



Pigeonpea Research For Enhancing Crop Productivity

Rachit K Saxena¹, CV Sameerkumar¹,
Abhishek Bohra², I P Singh², N P Singh²
and Rajeev K Varshney^{1,*}

¹International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru - 502324, India

²ICAR- Indian Institute of Pulses Research (IIPR), Kanpur 208 017, India

*r.k.varshney@cgiar.org

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.iipr.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 3-4t 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 rainfed 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 (urad) bean (*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 ICRISAT with a global mandate of crop improvement of select dryland crops. ICRISAT started working globally as well as with ICAR and other partners in India and the actual breeding program in pigeonpea at ICRISAT started in 1974. ICRISAT 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 ICRISAT 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 Pazhamala 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 48,680 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 is 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

- AeN, Arihara J, Okada K, Yoshihara T, Johansen C (1990) Phosphorus uptake by pigeonpea and its role in cropping systems of the Indian subcontinent. *Science* 248:477–480
- Bohra A, Dubey A, Saxena RK, Penmetsa RV, Poornima KN, Kumar N, Farmer AD, Srivani G, Upadhyaya HD, Gothwal R, Ramesh S, Singh D, Saxena K, Kishor PB, Singh NK, Town CD, May GD, Cook DR, Varshney RK (2011) Analysis of BAC-end sequences (BESs) and development of BES-SSR markers for genetic mapping and hybrid purity assessment in pigeonpea (*Cajanus* spp.). *BMC Plant Biol* 11:56
- Bohra A, Saxena RK, Gnanesh BN, Saxena KB, Byregowda M, Rathore A, Kavikishor PB, Cook DR, Varshney RK (2012) An intra-specific consensus genetic map of pigeonpea (*Cajanus cajan* (L.) Millsp) derived from six mapping populations. *Theor Appl Genet* 125:1325–13
- Gnanesh BN, Bohra A, Sharma M, Byregowda M, Pande S, Wesley V, Saxena RK, Saxena KB, Varshney RK (2011) Genetic mapping and quantitative trait locus analysis of resistance to sterility mosaic disease in pigeonpea (*Cajanus cajan* (L.) Millsp). *Field Crop Res* 123:53–61
- Mahata DN, Dave BB (1931) Studies in *Cajanus indicus*. *Botany* 19:1–25
- Morton JF, Smith RE, Lugo-Lopez MA, Abrams R (1982) Pigeonpea (*Cajanus cajan* Millsp.). A valuable crop of the tropics. Department of Agronomy and Soils, Mayaguez, Puerto Rico 123
- Mula MG, Saxena KB (2010) Lifting the level of awareness on pigeonpea – A global perspective. ICRISAT, Patancheru, Andhra Pradesh, India.
- Pazhamala LT, Saxena RK, Singh VK, Samer Kumar CV, Kumar V, Sinha P, Patel K, Obala J, Kaoneka SR, Tongoon P, Shimelis HA, Gangarao NVPR, Odeny DA, Rathore A, Dharmaraj PS, Yamini KN, Varshney RK (2015) Genomics-assisted breeding for boosting crop improvement in pigeonpea (*Cajanus cajan*). *Front Plant Sci* 6:50
- Ramanujam S, Singh SP (1981) Pigeonpea breeding in the All India coordinated programme. Pages 403–414. In: Proceedings international workshop on pigeonpeas. vol. 1. ICRISAT, Patancheru, India, 502324

Rao JVDKK, Dart PJ, Sastry PVSS (1983) Residual effect of pigeonpea (*Cajanus cajan*) on yield and nitrogen response of maize. *Exp Agric* 19:131–141

Saxena RK, Kale SM, Kumar V, Parupali S, Joshi S, Singh V, Garg V, Das RR, Sharma M, Yamini KN, Ghanta A, Rathore A, Sameerkumar CV, Saxena KB, Varshney RK (2017) Genotyping-by-sequencing of three mapping populations for identification of candidate genomic regions for resistance to sterility mosaic disease in pigeonpea. *Sci Rep* 7:1813

Saxena RK, Prathima C, Saxena KB, Hoisington DA, Singh NK, Varshney RK (2010) Novel SSR markers for polymorphism detection in pigeonpea (*Cajanus* spp.). *Plant Breed* 129:142–148

Saxena RK, Thudi M, Varshney RK (2016) Genomics, trait mapping and molecular breeding in pigeonpea and chickpea. *Indian J Genet* 76:504–511

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

Shaw FJF, Khan AR, Singh H (1933) Studies on Indian Pulses. The type of *Cajanus indicus*. *Indian J Agr Sci* 3:1–36

Singh VK, Khan AW, Saxena RK, Kumar V, Kale SM, Chitkineni A, Lekha TP, Garg V, Sharma M, Kumar CVS, Parupalli S, Vechalapu

S, Patil S, Muniswamy S, Ghanta A, Yamini KN, Dharmaraj PS, Varshney RK (2016) Next-generation sequencing for identification of candidate genes for Fusarium wilt and sterility mosaic disease in pigeonpea (*Cajanus cajan*). *Plant Biotechnol J* 14:1183–1194

Varshney RK, Graner A, Sorrells ME (2005) Genomics assisted breeding for crop improvement. *Trends Plant Sci* 10:621–630

Varshney RK, Saxena RK, Upadhyaya HD, Khan AW, Yu Y, Kim C, Rathore A, Kim D, Kim J, An S, Kumar V, Anuradha G, Yamini KN, Zhang W, Muniswamy S, Kim JS, Penmetsa RV, Von WE, Datta SK (2017) Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. *Nat Genet* 49:1082–1088

Varshney RK, Chen W, Li Y, Bharti AK, Saxena RK, Schlueter JA, Donoghue MT, Azam S, Fan G, Whaley AM, Farmer AD, Sheridan J, Iwata A, Tuteja R, Penmetsa RV, Wu W, Upadhyaya HD, Yang SP, Shah T, Saxena KB, Michael T, McCombie WR, Yang B, Zhang G, Yang H, Wang J, Spillane C, Cook DR, May GD, Xu X, Jackson SA (2012) Draft genome sequence of pigeonpea (*Cajanus cajan*), an orphan legume crop of resource-poor farmers. *Nat Biotechnol* 30:83–89

Varshney RK, Langridge P, Graner A (2007) Application of genomics for molecular breeding of wheat and barley. *Adv Genet* 58:122–155

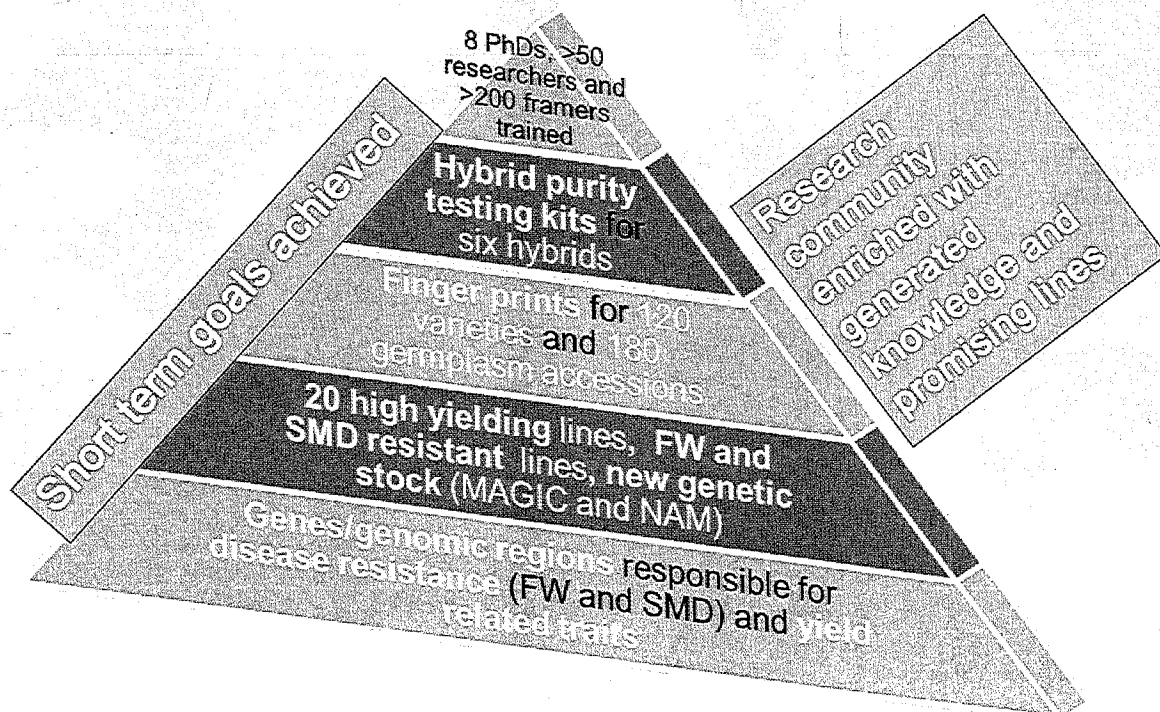


Figure 1. Key accomplishments in phase I of the pigeonpea genomics project entitled "Pigeonpea improvement using molecular breeding".