The pulses requirement for the year 2030 has been estimated at 32 million tons and by year 2050 at 50 million tons. In order to meet this requirement, additional 3 to 5 million hectares need to be brought under pulse cultivation and productivity has to be increased besides reducing post-harvest losses (Vision 2050: Indian Institute of Pulses Research, 2013, www.ipr.res.in). In this direction pigeonpea (Cajanus cajan) also known as poor man’s meat holds the promise to uplift the pulse production in India if genetic yield potential of this crop fully exploited. In addition to the main use of pigeonpea as de-hulled split peas (Dhal), immature green seeds and pods are also consumed fresh as a green vegetable. It’s crushed dry seeds are also serving as feed to animals while the green leaves form a quality fodder. In rural areas, dry stems of pigeonpea are used for fuel. In single cropping season, pigeonpea plants fix 40 kg ha-1 atmospheric nitrogen (Kumar Rao et al. 1983) and add valuable organic matter to the soil through fallen leaves. Its roots help in releasing soil-bound phosphorus to make it available for plant growth (Ae et al. 1990). The average yield of pigeonpea in India is currently 695 kg ha-1 significantly below its potential of around 3-4 t ha-1 (Mula and Saxena 2010). The estimated globally-sown pigeonpea area now stands at over 7.03 m ha, with a production of 4.89 m t and average yield of 695 kg/ha (FAOSTAT, 2017). The crop is well adapted to rainfall areas of India (5.60 m ha), Myanmar (0.6 m ha), Kenya (0.28), and Tanzania (0.25 m ha) and is intercropped either with cereals such as sorghum (Sorghum bicolor), pearl millet (Pennisetum glaucum) and maize (Zea mays) or legumes like soybean (Glycine max), mung bean (Vigna radiata) and urd (Vigna mungo). Few countries in the South American region and Caribbean islands also have(a/the) considerable area under pigeonpea production.

The genetic improvement of pigeonpea initiated in 1919 at the University of Hawaii. This program released the fodder variety ‘New Era’ (Morton et al. 1982). However, this program could survive for a decade and abounded due to introduction of more efficient forage legumes. Similarly, pigeonpea breeding programs in Australia, Malaysia, and Nigeria were also short-lived and failed to create an impact on the total production and average productivity world-wide. As compared to other countries pigeonpea improvement program in India are extensive. The first structured pigeonpea breeding effort in India was made by Shaw (1933) who described morphological and agronomic traits of 86 elite field collections. Almost at the same time, Mahata and Dave (1931) identified a few elite early and late maturing high yielding types. However, these efforts were just focusing on evaluation of field collection and had no significant impact on productivity. Considering the importance of pigeonpea in India, Indian Council of Agricultural Research (ICAR) started an All India Coordinated Pigeonpea Improvement Project in 1965. Under this mega program, crop improvement activities were simultaneously launched at 31 research centres in diverse agro-ecological zones (Ramanujam and Singh 1981). In 1972, CGIAR, an international body established ICARISAT with a global mandate of crop improvement of select dryland crops. ICARISAT started working globally as well as with ICAR and other partners in India and the actual breeding program in pigeonpea at ICARISAT started in 1974. ICARISAT and ICAR have been working very closely for more than 40 years. So far from these efforts ~100 varieties have been released. The impact of these efforts has been impressive with 56% increase in area and 54% increase in total grain production, however, it could not achieve the maximum yield potential of the crop. Further ICARISAT and ICAR are working in the direction of cytoplasmic male-sterility based hybrids and could achieve >40% yield advantage over checks (Saxena 2015).

Narrow genetic base in the cultivated pigeonpea and complex nature of abiotic and biotic stresses are the main causing elements in yield stagnation of pigeonpea which is less than 1 t ha-1 for several decades. The evolution of genomics and particularly genomics-assisted breeding (GAB) in early 21st century demonstrated enhanced yields in cereals like rice by minimizing losses due to biotic and abiotic stresses (Varshney et al. 2005, 2007). However, for deploying GAB, genomic resources are required and they were not available until 2005 in the pigeonpea crop. In the last decade the concerted efforts in
consortium mode has transformed pigeonpea from “orphan crop” to “genomics resources rich crop” (please see Pachamala et al. 2015). The development and application of genomics information particularly DNA markers and draft genome represent major achievements in recent years (Saxena et al. 2016; Varshney et al. 2012). In the draft genome, a total of 49,680 genes were predicted and also showed the potential role that certain gene families, for example, drought tolerance-related genes, have played throughout the domestication of pigeonpea and the evolution of its ancestors (Varshney et al. 2012). A number of marker systems including restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms (AFLPs), random amplified polymorphic DNA (RAPD), single feature polymorphism (SFP) and simple sequence repeats (SSRs) have been developed and utilized to assess genetic diversity (Saxena et al. 2010), construct genetic maps (Bohra et al. 2011) and quantitative trait loci (QTL) analysis (Gnanesh et al. 2011; Bohra et al. 2012) in pigeonpea. Recently, single nucleotide polymorphisms (SNPs) have been identified in a large number of pigeonpea lines especially due to the next generation sequencing (NGS) based re-sequencing of diverse germplasm (the reference set of pigeonpea) (Varshney et al. 2017).

Comprehensive application of genomics for crop improvement begins with the availability of large amount of markers, mapping populations and draft genome sequence (Varshney et al. 2012) as mentioned above. The reference genome sequence has been the base of re-sequencing based mapping studies (Saxena et al. 2017; Singh et al. 2016), which has enabled us to develop trait-associated markers quickly which in turn facilitating the identification of the genetic basis of agronomically important traits, and acceleration of the development of improved pigeonpea varieties.

In order to deploy available sequence information for pigeonpea improvement, Department of Agriculture Cooperation & Farmers Welfare, Ministry of Agriculture and Farmers Welfare and United States Agency for International Development (USAID)-India facilitated these efforts through funding research projects with the major emphasis on identification and delivering genetic improvements in pigeonpea. One of such projects entitled “Pigeonpea improvement using molecular breeding” was planned for three phases, phase I (generating basic information/material to initiate molecular breeding), phase II (molecular breeding, multi-location evaluation, development and extension) and phase III (coordinated research project trials and extension). Phase I was initiated in year 2012 with the funding from USAID-India. Key accomplishments in phase I of the pigeonpea genomics project have been summarized in Figure 1. In view above, it is essential to continue and expand research efforts in pigeonpea improvement especially in use of modern approaches in India to achieve daunting task of self-sufficiency in pulses as well as international level for sustainable pigeonpea production to meet the demand of ever growing population and to ensure food and nutritional security.

Acknowledgements

Authors are thankful to the Department of Agriculture Cooperation & Farmers Welfare, Ministry of Agriculture and Farmers Welfare and United States Agency for International Development (USAID)-India; and ICRISAT for funding. This work has been undertaken as part of the CGIAR Research Program on Grain Legumes. ICRISAT is a member of CGIAR Consortium.

References


Mula MG, Saxena KB (2010) Lifting the level of awareness on pigeonpea—a global perspective. ICRISAT, Patancheru, Andhra Pradesh, India.


Saxena KB (2015) From concept to field: evolution of hybrid pigeonpea technology in India. Indian J Genet Plant Breed 75:279–293


![Image of key accomplishments in phase I of the pigeonpea genomics project entitled “Pigeonpea improvement using molecular breeding”]

- 10 - Pulse India - Vol: II / Issue 07 / Sept-Oct 2017