



An Overview Of Chickpea Research: From Discovery To Delivery

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Rapid changes in climate coupled with population explosion and limited arable land are the greatest challenges before the humanity in attaining future food and nutritional security across the globe. In this context, being rich in grain protein, food legumes play an important role in reducing hunger and malnutrition especially in developing countries along with major cereals like maize, rice and wheat. Among more than a dozen legumes, chickpea (*Cicer arietinum* L.), a cool season crop, is the most important food legume in India. It is a self-pollinated crop with a basic chromosome number eight and a 738 Mb genome size (Varshney et al. 2013a). Based on seed market type, chickpea is classified into two groups namely *desi* and *kabuli*. Anthocyanin pigmentation can be seen on one or other parts of the *desi* chickpea whereas anthocyanin pigments are absent in *kabuli* types. Grains of *desi* chickpea are small in size, light to dark brown in color and have a thick seed coat. Grains of *kabuli* chickpea are bigger in size, have a whitish-cream color and thin seed coat. The *desi* type is more prominent and accounts up to 80% of global chickpea production. Chickpea is a highly nutritious grain legume crop and is one of the cheapest sources of protein. It is an important source of energy, protein, soluble and insoluble fiber. Further, the seed protein contains essential amino acids like lysine, methionine, threonine, valine, isoleucine and leucine. On an average, chickpea grains contain 60-65% carbohydrates, 6% fat, and between 12% and 31% protein – higher than any other pulse crop. It is also a good source of vitamins (rich in B vitamins) and minerals like potassium and phosphorus. Chickpea like other legume crops also replenishes soil fertility through biological nitrogen fixation.

Chickpea is grown mostly in South Asia and Sub-Saharan Africa, which accounts for more than 75% of the world chickpea area. Global chickpea production has increased from 7.68 million tonnes (1961) to 13.73 million tonnes (2014) (FAOSTAT, 2016). India ranks first in terms of cultivated area and production. However, there is a slight increase in the chickpea cultivation area in India from 9.27 million hectares (1961) to 9.92 million hectares (2014), but production increased significantly from 6.25 million

tonnes (1961) to 9.88 million tonnes (2014) due to significant increase in the productivity from 0.67 t/ha (1961) to 0.99 t/ha (2014). Other major chickpea producing countries are Australia (629,400 tonnes), Myanmar (562,163 tonnes), Ethiopia (458,682 tonnes), Turkey (450,000 tonnes), and Pakistan (399,030 tonnes) (2014) (FAOSTAT, 2016).

Chickpea has a long history of research in India. It started as early as 1905, when formerly Imperial Agricultural Research Institute, Pusa (now known as Indian Agricultural Research Institute (IARI)) made a modest beginning by taking up breeding work on chickpea. Systematic research on chickpea started with the establishment of the All India Coordinated Pulses Improvement Project (AICPIP) in 1967 (<http://www.aicrpchickpea.res.in>). In 1972, CGIAR, an international body established ICRISAT with a global mandate of crop improvement of select dryland crops including chickpea. ICRISAT started working globally as well as with ICAR and other partners in India. Realizing the importance of crop and providing focused attention on every aspect of chickpea, ICAR established a separate All India Coordinated Research Project (AICRP) on Chickpea in 1993. ICRISAT and ICAR have been working very closely for more than 40 years. More than 190 chickpea varieties for important traits have been released in India (Chaturvedi et al. 2016). In this article we provide an overview of chickpea research and highlight some research activities in chickpea research undertaken by ICRISAT and its partners during last 10 years or so. These activities are contributing to develop climate resilient chickpeas for ensuring food and nutritional security in India and across the globe.

Narrow genetic base in the cultivated genepool of chickpea and the complex nature of the abiotic and biotic stresses kept the productivity less than 1 t/ha⁻¹ for several decades. In addition, enhanced occurrences of abiotic (drought, heat, salinity, frost etc.) and biotic (*Fusarium* wilt, *Ascochyta* blight, insect pest, nematodes) stresses also contributed to significant production losses. During the last decade conventional breeding efforts coupled with genomics-assisted breeding (GAB) (Varshney et al. 2005, 2007) demonstrated enhanced yields in cereals like rice by minimizing losses due to biotic and abiotic stresses. In order to



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attain faster genetic gains, the availability of genomic resources and their deployment in breeding programs is a prerequisite. Although chickpea was considered as “orphan legume”, recent research efforts globally transformed it to a genomics resource rich crop. Several thousands of molecular markers (Nayak et al. 2010), high density genetic maps (Thudi et al. 2011; Gujaria et al. 2011; Jaganathan et al. 2014; Kale et al. 2015), transcriptomic resources (Varshney et al. 2009; Hiremath et al. 2012; Kudapa et al. 2014) and physical map (Varshney et al. 2014a) are now available for trait dissection and crop improvement. In recent years, genetics of complex abiotic stresses like drought (Varshney et al. 2014b), heat (P. M. Gaur, personal communication), salinity (Vadez et al. 2012; Pushpavalli et al. 2016) and biotic stresses like Fusarium wilt, Ascochyta blight (Sabbavarapu et al. 2013) have been understood and the genomic regions/QTLs have been identified. Furthermore, several functional genomics approaches such as RNA-seq, Massive Analysis of cDNA Ends (MACE) with parental genotypes of mapping populations as well near isogenic lines (NILs) have provided some candidate genes for drought tolerance that are being validated through genetical, genomics and/or TILLING approaches.

In 2013, International Chickpea Genome Sequencing Consortium (ICGSC <http://ceg.icrisat.org/gt-bt/ICGGC/ICGSC.htm>) co-led by ICRISAT, University of California-Davis (USA) and BGI-Shenzhen (China) assembled the draft genome of *kabuli* chickpea genotype CDC Frontier, while Next Generation Challenge Programme on Chickpea Genomics (NGCPCG), India assembled genome sequence of *desi* genotype ICC 4958. After assembling the draft chickpea genomes, efforts to exploit the potential of next generation sequencing (NGS) technology to understand the genome architecture of chickpea were initiated. As part of these initiatives NGS based whole genome re-sequencing (WGRS) of chickpea parental lines were undertaken, which led to identification of 2 million Single Nucleotide Polymorphisms (SNPs) and more than 290K Indels. These SNPs are valuable resource providing enough markers to undertake the genetics research (Thudi et al. 2016a). In addition, NGS based WGRS was used to understand the impact of breeding on genetic diversity and temporal diversity trends in chickpea. For this, WGRS was used to re-sequence more than 100 chickpea varieties released in last five decades and identified 1.2 million SNPs. These SNPs were used to identify the genomic changes during the history of chickpea breeding suggesting increase in diversity in the primary gene pool as result of recent chickpea breeding programs (Thudi et al. 2016b). In addition to parental lines and varieties, chickpea reference set (comprising 300 accessions) were also re-sequenced using WGRS approach and led to identification of 4.9 million SNPs. These SNPs are being used to undertaking the genome wide association study (GWAS) for identifying the markers associated with traits of interest and understanding the domestication and post domestication divergence in chickpea (unpublished data). Global genebanks store the huge germplasm wealth that has the potential to contribute significantly towards the goal of enhancing the rate of genetic gain. In order to exploit the potential of genebanks, ICRISAT along with its partners have launched the large scale resequencing initiative “The 3000

Chickpea Genome Sequencing Initiative” to re-sequence 3000 lines from Global Chickpea Composite Collection (Varshney, 2016). This is the first time in the chickpea research history that 3000 lines have been evaluated at six different locations in India for two seasons for several traits of agronomic importance.

The genomic resources generated have been successfully deployed for developing superior lines for different traits of interest. Trait mapping and molecular breeding such as marker-assisted backcrossing (MABC), marker-assisted recurrent selection (MARS) and advanced backcross quantitative trait loci (AB-QTL) analysis, which are routine in breeding programs for major crops, are also being practiced in chickpea. For example, superior lines with enhanced drought tolerance (Varshney et al. 2013b), fusarium wilt and ascochyta blight (Varshney et al. 2014c) have been developed. Introgression of the “QTL-hotspot” into several elite varieties in India as well as Kenya and Ethiopia led to development of superior lines with enhanced tolerance to drought and increased yield under rainfed and irrigated conditions irrespective of genetic background (Table 1). Further, the available genomic resources also enabled the successful deployment of modern breeding approaches like genomic selection for faster genetic gains (Roorkiwal et al. 2016).

For effective utilization of the available genomic resources in crop improvement cost effective genotyping platforms also play a major role. Towards this direction, for use in foreground and background selection, cost effective SNP genotyping assays like VeraCode assays (Roorkiwal et al. 2014), KASPar assays (Hiremath et al. 2012) were developed. Recently, a precise and cost effective SNP genotyping platform, with 50,590, high quality non-redundant SNPs on Affymetrix Axiom® *Cicer* SNP array has been developed and is being used for high resolution genetic mapping (unpublished data). This array will also be useful for fingerprinting the released varieties as well as assessing their adoption in addition to genetics and breeding applications. In summary, during last 12 years significant progress has been made in terms of developing genomic resources and these resources have been effectively used for attaining faster genetic gains in chickpea.

This article provides a “bird’s eye view” of about 10 years research efforts at ICRISAT using modern technologies towards developing climate resilient chickpeas. To date, besides conserving ~20,000 germplasm accessions, several advanced breeding lines were developed and shared with NARS partners through integrated crop improvements. As a result, in collaboration with different partners across the world, ~350 varieties were released in different parts of the world (Gaur et al. 2014). Further, for making better use of the germplasm lines in chickpea improvement composite collection, reference set and mini-core collections were developed at ICRISAT (see Upadhyaya et al. 2011). Genomic resources developed in recent past enabled trait dissection as well as trait improvement through modern molecular breeding approaches (Varshney, 2016). In addition to ICRISAT, NARS partners also deployed these resources for developing superior lines using MABC approach and several MABC lines have been tested for their yield performance in Advanced Varietal trials during 2016-17 crop season by AICRP on chickpea (Table 2). Ever since the announcement of draft genome, ICRISAT in collaboration



with premier research institutes in India developed a road map for deploying the available sequence information for chickpea improvement. In this direction, Department of Agriculture Cooperation & Farmers Welfare, Ministry of Agriculture and Farmers Welfare and Indo-Australian Biotechnology Fund, Ministry of Science and Technology of Government of India facilitated these efforts through funding research projects with major emphasis on identification and delivering genetic improvements in chickpea. In view above, it is essential to continue and expand research efforts in chickpea improvement especially in use of modern approaches in India as well as international level for sustainable chickpea production to meet

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Table 1: List of elite varieties targeted for molecular breeding to enhance tolerance/resistance to drought, Fusarium wilt and Ascochyta blight by select partners in India and Sub-Saharan Africa

For drought tolerance	For Fusarium wilt resistance	For Ascochyta blight resistance	Institute*
JG 11	C 214	C 214	ICRISAT, India
ICCV 10			
DCP92-3	Pusa 256		IIPR, India
KWR 108			
Pusa 362			IARI, India
	JG 74		JNKVV, Jabalpur
	Phule G12		MPKV, Rahuri
	Annigeri-1		ARS- Kalaburagi
Ejere			EIAR, Ethiopia
Arerti			
ICCV 97105			EU, Kenya
ICCV 95423			

*IIPR = Indian Institute of Pulses Research; JNKVV = Jawaharlal Nehru Krishi Vishwa Vidyalaya; MPKV = Mahatma Phule Krishi Vidyapeeth; ARS = Agricultural Research Station;

EU= Egerton University; EIAR= Ethiopian Institute of Agricultural Research

Table 2: Superior molecular breeding lines in the genetic background of JG 11 and ICCV 10 evaluated in Advanced Varietal Trials of AICRP on chickpea during 2016-17

S No.	Name of the entry	Pedigree	Source†
1.	DIBG 203	[(JG 11 × ICC 4958) × 3*JG 11] - 1	UAS, Dharwad
2.	DIBG 204	[(JG 11 × ICC 4958) × 3*JG 11] - 11	UAS, Dharwad
3.	DIBG 205	[(ICCV 10 × ICC 4958) × 3*ICCV 10] - 21	UAS, Dharwad
4.	NBeG 506	[(JG 11 × ICC 4958) × 3*JG 11] - 35	RARS, Nandyal
5.	NBeG 786	[(JG 11 × ICC 4958) × 3*JG 11] - 40	RARS, Nandyal
6.	NBeG 1004	[(ICCV 10 × ICC 4958) × 3*ICCV 10] - 9	RARS, Nandyal
7.	RKD 1	[(JG 11 × ICC 4958) × 3*JG 11] - 13	ARS-Kalaburagi
8.	RKD 4	[(ICCV 10 × ICC 4958) × 3*ICCV 10] - 2	ARS-Kalaburagi
9.	RVSS 51	[(JG 11 × ICC 4958) × 3*JG 11] - 34	RAKCA, Sehore
10.	RVSSG 52	[(ICCV 10 × ICC 4958) × 3*ICCV 10] - 13	RAKCA, Sehore

†UAS= University of Agricultural Sciences; RARS = Regional Agricultural Research Station; RAKCA = RAK College of Agriculture