
The Chickpea Genome: An Introduction

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Abstract

Chickpea is the second most important cool season grain legume cultivated by small holder farmers in 59 countries across the globe. Chickpea production is adversely affected by several abiotic stresses like drought, temperature extremes (high and low temperatures), salinity, and biotic stresses, e.g., insect, fungal and viral diseases. Until recently breeding for tolerance/resistance to these stresses has been challenged by lower level of natural variation and lack of genomics tools to adopt genomics-assisted breeding. Nevertheless, during recent years large-scale genomic resources like molecular markers, genetic maps, draft genome sequence of both desi and kabuli chickpea have become available as a result of partnership among different institutes and advances in sequencing technologies. The chickpea genome book provides an up-to-date account on developments made over past ten years and presents the road map for future chickpea research. This chapter introduces the book and provides brief summary of 11 chapters included in the book.

1.1 Introduction

Chickpea is the most important cool season food legume cultivated on marginal soils by resource poor farmers in the semi-arid regions of the world. Besides increasing soil fertility, it plays a key role in supplying protein requirements of human population. Chickpea or *chana* (called in Hindi) is used as an edible seed and is also used for making flour throughout the globe. In addition, it is consumed in various forms like roasted as snacks, raw, carbonized, or in broth. The acid exudates from leaves can be applied medicinally

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or used as vinegar, and its starch is suitable for textile sizing, giving a light finish to silk, wool, and cotton cloths. Archeological and botanical evidences suggest that it was used by the “hunter-gatherer societies” for eating and sustaining their communities even before 10,000 B.C (Ladizinsky 1975). Chickpea has its origin in southeastern Turkey, and after its domestication in Middle East, this crop progressed further throughout the Mediterranean region, India, and Ethiopia (Ladizinsky 1975; van der Maesan 1987). Although chickpea is cultivated in 59 countries and on about 13.98 million ha, the productivity is less than 1 ton per ha (FAO 2016; Fig. 1.1). Several abiotic and biotic stresses have been constrained to realization of production potential of chickpea. Further, recent climate changes increased the incidence of droughts, pest (pod borer), and diseases (Fusarium wilt, Ascochyta blight, dry root rot, etc.). Owing to the complexity of these stresses, breeding efforts in past were not much rewarding due to poor understanding of the genetics of the traits. For enhancing the awareness on the economic importance of pulses in food and nutritional security, Food and Agriculture Organization (FAO) has declared the year 2016 as the International Year of Pulses. Chickpea being the most important pulse crop, to meet the growing demand to reduce malnutrition, development of climate-resilient chickpea varieties with sustainable production is challenging task before the chickpea scientific community. Chickpea was

considered as an orphan crop before 2005 for not having sufficient genomic resources to take up genomics-assisted breeding which supplements the conventional breeding programs for crop improvement (Varshney et al. 2005). As a result of several efforts at national and international level, the chickpea is now considered as genomics resources-rich crop (Thudi et al. 2014; Varshney et al. 2016). This book provides an up-to-date information on different areas of chickpea including economic importance, biology, development of genomic resources, and the draft genomes of chickpea and their utilization in chickpea improvement.

1.2 Importance, Botanical Description, and Cytogenetics

Chapter 2 entitled “Economic importance of chickpea: production, value and world trade” written by Muehlbauer and Sarker provides information on chickpea production, value, and trade on a global, regional, and country basis to determine trends in production and product availability through domestic and international export markets. In addition, the chapter also describes the importance of chickpea in supplying human nutrition and its wide use in different dishes across the globe. In Chap. 3 entitled “Botany of chickpea,” Sajja et al. provide insights into origin, distribution, and taxonomic classification of chickpea. Further, a detailed

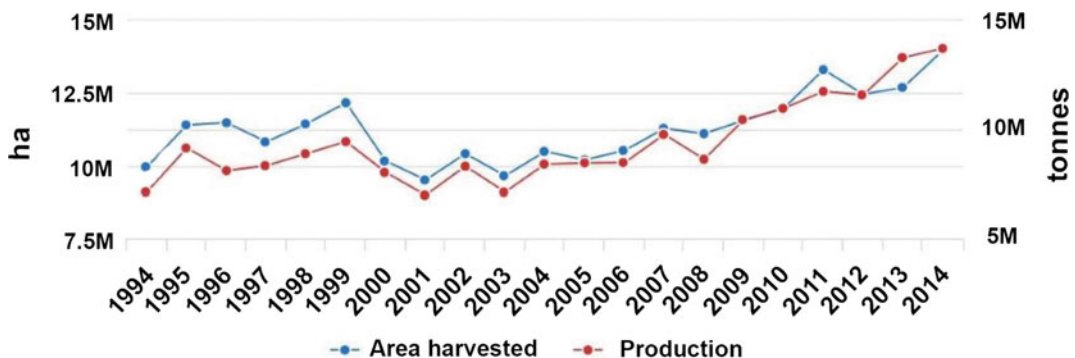


Fig. 1 Chickpea production in last two decades. The graph represents the area under cultivation in million hectares and production in million tons from 1994–2014

botanical description of the species has been provided in this chapter. Cytogenetic research is essential to establish the base information with respect to the karyotype (chromosome number, length, and morphology; and some limited descriptions based on banding) and an estimate of nuclear genome size. Efforts toward understanding the karyotypes and chromosome behavior at meiosis have been summarized by Karafiátová Miroslava and colleagues in Chap. 4 entitled “**Cytogenetics of *Cicer*.**” The chapter also emphasizes the use of flow cytometry as a means to explore the chickpea genome.

1.3 Germplasm, Genomic Resources, and Trait Mapping

Conservation of germplasm and existing variability in the germplasm lines is the key towards addressing new challenges that arise in coming future to feed the millions of people across the globe. Hari Upadhyaya and colleagues provide the details on conservation and management of germplasm resources in breeding programs in Chap. 5 entitled “**Managing and Discovering Agronomically Beneficial Traits in Chickpea Germplasm Collections.**” The chapter also provides the information on the essence of developing the germplasm subsets in the form of core/mini-core collections and genotyping-based reference set to harness the existing germplasm diversity in chickpea improvement programs. In Chap. 6 entitled “**Advances in Chickpea Genomic Resources for Accelerating the Crop Improvement,**” Manish Roorkiwal and colleagues summarize the development of various kinds of genomics tools like molecular markers, genetic maps, and efforts toward dissecting complex traits that hamper the chickpea production and productivity. The chapter also highlights the cost-effective utilization different marker genotyping platforms. Chapter 7 entitled “**Classical Genetics and Gene Mapping**” authored by Deokar and Taran has a major focus on linkage (and QTL) mapping and candidate

gene approaches for trait dissection, understating the genetics of the trait and validity of the genetic basis of the traits. It also provides the historical perspective of markers used for developing various kinds of genetic maps (i.e., sparse genetic maps to high-density genetic maps), and their genetic distances and traits mapped. Chapter 8 authored by Millan et al., as mentioned in the title of the chapter, has a special focus on “**Genetic Mapping and Quantitative Trait Loci.**” Reduced cost of sequencing and resequencing in recent years owing to advances in NGS technologies is bringing a paradigm shift in trait mapping and breeding approaches from marker-based genotyping to sequencing-based genotyping (Elshire et al. 2011). Genotyping by sequencing, skim sequencing, and bin mapping approaches have also been summarized in this chapter.

1.4 Genome Sequence and Beyond

Chapter 9 entitled “**Requirement of Whole-Genome Sequencing and Background History of the National and International Genome Initiatives**” authored by Thudi and Varshney summarizes the background history of two independent efforts to generate draft genome sequence of kabuli and desi chickpea genomes in addition to discussing the requirements of whole-genome sequencing and its importance for crop improvement. Aamir Khan and colleagues summarize the methods adopted and the analysis tools utilized in assembling the kabuli chickpea genome in Chap. 10 entitled “**Sequencing the Chickpea Genome.**”

For faster genetic gains, the use of modern breeding approaches like marker-assisted backcrossing (MABC), marker-assisted recurrent selection (MARS), and genomic selection (GS) has been proven in several crops. Srinivasan Samineni and colleagues in Chap. 11 entitled “**Impact of Genomics on Chickpea Breeding**” summarize molecular breeding efforts of developing improved lines for stresses like

drought tolerance, Fusarium wilt (FW), and Ascochyta blight (AB) resistance. Authors have presented utility of MABC as well as reasons for MARS not being effective in chickpea improvement. The chapter also discusses the usefulness of multi-parent advanced generation inter-cross (MAGIC) populations for trait dissection and harnessing the variability in chickpea improvement. Finally, Editors provide challenges and opportunities for future chickpea research in Chap. 12 entitled “**Future Prospects for Chickpea Research.**”

1.5 Conclusion

In summary, the volume contains useful articles written by eminent scientists in the area of cytogenetics, classical genetics, genomics, and molecular breeding. The successful efforts to breed for drought tolerance, FW, and AB through MABC in chickpea are summarized and well discussed. These efforts need to be extended to other important emerging disease like dry root rot beside enhancing stress resilience in elite cultivars in different chickpea growing regions of the world. Several genomes of thousands of chickpea will enable estimation of genome-wide diversity and untapped benefits of the genomic selection (GS) initially proposed in animal breeding for enhancing the genetic gains in

chickpea (Roorkiwal et al. 2016). Editors are hopeful that readers will enjoy reading the book.

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