The current status is dealt with in Chap. 7.

Although sorghum is relatively stress tolerant, like other crop plants its productivity is affected by various stresses, including biotic and abiotic stresses. Chapter 8 explores the application of genomic approaches such as large-scale genotyping and high-throughput sequencing towards genetic linkage mapping, association studies, and marker-assisted selection for biotic stresses. Chapter 9 describes similar progress for abiotic stresses, for which less success have been recorded. Chapter 10 provides the current status of the application of genomics tools in improving sorghum grain quality, be it starch quality or composition of seed proteins and nonstarch polysaccharides. Underground root architecture plays a vital role in moisture and nutrient acquisition by the plants from the soil, which most commonly remains...
unexplored. Chapter 11 focuses on sorghum root architecture, its screening tools, and the status of QTL analysis.

Overexpression and gene knockout studies play a vital role in gene discovery and their characterization; both are dependent on efficient transformation protocols. Chapter 12 examines studies that improve transformation efficiency in sorghum and enhance biotic and abiotic stress tolerance and nutritional quality using transgenic approaches. Chapter 13 reviews positional or map-based cloning of economically important genes/alleles and their characterization leading to their effective deployment in improvement of sorghum. The chapter further describes cloning strategies used to identify the underlying mutations of economic significance. TILLING, a reverse genomics tool, and its variant eco-TILLING, are novel tools for the discovery of genes and/or their mutant forms. Chapter 14 provides an account of this new dimension in TILLING/Eco-TILLING and its implication in sorghum genomics. Plant–microbiome interaction is a very dynamic phenomenon, being influenced by environmental stimuli. Such studies are limited in sorghum, which are elaborated in Chap. 15. Genomics and transcriptomics studies, which can be designed to understand the microbial communities associated with sorghum, are also described in this chapter.

The chapters of this book have been authored by a team of scientists who are expert in their respective fields of research in sorghum involving both conventional and genomics tools. Sincere efforts have been made to avoid overlapping in contents, however, some overlapping in isolated spots is unavoidable.

Some books in this area have already been published in the recent past by an international group of scientists. We have made efforts to include updated information in the chapters, and we believe that this book will be of much use to the sorghum research community. Any omission in the book is our responsibility and will be addressed in future editions.

We express our sincere thanks to the 42 contributors for their chapters. We sincerely appreciate their continuous cooperation starting from first submission of drafts to revision of their chapters matching with the reviews. We also thank our family members for bearing with us throughout the process of editing and finalization of this book.

Finally, we put on record our most sincere thanks to the series editor, Prof. C. R. Kole for giving us this opportunity to edit this book and Springer-Verlag and its entire staff, particularly Dr. Jutta Lindenborn and Ms. Abirami Purushothaman, for their kind understanding and help in publication and promotion of this book. We hope that this book will be useful to students, scientists both in academia and industry, and policy makers.

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