
Preface to the Volume

Soybean [*Glycine max* (L.) Merr.] is the most important legume crop, which is a great source of both protein and oil. Soybean seeds contain approximately 40% protein and 20% oil. Soybean is an important source of protein in animal and fish feed in addition to human nutrition. In recent years, soybean is also becoming a source of biodiesel. Soybean root fixes nitrogen through symbiosis with a rhizobacterium, *Bradyrhizobia japonicum*, improving soil health. More than 30% of the world's soybean crop is produced in the USA and is valued at around \$40 billion annually. Brazil and Argentina are other two major soybean-growing countries, followed by China and India.

Soybean was originated in East Asia. It was first domesticated over 8000 years ago in China, 5000 years ago in Japan, and 3000 years ago in Korea. It was introduced to Asian countries, such as India, Indonesia, the Philippines, Vietnam, Thailand, Cambodia, Malaysia, Burma, and Nepal between 1 AD and 1600 AD. To the major soybean-growing countries, soybean was introduced only in the recent years viz to the USA in 1765, Argentina in 1882, and Brazil in early 1950s. Over the last few years, there is a growing interest in expanding soybean cultivation in Africa. The soybean has a very narrow genetic base; most cultivars can be traced to the same handful progenitor lines. In recent years, wild species are utilized through hybridization to broaden the genetic base of modern soybean cultivars.

Considering economic importance and narrow genetic base of soybean, molecular genetics and genomics approaches are becoming vital to ensure steady increases in yield potential to meet the food and nutritional demands of over 9 billion people by 2050. Fortunately, with the advent of second- and now third-generation sequencing platforms, we are able to identify and use the genetic potentials of available germplasm in designing new soybean cultivars that are expected to meet the everincreasing nutritional demands of billions of people under the changing growing conditions, anticipated from climate change. The objective of this book is to bring attention of the readers including students to the recent advances in soybean genetics, breeding, and genomics along with resources essential for highly needed genetic improvement in soybean.

The book comprises 13 chapters with Chaps. 1 and 2 describing the economic importance and botanical aspects of soybean, respectively; with the last chapter (Chap. 13) providing the description and navigation of the

SoyBase; the toolbox for molecular markers, genetic and physical maps, mutants, metabolic pathway, gene expression, a Gbrowse for the soybean reference genome, literature searches to facilitate soybean genomic, genetic, and breeding research. The next six chapters (Chaps. 3–8) provide in-depth reviews on molecular markers, molecular maps, structural and comparative genomics, genome-wide association, and application of molecular resources in breeding soybean. Molecular markers and molecular maps essential for developing predictive selection programs for complex traits such as seed, protein, and oil yield are described in Chap. 3. The chapter reviews classical markers, then RFLP, RAPD, AFLP, SSR, and then SNP molecular markers and maps. The chapter also reviews the use of second-generation sequencing in generating tens of thousands of SNP markers for developing SNP maps from crosses involving wild species and cultivars.

Chapter 4 describes detection, description, and development of structural variation in the soybean genome and how to incorporate these polymorphisms in ongoing soybean research and genetic improvement. Genome assemblies and structural variations among a large collection of soybean genotypes obtained from resequencing are presented in Chap. 5. The Chap. 6 reviews comparative genomics in soybean and that of cultivars with accessions of a wild relative for identifying genes involved in defense response, cell growth, and photosynthesis.

In the USA, soybean germplasm collection is composed of nearly 22,000 accessions including 19,648 modern and landrace cultivars (*G. max*), 1168 wild relatives of soybean (*G. soja*), and 1184 perennial wild species. Most lines of the collection have been genotyped for 52,041 SNP loci making it feasible to conduct genome-wide association studies (GWAS). Chapter 7 reviews GWAS conducted for identification of candidate genes for various agronomical traits, seed composition, seed weight, nitrogen traits, photochemical reflectance index, resistance to soybean cyst nematode, and brown stem rot. The Chap. 8 describes progresses made in implementing tightly linked molecular markers in breeding and introgressing quantitative trait loci/genes that control important agronomic traits.

The next four chapters (Chaps. 9–12) review the recent advances in functional genomics of soybean through analyses of mutants created by the chemical mutagen ethyl methanesulfonate, gene silencing, or transposon-induced mutation. The Chap. 9 reviews application of targeted induced local lesions in genomes (TILLING) to identify mutations within soybean genes of interest. TILLING facilitates conducting both forward and reverse genetics in plant species, and this chapter reviews what has been accomplished in soybean with an example of functional characterization of a soybean cyst nematode resistance gene *Rhg4* encoding serine hydroxymethyltransferase (SHMT) involved in one carbon metabolism. The chapter also documents—the identification of suitable mutants through TILLING for improving quality of oil in soybean and the approach can be applicable also to any traits of interest. Chapter 10 describes the recent advances in virus-induced gene silencing, gene silencing through RNAi in stable transgenic plants, and gene editing systems in soybean.

In Chap. 11, landscape of the transposable elements (TEs) including retrotransposons and type II or DNA transposons in soybean is described. As in other crop species, retrotransposons with long terminal repeat retrotransposons are a major component of the soybean genome that are preferentially accumulated in the pericentromeric regions of all chromosomes and are inactive; but they can be activated under certain stressful conditions. In Chap. 12, application of heterologous transposon systems and an endogenous type II transposon element, *Tgm9*, in tagging and functional characterization of soybean genes is described.

The 13 chapters included in this book have been prepared by experts. We greatly appreciate their contributions. We expect that this book will be a useful reference—for graduate students as well soybean researchers and also researchers of other crop species.

We are grateful to all our colleagues for their contribution. We wish to record our thanks and appreciations for Prof. Chittaranjan Kole, the Series Editor, for his assistance and guidance right from the inception till publication of this book.

Columbia, USA
Ames, USA

Henry T. Nguyen
Madan Kumar Bhattacharyya



<http://www.springer.com/978-3-319-64196-6>

The Soybean Genome

Nguyen, H.T.; Bhattacharyya, M.K. (Eds.)

2017, XII, 211 p. 53 illus., 17 illus. in color., Hardcover

ISBN: 978-3-319-64196-6