The Pharma Innovation Journal 2022; SP-11(6): 36-39

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2022; SP-11(6): 36-39

www.thepharmajournal.com
Received: 13-04-2022
Accepted: 16-05-2022

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Achievements and opportunities in integrating genomics for chickpea improvement: A review

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Abstract
Recently, chickpeas have been improved via genetics and breeding. Faster chickpea improvement with modern breeding and genotyping methods It should considerably increase agricultural yields. Not surprisingly, conventional breeding has improved over 200 chickpea varieties. Rapid climate-resilient chickpea development requires new genetic resources and traditional breeding methods. Recent genomics tool and technology advancements have enabled sets of information for chickpea genotyping and sequencing on a big scale. Genomics-based breeding quality research reveals biological processes and genomes connected to Characteristics of breeding. Using genetics, several chickpea molecular breeding products have been created. It may be possible to generate superior chickpea varieties using functional omics, genomic sequence selection and forward breeding. Diagnostic markers for use in marker-assisted backcrossing programmes have been developed using genomic technology, resulting in many molecular breeding products in chickpea. A sequence-based holistic breeding method, which incorporates functional omics, parental selection, forward breeding, and genome-wide selection, is expected to result in a paradigm change in the generation of improved chickpea varieties. Genomics and molecular breeding must work together to close the gap between the genome and the phenome. Current developments in breeding population generation & screening are examined to improve selection efficiency and speed up Chickpea genetic improvement.

Keywords: Chickpea, genomics, molecular breeding, QTL mapping, marker assisted backcrossing

Introduction
Chickpea (*Cicer arietinum* L.) It is grown on 14.56 million hectares in 55 countries (FAOSTAT 2017). However, abiotic and biotic stresses reduce chickpea yielding to 1t ha–1 under optimum conditions. Since 1961, chickpea production has consistently grown, but its germplasm donor parents or accessions limited number employed in breeding programmes has increased its vulnerability to biotic and abiotic stresses. Chickpea yields can be reduced by up to 70percent due to heat and drought. Abiotic stressors such rot in the roots, fusarium wilt, collar rot, ascochyta blight, Helicoverpa, grey mould botrytis, Weeds that grow in the spring and summer limit yields.

Stressors abiotic and biotic should be managed to improve chickpea yielding. Crop growers must raise yields sufficient to feed the world's predicted ten billion residents by 2050. In the long run, breeding has failed to match expectations for output and nutrition. Micronutrient insufficiency affects 2 billion people worldwide and in nations with a lack of nutritional diversity, this is expected to rise in the future years according to UNICEF. Africa's Sub-Saharan and South Asia require new varieties of crop includes improved productivity & pest or disease tolerance to connect expanding demand. Nutritional deficiencies in chickpeas might lead to stunting. Fixation of N2 supplies soil with N2 (60 to 103 kg ha-1). Because of advancements in next-generation sequencing (NGS) technology, genotyping approaches have evolved from individual marker-based genotyping to whole-genome sequencing-based genotyping. Large-scale genomic resources, such as genome sequence assemblies, re-sequencing of a few thousand lines, high-resolution genetic maps, and a variety of low- to high-density genotyping platforms, have developed as a result of this. These include assembly of genomic sequences, a couple thousand lines re-sequenced, genetic maps with high resolution, and genotyping at low to high densities systems. GEO-based agronomic traits in chickpea these genetic resources were utilised to find alleles and haplotypes linked to chickpea agronomic characteristics. Examples of QTL-hotspots in chickpea include 7.74 Mb and Drought resistance traits are 300 kb in size [8, 9]. To develop rich genetic maps for chickpea breeding, the Axiom®CicerSNP Array SNP genotyping platform and has aided in the

creation of detailed genetic maps in order to boost chickpea genetics and breeding efforts. By utilising whole-genome resequencing (WGRS), these initiatives have revealed genetic diversity, domestication patterns, population structure, untapped genomic potential and linkage disequilibrium. Modern genomics techniques could speed up trait mapping, marker development, molecular breeding and gene discovery, improving chickpea yield. Abiotic stress resistance, disease resistance, and yield components are all qualities that genome-wide sequence data may capture along with phenotypic variation. Previously, chickpea breeding programmes aimed for crop yield and component qualities. Climate change has made raising yields difficult, in addition to providing consumer health benefits. Superior Chickpea cultivars that are resistant to the effects of climate change are urgently needed to get together people nutritional demands in developing countries. The technical developments that turned chickpea from an orphan crop to a genetic resource loaded crop in the post-genomics age are highlighted in this review article. We also explore next-generation mapping populations and techniques for tackling developing restrictions to chickpea production, as well as provide an update on the recently published molecular breeding variants for commercial farming. We also suggest a sequence-based holistic breeding method for developing superior chickpea varieties with increased genetic gains, which integrates genomics resources with breeding efforts.

Trait discovery and exploitation genetic resources

Genetic diversity is vital for crop selection and improvement. The global genebank contains huge amounts of germplasm that can enhance crop production globally. Around 100,000 chickpea accessions are held in 120 genebanks in 64 countries Of these, With 20,764 accessions from 59 countries, the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) genebank has the largest share (20.8 percent), followed by the ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR; 16 percent) and the International Center for Agricultural Research in the Dry Areas (ICARDA; 15 percent), accounting for more than half of the global chickpea collection. Basic features have been identified in the genetic resources stored at the ICRISAT and ICARDA genebanks, with germplasm subsets produced for breeding purposes. These subsets, which include the core collection (1956 accessions), mini-core collection (211 accessions), global composite collection (3000 accessions), trait-based FIGS (Focused Identification of Germplasm Strategy) sets, and reference set (300 accessions), are ideal for analysing allelic diversity, dissecting population structure, and mapping associations in chickpea. (Upadhyaya and Ortiz 2001; Upadhyaya *et al*. 2006, 2008). This will aid in the detection of QTLs that may be used in breeding programmes to create better chickpea types. Restricted genetic bases, long breeding cycles, sluggish acceptance of new technology, and limited seed distribution have impeded farmers' genetic advancements for decades (Varshney *et al*. 2018) [16]. Increasing genetic variety will help solve quantitative trait analysis difficulties. Chickpea, such example, has various QTLs (Varshney *et al*. 2014a; Roorkiwal *et al*. 2018a; Sivasakthi *et al*. 2018) [15, 10]. Multi-parent chickpea populations were created by combining various genetic parent contributions with a high amount of recombination to solve challenges linked to limiting genetic diversity and the incapacity of the biparental population to deal with many features (Varshney *et al*. 2019b). By intercrossing numerous (4, 8 as well as 16) various sources of paternal lines, scientists can develop haplotype combinations and novel genotype. The above qualities seem to be recorded to increase genetic diversity. This population combines bi-parental patterning communities' strengths with linkage maps to uncover novel genetic alleles relating to the interest trait. Each has two MAGIC populations in chickpea. MAGIC's founder parents were JG 11, JG 130, JG 16, ICC 4958, ICCV 00108, JAKI 9218, ICCV 10 and ICCV 97105. To collect recombination events, the eight parental lines were crossed in 28 two-way, 14 four-way, and seven eight-way crosses, yielding a MAGIC population of 1136 RILs, which were re-sequenced using the WGRS method. ICARDA's MAGIC population was created by crossing 12 different parents to create a population of 3053 RILs (Hamwieh *et al*. unpublished data). The protein diversity of 300 RILs from the ICARDA-MAGIC population ranged from 18 to 31 percent, with significant Fe and Zn levels (> 81 mg Kg1). The NAM and MAGIC populations are intended to speed up attempts to identify, isolate, and transfer critical candidate genes to help enhance chickpeas.

In chickpea, a high-throughput SNP genotyping platform with 50,590 SNPs was created and verified by genotyping two recombinant inbred line (RIL) populations [1]. High-density trait mapping is also possible with sequencing-based genotyping tools like WGRS and skim sequencing (Kale *et al*. 2015) [5], Optimal contribution selection (OCS)-based pre-breeding was used as a startergy to enhance crop productivity avoiding the erosion of genetic diversity. It was repoerted that CDC Frontier, a kabuli chickpea cultivar, has a 738-Mb draught whole genome shotgun sequence with an estimated 28,269 genes. (Varshney *et al*. 2019) [17]. For linkage mapping and QTL detection of ascochyta blight resistance, the GBS technique has been widely used. (Deokar *et al*. 2019) [1]. The RAD-Seq technology was utilised to create a high-density genetic map using an intraspecifc population, revealing new information on the frequency of recombination and hotspots throughout the chickpea genome. (Deokar *et al*. 2015). Pangenomes can distinguish between core (consistent across all individuals of a species) and dispensable (varying among individuals of a species) genome variants. In the coming years, the chickpea community will focus on developing cost-effective ultra-high-throughput genotyping systems. (Hurgobin *et al*. 2017) [3]. Chickpea pangenome and Cicer super pangenome development is expected to be a helpful resource for bridging the genome-to-phenome gap and utilising better alleles for chickpea improvement. Several molecular breeding approaches including MABC, MAS and forward breeding are being used to introgress genomic loci into elite and leading crop varieties including chickpea. (Varshney *et al*. 2018) [16].

Table 1: A summary of chickpea trait mapping attempts based on sequencing

S. No	Traits	Materials	Remark	References
1	QTL-hotspot" for Root Traits and Other Drought Tolerance Traits in JG 11	JG 11	Developed three inbreed lines (…)	Varshney *et al*. 2016
2	100-seed weight	221 specific chickpea genotypes And 48SSR Markers And 192 SNP Markers	CSN8 candidate gene at a major QTL interval regulating seed weight in chickpea.	Upadhyaya 2015
3	Using a recombinant inbred line FOR n Ascochyta blight in chickpea	Using a recombinant inbred line cross between C. arietinum And C. Reticulatum QTLs	Ascochyta blight were identified at 2 locations by interval mapping	Theor Appl Genet 2003
4	Drought tolerance	Donar parent ICC 4958	JG 11 Backcross lines that are stable in multi-location trials	Varshney *et al*. (2013)
5	Ascochyta blight resistance	Amit x ICCV 96029	Resistance QTLs on CaLG02, CaLG03, CaLG04, CaLG05, and CaLG06 account for up to 40% of phenotypic diversity (PVE)	Deokar *et al*. (2019) [1]
6	Heat tolerance	ICC 4567 × ICC 15614	QTLs having a cumulative PVE of 51.89 percent and 25.84 percent on CaLG05 and CaLG06, respectively.	Paul *et al*. (2018)
7	Seed trait	SBD377 x BGD112	QTLs that account for up to 29.71 percent of PVE, as well as candidate genes for seed characteristics	Verma *et al*. (2015)
8	Drought tolerance-related traits	ICC 4958 × ICC 1882	The "QTL- hotspot" area was refined from ca. 29 cM to 14 cM, and 49 SNPs were added to the region.	Jaganathan *et al*. (2015)
9	Photosynthetic efficiency and seed yield per plant	Cultivated and wild accessions	Photosynthetic efficiency and seed output per plant are linked by SNPs and candidate genes.	Basu *et al*. (2019)
10	Seed yield per plant	Cultivated accessions	A pentricopeptide repeat (PPR) gene linked to plant seed production	Basu *et al*. (2018)
11	Seed iron and zinc	Cultivated accessions	Seed-Fe and Zn concentrations	Upadhyaya *et al*. (2016)
			Were linked to genomic loci/genes (with a total PVE of 29%).	
12	Drought tolerance-related traits	ICC 4958 × ICC 1882 & ICC 283 × ICC 8261	Several drought component attributes have main-effect QTLs.	Roorkiwal *et al*. (2018b) [10]
13	Drought tolerance-related traits	ICC 4958 × ICC 1882	Identified 26 potential genes by limiting the "QTL-hotspot" area to 300 kb.	Kale *et al*. (2015) [5]
14	Plant vigour and canopy conductance	ICC 4958 × ICC 1882	CaLG04 and CaLG03 have QTLs for plant vigour and canopy conductance, respectively.	Sivasakthi *et al*. (2018)
15	Ascochyta blight resistance	ICCV 96029 × CDC Frontier and ICCV 96029 × Amit	Ascochyta blight resistance candidate genes	Deokar *et al*. (2019b) [1]
16	100-seed weight (100SDW) and root/total plant dry weight	ICC 4958 × ICC 1882	CaLG01 (1.08 Mb) and CaLG04 (2.7 Mb) genomic areas	Singh *et al*. (2016)
	ratio (RTR)		Were connected to 100-seed weight. 100SDW has two genes (Ca 04364 and Ca 04607), while RTR has one gene (Ca 04586).	
17	100-seed weight	ICC 7184 × ICC 15061	CaLG01 has a genomic area with six potential genes for 100- seed weight.	Das *et al*. (2015)
18	Drought tolerance	Released varieties and advanced breeding lines	Under drought, MTAs were strongly linked to yield and yield- related characteristics.	Li *et al*. (2018)
19	Fusarium wilt resistance	Donar parent WR 315	'Super Annigeri1' was released for commercial cultivation in India.	Mannur *et al*. (2019)

Technologies and Resources for genomics have improved

Until 2005, a chickpea was considered an orphan crop because to a lack of genetic and genomic resources. However, recent advances in NGS technology have Chickpea was turned from an infant plant to a crop with abundant genetic resources. Similarly, a chickpea has evolved from a minor crop to a major one due to its increasing socio-economic worth. Access to draught genome assemblies, high-throughput sequencing, molecular markers, as well asvalue control Translational genetics in crop production is now possible because to modules. In the coming years, the chickpea community will focus on developing cost-effective ultra-high-throughput genotyping systems.

Conclusion

Crop improvement relies heavily on genetic variation. It is possible to increase mutation amount accessible for the speed or selection, efficiency, but also the precision with which variants are created quickly with market-oriented features. Genetics has an ability to help both strategies. Chickpea genetic there are now materials available. for use in breeding programmes. We hope that MAS/MABC approaches will continue to improve elite/leading chickpea varieties for select traits through molecular breeding, and that parent selection, screening early generation, and GS will be integrated into chickpea breeding efforts, either in combination or separately, to accelerate the rate of genetic gains. Although genotyping

technology will become more economical in the next years, high-quality phenotyping data for these lines will be required to allow trait identification in the chickpea population. For the effective execution of breeding operations, additional resources like as mathematical models, data analytic abilities, field experiment design, barcode labelling, and databases for storing genotyping and phenotyping data would be required. Multi-institutional collaboration projects like the EiB platform (https://excel lence inbre eding.org/) and the Integrated Breeding platform (https://www.integ rated breed ing.net/) will be critical in tackling the issues in chickpea breeding. For chickpea development, incorporating a sequence-based holistic breeding method offers the potential to generate better varieties and give significant productivity benefits. In order to bridge the gap between genotype and phenotype, functional genomics methods and genome-wide selection will be used to capture genes and superior alleles for inclusion in molecular breeding programmes.

Finally, we believe that genomics technologies have huge potential to modernise breeding practises and offer next-generation chickpea varieties, which will have a significant influence in farmers' fields. In the coming years, genotyping procedures will become more economical, to identify these lines' traits, elevated phenotyping information will be required.

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