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Commentary

Innovative approach to further genetic gain in pulses

PS Basu

Former Head & Principal Scientist
Division of Basic Sciences
ICAR-Indian Institute of Pulses Research, Kanpur

Email: *psbsu59@gmail.com*

With more than 25 years of research experience in abiotic stress physiology in thermal microorganisms such as cyanobacteria and higher plants including legumes and vegetables, Dr PS Basu has made significant contributions in evolving varieties and donors tolerant to heat and drought in legumes and vegetables and deciphered the mechanisms of adaptation of pulses to diverse climatic conditions.

He is member of International Society of Drought Mitigation and Climate Change and has established active collaboration with CSIRO, Australia and JIRCAS Japan in .the field of stress physiology and evaluation of diverse legume germplasm through advanced molecular and physiological tools. His research interests include long term projections of climate change on agricultural productivity, developing varieties resilient to adverse climates and crop modeling.

Global production of grain legumes has the potential to provide a sustainable solution to food and protein security. The crops are indispensable for global food security and agricultural sustainability, however genetic improvement in these crops lagged behind cereals due to lack of genomic resources essential for deploying advanced breeding technologies. Recognizing the importance of grain legumes in human and soil health, some efforts were made to improve the yield and nutritional quality of legume crops by employing improved agronomy and crop rotation approaches. Several hundreds of varieties and a few hybrids have been developed in the legume crops using conventional breeding methods for traits like drought, heat, herbicide, low phosphorus tolerance, early maturity, insect resistance, machine harvestability and high nitrogen fixation. Nevertheless, the rate of genetic gains using the conventional approaches could not bridge the gap between the growing demands which is evident from only 60% increase in pulse production in last 50 years. Efforts are currently being made to increase genomic resources and adopt innovative breeding techniques to improve the yield and nutritional quality of legume crops along with enhanced climate resilience. Development of genetic resources will unleash untapped potential for genetic improvement. The development of effective phenotyping and breeding approaches is a challenge for the grain legumes. Modern breeding efforts are constrained by a low level of genetic diversity in breeding programmes. Large genetic diversity in seeds of grain legumes preserved in gene banks is not fully utilized in active breeding programmes. Therefore concept emerged towards evolving gene banks, applying optimal contribution selection to manage long.term genetic gain and genetic diversity in pre-breeding populations. The plant breeding method should be applied that captures valuable genes from wild relatives and moves them into the breeding programme by crossing the genetically diverse exotic lines with elite lines, creating evolving gene banks. The new rapid-cycle plant breeding method will have long-term benefits for all plant breeders, and could help to adapt and develop climate-ready pulse crops. The current genomic resources from functional sequences to epigenomics provided scope for improving the soybean resilience to different climate change. High-throughput genomic technologies including genome sequencing, genome re-sequencing (DNA-seq) and transcriptome sequencing (RNA-seq) are being applied to a range of legumes. The genetic and biotechnology resources are currently being applied to drought and water-logging using QTLs and breeding approaches. The crucial importance of root trait variability and its role in facilitating stress tolerance in chickpea has been well demonstrated. The mechanisms that underpin drought tolerance in legumes are further elaborated by an innovative analysis of root xylem plasticity and its role in improving water use efficiency in soybean plants subjected to water stress.

The mungbean is characterized for its small genome size, short life-cycle, selfpollinating, and close genetic relationship to other legumes. There have been several efforts to develop molecular markers and linkage maps associated with agronomic traits for the genetic improvement of mungbean and breeding for cultivar development to increase the average yields of mungbean. The recent release of a reference genome of the cultivated mungbean (V. radiata var. radiata VC1973A) and an additional de novo sequencing of a wild relative mungbean (V. radiata var. sublobata) has provided a framework for mungbean genetic and genome research, that can further be used for genome-wide association and functional studies to identify genes related to specific agronomic traits. Moreover, the diverse gene pool of wild mungbean comprises valuable genetic resources of beneficial genes that may be helpful in widening the genetic diversity of cultivated mungbean.

The availability of the draft genome sequences and re-sequencing of elite genotypes for several important legume crops have made it possible to identify structural variations at large scale. Availability of large-scale genomic resources and low-cost and high-throughput genotyping technologies are enhancing the efficiency and resolution of genetic mapping and marker-trait association studies. Most importantly, deployment of molecular breeding approaches has resulted in development of improved lines in some legume crops such as chickpea and groundnut. In order to support genomics-driven crop improvement at a fast pace, the deployment of breeder-friendly genomics and decision support tools seems appear to be critical in breeding programs in developing countries.

Although conventional breeding approaches have been successful to address the issue of low productivity in some legumes, but the desired success rate is not yet achieved. Therefore, it is very essential to intensify the legume genetic enhancement programs using advanced breeding approaches wherein the potential of genomics needs to be exploited for accelerated development of improved cultivars possessing high yield, genetic resilience against stresses, and enhanced nutritional quality. The next-generation sequencing (NGS) and genotyping technologies need to be used for precise marker-trait association, gene discovery, functional marker development, and their deployment in routine breeding programs. Efficiency of breeding programs of legume crops such as chickpea, pigeonpea and groundnut has been considerably improved over the past decade through deployment of modern genomic tools and technologies. For instance, next-generation sequencing technologies have facilitated availability of genome sequence assemblies, re-sequencing of several hundred lines, development of HapMaps, high-density genetic maps, a range of marker genotyping platforms and identification of markers associated with a number of agronomic traits in these legume crops. Although marker-assisted backcrossing and marker-assisted selection approaches have been used to develop superior lines in several cases, it is the need of the hour for continuous population improvement after every breeding cycle to accelerate genetic gain in the