Legume genomics: A perspective

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Abstract

Legumes such as chickpea, pigeonpea and groundnut are among the most important crops grown in Asia and Sub-Saharan Africa. India is the major grower as well as consumer of all these legume crops. In fact, India is also the biggest importer of chickpea and pigeonpea. The productivity of these three legumes has been stagnant and unacceptably low for decades as they are grown in marginal environments. Cereals have been the major beneficiary of utilizing genomics approaches in breeding and the above mentioned legumes have started to catch up very recently with cereals and other crops in terms of genomic interventions in their breeding. For instance, last ten years have witnessed significant progress in the area of development and deployment of genomic tools in crop improvement programs. Better genotypes with enhanced levels of resistance to biotic and abiotic stress as well as higher yields have been designed and developed in all three legume crops. Advances in sequencing and phenotyping technologies are expected to see the optimization and deployment of some modern genomics-assisted breeding approaches such as genomic selection, early generation screening, genome editing etc.

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We believe that by integrating genomics in breeding, better seeds can be developed and those seeds coupled with appropriate agronomy and management practices can provide better produce in the farmer's fields.

Introduction

Legumes belong to the family Leguminosae, with edible legumes being placed in the subfamily Papilionoideae. They play a vital role for food security and human health especially in developing countries besides maintaining soil health through biological nitrogen fixation. Legumes are often cultivated in a wide range of environments and soils. Based on cropping season, food legumes are broadly classified as (i) cool-season food legumes, comprised of chickpea (*Cicer arietinum*), pea (*Pisum sativum*), broad bean (*Vicia faba*) and lentil (*Lens culinaris*), (ii) temperate-season food legumes include common bean (*Phaseolus vulgaris*), runner bean (*Phaseolus multiflorus*), lima bean (*Phaseolus lunatus*), and hyacinth bean (*Lablab purpureus*), and (iii) warm-season food legumes include pigeonpea (*Cajanus cajan*), mung bean (*Vigna radiata*), black gram (*Vigna mungo*), adzuki bean (*Vigna angularis)*, cowpea (*Vigna unguiculata*), velvet bean (*Mucuna pruriens*) etc. Soybean (*Glycine max*) and groundnut (*Arachis hypogaea*), in most countries, are classified under oil seed crops as they are cultivated primarily for oil extraction.

Proteinacious legumes along with cereals play vital role in supplying nutritious diets to the vegetarian families around the globe. However, as compared to cereals, the extent of progress made in research and yield enhancement in legumes is far below than the expectation. This is basically due to the fact that cereals were considered as staple food and as a result the nutritious food was ignored in the past. Moreover, global population is expected to reach 8.5 billion by 2030. Therefore the world food production must rise by 50 percent by 2030 to meet the ever increasing demand. Enhancing legume production in the same proportion seems to be a daunting task as legumes are frequently exposed to several abiotic and biotic stresses, and there is less public funding support and limited private sector attention for R&D of legumes (Varshney *et al.* 2016a). On the other hand, many legumes have enormous genetic potential to overcome the yield stagnation and can be transformed in to climate-smart varieties.

Achievements

In terms of research innovations, a number of success stories have become possible in cereals starting from Green Revolution in the second half of 20th century to the modern genomics-assisted breeding products such as Swarna-Sub1 (Septiningsih *et al.* 2009) in early 21st century. Realizing the importance of legumes, a few concerted efforts were initiated recently and reasonable progress has been made. In recent years, legume genomics has been focused on the development of resources such as

molecular markers, genetic maps, transcriptomes etc. (Varshney *et al.* 2016). These resources have been used in enhancing our understanding on genetic control of various economically important traits and deploy them through genomics assisted breeding (GAB) (Pazhamala *et al.* 2016). With the advantage of next generation sequencing (NGS) the legume research is now catching up the pace with limited available resources. As a result of affordable NGS and available genomic resources, in the last decade major legume species have been sequenced and draft genome sequences have been assembled. For instance soybean (Schmutz *et al.* 2010), pigeonpea (Varshney *et al.* 2012), chickpea (Varshney *et al.* 2013a), mung bean (Kang et al. 2014), common bean (Schmutz *et al.* 2014), adzuki bean (Kang *et al.* 2015; Yang et al. 2015), groundnut (Bertioli *et al.* 2016, Chen *et al.* 2016), etc. are now equipped with the draft genome information. Accordingly, now there is a need to deploy the genome sequence information for crop improvement programs in respective legume species. In this direction, some efforts have been initiated in selected crops at different research organizations and universities.

ICRISAT, in collaboration with several partners, both at national and international levels, has been successful in developing and deploying genomic resources for enhancing the productivity of three most important legumes, *viz.,* chickpea, pigeonpea and groundnut, in arid and semiarid regions of the world (Varshney 2016). Besides unravelling the draft genomes in three legumes, several germplasm lines have also been

resequenced (Thudi *et al.* 2016a, b; Kumar *et al*. 2016). The generated genomics information has also been used in developing some superior lines/varieties. Using marker-assisted backcrossing (MABC) approach in chickpea, several improved lines for drought tolerance (Varshney *et al.* 2013b), *Fusarium* wilt and *Ascochyta* blight resistance have been developed (Varshney *et al.* 2014a). Three improved lines have been promoted for advanced varietal trials (AVT) from initial varietal trials (IVT) under All India Coordinated Research Project (AICRP) on chickpea. Similar efforts are also being carried out at Indian Agricultural Research Institute (IARI, New Delhi), Indian Institute of Pulse Research (IIPR, Kanpur) for developing drought tolerant lines in chickpea. In case of groundnut, several improved lines with enhanced resistance to foliar diseases like rust and late leaf-spot have been developed (Varshney *et al.* 2014b). Some of these lines have shown higher yields in multi-location trials conducted in India (Janila *et al.* 2016a). Similarly, using marker-assisted backcrossing, several lines with high Oleic acid/Linoleic acid ratio have been developed in groundnut (Janila *et al.* 2016b). Purity testing kits were developed for ensuring the purity of F_1 hybrids and parental lines, which is most important to realize the full production potential of pigeonpea. Furthermore, by using genomic-segment-introgression from wild species (*C. cajanifolius*, *C. acutifolius*, *C. scaraboides,* etc), some promising lines with enhanced resistance to sterility mosaic disease and higher yield have been developed in pigeonpea and are included in multi-location trials under AICRP-Pigeonpea in India.

Outlook

As mentioned above, the importance, bottlenecks in R&D, and recent developments in grain legumes, the time has come now to give due credit and support the legume research community as well as the farmers. Presently, this is visible in various developmental activities to enhance the legume production (Varshney *et al.* 2016). Hence, it is imperative to continue to invest in research with a long-term vision. There is a need to enhance the genetic gains made in legume breeding by focusing on factors like selection intensity, selection accuracy, genetic variance in the germplasm/breeding lines, heritability of the trait, besides management etc. Modernization of breeding by adopting genomic tools is the first step to enhance legume productivity in a systematic manner. Accordingly, research objectives should be redefined in consultation with the stakeholders. In short-term goals, genomics research should move in the direction of importing of easy assessable tools for making quick and accurate decisions for breeding. In the long-term, genomic selection approach should be deployed in other legumes as it has been done in the case of chickpea (Roorkiwal *et al*. 2016) and pea (Tayeh *et al.* 2015). On the other hand, early generation selection for desirable traits will reduce the time, efforts and resources invested in the development of improved lines/varieties (Varshney 2016). Most of the legume species are self-pollinating crops and thus suffer from low-level genetic diversity of

cultivated gene pools. Modern approaches such as multi-parent advanced-generation-intercross (MAGIC) populations and nested-association mapping (NAM) populations should be adopted for optimal utilization of genetic diversity. Moreover, efforts should also be directed towards utilization of genetic variation and useful traits available in many related wild species using introgression lines (ILs), backcross-inbred lines (BILs), chromosome-segment-substitution lines (CSSLs), etc. We visualize that in near future the use of NGS, early-generation screening, GS, genome editing, coupled with other advances, will revolutionize legume-breeding strategies which might pave way for the realization of their potential yield.

Acknowledgements

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