CROP BREEDING AND APPLIED BIOTECHNOLOGY

ARTICLE

Next generation breeding in pulses: Present status and future directions

Ashish Kumar[1], Abhishek Bohra[2], Reyazul Rouf Mir[3], Radheshyam Sharma[1], Abha Tiwari[2], Mohd Anwar Khan[3] and Rajeev K. Varshney[4,5*]

Crop Breeding and Applied Biotechnology
21(S): e394221S13, 2021
Brazilian Society of Plant Breeding.
Printed in Brazil
http://dx.doi.org/10.1590/1984-70332021v21Sa26

Abstract: *Human population growth in combination with changing patterns of global food consumption under climate change is posing formidable challenge to attaining sustainable global food security. Besides being economically viable sources of plant based protein for human consumption, pulses are also beneficial for the environment owing to their inherent capacity of nitrogen fixation. Hence, further development of pulses has become imperative in the vigorously transitional global scenario where flourishing anthropogenic activities are triggering irreplaceable depletion of natural resources. During past years, considerable attention has been given on the use of next generation sequencing for enriching the genomic resources in pulse crops including high-throughput DNA markers, candidate gene(s) and QTLs for predicting plant phenotypes, and whole genome sequences. With refinements in DNA sequencing technologies and computational analytical tools, the rapidly grown numbers of sequenced pulse genomes offer novel insights on crop evolution and breeding history. Integration of new-generation genomic and phenomic tools with generation acceleration procedures like genomic selection and speed breeding could greatly accelerate progress in pulses genetic improvement. The present review discusses current status and future scope of using next-generation breeding approaches in pulses that will cause not only an increase in the rate of developing climate-resilient superior cultivars but also help to reach to goal of global food security.*

Keywords: *Pulses, DNA marker, genome, gene, QTL, haplotype, genetic gain*

***Corresponding author:**
E-mail: r.k.varshney@cgiar.org/ rajeev.varshney@murdoch.edu.au
ORCID: 0000-0002-4562-9131

Received: 18 August 2021
Accepted: 24 August 2021
Published: 27 August 2021

[1] Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur (M.P.) 482 004, India
[2] ICAR-Indian Institute of Pulses Research (IIPR), Kanpur (U.P.) 208 024, India
[3] Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir (SKUAST-K), Wadura Campus, Sopore- 193 201, Kashmir, India
[4] International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Telangana, 502 324, India
[5] State Agricultural Biotechnology Centre, Crop Research Innovation Centre, Food Futures Institute, Murdoch University, Murdoch, Western Australia, Australia

INTRODUCTION

Pulses, defined as legumes that yield dry seed for human use, are agronomically valuable plants, both in the food system and in the field. Grain legumes used for human consumption especially pulses have witnessed a reinvigoration in the last decade as a way to tackle agricultural issues all around the world (Bohra et al. 2015, Varshney et al. 2015). Pulses are among the best plant-based sources of dietary protein and other nutrients such as iron, zinc, magnesium and of dietary fibre (Bohra et al. 2014, Kouris-Blazos and Belski 2016, Maphosa and Jideani 2017). A plant-based agrarian diet which is rich in fruit or legume fibre assists to enhance microbial diversity and exerts a positively influence in the levels of short-chain fatty acids, which are important for maintaining a good intestinal health (Simpson and Campbell 2015). Apart from providing nutritional health benefits, legumes also augment the soil's fertility owing to their characteristic feature of symbiotic

nitrogen fixation with the help of *Rhizobium* spp. in their root nodules (Graham and Vance 2003, Stagnari et al. 2017).

Pulses provide a sustainable option by plummeting the demand of chemical fertilization and several high protein containing pulses can be explored as a substitute of meat around the world (Maphosa and Jideani 2017). Food and nutritional security is a global issue, as indicated by nearly 800 million people suffering from chronic malnutrition worldwide (http://faostat.fao.org/). With the world's population expected to reach 9-10 billion people, the growing quest for sustainable food systems caused a paradigm shift in nutritious global diets (Godfray et al. 2010, Massawe et al. 2016, Varshney et al. 2021). Land-use alterations, which are one of the key forces affecting soil sustainability and biodiversity, will be exacerbated by global warming and anthropogenic campaign especially in agriculture (Houghton et al. 2012). In view of above, economically nutritious foods need to be introduced or created in order to eliminate all types of hunger and malnutrition, as stated by the United Nations (UN) Sustainable Development Goals (United Nations 2015). Pulses are harvested primarily for their dry grains resulting in a total of 11 pulse crops (http://faostat.fao.org/) (Cheng et al. 2019).

Leguminosae or Fabaceae, comprising 750 genera and 20,000 species (Polhill 1981), constitutes the third largest family of flowering plants after the orchid (Orchidaceae) and sunflower (Asteraceae) families (Walters 1960). Globally, a total of 93.23 million tons (m t) of pulses are harvested from 91.77 million (m) ha of land, with a productivity of 1016 kg ha^{-1} (http://faostat.fao.org/). In total, 92.82 % of the global pulse production (86.53 m t) with an acreage of 91.58% (84.05 million ha) is shared by major pulse crops, viz. dry beans (mainly common bean), chickpea, dry peas (pea), cowpea, pigeonpea, lentil and faba bean with cumulative average productivity of 1030 kg ha^{-1} (http://faostat.fao.org/).

Pulse crops are broadly categorized into two distinct groups based on their adaptability to tropical and temperate agro-climatic conditions, viz. 1) warm season crops (common bean, pigeonpea and cowpea), and 2) cool season crops (pea, chickpea, lentil and faba bean) (Cannon et al. 2009, Young et al. 2003, Zhu et al. 2005). Owing to domestication early in pre-history (c. 11,000 years ago), chickpea, pea and lentil are not only considered among the founder grain crops but also paved the way for establishment of modern agriculture (Zohary and Hopf 2000). Due to their high agricultural value, extensive research has been conducted on pulse improvement through conventional breeding, resulting in the development and release of several high-yielding varieties (Singh 2005, Saxena 2008, Pérez de la Vega et al. 2011, Torres et al. 2011, Gaur et al. 2012), as well as an increase in the global area under pulses from 64 to 91.77 million hectares over the last 60 years (http://faostat.fao.org/). However, productivity aspects of the above mentioned seven major pulse crops is still lacking and needs to be addressed in order to meet the growing protein calorie demand of the world (Figure 1). Factors like cultivation in risk prone environments, erratic rainfall, prolonged dry spells, vulnerability to variety of pest and disease limit pulse production and make them lag behind the other crops especially cereals (Borlaug 1973, Varshney et al. 2011, Varshney et al. 2013a). Concerted efforts are required to overcome the biotic and abiotic barriers hampering the yield of pulse crops (Table 1). This herculean task can be achieved by dynamic fusion of genomic tools with conventional breeding methods to augment the crop improvement progress.

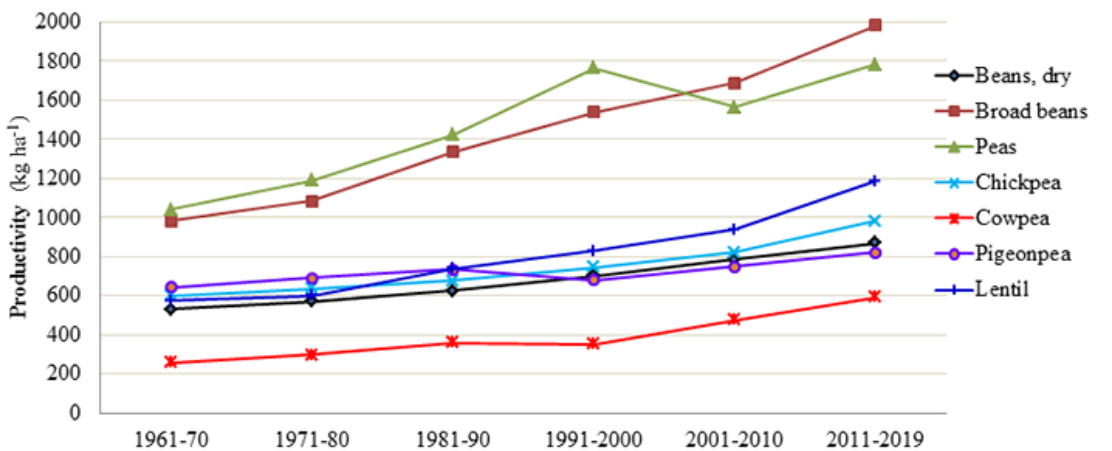

Figure 1. Global trends in productivity of seven major pulse crops. The Figure illustrates trends in productivity of major pulse crops witnessed over last six decades.

Table 1. Genome organization, productions areas, major constraints and anti-nutritional factors in key pulse crops

Pulse crop	Scientific name	Ploidy level/ chromosome count	Genome size [1C (Mbp)]*	Major growing areas	Production constraints		Major anti-nutritional factors
					Biotic	Abiotic	
Adzuki bean (Red bean)	*Vigna angularis*	2n = 22	490	Japan, Korean peninsula, and China,Nepal and Bhutan (Vaughan et al. 2005)	Brown stem rot *(Phialophora gregata*), phytophthora stem rot (*Phytophthora vignae* f.sp. *adzukicola*), wilt (*Fusarium oxysporum* f. sp. *adzukicola*), and bruchids (Vaughan et al. 2005)	Low temperature	Trypsin inhibitors, phylates and galactosides (Yoshida et al. 2010)
Bambara bean (Earth pea, groundbean)	*Vigna subterranea*	2n = 22	882	Mali, Burkina Faso, Cameroon, Niger, Togo and the Democratic Republic of Congo (Majola et al. 2021)	Cercospora leaf spot (*Cercospora canescens*), powdery mildew (*Erysiphe polygoni*), Fusarium wilt (*Fusarium oxysporum* f. sp. *voandzeia*), rust (*Puccinia graminis* f.sp. *tritici*), leaf blight *(Colletotrichum graminicola*), cowpea aphid-borne mosaic virus (CABMV), black-eye cowpea mosaic virus (BECMV), peanut mottle potyvirus (PMV), cowpea mottle comovirus (CMV), cowpea yellow mosaic virus (CYMV), cowpea weevil, bruchids, root-knot nematode (*Meloidogyne javanica*) (Majola et al. 2021)	Drought (Majola et al. 2021)	Condensed tannins (CTs), phytic acid phosphate (PAP), polyphenol, and trypsin inhibitor (Unigwe et al. 2018)
Chickpea (Gram)	Cicer arietinum	2n = 16	749.7	India, Australia, Pakistan, Myanmar, Turkey, Ethiopia, Iran, Mexico, Canada and USA (http://faostat.fao.org/)	Dry root rot (*Rhizoctonia bataticola*), Fusarium wilt (*Fusarium oxysporum* f. sp. *ciceris*), collar rot (*Sclerotium rolfsii*), wet root rot (*Rhizoctonia solani*) and black root rot (*Fusarium solani*), Ascochyta blight (*Ascochyta rabiei*), Botrytis gray mold (*Botrytis cinerea*), Stemphylium blight (*Stemphylium sarciniforme*), Bacterial blight (*Xanthomonas campestris* pv. *cassiae*) Beet armyworm (*Spodoptera exigua*), leafminer (*Liriomyza cicerina*), black aphid (*Aphis craccivora*), Pod borers (*Helicoverpa armigera*) (Nene et al. 2012)	Drought, heat and cold stress	Protease inhibitors, amylase inhibitors, phytolectins, polyphenols, and oligosaccarides
Common bean	*Phaseolus vulgaris*	2n = 22	588	Nigeria, Myanmar, India, Brazil, Niger, USA, Tanzania, Mexico, China, Uganda (FAOSTAT, 2019)	Web blight (*Thanatephorus cucumeris*), Cercospora leaf spot (*Cercospora cruenta*), Anthracnose (*Colletotrichum lindemuthianum*), rust (*Uromyces appendiculatus*), Angular leaf spot (*Pseudocercospora griseola*), Bacterial blight (*Xanthomonas axonopodis* pv *phaseoli*), Halo blight (P*seudomonas syringae* pv. *phaseolicola*), Bean common mosaic virus (BCMV), Aphids, Armyworms, Corn earworm , Cutworms, Leafminers, Mexican bean beetle, Stinkbugs (Degu et al. 2020, OECD 2016)	Low soil phosphorus (Beebe et al. 2014)	lectin, saponin, trypsin inhibitor and phytic acid (Rui et al. 2016)

Common vetch	*Vicia sativa*	2n = 12	2254	Turkey, Albania, Lebanon, India, China, North America, Spain, Australia (Ennenking and Tate 2006, Firincioglu et al. 2010)	Powdery mildew (*Erysiphe pisi*), pea aphid (*Acyrthosiphon pisum*)	Frost (Chung et al. 2013)	beta cyano L alanine and its derivatives (Tate and Ennenking 2006)
Cowpea (black eye bean)	*Vigna unguiculata*	2n = 22	1176	Nigeria, Niger, Burkina Faso, Tanzania, Cameroon, Mali, Myanmar, Kenya, Mozambique, Democratic Republic of the Congo (http://faostat.fao.org/)	Leaf smut or false smut (*Protomycopsis phaseoli),* Bacterial blight (*Xanthomonas campestris* pv *vignicola*), bacterial pustule (*Xanthomonas campestris* pv. *vigna euguiculatae),* cowpea aphid borne mosaic (CABMV), cucumber mosaic virus (CMV), cowpea mild mottle virus (CPMMV) and cowpea severe mosaic virus (CPSMV), Root-knot nematodes (*Meloidogyne incognita* and *M. jjavanica),*Koch (*Aphis craccivora*), bruchids (*Callosobruchus maculatus* (Fabricius)), beetles *(Ootheca mutabilis*), maruca (*Maruca vitrata*), leafhoppers and foliage beetles, *Parasitic weeds: Striga gesnerioides* (Willd.) Vatke and *Alectra vogelii* Benth (Horn and Shimelis 2020)	Drought and heat stresses and poor soil fertility (Horn and Shimelis 2020)	Phytate, polphenols, enzyme inhibitors (trypsin, chymotrypsin) (Frias et al. 1995)
Faba bean (Broad bean, horsebean)	*Vicia faba*	2n = 12	13034	China, Europe, Northern Africa, West Asia and Australia (http://faostat.fao.org/)	Ascochyta blight (*Ascochyta fabae*), chocolate spot (*Botrytis fabae)* rust (*Uromyces viciae-fabae*), faba bean necrotic yellows virus (FBNYV), bean yellow mosaic virus (BYMV), black root rot (*Fusarium solani*), faba bean root rot (*Aphanomyces euteiches*), powdery mildew (*Erysiphe pisi* var. *pisi*), stem rot (*Sclerotinia trifoliorum*), black bean aphid (*Aphis fabae*), pea leaf weevil (*Sitona lineatus*), broad bean weevil (*Bruchus rufimanus*) (Karkanis et al. 2018)	Drought and heat stress (Katerji et al. 2011)	phenol and condensed tannin/proanthocyanidin (Kumar et al. 2015)
Grass pea	*Lathyrus sativus*	2n = 14	8330	India, Pakistan, Bangladesh, Nepal, Ethiopia (Vaz Patto et al. 2006)	Powdery mildew (*Erysiphe pisi*), downy mildew (*Peronospora* spp) rust (*Uromyces* spp.), blight (*Mycosphaerella pinodes*), orobanche, root knot nematode (*Meloidogyne artiella*) and cyst nematode (*Heterodera ciceri*) (Vaz Patto et al. 2006)	-	ODAP, nitriles (Vaz Patto and Rubiales 2014)
Hyacinth bean (Lablab)	*Lablab purpureus*	2n = 22	367 (Iwata et al. 2013)	India, Nepal, China, Bagladesh, Thailand, Australia and Eastern Africa (Maass et al. 2010)	Bruchid (*Callosobruchus* spp.), pod borer (*Adisura atkinsoni*), anthracnose (*Colletotrichum lindemuthianum*), leaf spot (*Cercospora dolichi*) and powdery mildew (*Leveillula taurica*)	Drought (Maass et al. 2010)	Tannins, phylates and trypsin inhibitors (Murphy and Colucci 1999)

Lentil	*Lens culinaris*	2n = 14	4125.8	Canada, India, Turkey, Australia, Nepal, USA, China, Ethiopia, Bagladesh, Syrian Arab Republic (http://faostat.fao.org/)	Wilt (*Fusarium oxysporum* f. sp. *lentis*), Rust (*Uromyces viciae-fabae*), Ascochyta blight (*Ascochyta fabae* f.sp. *lentis*) Sitona weevil/bruchids, Aphids (Agrawal et al. 2013)	Drought, heat, cold and frost (Agrawal et al. 2013)	oligosaccharides, α-galactosides, trypsin inhibitors (Vidal-Valverde et al. 1994)
Lupins							
White	*Lupinus albus*	2n = 50	568.4	Australia, Poland, Ukraine (http://faostat.fao.org/)	Anthracnose (*Colletotrichum lupini*), Phomopsis stem blight (*Diaporthe toxica*), rust (*Urmyces lupinicolus*), gray mold (*Botrytis cinerea*),, cucumber mosaic virus (CMV), bean common mosaic virus (BYMV) (Clements et al. 2005)	Alkaline soil, frost	Alkaloids (Quinolizidine)
Yellow	*L. luteus*	2n = 52	980				
Narro-leafed	*L. angustifolius*	2n = 40	926.1				
Moth bean (Mat bean)	*Vigna aconitifolia*	2n = 22	1078				
Mungbean (Green gram)	*Vigna radiata*	2n = 22	588	India, Pakistan, China, Myanmar and Thailand (Isemura et al. 2012)	Leaf spot (*Cercospora canesens*), Powdery mildew (*Erysiphe polygoni*), anthracnose (*Colletotrichum* spp.), mungbean yellow mosaic virus (MYMV), bruchids, white fly (*Bemicia tabaci*), thrips (*Megalurothrips distalis*) (Nair et al. 2019)	Alkaline soil, iron deficiency chlorosis (Prathet et al. 2012)	Trypsin inhibitors, haemaglutinins and phylates (Lambrides and Godwin 2007, Sompong et al. 2012)
Pigeonpea	*Cajanus cajan*	2n = 22	784	Asia,Eastern and Southern Africa, Latin America and Caribbeancountries (Choudhary et al. 2011)	Fusarium wilt (*Fusarium udum*), sterlity mosaic (Pigeonpea Sterlity Mosaic Virus) and phytopthora blight (*Phytopthora drechslei* sp. *cajani*).Pod-bug (*Calvigralla gibbosa*, *C. scutellarius*), Pod borer (*H. Armigera*), leaf webbers, cutworms (*Agrotis ipsilon* and *Ochropleura flammatra*) and hairy caterpillars (*Amsacta moorei*, *A. albistriga* and *Spilosoma obliqua*) (Sharma et al. 2010)	Waterlogging, Drought, Low temperature, photoperiod, soil salinity, Al toxicity (Choudhary et al. 2011)	Protease inhibitors, amylase inhibitors, phytolectins, polyphenols, and oligosaccarides
Rice bean	*Vigna umbellata*	2n = 22	588	Eastern India, Myanmar, Thailand,Nepal and Southern China (Isemura et al. 2010)	Rust (*Uromyces appendiculatus*), cercospora leaf spot and web blight (*Rhizoctonia solani*) (Khadka and Acharya 2009)	-	Trypsin inhibitors and Phylates
Urd bean	*Vigna mungo*	2n = 22	588	India, Myanmar, Thailand, Phillipines and Pakistan (Gupta et al. 2013a)	Leaf crinkle virus, MYMV and bruchids (Sharma et al. 2011)	Salinity and drought	Trypsin inhibitors and Phylates

*Information used from http://data.kew.org/cvalues/.

Availability of economically viable next generation sequencing (NGS) technologies has led to remarkable advances in genomic resources of pulses including the whole genome sequencing (Varshney et al. 2013b, Varshney et al. 2017). NGS based protocols such as genotyping by sequencing (GBS) have been implemented for discovering and genotyping SNPs in large populations and germplasm collections (Bohra et al. 2020a, Jaganathan et al. 2020). Stupendous scope has been generated for forward genetics approaches like QTL mapping intending to decipher the gene(s)/QTLs underlying a particular phenotype. Further, exciting opportunities like marker development, trait mapping and molecular mapping have knocked on the door with the advent of application of genome-wide strategies like restriction-site associated DNA sequencing (RADSeq) in pulses (Yang et al. 2012, Yang et al. 2013a, Yang et al. 2013b). In consideration of the above, this review summarizes the production scenario and constraints, the available genomic resources and their downstream applications as well as prospects for genomics-assisted breeding (GAB) in selected pulse crops.

MOLECULAR MARKERS AND GENOTYPING ASSAYS IN PULSES

Since its discovery in 1980s, the DNA marker system has revolutionized the science of plant breeding. The molecular marker technology evolved remarkably since the discovery of first molecular marker system restriction fragment length polymorphism (RFLP). Several classifications have been proposed to classify DNA based molecular markers. For instance, classification based on their generation of development (First generation *vs* 2nd generation *vs* 3rd generation *vs* 4th generation *vs* 5th generation), hybridization *vs* non-hybridization, array based *vs* non-array based, sequence based *vs* non-sequence based, low-throughput *vs* high-throughput *vs* ultra-high throughput, past *vs* present *vs* future molecular markers (Mir et al. 2013a, Mir and Varshney 2013, Gupta et al. 2013, Kumar et al. 2021). The recent advances in genomics tools and techniques have helped in the development of variety of molecular markers in crop plants including legume crops. Legume crops like chickpea, pigeonpea, groundnut, lentil, etc. were once considered as "orphan crops" due to lack of sufficient or availability of insufficient genomic resources in these legume crops. However, in the last decade, tremendous progress was made and large repertoire of molecular markers has been developed in these important legume crops. The success in development of these markers could be attributed to the evolution of new sequencing technologies that led to the reduction in cost of DNA sequencing (Varshney et al. 2019). A number of marker types that are available include thousands of SSRs, diversity arrays technology (DArT) markers, single nucleotide polymorphism (SNP) markers, different SNP platforms, micro-array based markers, NGS-based markers, genotyping by sequencing (GBS), InDel markers etc. The marker resources available in chickpea and pigeonpea have been recently summarized (see Bohra et al. 2020a, Roorkiwal et al. 2020). Briefly, using different approaches, thousands of SSR (>3000 in chickpea, >3000 in pigeonpea) have become available over the years and DArT markers with >15360 features each for chickpea, pigeonpea and groundnut have been also developed by ICRISAT in collaboration with DArT Pvt Ltd, Australia. In addition to thousands of SSR and DArT markers, tens of thousands of SNP markers have also been developed by ICRISAT in collaboration with national/international partner's using variety of approaches.

The availability of marker resources has led to the development of different types of genotyping platforms/assays (including Kompetitive Alelle Specific PCR (KASP) assays, GoldenGate assays, Vera-code assays, 60K SNP chips using Affymetrix SNP platform and Axiom SNP array with thousands of SNPs) by public and private research organization/ companies for their research/commercial use. Most of these genotyping platforms developed are based on SNP markers, since SNP markers considered as markers of choice and are amenable to high-throughput genotyping. The genotyping platforms available can be classified into low-density (1-10 SNPs), medium-density (2-10 K SNPs) and high-density (>20K SNPs) genotyping platform (Varshney et al. 2019). The low density genotyping platforms can be used in early generation testing, marker-assisted selection (MAS) and testing hybridity. The medium and high-density genotyping platforms have been extensively used in genetic diversity studies, genomic selection (GS), background selection, mapping genes/QTLs in different crop plants through genome-wide association studies (GWAS) and linkage mapping/QTL mapping. ICRISAT in collaboration with Intertek company is extending low-density (10 SNPs) genotyping for many crop species, including chickpea, pigeonpea and groundnut for foreground selection in early generations of breeding program (Varshney 2016, Varshney et al. 2019). Among the high-density genotyping platforms, the most recent SNP Arrays with genome-wide SNPs tiled on these have been developed in crops like chickpea (Roorkiwal et al. 2018a), pigeonpea (Saxena et al. 2018), field pea (Tayeh et al. 2015a). Moderate density genotyping platforms including genotyping by sequencing (GBS) and restriction-site-associated sequencing (RAD-Seq) have been also used successfully in chickpea for genetic studies (Roorkiwal

et al. 2020). In summary, different molecular marker systems have been used in the study of genetic diversity, population structure, development of genetic maps and QTL mapping/ GWAS for key traits in pulse crops including chickpea, and pigeonpea. The genes/QTLs once identified are deployed in molecular breeding programs aimed at enhancing targeted traits in different crop plants through marker-assisted selection (MAS), marker-assisted recurrent selection (MARS) and GS. It is expected that the improved versions of next-generation crop varieties could be developed with enhanced quality traits, better yield and disease resistance (Varshney et al. 2021).

MOLECULAR GENETIC MAPS

The molecular genetic maps refer to linear arrangement of molecular markers (loci) on the chromosome that has been obtained on the basis of estimates of recombination fractions among the markers. These molecular genetic maps once developed can be used for different purposes including i) understanding genome organization, ii) study of evolution of species, iii) study of synteny between related species, iv) study of chromosomes/genome rearrangement across taxa, and more importantly v) discovery of genes/QTL through QTL interval mapping. During recent advances in genomics tools and technologies including advances in development of marker technologies, molecular genetic maps have been developed in almost all plants of significant academic and economic interest, and the list of plants is growing regularly. In many pulses also, linkage maps have been developed. For instance, in pigeonpea, the first genetic map was developed in year 2011 with 239 SSR loci (Bohra et al. 2012). Following this, several other maps were developed for pigeonpea (Bohra et al. 2012). However, these maps were not dense due to availability of less number of markers and due to less polymorphism available in the pigeonpea. However, with the availability of high-density genotyping platforms, the marker densities of the genetic maps in pigeonpea have now improved dramatically. The first high-density genetic linkage map of pigeonpea was developed using SNP markers and this map possess 910 marker loci with an average inter marker distance of 1.11 cM (Saxena et al. 2012). In addition to individual genetic maps, consensus genetic maps have also been developed in pigeonpea by merging more than one map (Arora et al. 2017). The genetic map with highest density in pigeonpea was constructed with 6818 SNP loci that span 974 cM of the genome (Yadav et al. 2019). A list of high-density genetic maps available in pigeonpea is available elsewhere (Bohra et al. 2020b).

In chickpea, narrow genetic base and low level of intra-specific genetic polymorphism, development of good high-density genetic mapping remained a challenge (Verma et al. 2015). However, advent of NGS technologies led to the development of thousands of markers and availability of high-density marker linkage maps in chickpea. For instance, one of the most comprehensive genetic map having 1,291 markers on eight linkage groups spanning a total of 845.56 cM distance was developed at ICRISAT (Thudi et al. 2011). Varshney et al. (2014a) after screening thousands of markers, could find only few hundred polymorphic markers and ultimately were able to map 241 and 168 markers on ICCRIL03 and ICCRIL04 mapping populations respectively. However, with the availability of NGS tools and technologies like genotyping-by-sequencing genotyping platform, several high-density genetic maps could be developed. For instance, using GBS, a high-density genetic map having 1007 mapped markers spanned around 727.29 cM was developed (Jaganathan et al. 2015). Similarly, using GBS technology, one of the most saturated/densest intra-specific linkage maps reported with 3,363 loci at an average marker density 0.33 cM (Verma et al. 2015). Several other linkage maps and consensus maps using multiple genetic mapping have been developed in chickpea (Mallikarjuna et al. 2017). In addition, integrated physical, genetic and genome sequence map of chickpea has also been developed (Varshney et al. 2014b).

More recently, using NGS-based genome sequencing and resequencing technologies, millions of SNP markers have been discovered in chickpea and used in preparation of high-density SNP array. Using high-density SNP array platform "Axiom CicerSNP Array", genetic maps for ICCRIL03 and ICCRIL04 populations were constructed. For ICCRIL03 mapping population, a total of 13679 SNPs were successfully placed on eight linkage groups covering 1033.67 cM (Roorkiwal et al. 2018a).

Like chickpea and pigeonpea, genetic linkage maps including medium-density and high-density linkage maps have been developed successfully in other legumes crops including groundnut and lentil. The development of these genetic linkage maps involved the use of a variety of molecular markers /genotyping platforms including SNP arrays.

Mapping of genes: from QTL mapping to sequence-based trait mapping

Identification of genes/QTLs through QTL interval mapping is now a routine. However, several inherent disadvantages are associated with QTL mapping including i) Time and labor intensive, ii) less recombination events and hence less

diversity sampled, iii) use of controlled crosses whose development takes several years, iv) problem of polymorphism while developing linkage maps, etc. Some of these disadvantages have been overcome through the use of recently emerged association mapping (genome-wide association studies; GWAS) as an alternative to QTL mapping. The use of association mapping/GWAS has become very popular in the last two decades and now GWAS has been used in almost all crop plants for discovery of gene/QTLs of all important traits. In grain legume crops both mapping approaches including QTL mapping and GWAS have been used for gene discovery and several important genes/QTLs have been discovered for important targeted traits. For instance, using QTL interval mapping, genes/QTLs have been identified for drought/ drought related traits and yield under drought (Mir et al. 2012, Varshney et al. 2014b). It is important to mention that a "*QTL-hotspot*" was identified on linkage group-4 that harbors 12 major QTLs for drought tolerance related traits explaining up to 58.20% phenotypic variation. This important hot-spot region was later fine mapped using important genotyping platform "genotyping-by-sequencing (GBS)", sliding window based bin mapping and GWAS based gene enrichment analysis of skim sequenced data of RIL population (Jaganathan et al. 2015, Kale et al. 2015). QTLs/genes for drought and heat responsive traits have also been identified using GWAS and candidate gene sequencing approaches (Thudi et al. 2014). Genes/QTLs have also been identified for important diseases in chickpea like Fusarium wilt (FW), Ascochyta blight (AB), botrytis gray mold (Anuradha et al. 2011, Sabbavarapu et al. 2013, Varshney 2016). In addition gene/QTLs have also been identified for phenology related traits, seed traits etc. (Verma et al. 2015, Ortega et al. 2019, Sivasakthi et al. 2019, Roorkiwal et al. 2020).

Similarly, in pigeonpea, genes/QTLs have been identified for variety of traits using different trait mapping approaches. For instance genes/QTLs have been identified for important diseases like Fusarium wilt (FW) and sterility mosaic disease (SMD) (see Raju et al. 2010, Dubey et al. 2011, Varshney 2016, Pazhamala et al. 2017, Mir et al. 2017, Bohra et al. 2020a, Saxena et al. 2021). Genes/QTLs have been also identified for plant height, growth habit, flowering, earliness and determinacy through candidate gene sequencing and whole genome scanning approaches (Bohra et al. 2011, Kumawat et al. 2012, Mir et al. 2013b, Mir et al. 2014, Mir et al. 2017). In addition, genes/QTLs have also been identified for drought, salinity, cold, agronomic traits such as fertility restoration (Priyanka et al. 2010, Bohra et al. 2011, Kumawat et al. 2012, Deeplanaik et al. 2013, Mir et al. 2017, Saxena et al. 2020). The use of wild relatives like *C. cajanifolius* and *C. acutifolius* through advance back-cross QTL mapping has also been attempted in pigeonpea to map genes for agronomically important traits including yield and yield contributing traits (Saxena et al. 2020).

In view of genomics revolution in legume crops, the NGS-based high-throughput genotyping approaches are being used for genetic/trait mapping. This sequence-based trait mapping has been used in chickpea, pigeonpea by either sequencing of the whole population or pooled samples belonging to two extreme bulks for the trait of interest (see Pandey et al. 2016, Varshney et al. 2019, Roorkiwal et al. 2020, Bohra et al. 2020b). The NGS-based trait mapping overcomes several disadvantages like time consuming and costly nature of traditional approaches of trait mapping and therefore preferred in recent times for trait mapping., Sequenced-based trait mapping approaches have also been used in chickpea, pigeonpea and groundnut for identification of candidate genes/genomic regions for rust and late leaf spot resistance (see Pandey et al. 2016, Varshney 2016, Roorkiwal et al. 2020, Bohra et al. 2020c).

GENOME SEQUENCING INITIATIVES IN PULSES

Whole genome sequencing

Chickpea

Chickpea is one of the most important legume crops with its small (desi) and large sized (kabuli) seeds constituting the main market types. Varshney et al. (2013d) reported 532-Mb genome assembly in CDC Frontier (Kabuli chickpea) by whole genome shotgun sequencing approach, and assembly contained a total of 28,269 genes. The assembly had 7,163 scaffolds greater than 1Kb and 3,659 scaffolds greater than 2 Kb. Nearly 73% of the assembly comprised of larger scaffold size, being N50 of 39.99 Mb. Of the total genes reported, 89.73% were annotated with 4.93 as the mean number of exon per gene and 236 bp as the average exon size. The assembly harboured 187 disease-resistance genes and large-scale DNA markers were discovered including 48,298 SSRs and 76,084 SNPs. Similarly, Jain et al. (2013) reported draft genome sequence of ICC 4958 (desi) having size of 520 Mb, capturing 70% of total genome size. Their genome assembly had 27,571 predicted genes and the repeat elements comprised of 210 Mb. During comparative analysis with other dicot genome

numbers of gene predicted were lower but the average transcript length was reported to be higher and nearly equal to soybean. Another genome assembly by Parween et al. (2015) captured 511 Mb of ICC 4958 (desi) and 327 Mb-genome was assembled for PI 489777, a wild chickpea (Gupta et al. 2017). Among all the assemblies, Varshney et al. (2013d) have sequenced most of the genome approximately 74% of the total. Further, Misra et al. (2014) developed a Chickpea Genomic Web Resource (CGWR) to visualize the desi genotype (ICC 4958) genome and have comparatively analyzed the wild and cultivated genotypes of chickpea and other legume crops. Following the availability of the whole genome assemblies, researchers have developed several databases to catalogue genome-wide DNA markers for applications in research and breeding such as chickpea microsatellite database (CicArMiSatDB) (Doddamani et al. 2014) and Microsatellite Database (CMsDB) (Parida et al. 2015). Other databases on chickpea genomic resources include CicArVarDB encompassing SNP and InDel (Doddamani et al. 2015), and ISM-ILP database (Srivastava et al. 2016) that provides information on 119,169 and 110,491 ISMs from protein-coding genes desi (23,129) and kabuli (20,386) chickpeas.

Pigeonpea

Pigeonpea was the first pulse and second legume crop whose genome was sequenced. Using a *de novo* assembly approach and based on Illumina sequencing platform, Varshney et al. (2012) assembled 605.78 Mb of the popular pigeonpea variety ICPL 87119 (Asha), representing 72.7% the total genome size of pigeonpea (833.07 Mb). This assembly contained a total of 137,543 scaffolds with N50 of 516.06 Kb. Of the total scaffolds, 6,534 were longer than 2kb. In this draft genome assembly, 51.67% of the total genome was represented by the transposable elements (TE) whereas the total GC content was 32.8%. The genome assembly had 48,680 genes with coding sequence size of 959.39 bp and 3.59 exons per gene. Besides protein-coding genes, further annotation identified 862 microRNAs, 763 tRNA, 329rRNA and 363 small nuclear RNA (snRNA) in the pigeonpea genome. On comparative analysis with soybean genome (Schmutz et al. 2010), the number of exons per gene was 3.59 which was less than that of soybean (5), whereas lengths of exon (267.39 bp) and intron (536.89 bp) were found to be higher. Another draft genome assembly of pigeonpea by Singh et al. (2012) based on 454 GS-FLX technology. They identified 1,213 defence-responsive genes and 152 genes having possible association tolerance against abiotic stress. The availability of the reference genome sequence has opened enormous opportunity for the development of large-scale DNA markers, such as 309,052 SSRs and 28,104 SNPs across 12 genotypes. Varshney et al. (2017) have resequenced the genomes (with the coverage depth of 5X to 12X) of 292 pigeonpea accessions including wild species, cultivated breeding lines and landraces. Following the whole genome sequencing approach, Kumar et al. (2016) have reported the first hap map using 20 accessions representing parents of MAGIC, NAM, RIL, 18 wild and 2 cultivated lines. Similarly, first pangenome of pigeonpea contained 86.6% core genes and 13.4% variable genes.

Field pea

Field pea is used as a genetic model for genetic studies since 1980s, however its large genome size (4.45 Gb) has hampered the progress of pea genomics as compared to the other pulse crops. Earlier researches have reported that this difficulty occurs because pea genome is mostly dominated by mobile and repetitive elements mainly Ty3/gypsy family of transposons (Macas et al. 2007). More recently, Kreplak et al. (2019) have built a high-quality chromosomal-level genome assembly of the reference genotype 'Caméor' that spanned 3.92 Gb of the genome. The genome assembly was made using a combination of short read sequences (Illumina sequences) with 281X genome coverage and long read sequences (PacBio RSII) with 13X genome coverage. The key features of this assembly included N50 of scaffolds being with 415,920 bp, total length of pseudomolecules was 3.23 Gb, and the lengths of transposon regions were 2.45 Gb and 171 Mb of class II and class I, respectively. The genome pea assembly consisted of 44,756 genes, 30,687 of which were annotated. The reference pea genome provides a strong foundation to elucidate the phylogeny and evolutionary relationship of pea with other crops, and a variety of important genes for future improvement.

Common bean

Common bean is a short-day plant grown mainly in African and American countries. Nearly 8,000 years ago, wild pools independently isolated themselves in two geographical locations i.e., Mexican and South American. Schmutz et al. (2014) presented a genome analysis of an Andean ecotype common bean (G19833) to cover accessions ranging from Mexico to Argentina. Using whole genome shotgun approach, the authors assembled common bean genome on

11 psuedomolecules, with a mean coverage of 21X. The assembly size was reported to be 472.5 Mb, of which 468.2 Mb was assigned to psuedomolecules. By resequencing 60 wild accessions and 100 landraces the study confirmed the evolutionary relationship of the Mesoamercian and Andean gene pools.

Mungbean

Mungbean is a warm season fast growing legume in Asia belonging to subgenus *Ceratotropis* of genus *Vigna.* Kang et al. (2014) assembled 431-Mb of the diploid *V. radiata* var. *radiata* (VC 1973) using Illumina and GS FLX platforms, with the corresponding libraries providing 320-fold and five-fold coverage of the total genome. Furthermore, a wild relative (*V. radiata* var. *sublobata*, accession *TC1966*) of the domesticated mungbean was sequenced covering 82% (423-Mb) of the total 501 Mb genome. Similarly, a 792-Mb genome of the tetraploid *V. reflexo-pilosa var. glabra* (accession V1160) was assembled into 29,166 scaffolds. A total of 22,427 genes were predicted based on homology-based search and RNA-Seq data of different tissues.

Adzuki Bean

Adzuki bean (*V. angularis* var. *angularis*) is grown in 30 countries worldwide. To accelerate the genomic research, Kang et al (2015) built a genomic assembly of Chinese cultivar "Jingnong 6". With 168X coverage of the total genome, 443 Mb representing 75% of the total genome (591 Mb) was assembled into 3,883 scaffolds having N50 of 703 Kb. The repetitive content of the genome comprised of 207 Mb (44.51%), which was lower than other pulse crops such as chickpea, pigeonpea but almost similar to that of common bean. A total of 26,857 genes were predicted with high confidence and of these, 15,976 genes were assigned to pseudo chromosomes. Salient features of the genomic assemblies among selected legume crops are given in Table 2.

Another draft genome assembly of adzuki bean by Yang et al. (2015) based on HiSeq 2000 sequencing platform assembled 450 Mb contig sequences with N50 of 38 kb (168X coverage of total genome) representing 83% of the total genome size of adzuki bean (542 Mb). This assembly contained a total of 466.7 Mb scaffolds with N50 of 1.29 Mb, representing 86.11% of the total genome size. Of the total scaffolds, 6,534 were longer than 2kb. In this draft genome assembly, 34.57% of the total genome was represented by the retrotransposons whereas the total GC content was 34.8%. Besides 34,183 protein-coding genes, further annotation identified 312 microRNAs, 307 tRNAs, 3730 rRNAs and 314 small nuclear RNAs (snRNA) in the adzuki bean genome.

Table 2. Salient features of the genome assemblies of some pulse crops

Assembly features	Chickpea	Pigeonpea	Field Pea	Common Bean	Mungbean	Adzuki Bean
Genome Size	738 Mb	858 Mb	4.45 Gb	587 Mb	579 Mb	538 Mb
Genome sequenced	544.3 Mb	605.78 Mb	3.92 Gb	473 Mb	473 Mb	450 Mb
Number of Scaffold	7,163	137,542	24,623	708	2,800	37,533
N50 of (Scaffolds)	39.99 Mb	516 Kb	415,940 bp	50.4 Mb	1507 Kb	1.29 Mb
Number of exon per gene	4.93	3.59	4.33	5.5	-	-
Number of predicted genes	28,269	48,680	44,756	27,197	22,427	34,183
Transposable elements	49.41%	51.67%	84%	45.42%	43%	44.51%
GC% content	30.78%	32.80%	37.60%	-	33%	34.80%
References	Varshney et al. (2013d)	Varshney et al. (2012)	Kreplak et al. (2019)	Schmutz et al. (2014)	Kang et al. (2014)	Kang et al. (2015)

TRANSCRIPTOMIC RESOURCES IN PULSES

To leverage legume functional genomics and to provide genes controlling important traits, transcriptomic resources have been developed in recent past. The global expression analysis in combination with gene expression atlas (Table 3), have elucidated the molecular mechanism underlying important plant responses that contribute towards sustainable agriculture production. Earlier, transcriptome assemblies were developed in pulse crops using a combination of Sanger and next generation sequencing platforms. For example, Dubey et al. (2011) developed a transcriptome assembly (CcTA)

Table 3. Gene expression atlas built in some pulse crops

Crop	Resource	Number of genes catalogued	References
Chickpea	*Cicer arietnium* gene expression atlas *(CaGEA)*	32,873	Kudapa et al. (2018)
Pigeonpea	*Cajanus cajan* gene expression Atlas *(CcGEA)*	28,793	Pazhmala et al. (2017)
Common bean	*Phaseolus vulgaris* gene Expression Atlas *(Pv GEA)*	11,010	O' Rourke et al. (2014)

comprising of 127,754 tentative unique sequences (TUSs) and the transcriptome assembly offered sets of DNA markers including 8137 SSRs, 12,141 SNPs and 5845 ISR. Similarly, Dutta et al. (2011) developed a set of 3,771 genic SSR markers. Sinha et al. (2015a, b) in pigeonpea identified, sequenced and validated the set of 10 housekeeping genes in pigeonpea under salt and heat stress conditions. The study by Raju et al. (2010) reported 9,468 high quality ESTs and identified genes responsive to Fusarium wilt (19) and sterility mosaic disease (20), the two most prominent diseases of pigeonpea. More recently, transcriptome assemblies have been developed in pigeonpea based on RNA-Seq of transcriptomes from unopened flower buds of male sterile lines and cognate fertile lines (Bohra et al. 2021a, Bohra et al. 2021b).

Similarly in chickpea, 21,491 ESTs were developed as a rich resource for the identification of drought-responsive genes (Hiremath et al. 2011). A variety of DNA markers were identified including SSRs (728), SNPs (495), COS (387), and ISR (2088). Other transcriptome based studies in chickpea include Varshney et al. (2009) (20,162 ESTs) and Garg et al. (2011) (34,760 transcripts reads). In chickpea, SAGE combined with NGS has also been used for genome-wide high quality transcriptome profiling, which led to the identification of 3,858 drought-responsive genes in chickpea. Another SAGE analysis study by Afonso-Grunz et al. (2015) elucidated strongly upregulated gene glutathione S-transferases or genes implicated in phenylpropanoid and flavonoid biosynthesis pathway. A microarray based transcriptome analysis in root and leaf tissues have revealed 4,815 differentially expressed genes, out of which 88 and 52 genes were found to be differentially expressed in root and leaf tissues respectively. Another microarray based transcript study has confirmed a set of 109,210 and 386 genes expressed differentially in drought, cold and salinity stress respectively (Mantri et al. 2007). Advances in sequencing technologies in combination with improved computations tool have facilitated the development of gene expression atlas in different pulse crops such as common bean (O'Rourke et al. 2014) pigeonpea (Pazhmala et al. 2017) and chickpea (Kudapa et al. 2018).

GEMOMIC BREEDING METHODS IN PULSE CROP IMPROVEMENT

Marker-assisted backcrossing

Among various GAB (Varshney et al. 2021) approaches, marker assisted backcrossing (MABC) has been used to introgress major-effect QTL controlling a variety of biotic and abiotic stresses such as disease resistance and drought tolerance. For instance, Geletu, a drought tolerant line derived from MABC scheme in chickpea was released for cultivation in Ethiopia. The QTL hotspot genomic region harbouring a variety of drought tolerance associated traits was introgressed into an Indian chickpea cultivar from the donor ICC 4958 (Varshney et al. 2013c). Similarly, QTL controlling resistance against Fusarium wilt and Ascochyta blight were introgressed to chickpea cultivar C 214 following MABC approach (Varshney et al. 2014c). More recently, fast-track development of drought tolerant 'Pusa chickpea 10216' was demonstrated by transferring "*QTL-hotspot*" genomic region from ICC 4958. Development of various molecular breeding products in chickpea has been discussed in detail elsewhere (Bohra et al. 2019, Roorkiwal et al. 2020).

In field pea, application of GAB approach was demonstrated for selection of lodging resistance in early segregating generations, and the GAB approach was found to be more efficient than conventional phenotypic selection (Zhang et al. 2006). Other traits that have been introgressed in field pea using GAB approach include *Aphanomyces* root rot resistance (Hamon et al. 2013), frost tolerance (Lejeune-Hénaut et al. 2008, Tayeh et al. 2015b). Advanced backcross-QTL (AB-QTL) proposed by Tanksley and Nelson (1996), facilitates variety development and QTL introgression in a simultaneous manner. In field pea, an AB population was made by back crossing (BC_2F_6) an accession ATC 113 to a susceptible cultivar Pennant (Aryamanesh et al. 2012). Similar examples were reported in common bean for agronomic traits (Blair et al. 2006). Some examples of fast-track trait introgression using MABC/MAS approaches in pulse crops are provided in Table 4.

Table 4. Some examples of fast-track trait introgression using MABC/ MAS in some pulse crops

Crop	Donor Parent	Recipient	Trait	DNA Marker	References
Chickpea	Vijay	Pusa 256	Resistance against Fusarium wilt *(foc2)*	SSR	Pratap et al. (2017)
Chickpea	WR 315	C 214	Resistance against Fusarium wilt *(foc1)*	SSR	Varshney et al. (2014c)
Chickpea	ILC 3279	C 214	Ascochyta blight *(ABQTL-I and ABQTL-II)*	SSR	Varshney et al. (2014c)
Common bean	AND 277	Rudá	Resistance against angular leaf spot	STR	Gonçalves-Vidigal et al. (2011)
Common bean	AND 277	IAC-Milênio	Resistance against angular leaf spot	SNP	De Almeida et al. (2021)
Common Bean	BAT93	Jalo EEP558	Resistance against anthracnose and rust	SSR, RGA, AFLP	Hanai et al. (2010)
Common Bean	Bunsi	Midland	Resistance against white mold	AFLP, RAPD	Ender et al. (2008)
Common Bean	R31-83	Orion	Resistance against white mold	SNP	Vasconcellos et al. (2017)
Common Bean	G21212	BAT 881	Drought tolerance	RFLP,SSR,SNP	Diaz et al. (2018)
Lentil	*L. odemensis*	*L. culinaris* cv. alpo	Ascochyta blight resistance	SNP	Polanco et al. (2019)
Lentil	ILL2024	Cassab	Boron toxicity tolerance	SNP	Kaur et al. (2014)
Lentil	L 4149	PL 8	Rust resistance	SRAP , SSR	Dikshit et al. (2016)
Lentil	PDL-1 and PSL-9	L-4147 and L-4076	Salt Tolreance	SSR	Singh et al. (2020)
Pea	00-2067	Reward	Resistance against Aphanomyces root rot (ARR)	SSR, SNP	Wu et al. (2021)
Pea	Eritreo	Messire	Resistance against powdery mildew	SCAR, RAPD	Cobos et al. (2018)
Pea	955180	Majoret	Resistance against powdery mildew	SSR	Ek et al. (2005)
Pea	JI2480	Lincoln	Resistance against powdery mildew	RAPD, SSR	Katoch et al. (2010)
Pea	955180	Majoret	Resistance against powdery mildew	SSR	Ek et al. (2005)
Pea	Parafield	Kaspa	Salt tolerance	SNP	Leonforte et al. (2013)

Genomic selection

In the post-NGS era, the availability of references genome sequence has provided the breeders with a variety of genome-wide DNA markers that are indispensable to effective plant selections and GAB. Several high-density genotyping systems are now available to assay a large number of genotypes in a cost and time-efficient manner (Rasheed et al. 2017). The development of cost-effective and customized genotyping platforms are all the more relevant in view of the concurrent refinements in plant breeding methods. For instance, genomic selection (GS) has recently emerged as a new breeding tool to improve genetic gain of plant breeding programs (Crossa et al. 2017). The genetic gain per unit time can be predicted based on the breeder's equation (Moose and Mumm 2008). The genetic gain of a breeding program can be enhanced by improving selection intensity (i) and selection accuracy (r) while shortening the length (l) of the breeding cycle (Santantonio et al. 2020, Sinha et al. 2021). The application of GS has shown encouraging results in legume crops. In chickpea, Roorkiwal et al. (2016) performed phenotyping of 320 elite breeding lines genotyped with 3,000 DArT Seq markers at two different locations, and the accuracies of GS models ranged from 0.13 (seed yield) to 0.91 (100-seed weight). A later GS study in chickpea by the same group incorporated G×E interactions into GS prediction models and also compared the impact of population structure and different genotyping platforms (GBS and DArT-Seq) on prediction accuracies (Roorkiwal et al. 2018b). In field pea, Tayeh et al. (2015c) reported prediction accuracies in the range of 0.65 (days to flowering) and 0.83 (1000-seed weight) based on the GS study involving 339 accessions genotyped using 13.2K SNP array. The study reported higher effect of size and composition of the training population on prediction accuracies than that of the GS prediction models and genotyping platforms. Another GS study performed on 215 field pea lines (assayed by the GBS) reported 0.56 as the highest prediction accuracy for ascochyta blight resistance. GBLUP and RKHS models performed better than the other models employed (RR-BLUP, Bayes A, Bayes B, Bayes C, BRR) (Carpenter et al. 2018). Recently, Annicchiarico et al. (2019) applied genomic prediction approach for improving grain yield, flowering initiation, lodging susceptibility, seed weight and winter plant survival for three environments, with GS models trained on 306 interconnected RILs. The study established the superiority of GS over the phenotypic selection. The utility of WGRS data in predicting hybrid performance and identification of high-yielding heterotic pattern has been demonstrated in pigeonpea (Saxena et al. 2021). The genome-wide predictions have been elucidated to be crucial for long term gain in hybrid breeding.

Rapid generation turnover (RGT) technologies

As mentioned in the previous section, approaches that reduce the length of the breeding cycle can contribute to accelerate the rate of genetic gain. These breeding protocols are collectively termed as speed breeding (SB). From the breeder's equation, the response to selection shows an inverse relation with the length of the breeding cycle (Moose and Mumm 2008). Hickey et al. (2019) have discussed the benefits of SB using artificial lighting and other rapid generation advancement (RGA) technologies with other modern breeding tools (genome editing, high-throughput phenotyping and GS) to accelerate the yield gains. The study by Watson et al. (2019) has demonstrated a considerable reduction in the breeding cycle time (up to 6 generation in a year) of cool season legumes such as chickpea and field pea (Watson et al. 2019). A more recent study by Samineni et al. (2020) applied RGA protocol on six chickpea accessions, two each from early, medium and late categories and the authors reported production of seven generations in a single year. Earlier in pea, RGA protocol (20-hr photoperiod, 21/16 ligh/dark, hydroponic system etc.) accelerated the development of mapping population of pea by 30–45 days per generation faster over standard single seed descent method (Mobini and Warkentine 2016). Exogenous application of plant growth regulators such as benzylaminopurine (BAP; cytokinin) in combination with cold treatment (8/4 °C day/night for 2 days) considerably reduced the generation time in faba bean through improving pollen viability and enhanced pod and seed setting (Mobini et al. 2015).

In pigeonpea, four genotypes from early maturity groups namely, ICPL 4, ICPL 151, ICPL 85024 and ICPL 87093 were subjected to RGA protocol under controlled conditions, and four generations were obtained in 349, 367, 313 and 338 days, respectively (Saxena et al. 2017). The study demonstrated shortening of generation time by combining harvesting of immature seeds and single pod descent method. Another SB-based strategy by Saxena et al. (2019) employed early maturating photoperiod-insensitive genotypes, and showed its potential to deliver new early maturing cultivars with the successful reduction of up to 4-5 years. SB recipes combined with single seed descent and MAS or GS will provide greater genetic gains over conventional methods of plant breeding (Varshney et al. 2021).

Haplotype-based breeding

While the concept of haplotype assembly was proposed by Bevan et al. (2017), based on haplo-pheno analysis, superior haplotypes were identified in rice (Abbai et al. 2019) and pigeonpea (Sinha et al. 2020). Based on these superior haplotypes, Varshney et al. (2020) outline the concept of of haplotype-based breeding for faster development of designer cultivars. This approach has tremendous advantages over MABC, which takes years and generations to transfer superior genes, and the process creates bottleneck effects and reduction of genetic diversity. Developing improved cultivars for future climate will require assembling gene(s) scattered throughout the genome, and efficient accumulation of such gene(s) will rely on approaches that exploit haplotypes. Haplotype-based breeding aimed at transferring superior haplotypes underlying genetic variations that are in strong linkage disequilibrium (LD) with the candidate genomic regions associated with the traits of interest (Varshney et al. 2021).

To accelerate future crop breeding, breeders need to shift from traditional DNA marker systems to haplotypes and pyramid them into a variety, opening doors to transfer novel genetic diversity from wild species, landraces and diverse accessions. More recently, the haplotype-based approach has been implemented in pigeonpea. For instance, Sequencing data of 292 accessions were mined to find superior haplotypes for 10 drought-responsive candidate genes (Sinha et al. 2020). Total five genes showed positive linkage disequilibrium for the seven drought responsive traits. A haplo-pheno analysis targeting candidate genomic regions/genes of association analysis revealed the superior haplotypes *viz*., *C. cajan_23080-H2*, *C. cajan_30211-H6*, *C. cajan_26230-H11* and *C. cajan_26230-H5* for plant traits that control drought response of pigeonpea. Identification of haplotypes creates novel avenues to tailor future cultivars harnessing growing genome-wide sequence information and historical phenotypic records (Varshney et al. 2021).

FINAL CONSIDERATIONS

Pulses are crucial to provide affordable protein to growing human population worldwide. The pace of genetic improvement of pulses has lagged behind in comparison to cereal crops. Nevertheless, remarkable success has been made in recent years in developing modern genomic tools and breeding approaches that underpin genetic improvement of pulses. Trait discovery has been revolutionized following sequencing of multiple genomes, and elucidation of crop evolution and breeding history has offered novel breeding targets to hasten crop breeding progress. Improved pulses

cultivars resulting from GAB are now ready for cultivation in famers' field. Initial examples of application of GS and SB for enhancing generation turnover in pulses breeding programs are encouraging, and enhanced adoption of these modern approaches will be crucial to improve the rate of genetic gain in pulses breeding programs. Besides SB and GS, application of HBB will pave the way for next generation breeding in pulses for the rapid delivery of ideal cultivars that adequately cater to the future needs in a timely manner.

ACKNOWLEDGEMENTS

RKV is thankful to Bill & Melinda Gates Foundation (#OPP1114827, OPP1130244) for financial support and Science & Engineering Research Board (SERB) of Department of Science & Technology (DST), Government of India for providing the J C Bose National Fellowship (SB/S9/Z-13/2019).

REFERENCES

Abbai R, Singh VK, Nachimuthu VV, Sinha P, Selvaraj R, Vipparla AK, Singh AK, Singh UM and Varshney RK and Kumar A (2019) Haplotype analysis of key genes governing grain yield and quality traits across 3K RG panel reveals scope for the development of tailor-made rice with enhanced genetic gains. **Plant Biotechnology Journal 17**: 1612-1622.

Afonso-Grunz F, Hoffmeier K, Müller S, Westermann AJ, Rotter B, Vogel J, Winter P and Kahl G (2015) Dual 3'Seq using deepSuperSAGE uncovers transcriptomes of interacting *Salmonella enterica typhimurium* and human host cells. **BMC Genomics 16**: 323.

Agrawal SK, Barpete S, Kumar J, Gupta P and Sarker A (2013) Global Lentil Production: Constraints and Strategies. SATSA Mukhapatra **Annual Technical Issue**: 1-13.

Annicchiarico P, Nazzicari N, Pecetti L, Romani M and Russi L (2019) Pea genomic selection for Italian environments. **BMC Genomics 20**: 603.

Anuradha C, Gaur PM, Pande S, Gali K, Ganes M, Kumar J and Varshney RK (2011) Mapping QTL for resistance to botrytis grey mould in chickpea. **Euphytica 182**: 1-9.

Arora S, Mahato AK, Singh S, Mandal P, Bhutani S, Dutta S, Kumawat G, Singh BP, Chaudhary AK, Yadav R, Gaikwad K, Sevanthi AM, Datta S, Raje RS, Sharma TR and Singh NK (2017) A high density intraspecific SNP linkage map of pigeonpea (*Cajanas cajan* L. Millsp.). **PLoS One 12**: e0179747.

Aryamanesh N, Byrne O, Hardie DC, Khan T, Siddique KHM and Yan G (2012) Large-scale density-based screening for pea weevil resistance in advanced backcross lines derived from cultivated field pea (*Pisum sativum*) and *Pisum fulvum***. Crop and Pasture Science 63**: 612-618.

Beebe SE, Rao IM, Devi MJ and Polania J (2014) Common beans, biodiversity, and multiple stresses: Challenges of drought resistance in tropical soils. **Crop and Pasture Science 65**: 667-675.

Bevan MW, Uauy C, Wulff BBH, Zhou J, Krasileva K and Clark MD (2017) Genomic innovation for crop improvement. **Nature 543**: 346-354.

Blair MW, Iriarte G and Beebe S (2006) QTL analysis of yield traits in an advanced backcross population derived from a cultivated Andean x wild common bean (*Phaseolus vulgaris* L.) cross. **Theoretical and Applied Genetics 112**: 1149-1163.

Bohra A, Dubey A, Saxena RK, Penmetsa RV, Poornima KN, Kumar N, Farmer AD, Srivani G, Upadhyaya HD, Gothalwal R, Ramesh R, Singh D, Saxena KB, Kavi Kishor PB, Singh NK, Town CD, May GD, Cook DR and 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 Biology 11**: 56.

Bohra A, Jha UC, Godwin I and Varshney RK (2020a) Genomic interventions for sustainable agriculture. **Plant Biotechnology Journal 18**: 2388-2405.

Bohra A, Jha UC, Kavi Kishor PB, Pandey S and Singh NP (2014) Genomics and molecular breeding in lesser explored pulse crops: Current trends and future opportunities. **Biotechnology Advances 32:** 1410-1428.

Bohra A, Mir RR, Jha R, Maurya AK and Varshney RK (2020c) Advances in genomics and molecular breeding for legume improvement. In Tuteja N, Tuteja R, Passricha N and Saifi SK (eds) **Advancement in crop improvement techniques**. Woodhead Publishing, New York, p. 129-189.

Bohra A, Prasad G, Rathore A, Saxena RK, Satheesh Naik SJ, Pareek S, Jha R, Pazhamala L, Datta D, Pandey G, Tiwari A, Maurya AK, Soren KR, Akram M, Varshney RK and Singh NP (2021a) Global gene expression analysis of pigeonpea with male sterility conditioned by A_2 cytoplasm. **The Plant Genome.** DOI: 10.1002/tpg2.20132.

Bohra A, Sahrawat KL, Kumar S, Joshi R, Parihar AK, Singh U, Singh D and Singh NP (2015) Genetics- and genomics-based interventions for nutritional enhancement of grain legume crops: Status and outlook. **Journal of Applied Genetics 56**: 151-161.

Bohra A, Saxena KB, Varshney RK and Saxena RK (2020b) Genomics assisted breeding for pigeonpea improvement. **Theoretical and Applied Genetics 133**: 1721-1737

Bohra A, Saxena RK, Gnanesh BN, Saxena KB, Byregowda M, Rathore A, Kavi Kishor PB, Cook DR and Varshney RK (2012) An intra-specific consensus genetic map of Pigeonpea [*Cajanus cajan* (L.) Millspaugh] derived from six mapping populations. **Theoretical and Applied Genetics 125**: 1325-1338.

Bohra A, Bharadwaj C, Radhakrishnan T, Singh NP and Varshney RK (2019) *Translational genomics and molecular breeding for enhancing precision and efficiency in crop improvement programs: Some examples in legumes.* **Indian Journal of Genetics and Plant Breeding 79**: 227-240.

Bohra A, Rathore A, Gandham P, Saxena RK, Satheesh Naik SJ, Dutta D, Singh IP, Singh F, Rathore M, Varshney RK and Singh NP (2021b) Genome-wide comparative transcriptome analysis of the A4-CMS line ICPA 2043 and its maintainer ICPB 2043 during the floral bud development of pigeonpea. **Functional & Integrative Genomics 21**: 251-263.

Borlaug NE (1973) Building a protein revolution on grain legumes. In Milner M (ed) **Nutritional improvement of food legumes by breeding**. Protein Advisory Group of the United Nations, Rome, p. 390

Cannon SB, May GD and Jackson SA (2009) Three sequenced legume genomes and many crop species: rich opportunities for translational genomics. **Plant Physiology 151:** 970-977.

Carpenter MA, Goulden DS, Woods CJ, Thomson SJ, Kenel F, Frew TJ, Cooper RD and Timmerman-Vaughan GM (2018) Genomic selection for ascochyta blight resistance in pea. **Frontiers in Plant Science 9**: 1878.

Cheng A, Raai MN, Zain NAM, Massawe F, Singh A and Wan MW (2019) In search of alternative proteins: Unlocking the potential of underutilized tropical legumes. food security: the science, sociology and economics of food production and access to food. **The International Society for Plant Pathology 11**: 1205-1215.

Choudhary AK, Sultana R, Pratap A, Nadarajan, N Jha and UC (2011) *Breeding for abiotic stresses in pigeonpea.* **Journal of Food Legumes 24**: 165-174.

Chung JW, Kim TS, Suresh S, Lee SY and Cho GT (2013) Development of 65 novel polymorphic cDNA-SSR markers in common vetch (*Vicia sativa* subsp. sativa) using next generation sequencing. **Molecules 18**: 8376-8392.

Clements JC, Buirchel BJ, Yang H, Smith PMC, Sweetingham MW and Smith CG (2005) Lupin. In Singh RJ and Jauhar PP (eds) **Genetic resources, chromosome engineering and crop improvement**. CRC Press, Boca Raton, p. 223-331.

Cobos M, Satovic Z, Rubiales D and Fondevilla S (2018) Er3 gene, conferring resistance to powdery mildew in pea, is located in pea LGIV. **Euphytica 214**: 203.

Crossa J, Perez-Rodriguez P, Cuevas J, Montesinos-Lopez O, Jarquin D, de los Campos G, Burgueno J, Gonzalez-Camacho JM, Perez-Elizade S, Beyene Y, Dreisigacker S, Singh R, Zhang X, Gowda M, Roorkiwal M, Rutkoski J and Varshney RK (2017) Genomic selection in plant breeding: methods, models, and perspectives. **Trends in Plant Science 22**: 961-975.

De Almeida CP, de Carvalho Paulino JF, Bonfante GFJ, Perseguini JMKC, Santos IL, Gonçalves JGR, Patrício FRA, Taniguti CH, Gesteira GS, Garcia AAF, Song Q, Carbonell SAM, Chiorato AF and Benchimol-Reis LL (2021) Angular leaf spot resistance loci associated with different plant growth stages in common bean. **Frontiers in Plant Science 12**: 647043.

Deeplanaik N, Kumaran RC, Venkatarangaiah K, Shivashankar SKH, Doddamani D and Telkar S (2013) Expression of drought responsive genes in pigeonpea and in silico comparison with soybean cDNA library. **Journal of Crop Science and Biotechnology 16**: 243-251.

Degu T, Yaregal W and Gudisa T (2020) Status of common bean (*Phaseolus vulgaris* L.) diseases in metekel zone, north west Ethiopia. **Journal Plant Pathology Microbiology 11**: 494.

Diaz LM, Ricaurte J, Tovar E, Cajiao C, Teran H, Grajales M, Polanía J, Rao I, Beebe S and Raatz B (2018) QTL analyses for tolerance to abiotic stresses in a common bean (*Phaseolus vulgaris* L.) population. **PLoS One 13**: e0202342.

Dikshit H, Singh A, Singh D, Aski M, Jain N, Hegde VS, Basandrai A, Basandrai D and Sharma T (2016) Tagging and mapping of SSR marker for rust resistance gene in lentil (*Lens culinaris* Medikus subsp. *culinaris*). **Indian Journal of Experimental Biology 54**: 394-399.

Doddamani D, Katta MA, Khan AW, Agarwal G, Shah TM and Varshney RK (2014) CicArMiSatDB: the chickpea microsatellite database. **BMC Bioinformatics 15**: 212.

Doddamani D, Khan AW, Katta MA, Agarwal G, Thudi M, Ruperao P, Edwards D and Varshney RK (2015) CicArVarDB: SNP and InDel database for advancing genetics research and breeding applications in chickpea. Database (Oxford): bav078. doi: 10.1093/database/bav078

Dubey A, Farmer A, Schlueter J, Cannon SB, Abernathy B, Tuteja R, Woodward J, Shah T, Mulasmanovic B, Kudapa H, Raju NL, Gothalwal R, Pande S, Xiao Y, Town CD, Singh NK, May GD, Jackson S and Varshney RK (2011) Defining the transcriptome assembly and its use for genome dynamics and transcriptome profiling studies in pigeonpea (*Cajanus cajan* L.). **DNA Research 18**: 153-164.

Dutta S, Kumawat G, Singh BP, Gupta DK, Singh S, Dogra V, Gaikwad K, Sharma TR, Raje RS, Bandhopadhya TK, Datta S, Singh MN, Bashasab F, Kulwal P, Wanjari KB, K Varshney R, Cook DR and Singh NK (2011) Development of genic-SSR markers by deep transcriptome sequencing in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. **BMC Plant Biology 11**: 17.

Ek M, Eklund M, Von Post R, Dayteg C, Henriksson T, Weibull P, Ceplitis A, Isaac P and Tuvesson S (2005) Microsatellite markers for powdery mildew resistance in pea (*Pisum sativum* L.). **Hereditas 142**: 86-91.

Ender M, Terpstra K and Kelly JD (2008) Marker-assisted selection for white mold resistance in common bean. **Molecular Breeding 21**: 149-157.

Ennenking D and Tate M (2006) Global vetch production. **Grain Legumes 47**: 14-15.

Firincioglu HK, Unal S, Erberkas E and Dogruyol L (2010) Relationships between seed yield and yield components in common vetch (*Vicia sativa* ssp. *sativa*) populations sown in spring and autumn in central Turkey. **Field Crops Research 116**: 30-37.

Frias J, Diaz-Pollan C, Hedley CL and Vidal-Valverde C (1995) Evolution of trypsin inhibitor. activity during germination of lentils. **Journal of Agriculturual and Food chemistry 43**: 2231-2234.

Garg R, Patel RK, Jhanwar S, Priya P, Bhattacharjee A, Yadav G, Bhatia S, Chattopadhyay D, Tyagi AK and Jain M (2011) Gene discovery and

tissue-specific transcriptome analysis in chickpea with massively parallel pyrosequencing and web resource development. **Plant Physiology 156**: 1661-1678.

Gaur PM, Jukanti AK and Varshney RK (2012) Impact of genomic technologies on chickpea breeding strategies. **Agronomy 2**: 199-221.

Godfray HCJ, Beddington JR, Crute IR, Haddad L, Lawrence D and Muir JF (2010) Food security: the challenge of feeding 9 billion people. **Science 327**: 812-818.

Gonçalves-Vidigal MC, Cruz AS, Garcia A, Kami J, Filho PSV, Sousa LL , McClean P, Gepts P and Pastor-Corrales MA (2011) Linkage mapping of the Phg-1 and Co-14 genes for resistance to angular leaf spot and anthracnose in the common bean cultivar AND 277. **Theoretical and Applied Genetics 122**: 893–903.

Graham PH and Vance CP (2003) Legumes: importance and constraints to greater use. **Plant Physiology 131**: 872-877.

Gupta PK, Rustgi S and Mir RR (2013) Array-based high-throughput DNA markers and genotyping platforms for cereal genetics and genomics. In Gupta PK and Varshney RK (eds) **Cereal genomics II**. Springer, Netherlands, p. 11-55.

Gupta S, Gupta DS, Anjum TK, Pratap A and Kumar J (2013a) Inheritance and molecular tagging of MYMIV resistance gene in blackgram (*Vigna mungo* L. Hepper). **Euphytica 193**: 27-37.

Gupta S, Nawaz K, Parween S, Roy R, Sahu K, Kumar Pole A, Khandal H, Srivastava R, Kumar Parida S and Chattopadhyay D (2017) Draft genome sequence of *Cicer reticulatum* L., the wild progenitor of chickpea provides a resource for agronomic trait improvement. **DNA Research 24**: 1-10.

Hamon C, Coyne CJ, McGee RJ, Lesne A, Esnault R, Mangin P and Pilet-Nayel ML (2013) QTL meta-analysis provides a comprehensive view of loci controlling partial resistance to *Aphanomyces euteiches* in four sources of resistance in pea. **BMC Plant Biology 13**: 45.

Hanai LR, Santini L, Camargo LE, Fungaro MH, Gepts P, Tsai SM and Vieira ML (2010) Extension of the core map of common bean with EST-SSR, RGA, AFLP, and putative functional markers. **Molecular Breeding 25**: 25-45.

Hickey LT, N Hafeez A, Robinson H, Jackson SA, Leal-Bertioli SCM, Tester M, Gao C, Godwin ID, Hayes BJ and Wulff BBH (2019) Breeding crops to feed 10 billion. **Nature Biotechnology 37**: 744-754.

Hiremath PJ, Farmer A, Cannon SB, Woodward J, Kudapa H, Tuteja R, Kumar A, Bhanuprakash A, Mulaosmanovic B, Gujaria N, Krishnamurthy L, Gaur PM, Kavikishor PB, Shah T, Srinivasan R, Lohse M, Xiao Y, Town CD, Cook DR, May GD and Varshney RK (2011) Large-scale transcriptome analysis in chickpea (*Cicer arietinum* L.), an orphan legume crop of the semi-arid tropics of Asia and Africa. **Plant Biotechnology Journal 9**: 922-931.

Horn LN and Shimelis H (2020) Production constraints and breeding approaches for cowpea improvement for drought prone agro-ecologies in Sub-Saharan Africa. **Annals of Agricultural Sciences 65**: 83-89.

Houghton RA, House JI, Pongratz J, Vander Werf G, DeFries RS and Hansen MC (2012) Carbon emissions from land use and land-cover change. **Biogeosciences 9**: 5125-5142.

Isemura T, Kaga A, Tabata S, Somta P, Srinives P, Shimizu T, Uken Jo, Duncan AV and Norihiko T (2012) Construction of a genetic linkage map and genetic analysis of domestication related traits in mungbean (*Vigna radiata*). **PLoS One 7**: e41304.

Isemura T, Kaga A, Tomooka N, Shimizu T and Vaughan DA (2010) Construction of a genetic linkage map and genetic analysis of the domestication related traits in rice bean (*Vigna umbellata*). **Annual Botany 106**: 927-944.

Iwata A, Greenland CM and Jackson SA (2013) Cytogenetics of legumes in the Phaseoloid clade. **The Plant Genome 6**: 1-8.

Jaganathan D, Bohra A, Thudi M and Varshney RK (2020) Fine mapping and gene cloning in the post-NGS era: Advances and prospects. **Theoretical and Applied Genetics 133**: 1791-1810.

Jaganathan D, Thudi M, Kale S, Azam S, Roorkiwal M, Gaur PM, Kishor PB, Nguyen H, Sutton T and Varshney RK (2015) Genotyping- by-sequencing based intra-specific genetic map refines a "*QTL-hotspot*" region for drought tolerance in chickpea. **Molecular Genetics and Genomics 290**: 559-571.

Jain M, Misra G, Patel RK, Priya P, Jhanwar S, Khan AW, Shah N, Singh VK, Garg R, Jeena G, Yadav M, Kant C, Sharma P, Yadav G, Bhatia S, Tyagi AK and Chattopadhyay D (2013) A draft genome sequence of the pulse crop chickpea (*Cicer arietinum* L.). **The Plant Journal 74**: 715-29.

Kale SM, Jaganathan J, Ruperao P, Chen C, Punna R, Kudapa H, Thudi M, Roorkiwal M, Mohan AVSKK, Doddamani D, Garg V, Kavikishor PB, Gaur PM, Nguyen HT, Batley J, Edwards D, Sutton T and Varshney RK (2015) Prioritization of candidate genes in QTL hotspot region for drought tolerance in chickpea (*Cicer arietinum* L.). **Scientific Reports 5**: 15296

Kang Y, Kim S, Kim M, Lestari P, Kim K, Ha B and Lee S (2014) Genome sequence of mungbean and insights into evolution within *Vigna* species. **Nature Communications 5**: 5443.

Kang YJ, Satyawan D, Shim S, Lee T, Lee J, Hwang WJ, Kim SK, Lestari P, Laosatit K, Kim KH, Ha TJ, Chitikineni A, Kim MY, Ko JM, Gwag JG, Moon JK, Lee YH, Park BS, Varshney RK and Lee SH (2015) Draft genome sequence of adzuki bean, *Vigna angularis*. **Scientific Reports 5**: 8069.

Karkanis A, Ntatsi G, Lepse, L, Fernandez JA, Vagen IM, Rewald B, Alsina I, Kronberga A. Balliu A, Olle M, Bodner G, Dubova L, Rosa E and Savva D (2018) Faba bean cultivation-revealing novel managing practices for more sustainable and competitive European cropping systems. **Frontier in Plant Sciences 9**: 1115.

Katerji N, Mastrorilli, M, Lahmer FZ, Maalouf F and Oweis T (2011) Faba bean productivity in saline-drought conditions. **European Journal of Agronomy 35**: 2-12.

Katoch V, Sharma S, Pathania S, Banyal D, Sharma S and Rathour R (2010) Molecular mapping of pea powdery mildew resistance gene er2 to pea linkage group III. **Molecular Breeding 25**: 229-237.

Kaur S, Cogan NO, Stephens A, Noy D, Butsch M, Forster JW and Materne M (2014) EST-SNP discovery and dense genetic mapping in lentil (*Lens culinaris* Medik.) enable candidate gene selection for boron tolerance. **Theoretical and Applied Genetics 127**: 703-713.

Khadka K and Acharya BD (2009) **Cultivation practices of ricebean**. Local Initiatives for Biodiversity, Research and Development (LI-BIRD), Pokhara, 31p.

Kouris-Blazos A and Belski R (2016) Health benefits of legumes and pulses with a focus on Australian sweet lupins. **Asia Pacific Journal of Clinical Nutrition 25**: 1-17.

Kreplak J, Madoui MA, Capal P, Winker P and Burstin J (2019) A reference genome for pea provides insight into legume genome evolution. **Nature Genetics 51**: 1411-1422.

Kudapa H, Garg V, Chitikineni A and Varshney RK (2018) The RNA-Seq-based high resolution gene expression atlas of chickpea (*Cicer arietinum* L.) reveals dynamic spatio-temporal changes associated with growth and development. **Plant, Cell & Environment 41**: 2209-2225.

Kumar A, Nidhi, Prasad N and Sinha SK (2015) Nutritional and antinutritional attributes of faba bean (*Vicia faba* L.) germplasms growing in Bihar, India. **Physiology and Molecular Biology of Plants 21**: 159-162.

Kumar S, Kumar M, Mir RR, Kumar R and Kumar S (2021) Advances in molecular markers and their use in genetic improvement of wheat. In Wani SH, Mohan A and Singh GP (eds) **Physiological, molecular and genetic perspectives of wheat improvement.** Springer International Publishing, Switzerland, p. 139-174.

Kumar V, Khan AW, Saxena RK, Garg V and Varshney RK (2016) First-generation HapMap in *Cajanus* spp. reveals untapped variations in parental lines of mapping populations. **Plant Biotechnology Journal 14**: 1673-1681.

Kumawat G, Raje RS, Bhutani S, Pal JK, Mithra SVCR, Kishor Gaikwad K, Sharma TR and Singh NK (2012) Molecular mapping of QTLs for plant type and earliness traits in pigeonpea (*Cajanus cajan* L. Millsp.). **BMC Genetics 13**: 84.

Lambrides CJ and Godwin ID (2007) Mungbean. In Kole C (ed) **Genome mapping and molecular breeding in plants. Pulses, sugar and tuber crops Heidelberg**. Springer, Verlag, p. 69-90.

Lejeune-Henaut I, Hanocq E, Bethencourt L, Fontaine V, Delbreil B, Morin J, Petit A, Devaux R, Boilleau M, Stempniak JJ, Thomas M, Laine AL, Foucher F, Baranger A, Burstin J, Rameau C and Giauffret C (2008) The flowering locus Hr colocalizes with a major QTL affecting winter frost tolerance in *Pisum sativum* L. **Theoretical and Applied Genetics 116**: 1105-1116.

Leonforte A, Sudheesh S, Cogan NO, Salisbury PA, Nicolas ME, Materne M, Forster JW and Kaur S (2013) SNP marker discovery, linkage map construction and identification of QTLs for enhanced salinity tolerance in field pea (*Pisum sativum* L.). **BMC Plant Biology 13**: 161.

Maass BL, Knox MR, Venkatesha SC, Angessa TT, Ramme S and Pengelly BC (2010) *Lablab purpureus*-a crop lost for Africa? **Tropical Plant Biology 3**: 123-135.

Macas J, Neumann P and Navratilova A (2007) Repetitive DNA in the pea (*Pisum sativum* L.) genome: comprehensive characterization using 454 sequencing and comparison to soybean and *Medicago truncatula*. **BMC Genomics 8**: 427.

Majola NG, Gerrano AS and Shimelis H (2021) Bambara groundnut (*Vigna subterranea* [L.] Verdc.) production, utilisation and genetic improvement in Sub-Saharan Africa. **Agronomy 11**: 1345.

Mallikarjuna BP, Samineni S, Thudi M, Sajja SB, Khan AW, Patil A, Viswanatha KP, Varshney RK and Gaur PM (2017) Molecular mapping of flowering time major genes and QTLs in chickpea (*Cicer arietinum* L.). **Frontiers in Plant Science 8:** 1140.

Mantri NL, Ford R, Coram TE and Pang EC (2007) Transcriptional profiling of chickpea genes differentially regulated in response to high-salinity, cold and drought. **BMC Genomics 8**: 303.

Maphosa Y and Jideani VA (2017) The role of legumes in human nutrition. In Hueda MC (ed) **Functional food**: Improve health through adequate food. Intech Open, London, p.103-121.

Massawe F, Mayes S and Cheng A (2016) Crop diversity: an unexploited treasure trove for food security. **Trends in Plant Science 21**: 365-368.

Mir RR and Varshney RK (2013) Future prospects of molecular markers in plants. In Henry RJ (ed) **Molecular markers in plants**. Blackwell Publishing Ltd, Oxford, p.169-190.

Mir RR, Hiremath PJ, Riera-Lizarazu O and Varshney RK (2013a) Evolving molecular marker technologies in plants: From RFLPs to GBS. In Lübberstedt T and Varshney RK (eds) **Diagnostics in plant breeding**. Springer Science, New York, p. 229-247.

Mir RR, Kudapa H, Srikanth S, Saxena RK, Sharma A, Sarwar A, Saxena K, Penmesta RV and Varshney RK (2014) Candidate gene analysis for determinacy in pigeonpea (*Cajanus spp*.). **Theoretical and Applied Genetics 127**: 2663-2678.

Mir RR, Rather IA, Bhat MA, Parray GA and Varshney RK (2017) Molecular mapping of genes and QTLs in pigeonpea. In Varshney R, Saxena R and Jackson S (eds) **The pigeonpea genome. Compendium of plant genomes**. Springer, Cham, p. 55-64.

Mir RR, Saxena RK, Saxena KB, Upadhyaya HD, Kilian A, Cook DR and Varshney RK (2013b) Whole-genome scanning for mapping determinacy in pigeonpea (*Cajanus* spp.). **Plant Breeding 132**: 472-478.

Mir RR, Zaman-Allah M, Sreenivasulu N, Trethowan R and Varshney RK (2012) Integrated genomics, physiology and breeding approaches for improving drought tolerance in crops. **Theoretical and Applied Genetics 125**: 625-645.

Misra G, Priya P, Bandhiwal N, Bareja N, Jain M, Bhatia S, Chattopadhyay D, Tyagi AK and Yadav G (2014) The chickpea genomic web resource: visualization and analysis of the desi-type *Cicer arietinum* nuclear genome for comparative exploration of legumes. **BMC Plant**

Biology 14: 315.

Mobini SH and Warkentine TD (2016) A simple and efficient method of in vivo rapid generation technology in pea (*Pisum sativum* L.). **In Vitro Cellular & Developmental Biology Plant 52**: 530-536.

Mobini SH, Lulsdorf M, Warkentin TD and Vandenberg A (2015) Plant growth regulators improve in vitro flowering and rapid generation advancement in lentil and faba bean**. In Vitro Cellular & Developmental Biology 51**: 71-79.

Moose SP and Mumm RH (2008) Molecular plant breeding as the foundation for 21st century crop improvement. **Plant Physiology 147**: 969-977.

Murphy AM and Colucci PE (1999) A tropical forage solution to poor quality ruminant diets: a review of *Lablab purpureus*. **Live stock Research Rural Development 11**: 2.

Nair RM, Pandey AK, War AR, Hanumantharao B, Shwe T, Alam A, Pratap A, Malik SR, Karimi R, Mbeyagala EK, Douglas CA, Rane J and Schafleitner R (2019) Biotic and abiotic constraints in mungbean production-progress in genetic improvement. **Frontiers in Plant Science 25**: 1340.

Nene YL, Reddy MV, Haware MP, Ghanekar AM, Amin KS, Pande S and Sharma M (2012) **Field diagnosis of chickpea diseases and their control**. AP, India, 60p.

OECD (2016) **Common bean (*Phaseolus vulgaris*)", in safety assessment of transgenic organisms in the environment, OECD consensus documents**. OECD Publishing, Paris, p. 187-210.

O'Rourke JA, Iniguez LP, Fu F, Bucciarelli B, Miller SS, Jackson SA, McClean PE, Li J, Dai X, Zhao PX, Hernandez G and Vance CP (2014) An RNA-Seq based gene expression atlas of the common bean. **BMC Genomics 15**: 866.

Ortega R, Hecht VFG, Freeman JS, Rubio J, Carrasquilla-Garcia N, Mir RR, Penmetsa RV, Cook DR, Millan T and Weller JL (2019) Altered expression of an FT cluster underlies a major locus controlling domestication-related changes to chickpea phenology and growth habit. **Frontiers in Plant Science 10**: 824.

Pandey MK, Roorkiwal M, Singh VK, Ramalingam A, Kudapa H, Thudi M, Chitikineni A, Rathore A and Varshney RK (2016) Emerging genomic tools for legume breeding: current status and future prospects. **Frontiers in Plant Science 7**: 455.

Parida SK, Verma M, Yadav SK, Ambawat S, Das S, Garg R and Jain M (2015) Development of genome-wide informative simple sequence repeat markers for large-scale genotyping applications in chickpea and development of web resource. **Frontiers in Plant Science 6**: 645.

Parween S, Nawaz K, Roy R, Pole AK, Venkata Suresh B, Misra G, Jain M, Yadav G, Parida SK, Tyagi AK, Bhatia S and Chattopadhyay D (2015) An advanced draft genome assembly of a desi type chickpea (*Cicer arietinum* L.). **Scientific Reports 11**: 12806.

Pazhamala LT, Purohit S, Saxena RK, Garg V, Krishnamurthy L, Verdier J and Varshney RK (2017) Gene expression ATLAS of pigeonpea and its application to gain insights into genes associated with pollen fertility implicated in seed formation. **Journal of Experimental Botany 68**: 2037-2054

Perez de la Vega M, Fratini RM and Muehlbauer FJ (2011) Lentil. In Perez de la Vega M, Torres AM, Cubero JI and Kole C (eds) **Genetics, genomics and breeding of cool season grain legumes (genetics, genomics and breeding in crop plants).** Science Publishers, New Hampshire, p. 98-150.

Polanco C, Saenz de Miera LE, Gonzalez AI, Garcia P, Fratini R, Vaquero F, Vences FJ and Perez de la Vega M (2019) Construction of a high-density interspecific (*Lens culinaris* x *L. odemensis*) genetic map based on functional markers for mapping morphological and agronomical traits, and QTLs affecting resistance to Ascochyta in lentil. **PLoS One 14**: e0214409.

Polhill RM (1981) Papilionoideae. **Advances in Legume Systematics 1**: 191-208.

Pratap A, Chaturvedi SK, Tomar R, Rajan N, Malviya N, Thudi M, Saabale PR, Prajapati U, Varshney RK and Singh NP (2017) Marker-assisted introgression of resistance to fusarium wilt race 2 in Pusa 256, an elite cultivar of desi chickpea. **Molecular Genetics and Genomics 292**: 1237-1245.

Prathet P, Somta P and Srinives P (2012) Mapping QTL conferring resistance to iron deficiency chlorosis in mungbean *Vigna radiata* (L.) Wilczek. **Field Crops Research 137**: 230-236.

Priyanka B, Sekhar K, Sunitha T, Reddy VD and Rao KV (2010) Characterization of expressed sequence tags (ESTs) of pigeonpea (*Cajanus cajan* L.) and functional validation of selected genes for abiotic stress tolerance in *Arabidopsis thaliana*. **Molecular Genetics and Genomics 283**: 273-287.

Raju NL, Gnanesh BN, Lekha P, Jayashree B, Pande S, Hiremath PJ, Byregowda M, Singh NK and Varshney RK (2010) The first set of EST resource for gene discovery and marker development in pigeonpea (*Cajanus cajan* L.). **BMC Plant Biology 10**: 45.

Rasheed A, Hao Y, Xia X, Khan A, Xu Y, Varshney RK and He Z (2017) Crop breeding chips and genotyping platforms: progress, challenges, and perspectives. **Molecular Plant 10**: 1047-1064.

Roorkiwal M, Bharadwaj C, Barmukh R, Dixit GP, Thudi M, Gaur PM, Chaturvedi SK, Fikre A, Hamwieh A, Kumar S, Sachdeva S, Ojiewo CO, Taran B, Wordofa NG, Singh NP, Siddique KHM and Varshney RK (2020) Integrating genomics for chickpea improvement: achievements and opportunities. **Theoretical and Applied Genetics 133**: 1703-1720.

Roorkiwal M, Jain A, Kale SM, Doddamani D, Chitikineni A, Thudi M and Varshney RK (2018a) Development and evaluation of high density SNP array (*Axiom®CicerSNP Array*) for high resolution genetic mapping and breeding applications in chickpea. **Plant Biotechnology Journal 16**: 890-901.

Roorkiwal M, Jarquin D, Singh MK, Gaur PM, Bharadwaj C, Rathore A, Howard R, Srinivasan S, Jain A, Garg V, Kale S, Chitikineni A, Tripathi S, Jones E, Robbins KR, Crossa J and Varshney RK (2018b) Genomic-enabled prediction models using multi-environment trials to estimate

the effect of genotype × environment interaction on prediction accuracy in chickpea. **Scientific Reports 8**: 11701.

Roorkiwal M, Rathore A, Das RR, Singh MK, Jain A, Srinivasan S, Gaur PM, Chellapilla B, Tripathi S, Li Y, Hickey JM, Lorenz A, Sutton T, Crossa J, Jannink JL and Varshney RK (2016) Genome-enabled prediction models for yield related traits in chickpea. **Frontiers in Plant Science 7**: 1666.

Rui S, Hua W, Rui G, Qin L, Lei P, Jianan L, ZhiHui H and Chanyou C (2016) The diversity of four anti-nutritional factors in common bean. **Horticultural Plant Journal 2**: 97-104.

Sabbavarapu MM, Sharma M, Chamarthi SK, Swapna N and Rathore A (2013) Mapping of QTLs for resistance to *Fusarium* wilt (race 1) and *Ascochyta* blight in chickpea (*Cicer arietinum* L.). **Euphytica 93**: 121-133.

Samineni S, Sen M, Sajja SB and Gaur PM (2020) Rapid generation advance (RGA) in chickpea to produce up to seven generations per year and enable speed breeding. **The Crop Journal 8**: 164-169.

Santantonio N, Atanda SA, Beyene Y, Varshney RK, Olsen M, Jones E, Roorkiwal M, Gowda M, Bharadwaj C, Gaur PM, Zhang X, Dreher K, Ayala-Hernandez C, Crossa J, Perez-Rodríguez P, Rathore A, Gao SY, McCouch S and Robbins KR (2020) Strategies for effective use of genomic information in crop breeding programs serving Africa and South Asia. **Frontiers in Plant Science 11**: 353.

Saxena KB (2008) Genetic improvement of pigeonpea: a review. **Tropical Plant Biology 1**: 159-178.

Saxena KB, Saxena RK and Varshney RK (2017) Use of immature seed germination and single seed descent for rapid genetic gains in pigeonpea. **Plant Breeding 136**: 954-957.

Saxena KB, Saxena RK, Hickey LT and Varshney RK (2019) Can a speed breeding approach accelerate genetic gain in pigeonpea. **Euphytica 215**: 202.

Saxena RK, Hake A, Bohra A, Khan A, Hingane A, Sultana R, Singh IP, Satheen Naik SJ and Varshney RK (2021) A diagnostic marker kit for Fusarium wilt and sterility mosaic diseases resistance in pigeonpea. **Theoretical and Applied Genetics 134**: 367-379.

Saxena RK, Jiang Y, Khan A, Zhao Y, Singh VK, Bohra A, Sonappa M, Rathore A, Sameerkumar CV, Saxena CV, Reif J and Varshney RK (2021) Characterization of heterosis and genomic prediction based establishment of heterotic pattern for developing better hybrids in pigeonpea. **Plant Genome 2021**: e20125.

Saxena RK, Kale S, Mir RR, Mallikarjuna N, Yadav P, Das RR, Molla J, Sonnappa M, Ghanta A, Narasimhan Y, Rathore A, Kumar CVS and Varshney RK (2020) Genotyping-by-sequencing and multi-location evaluation of two interspecific backcross populations identify QTLs for yield-related traits in pigeonpea. **Theoretical and Applied Genetics 133**: 737-749**.**

Saxena RK, Penmetsa RV, Upadhyaya HD, Kumar A, Carrasquilla-Garcia N, Schlueter JA, Farmer A, Whaley AM, Sarma BK, May GD, Cook DR and Varshney RK (2012) Large-scale development of cost-effective single-nucleotide polymorphism marker assays for genetic mapping in pigeonpea and comparative mapping in legumes. **DNA Research 19**: 449-461.

Saxena RK, Rathore A, Bohra A, Yadav P, Das RR, Khan AW, Singh VK, Chitikineni A, Singh IP, Sameer Kumar CV, Saxena KB and Varshney RK (2018) Development and application of high density Axiom®CajanusSNP Array with 56K SNPs for understanding genome architecture of released varieties and founder genotypes for redefining future pigeonpea breeding programmes. **The Plant Genome 11**: 180005.

Schmutz J, Cannon SB, Schlueter J, Ma J, Mitros T, Nelson W, Hyten DL, Song Q, Thelen JJ, Cheng J, Xu D, Hellsten U, May GD, Yu Y, Sakurai T, Umezawa T, Bhattacharyya MK, Sandhu D, Valliyodan B, Lindquist E, Peto M, Grant D, Shu S, Goodstein D, Barry K, Futrell-Griggs M, Abernathy B, Du J, Tian Z, Zhu L, Gill N, Joshi T, Libault M, Sethuraman A, Zhang XC, Shinozaki K, Nguyen HT, Wing RA, Cregan P, Specht J, Grimwood J, Rokhsar D, Stacey G, Shoemaker RC and Jackson SA (2010) Genome sequence of the palaeopolyploid soybean. **Nature 463**: 178-183.

Schmutz J, McClean PE, Mamidi S, Wu GA, Cannon SB, Grimwood J, Jenkins J, Shu S, Song Q, Chavarro C, Torres-Torres M, Geffroy V, Moghaddam SM, Gao D, Abernathy B, Barry K, Blair M, Brick MA, Chovatia M, Gepts P, Goodstein DM, Gonzales M, Hellsten U, Hyten DL, Jia G, Kelly JD, Kudrna D, Lee R, Richard MM, Miklas PN, Osorno JM, Rodrigues J, Thareau V, Urrea CA, Wang M, Yu Y, Zhang M, Wing RA, Cregan PB, Rokhsar DS and Jackson SA (2014) A reference genome for common bean and genome-wide analysis of dual domestications. **Nature Genetics 46**: 707-713.

Sharma OP, Bambawale OM, Gopali JB, Bhagat S, Yelshetty S, Singh SK, Anand R and Singh OP (2011) **Field guide mungbean and urdbean**. Government of India, Department of Agricultural and Co-operation, New Delhi, p. 1-40.

Sharma OP, Gopali JB, Yelshetty S, Bambawale OM, Garg DK and Bhosle BB (2010) Pests of pigeonpea and their management. NCIPM, LBS Building, IARI Campus, New Delhi.

Simpson HL and Campbell BJ (2015) Review article: Dietary fibre-microbiota interactions aliment. **Pharmacology Therapeutics 42**: 158-179.

Singh BB (2005) Cowpea (*Vigna unguiculata* (L.) Walp). In Singh RJ and Jauhar PP (eds) **Genetic resources, chromosome engineering and crop improvement**. CRC Press, Boca Raton, p. 117-162.

Singh D, Singh C, Tomar RS, Karwa S, Singh MP, Singh V, Sanwal S and Sharma P (2020) Genetics and molecular mapping for salinity stress tolerance at seedling stage in lentil (*Lens culinaris* Medik). **Crop Science 60**: 1254-1266.

Singh NK, Gupta DK, Jayaswal PK, Mahato AK, Dutta S, Singh S, Bhutani S, Dogra V, Singh BP, Kumawat G, Pal JK, Pandit A, Singh A, Rawal H, Kumar A, Prashat GR, Khare A, Yadav R, Raje RS, Singh MN, Datta S, Fakrudin B, Wanjari KB, Kansal R, Dash PK, Jain PK, Bhattacharya R, Gaikwas K, Mohapatra T, Srinivasan R and Sharma TR (2012) The

first draft of the pigeonpea genome sequence. **Journal of Plant Biochemistry and Biotechnology 21**: 98-112.

Sinha P, Saxena RK, Singh VK and Varshney RK (2015b) Selection and validation of housekeeping genes as reference for gene expression studies in pigeonpea (*Cajanus cajan*) under heat and salt stress conditions. **Frontier in Plant Science 6**: 1071.

Sinha P, Singh VK, Bohra A, Kumar A, Reif JC and Varshney RK (2021) Genomics and breeding innovations for enhancing genetic gain for climate resilience and nutrition traits. **Theoretical and Applied Genetics 134**: 1829-1843.

Sinha P, Singh VK, Saxena RK, Khan AW, Abbai R, Chitikineni A, Desai A, Molla J, Upadhyaya HD, Kumar A and Varshney RK (2020) Superior haplotypes for haplotype-based breeding for drought tolerance in pigeonpea (*Cajanus cajan* L.). **Plant Biotechnology Journal 18**: 2482-2490.

Sinha P, Singh VK, Suryanarayana V, Krishnamurthy L, Saxena RK and Varshney RK (2015a) Evaluation and validation of housekeeping genes as reference for gene expression studies in pigeonpea (*Cajanus cajan*) under drought stress conditions. **PLoS One 10**: e0122847.

Sivasakthi K, Marques E, Kalungwana N, Carrasquilla-Garcia N, Chang PL, Bergmann EM, Bueno E, Cordeiro M, Sani SGAS, Udupa SM, Rather IA, Mir RR, Vadez V, Vandemark GJ, Gaur PM, Cook DR, Boesch C, Wettberg EJBV, Kholova J and Penmetsa RV (2019) Functional dissection of the chickpea (*Cicer arietinum L.*) stay-green phenotype associated with molecular variation at an ortholog of Mendel's i gene for cotyledon color: implications for crop production and carotenoid biofortification. **International Journal of Molecular Sciences 20**: 5562.

Sompong U, Somta P, Raboy V and Srinives P (2012) Mapping of quantitative trait loci for phytic acid and phosphorus contents in seed and seedling of mungbean (*Vigna radiata* (L.) Wilczek). **Breeding Science 62**: 87-92.

Srivastava R, Bajaj D, Sayal YK, Meher PK, Upadhyaya HD, Kumar R, Tripathi S, Bharadwaj C, Rao AR and Parida SK (2016) Genome-wide development and deployment of informative intron-spanning and intron-length polymorphism markers for genomics-assisted breeding applications in chickpea. **Plant Science 252**: 374-387.

Stagnari F, Maggio A, Galieni A and Pisante M (2017) Multiple benefits of legumes for agriculture sustainability: an overview. **Chemical and Biological Technologies in Agriculture 4**: 2.

Tanksley SD and Nelson JC (1996) Advanced backcross QTL analysis: a method for the simultaneous discovery and transfer of valuable QTLs from unadapted germplasm into elite breeding lines. **Theoretical and Applied Genetics 92**: 191-203.

Tate M and Ennenking D (2006) Common vetch (*Vicia sativa* ssp. sativa): feed or future food. **Grain Legumes 47**: 16-17.

Tayeh N, Aluome C, Falque M, Jacquin F, Klein A, Chauveau A, Bérard A, Houtin H, Rond C, Kreplak J, Boucherot K, Martin C, Baranger A, Pilet-Nayel ML, Warkentin TD, Brunel D, Marget P, Le Paslier MC, Aubert G and Burstin J (2015a) Development of two major resources for pea genomics: the GenoPea 13.2K SNP Array and a high-density, high-resolution consensus genetic map. **The Plant Journal 84**: 1257-1273.

Tayeh N, Aubert G, Pilet-Nayel ML, Lejeune-Hénaut I, Warkentin TD and Burstin J (2015b) Genomic tools in pea breeding programs: Status and perspectives. **Frontiers in Plant Science 6**: 1037.

Tayeh N, Klein A, Le Paslier MC, Jacquin F, Houtin H, Rond C, Chabert-Martinello M, Magnin-Robert JB, Marget P, Aubert G and Burstin J (2015c) Genomic prediction in pea: effect of marker density and training population size and composition on prediction accuracy. **Frontiers in Plant Science 6**: 941.

Thudi M, Bohra A, Nayak SN, Varghese N, Shah TM, Penmetsa RV, Thirunavukkarasu N, Gudipati S, Gaur PM, Kulwal PL, Upadhyaya HD, KaviKishor PB, Winter P, Kahl G, Town CD, Kilian A, Cook DR and Varshney RK (2011) Novel SSR markers from BAC-end sequences, DArT arrays and a comprehensive genetic map with 1291 marker loci for chickpea (*Cicer arietinum* L.). **PLoS One 6**: e27275.

Thudi M, Gaur PM, Krishnamurthy L, Mir RR, Kudapa H, Fikre A, Kimurto P, Tripathi S, Soren KR, Mulwa R, Bharadwaj C, Datta S, Chaturvedi SK and Varshney RK (2014) Genomics-assisted breeding for drought tolerance in chickpea. **Functional Plant Biology 41**: 1178-1190.

Torres AM, Avila CM, Stoddard FL andCubero JI (2011) Faba bean. In Perez de la Vega M, Torres AM, Cubero JI and Kole C (eds) **Genetics, genomics and breeding of cool season grain legumes (genetics, genomics and breeding in crop plants)**. Science Publishers, New Hampshire, p. 50-97.

Unigwe AE, Doria E, Adebola P, Gerrano AS and Pillay M (2018) Anti-nutrient analysis of 30 Bambara groundnut (*Vigna subterranea*) accessions in South Africa. **Journal of Crop Improvement 32**: 208-224.

United Nations (2015) **Transforming our world: The 2030 agenda for sustainable development**. United Nations, New York, 41p.

Varshney RK (2016) Exciting journey of 10 years from genomes to fields and markets: some success stories of genomics- assisted breeding in chickpea, pigeonpea and groundnut. **Plant Science 242**: 98-107.

Varshney RK, Bohra A, Yu J, Graner A, Zhang Q and Sorrells ME (2021) Designing future crops: genomics-assisted breeding comes of age. **Trends in Plant Science 26:** 631-649.

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

Varshney RK, Gaur PM, Chamarthi SK, Krishnamurthy L, Tripathi S, Kashiwagi J, Samineni S, Singh VK, Thudi M and Jaganathan D (2013c) Fast-track introgression of "*QTL-hotspot*" for root traits and other drought tolerance traits in JG 11, an elite and leading variety of chickpea. **The Plant Genome 6**: 1-9

Varshney RK, Hiremath PJ, Lekha P, Kashiwagi J, Balaji J, Deokar AA, Vadez V, Xiao Y, Srinivasan R, Gaur PM, Siddique KH, Town CD and Hoisington DA (2009) A comprehensive resource of drought- and salinity- responsive ESTs for gene discovery and marker development in chickpea (*Cicer arietinum* L.). **BMC Genomics 10**: 523.

Varshney RK, Kudapa H, Pazhamala L, Chitikineni A, Thudi M, Bohra A, Gaur PM, Janila P, Fikre A, Kimurto P and Ellis N (2015) Translational genomics in agriculture: some examples in grain legumes. **Critical Reviews in Plant Sciences 34**: 169-194.

Varshney RK, Mir RR, Bhatia S, Thudi M, Hu Y, Azam S, Zhang Y, Jaganathan D, You FM, Gao J, Riera-Lizarazu O and Luo M-C (2014a) Integrated physical, genetic and genome map of chickpea (*Cicer arietinum L.*). **Functional & Integrative Genomics 14**: 59-73.

Varshney RK, Mohan SM, Gaur PM, Chamarthi SK, Singh VK, Srinivasan S, Swapna M, Sharma S, Pande S, Singh S and Kaur L (2014c) Marker-assisted backcrossing to introgress resistance to Fusarium wilt race 1 and Ascochyta blight in C 214, an elite cultivar of chickpea. **The Plant Genome 7**: 1-11.

Varshney RK, Murali Mohan S, Gaur PM, Gangarao NVPR, Pandey MK, Bohra A, Sawargaonkar SL, Chitikineni A, Kimurto PK, Janila P, Saxena KB, Fikre A, Sharma M, Rathore A, Pratap A, Tripathi S, Datta S, Chaturvedi SK, Mallikarjuna N, Anuradha G, Babbar A, Choudhary AK, Mhase MB, Bharadwaj Ch, Mannur DM, Harer PN, Guo B, Liang X, Nadarajan N and Gowda CL (2013a) Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics. **Biotechnology Advances 31**: 1120-1134.

Varshney RK, Pandey MK, Bohra A, Singh VK, Thudi M and Saxena RK (2019) Towards sequence-based breeding in legumes in the post-genome sequencing era. **Theoretical and Applied Genetics 132**: 797-816.

Varshney RK, Roorkiwal M Nguyen HT (2013b) Legume genomics: from genomic resources to molecular breeding. **Plant Genome 6**: 1-7.

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-wettberg E and Datta SK (2017) Whole-genome resequencing of 292 pigeonpea accessions identifies genomic regions associated with domestication and agronomic traits. **Nature Genetics 49**: 1082-1088.

Varshney RK, Sinha P, Singh VK, Kumar A, Zhang Q and Bennetzen (2020) 5Gs for crop genetic improvement. **Current Opinion in Plant Biology 56**: 190-196.

Varshney RK, Song C, Saxena RK , Azam S, Yu S , Sharpe AG, Cannon S, Baek J, Rosen B D, Tar'an B, Millan T, Zhang X, Ramsay LD, Iwata A, Wang Y, Nelson W, Farmer AD, Gaur PM, Soderlund C, Penmetsa RV, Xu C, Bharti AK, He W, Winter P, Zhao S, Hane JK, Carrasquilla-Garcia N, Condie JA, Upadhyaya HD, Luo M-C, Thudi M, Gowda CLL, Singh NP, Lichtenzveig J, Gali KK, Rubio J, Nadarajan N, Dolezel J, Bansal KC, Xu X, Edwards D, Zhang G, Kahl G, Gil J, Singh KB, Datta SK, Jackson SA, Wang J and Cook DR (2013d) Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. **Nature Biotechnology 31**: 240-246.

Varshney RK, Thudi M, Nayak SN, Gaur PM, Kashiwagi J, Krishnamurthy L, Jaganathan D, Koppolu J, Bohra A, Tripathi S, Rathore A, Jukanti AK, Jayalakshmi V, Vemula A, Singh SJ, Yasin M, Sheshshayee MS and Viswanatha KP (2014b) Genetic dissection of drought tolerance in chickpea (*Cicer arietinum* L.). **Theoretical and Applied Genetics 127**: 445-462.

Vasconcellos RC, Oraguzie OB, Soler A, Arkwazee H, Myers JR, Ferreira JJ, Song Q, McClean P and Miklas PN (2017) Meta-QTL for resistance to white mold in common bean. **PLoS One 12**: e0171685.

Vaughan DA, Tomooka N and Kaga A (2005) Azuki bean [*Vigna angularis* (L.) Ohwi and Ohashi]. Genetic resources, chromosome engineering and crop improvement. In Singh RJ and Jauhar PP (eds) **Grain legumes Boca Roca (FL)**. CRC Press, Boca Raton, p. 347-359.

Vaz Patto MC and Rubiales D (2014) Lathyrus diversity: available resources with relevance to crop improvement- *L sativus* and *L cicera* as case studies. **Annals of Botany 113**: 895-908.

Vaz Patto MC, Skiba B, Pang ECK, Ochatt SJ, Lambein F and Rubiales D (2006) Lathyrus improvement for resistance against biotic and abiotic stresses: from classical breeding to marker assisted selection **Euphytica 147:** 133-147.

Verma S, Gupta S, Bandhiwal N, Kumar T, Bharadwaj C and Bhatia S (2015) High-density linkage map construction and mapping of seed trait QTLs in chickpea (*Cicer arietinum* L.) using genotyping-by-sequencing (GBS). **Scientific Reports 5**: 17512.

Vidal-Valverde C, Frias J, Estrella I, Gorospe MJ, Ruiz R and Bacon J (1994) Effect of processing on some anti-nutritional factors of lentils. **Journal of Agricultural and Food Chemistry 42:** 2291-2295.

Walters SM (1960) The shaping of angiosperm taxonomy. **New Phytologist 60**: 74-84.

Watson A, Hickey LT, Christopher J, Rutkoski J, Poland J and Hayes BJ (2019) Multivariate genomic selection and potential of rapid indirect selection with speed breeding in spring wheat. **Crop Sciences 59**: 1945-1959.

Wu L, Fredua-Agyeman R, Hwang SF, Chang KF, Conner RL, McLaren DL and Strelkov SE (2021) Mapping QTL associated with partial resistance to Aphanomyces root rot in pea (*Pisum sativum* L.) using a 13.2 K SNP array and SSR markers. **Theoretical and Applied Genetics 134**: 2965-2990

Yadav P, Saxena KB, Hingane A, Kumar C, Kandalkar VS, Varshney RK and Saxena RK (2019) An "Axiom Cajanus SNP Array" based high density genetic map and QTL mapping for high-selfing flower and seed quality traits in pigeonpea. **BMC Genomics 20**: 235.

Yang H, Tao Y, Zheng Z, Shao D, Li Z, Sweetingham MW, et al. (2013b) Rapid development of molecular markers by next-generation sequencing linked to a gene conferring phomopsis stem blight disease resistance for marker-assisted selection in lupin (*Lupinus angustifolius* L.) breeding. **Theoretical and Applied Genetics 126**: 511-522.

Yang H, Tao Y, Zheng Z, Zhang Q, Zhou G, Sweetingham MW, Howieson JG and Li C (2013a) Draft genome sequence, and a sequence-defined genetic linkage map of the legume crop species *Lupinus angustifolius* L. **PloS One 8**: e64799.

Yang K, Tian Z, Chen C, Luo L, Zhao B, Wang Z, Yu L, Li Y, Sun Y, Li W, Chen Y, Li Y, Zhang Y, Ai D, Zhao J, Shang C, Ma Y, Wu B, Wang M, Gao L, Sun D, Zhang P, Guo F, Wang W, Li Y, Wang J, Varshney RK, Wang J, Ling HQ and Wan P (2015) Genome sequencing of adzuki bean. **Proceedings of the National Academy of Sciences 112**: 13213-13218.

Yang T, Bao SY, Ford R, Jia TJ, Guan JP, He YH, Sun XL, Jiang JY, Hao JJ, Zhang XY and Zong XX (2012) High-throughput novel microsatellite marker of faba bean via next generation sequencing. **BMC Genomics 13**: 602-613.

Yoshida H, Tomiyama Y, Yoshida N, Shibata K and Mizushina Y (2010) Regio specific profiles of fatty acids in triacylglycerols and phospholipids from Adzuki beans (*Vigna angularis*). **Nutrients 2:** 49-59.

Young ND, Mudge J and Noel Ellis TH (2003) Legume genomes: more than peas in a pod. **Current Opinion Plant Biology 6:** 199-204.

Zhang C, Taran B, Warkentin T, Tullu A, Bett KE, Vandenberg B and Somers DJ (2006) Selection for lodging resistance in early generations of field pea by molecular markers. **Crop Science 46**: 321-329.

Zhu H, Choi HK, Cook DR and Shoemaker RC (2005) Bridging model and crop legumes through comparative genomics. **Plant Physiology 137**: 1189-1196.

Zohary D and Hopf M (2000) **Domestication of plants in the old world**. Oxford University Press, New York, 316p.