
The Pigeonpea Genome: An Overview

1

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Abstract

First two decades of twenty-first century have witnessed a number of advances in genetics and genomics research of pigeonpea. These advances have enhanced our understanding of structural and functional aspects of genome and also provided us opportunities to deal with constraints impeding production of pigeonpea in precise and faster manner. Availability of the draft genome sequence and large-scale molecular markers has made it possible to map traits of interest in speedy manner. Although germplasm re-sequencing has already been started in pigeonpea, large-scale germplasm including elite breeding line, landraces and wild species is expected to be fully sequenced very soon. These sequencing efforts coupled with functional genomics and systems biology will facilitate the identification of genes/gene networks that are involved in expression of agronomically valuable traits. For accelerating genetic gains in the crop breeding, selection efficiency needs to be enhanced by integrating modern genomics in breeding efforts. This book provides a critical assessment on current status as well as future prospects on different aspects of genome, trait mapping, germplasm research and genomics-assisted breeding. This chapter introduces and provides highlights of different chapters of the book.

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1.1 Introduction

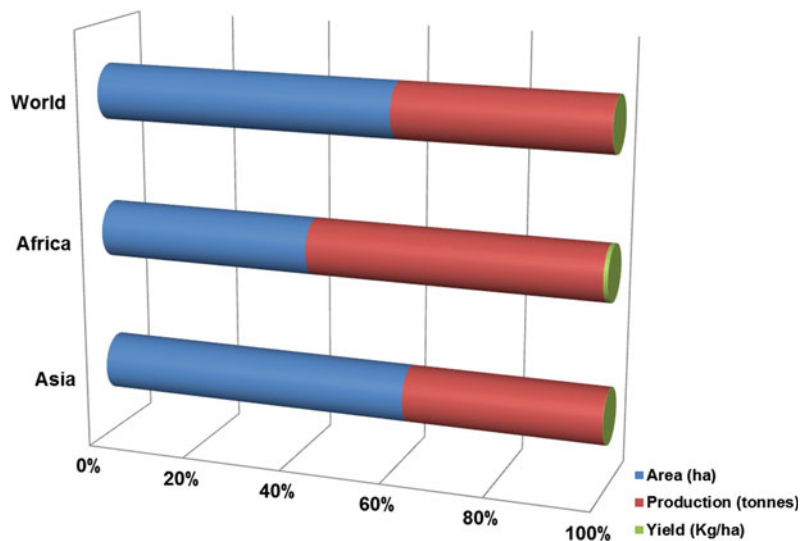
Pigeonpea is considered a resilient crop to environmental constraints and climate changes. It is an important crop for providing proteins in food to the poor people especially in Asia. In present-day scenario, agricultural focus is shifting to “nutritional food security” from just “food security”. Therefore, pulse crops such as

pigeonpea have potential for sustainable agriculture to meet the needs of a fast-growing human population worldwide. However, pigeonpea suffers with a low yield levels due to the exposure of the crop to a number of biotic and abiotic stresses (Saxena et al. 2014). On the other hand, lack of systematic public funding and minimal or no industrial funding support to pigeonpea research and development have also contributed to slow development of varieties with the limited genetic gains in the past. As a result, the crop productivity has remained stagnant for about last six decades (Fig. 1.1). Emphasis of research and funding and support of private sector in pigeonpea was also highlighted by Mr. Bill Gates during his visit to ICRISAT in his blog entitled “Making a Better Pigeonpea” as following: “*It’s also an example of what agricultural development people call an orphan crop, a crop that’s important to many of the world’s poorest people yet largely ignored by the big agriculture companies. Those companies focus on high-value crops like corn and soy that are building blocks of rich-world diets and industry. As a result, their research has boosted yields of those crops by making them more resistant to insects, disease, and drought. The orphans haven’t seen many, if any, of those kinds of improvements*” (<https://www.gatesnotes.com/Development/Visiting-ICRISAT-Agricultural-Research-Center>).

Genomics has made positive interventions on enhancing yield and developing better varieties in many cereals and few legume crops (Varshney et al. 2011). However, the pigeonpea crop, until recently, has largely been untouched with this genomic revolution. As a result, pigeonpea has often referred as “orphan crop”. However, due to the decline in sequencing cost and strong partnerships across different continents, draft genome was assembled for pigeonpea (Varshney et al. 2012) that has provided tools and opportunities for pigeonpea improvement. These tools can be used in a number of ways such as deployment of early generation screening of large segregating populations for must-have traits, gene pyramiding for multiple resistance to specific pathogens and pests within the same cultivar, introgression of superior alleles from landraces and wild species in cultivated material.

In recent years, significant progress has been achieved in the area of pigeonpea genomics. For instance, large-scale genomic and transcriptome resources have been developed and used in germplasm research, trait mapping, molecular breeding as well as functional genomics research (Pazhamala et al. 2015). The present book entitled “The Pigeonpea Genome” therefore aims to present available information on different aspects of research in the area of germplasm, genetics, genomics and breeding. The book also provides

Fig. 1.1 Pigeonpea area, production and productivity in different regions during 2014



approaches and strategies to apply in breeding. Furthermore, in addition to achievements, constraints and future prospects of applications of modern genomics in pigeonpea improvement have also been appraised. The introductory chapter provides an overview of all the chapters of the book in following sections.

1.2 Crop Characteristics, Botanical Description and Wide Crossing

Chapter 2 entitled “Key Plant and Grain Characteristics and Their Importance in Breeding and Adaptation of Pigeonpea Cultivars” by KB Saxena and colleagues provides detailed information on the potential role of different plant and grain characteristics in determining yield and stability of pigeonpea. Yield enhancement is an ultimate target for any crop improvement program, however; there is no straight route for breeding high-yielding cultivars. Breeders have relied on selecting individual traits, which contributing to yield directly or indirectly and limited success has been achieved in pigeonpea. Therefore, in Chap. 2, authors have highlighted various qualitative and quantitative traits related to seed yield, quality and those preferred for marketing and milling. A brief description about their inheritance and association with yield in pigeonpea has also been provided.

Chapter 3, Botanical Description of Pigeonpea authored by Sameer Kumar et al., provides information on the genetic structure of the genus including its origin, variability and geographical distribution of various species. The detailed description on pollination behaviour, adaptability to a range of soil types, temperature and rainfall, ability of nitrogen fixation, root system, branching pattern, growth habit or plant architecture has been provided in this chapter.

Nalini Mallikarjuna and colleagues provide detailed information on the importance and utilization of rich source of genetic variations in Chap. 4 entitled Wide Crossing Technology for Pigeonpea Improvement. This chapter also summarized a thorough knowledge of crossability and concerted efforts to effectively utilize the

immense variation present in the secondary, tertiary and quaternary gene pool. In the end of this chapter, an emphasis has been given to use advances in genomics wide crossing program.

1.3 Genetic Resources and Trait Mapping

Bohra et al. provide information on the modern genomic tools for pigeonpea improvement in Chap. 5. This chapter reviews the progress on generation of genomic resources and highlights their importance in designing future crop breeding schemes. This chapter has assembled the information on the collaborative research efforts which have facilitated development of genomic tools (mapping populations, molecular markers, genome sequence, transcriptome, etc.) for pigeonpea improvement during the last ten years (Pazhamala et al. 2015). Subsequently, Irshad Ahmad Rather and colleagues in Chap. 6 compile molecular mapping efforts on genes and quantitative trait loci (QTL) in pigeonpea. Chapter 7 entitled “Germplasm Characterization and Trait Discovery” authored by Christopher P Krieg and colleagues discusses development of core and minicore collections for better utilization of diverse germplasm in routine pigeonpea breeding program. The chapter also presents about the research priorities for important traits such as yield, resistance to biotic and abiotic stress. Further deployment of modern genomics approaches has been suggested for accelerated trait/gene discovery and development of appropriate genomics tools for key traits to deploy them in routine breeding program to utilize germplasm collection.

1.4 Genome Sequence and Beyond

Two chapters, i.e. Chaps. 8 and 9, explain about various efforts undertaken for *de novo* genome sequencing of pigeonpea and provide background history on genome sequencing efforts and current status on deployment of genome sequence information for crop improvement.

These chapters related to genome sequencing have also discussed about recent advances in establishing high-density genotyping platforms such as genotyping by sequencing (GBS) and Axiom[®] *Cajanus* SNP Array: 56 K, whole genome re-sequencing efforts, etc. In the last chapter (Chap. 10) entitled “Future Prospects”, the editors of book have presented a concise view on future prospects of pigeonpea research. Next-generation breeding including use of next-generation sequencing and high-throughput genotyping for early generation screening, marker-assisted selection, marker-assisted backcrossing and genomic selection as well as genome editing coupled with other advances has been proposed to achieve rapid genetic gains for pigeonpea improvement.

1.5 Conclusion

This book provides up-to-date information about pigeonpea genome and its utilization for germplasm research, advancing genetics, genomics and accelerating breeding practices by a panel of lead pigeonpea scientists across the world. This book does not provide only current landscape of pigeonpea genomics at international level in terms of tools and strategies employed in genome sequencing, transcriptomics, functional analysis,

trait mapping and molecular breeding but also present a road map for accelerating genetics and genomics research for enhancing genetic gains in pigeonpea improvement.

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