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Genetic resources of pulse crops in India: An overview

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Abstract

India is rich in genetic diversity of major pulse crops, but the productivity and the production of pulse crops remains low compared to the world and hence, there is a need to enhance the utilization for increasing the production. Major pulse species for which genetic diversity is occurring in India include *Vigna, Cajanus, Cicer, Pisum, Lens, Phaseolus* and few minor pulses such as *Macrotyloma*, *Canavalia, Lathyrus, Vicia, Mucuna*, *Moghania* and *Rhynchosia* etc. National Bureau of Plant Genetic Resources (NBPGR) is the nodal institute for the management of plant genetic resources in India. It has assembled ~70,000 accessions of different pulse crops majoring *Cajanus cajan*, *Cicer arietinum*, *Phaseolus vulgaris*, *Pisum sativum*, *Vigna mungo*, *Vigna radiata*, *Vigna umbellata*, *Vigna unguiculata*, *Vicea* sp. and *Lens* sp. through collection and introduction from India and from >70 other countries of the world. Several pests of quarantine significance have been identified and salvaged from the exotic germplasm. The *ex situ* base collection at NBPGR conserve 64,744 accessions of 20 genera and 61 species of pulses. This germplasm has been characterized for agro-morphological, quality and biochemical traits, biotic and abiotic stresses for identifying trait-specific reference sets and 28 catalogues describing about 45,000 accessions of 14 pulse crops. A total of 121 accessions of various pulse crops have been registered as unique/potential donors. Core and mini cores have been developed in chickpea, pigeonpea, common bean, mungbean, adzuki bean, cowpea, lentil, moth bean and pea both nationally and internationally. Wild species of pulse crops have been utilized for transferring desirable traits into cultivated species. Application of modern tools and technologies of molecular biology will accelrate the process of gene transfer for improvement of pulse crops.

Key words: Genetic resources, pulses, species, core collection, conservation

Introduction

Pulses are an important constituent of the food basket and a cost-effective and nutritionally rich source of protein. Although, India is a key player in pulses production, contributing significantly to the global production, however, low production and productivity of pulses coupled with increasing demand has been a great concern. This situation has created a demand and supply disequilibrium; consequently the prices of pulses have risen sharply. Realizing and recognizing that India is deficit in pulse production and not able to meet the domestic requirements from its own, it is essential to strategize boosted and sustained domestic production of pulses to attain self-sufficiency. This required concerted breeding efforts to develop varieties, which give not only high yield but also sustain the climatic vagaries (Upadhyaya et al. 2016). To meet these challenges management and enhanced utilization of genetic resources has always been in forefront.

India is one of the eight centres of origin (Vavilov 1951) and is one of the twelve-mega gene centres/ regions of diversity of crop plant in the world (Zeven and Zhukovsky 1975). The cultivation of legume crops is ancient and their centres of origin or area of diversity are correlated with development of ancient human societies and their agricultural needs. Species like *Pisum arvense, Lens and Lathyrus* were domesticated in India in Neolithic and Chalcolithic periods (Vishnu-Mittrre 1974). India is considered a primary centre of diversity for urdbean, moth bean and pigeon pea, secondary centre of diversity for cowpea and regional diversity centre for chickpea and mungbean (Arora 1988). The genus *Vigna* has 07 subgenera and 150 species, which are naturally distributed across Africa and Asia while subgenus *Ceratotropis* is referred to as Asiatic *Vigna* followed by *Lathyrus* (150 species), *Vicia* (140), *Phaseolus* (50), *Cicer* (43), *Cajanus* (32),

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Macrotyloma (24), *Lens* (5) and *Pisum* (2). The two species are African originated (*Vigna unguiculata* and *Vigna subterranean* and five species are from Asiatic group known to be originated in Indian subcontinent (*V. radiata*, *V. mungo*, *V. aconitifolia, V. angularis, V. umbellata*) while the major gene pools of *P. vulgaris* occur in Latin America namely in Central America and Mexico (Mesoamerican) and in the Andean mountains of South America (Bitocchi et al. 2013; Takahashi et al. 2016). In India, *Vigna* and *Cajanus* are the largest genera with maximum number of species diversity occurring in the Western Ghats, North eastern region and Eastern peninsular tract. Besides, there are other wild relatives enumerated in Indian Floras include *Phaseolus coccineus, P. lunatus, Cicer microphyllum, Macrotyloma sargarwalensis*, *Canavalia virosa, C. obtusifolia, C. maritime, C. stocksii, Lathyrus aphaca, Vicia* sp., *Lathyrus* sp., *Mucuna* sp., *Moghania* sp. and *Rhynchosia* sp.

Germplasm collection and introduction

Historically, the management of pulses genetic resources was initiated in India in 1946 under the aegis of Division of Botany, Imperial Agricultural Research Institute, New Delhi and later AICRP on Pulses Improvement in 1966-67. Internationally, pulse improvement was initiated in 1962 under Regional Pulse Improvement Project (RPIP) between India and Iran. Afterwards, International Crops Research Institute for Semi-Arid Tropics (ICRISAT) came into existence in 1972 and assumed the responsibilities as the World Repository for genetic resources of chickpea and pigeon pea. Later, National Bureau of Plant Genetic Resources (NBPGR) that came into existence in 1976 and started systematic management and utilization of plant genetic resources. Till now, NBPGR in collaboration with other crops based institutes and State Agriculture Universities has collected >70,000 accessions of different pulses crops. The major species collected represents *Cajanus cajan* (13407), *Cicer arietinum* (15614), *Macrotyloma uniflorum* (3615), *Phaseolus vulgaris* (6483), *Pisum sativum* (4806), *Vigna aconitifolia* (2633), *Vigna mugo* (5675), *Vigna radiata* (7163), *Vigna umbellata* (2951), *Vigna unguiculata* (3220) and *Lens* sp. (4994). Besides, several wild species have also been collected and conserved in the genebnak (Table 4).

The indigenous genetic diversity has been further enriched by introducing around 50,000 germplasm accessions of various genera *viz*., *Cajanus* (3,732), *Cicer* (20,178), *Vigna* (10,110), *Vicia* (2,350) *Lens* (14,049), *Cyamopsis* (152), and *Macrotyloma* (45) from >70 countries of the world. The paucity of space is not allowing authors to mention detail of species here but can be obtained from NBPGR. Core and mini core collections of pigeon pea, chickpea, cowpea and lentil have also been introduced. Trait specific germplasm accessions introduced in various crops are given in Table 1.

Characterization and evaluation

Detailed evaluation of germplasm for good agronomy and quality and tolerance to biotic and abiotic stresses helps in the identification of superior genetic stocks and subsequently for their utilization in breeding programmes. ICAR-NBPGR has also developed minimal descriptors for systematic evaluation in 14 pulse crops. Over the years, NBPGR has characterized and evaluated >50,000 germplasm accessions of various pulse crops individually and in collaboration with other institutes for agro-morphological, quality and biochemical traits, biotic and abiotic stresses. The promising accessions have been identified and traits specific reference sets have been developed in various crops and few of the accessions of these sets are given in table 2. We assume that information would be of potential value as these could serve as important donors in crop improvement programmes. NBPGR has published 28 catalogues describing about 45,000 accessions of 14 pulse crops. ICRISAT has published catalogues on worlds' collection on chickpea (Pundir et al. 1988) and pigeonpea (Remanandan et al. 1988); ICARDA on kabuli chickpea (Singh et al. 1983; Singh et al. 1991), lentil (Erskine and Witcombe 1984) and fababean (Robertson and Sherbeeny 1988); on mung bean by AVRDC (Tay et al. 1989), urdbean by CSIRO (Imrie et al. 1981) and cowpea by IITA, Nigeria (IITA 1974).

In India, germplasm of pulses has also been evaluated by several other institutions for various traits. For instance, inheritance and molecular tagging of mosaic virus resistance gene in black gram (Gupta et al. 2013; Basamma et al. 2015; Akthar et al. 2016), powdery mildew, heat stress in mung bean (Alagupalamuthirsolai et al. 2015), nutritional and chemical evaluation in *Vigna trilobata* (Siddhuraju et al. 1992), Phytophthora stem bight, Fusarium wilt and sterility mosaic disease in pigeon pea (Sharma et al. 2015; Yadav et al. 2016), drought tolerance, agro-morphological traits, high carotenoids in chick pea (Kaneni et al. 2013; Kumar et al. 2015; Kahraman et al. 2016), agronomy characters, micronutrients

Table1. Trait specific germplasm introduced by ICAR-NBPGR

Crop/traits	Accessions
Chickpea	
Resistance to *Ascochyta* blight	EC303580-EC303630, EC382339-343, EC382361-64, EC382366-74
Fusarium Wilt	EC382338, EC382346-49, EC382354, EC382413-14
Blight	EC382352–53, EC382393–97, EC382404-408
Leaf minor	EC382357–59, EC382365, EC382375, EC382379, EC382375, EC382418-20
Cold	EC382360, EC382376-78, EC382383-84, EC382388-90, EC530806-808
Cyst nematode	EC382421-429, EC382432-34
Drought	EC382409-410, EC382446-47
Lentil	
Ascochyta and wilt resistance	EC267526–EC267712
Winter hardiness and multiple disease resistance	EC382715-725
Drought tolerance	ET157075-ET157122
Urdbean	
High yield, flood tolerance	EC319031–33
Drought tolerance	EC319034-37
Mungbean	
Resistance to *Cercospora* leaf spot	EC118895-96, EC124083A, EC124084A, EC124089A, EC245968–975
Powdery mildew	EC118898, EC155745, EC155747, EC318985–698
Mottle virus	EC124098– EC124104; EC124111-115, EC245968–975
Root rot disease	EC124105–108
Charcoal rot	EC245968–975, EC319008-10
Leaf crinkle virus	EC319011-12
Mung bean yellow moasic virus	EC319013-17, EC501570, EC565626-33
Early maturity	EC501566-68
Cowpea	
Bacterial canker resistance	EC4209- EC4235
Cercospora leaf spot	EC120745-46
100-seed weight	EC384918, EC384921
Draught tolerance	EC384928
Faba bean	
Chocolate spot resistance	EC303649-671
Ascochyta blight	EC303672-691
Rust	EC303692-706

profiling, stored pest (*Callosobruchus chinensis*), heat stress tolerance, gene effects, seed traits, nature and magnitude of variation in lentil (Rana and Gupta 1993b,d, 1995b; Kumar, 2015; Sengupta et al. 2016; Gore et al. 2015; Singh et al. 2016), agronomic traits, genetic diversity and architecture, powdery mildew, response to selection, physiological traits, seed quality and protein profiling in pea (Rana and Gupta 1993c, a, 1995a, 1998; Singh et al. 2010; Sharma et al. 2015; Rana et al. 2013, 2016), morphological and yield parameters, multivariate analysis, fatty acids, flavonols and minerals, seed coat, cotyledon and embryonic axe fractions for their phenolic composition in relation to antioxidant activities, drought tolerance in horse gram (Morris 2013; Sreerama et al. 2010; Sharma et al. 2015a,b), genetic diversity analysis, seed, flour and starch properties, screening against anthracnose, mineral and protein profiling, phenotyping for agronomic traits in kidney bean (Sharma et al. 2006; Singh et al. 2012; Sharma et al. 2012; Parmar et al 2014; Rana et al. 2015), agronomic traits, grain, starch and protein characteristics, resistant to stored pest in rice bean (Singh et al. 2012; Chandel et al. 1988), genotype × environment interaction, and genetic diversity in adzuki bean (Dobhal and Rana 1994, 97).

Many International Institutes have also evaluated germplasm for various traits such as phylogenetic relationship, agronomic traits, powdery mildew, antioxidants in mung bean (Chotechung et. al. 2016; Liu et al. 2016; Chaitieng et al. 2002; Ghafoor et al. 2001), photo-thermo sensitivity, high temperature tolerance, flower bud thrips, *Striga gesnerioides*, protein and minerals, black eye cowpea mosaic virus, cowpea aphid-borne mosaic virus, drought tolerance, morphological traits in cowpea (Gumedzoe et al. 1998; Boukar et al. 2016; Fatokun et al. 2012; Boukar et al. 2011; Stoilova and Pereira 2013; Pratap et al. 2014; Kaur et al. 2015), resistance against the yellow and orange variants of the bacterial wilt, white mold, halo blight, salt stress, drought stress, chilling stress in common bean (Parkin et al. 2011; Mkwaila et al. 2011; Porch et al. 2009; Hsieh et al. 2005; Khan et al. 2014; Nahar et al. 2016), protein and amino acids content, genetic diversity using SNP in lentil (Kahraman et al. 2016; Khazaei et al. 2016), agronomic traits, pea weevil, powdery mildew, rust, genetic diversity, cold tolerance (Buckseth et al. 2016; Sun et al. 2016; Aryamanesh et al. 2012; Teshome et al. 2015; Wu et al. 2016; Zhang et al. 2016), agro-morphological traits, phylogenetic relationship and domestication, population structure using SSR, nutritional and

Table 2. Traits specific promising germplasm identified in various pulse crops

Trait /stress	Promising germplasm
Chickpea	
100 seed weight	IC269131, IC269064, IC268945, IC269012,IC327727
No of pods/plant	IC269146, IC268949, IC269191, IC269186, IC269218
Seed yield	IC275465, IC251669, IC251858, EC548039, IC251788
Wilt	IC327035, IC327044, IC327060, IC327062, IC327063
Dry root rot	IC327074, IC327701, IC327049, IC327031, IC327100
Wet root rot	IC327906, IC327414, IC327055, IC327104, IC327904
Ascochyta blight	IC327352, IC327414, IC327231, IC327737, IC327229
Collar rot	IC327736, IC327081, IC327745, IC327046, IC327259
Botrytis grey mould	IC327288, IC327583, IC327933, IC327446, IC327749
Foot rot	IC327201, IC327276, IC327200, IC327692, IC327034
Pod borer	IC327744 IC327293, IC327172, IC327150, IC327188
Cold tolerance	IC327361, IC327109,IC327327, IC327306, IC327639
Drought tolerance	IC327289, IC327290, IC327730, IC327732, IC327330
Protein content	IC327246, ICC10948, IC116373, IC83860, IC116380
Pigeonpea	
Early maturity	IC245518, IC245319, IC245149,IC245183, IC245218
Number of pods/plant	IC73318, IC74015, IC490447, NIC-23578, IC139739
100 -seed weight	IC73796, IC73995, EC100467, C139635, D379
Wilt	IC73727, IC73735, IC73321, IC73726, IC73832
Sterility mosaic disease	IC245198, IC45768, IC73313, IC73332, IC73336
Pod borer (Moderate resistance)	IC245130, IC245131, IC245132, IC245134, IC245136
Protein content	IC245543, IC525519, IC525504, IC525445, IC424779
Lentil	
High pods/plant	IC208351-1, IC559608, IC560182, IC321535, IC560033, EC299646
Bold seeded	IC201676, IC560182, IC208351
Rust resistant	IC212676, IC241783, IC361296, IC558919, IC559647
Highly resistant (Rust)	IC208336, IC346091, IC559894, IC560250, ILL 4605
Wilt	IC266840, IC406527, IC558919, IC559792, IC560343, IC315962
Nematode resistance	IC559573, IC559890, IC559744, IC282863
Protein	IC201674, IC201751, IC560209, IC560206
Cowpea	
Pods/plant	EC724307, EC724366, EC725116, EC724547, EC724770
Pod length	EC723681,EC725162, EC724327, EC724045, EC724536
Seed/pod	EC725164, EC723741, EC723971, EC725180
Nematode resistance	IC253277, EC528391, EC517140, EC149444, IC402090
Protein content	IC536626, IC536637, IC397807
Urdbean	
High pods/plant	IC140822, IC250226, IC250229, IC-250245
Pod length	IC146954, IC250256, IC20818, IC24129
Seeds/pod	IC396032, IC48553, IC485550
100 seed weight	IC485552, IC485550, IC485665
MYMV (High resistance)	IC144901, IC001572, IC011613, IC485638
Mungbean	
Extra early flowering	IC39335, IC39332
Nematode resistance	IC212049
Protein content	EC251557, PLM-350
French bean	
Number of pods	IC311085, IC274526, IC313279, EC537981, EC537998
Pod length	IC313281, IC280000, IC311083EC537993, IC381022
Seeds per pod	
100-seed weight	EC500458, EC500459, EC500759, IC326623, IC329375

Protein content	EC398518, EC405211, EC398571, IC274526, IC313279
Lysine	IC415266, IC38312, IC415318, IC415290, IC418280
Ash	IC5195541 IC415282, IC515387, IC515448, IC467901
Resistance to anthracnose	IC326964, IC326981, EC77006, EC500944 EC537965, EC537998, EC537975, EC537996, EC50218, EC537990
Pod/plant and seed/pod	EC530886, EC500298, EC500482, EC500278, EC530884
Web blight	EC50218, EC385254, EC214425, EC537972, EC530920
BCMV	IC328665, IC329154, IC329505, IC 415334, IC415486, IC415517
Pea	
Pod length	IC278701, IC469139, IC469147, IC469167
No. of pods	IC342026, IC342033, IC469164, IC469137 IC342028
100-seed weight	IC469135, IC279125, IC279082, IC469146, IC291541, IC279082
Resistance to powdery mildew	IC469165, IC394026, IC469155, IC394027, IC381445, IC381054, IC311066
Adzuki bean	
Seed yield/plant	IC341952, IC341954, EC108080, IC15256, EC254, IC469172, EC340280
Pod number	IC469171, IC341960, EC120460, EC87896, EC15257, EC390255
100-seed weight	EC500458, EC500459, EC500639, EC500280, EC500909,
Ash (%)	IC469173, IC341953, IC341952, IC341949, IC240105, IC24522
Phenol	IC341944, IC341952, IC341949, IC341953, IC469173
Rice bean	
Seed/pod	LRB-477, LRB-448, LRB-488, LRB-322, LRB-482
Pod/length	LRB-477, LRB-457, LRB-461, LRB-458
No. of pods/plant	LRB-475
100-seed weight	LRB-474, 476, 493, EC281186, EC340240
Pods/cluster	EC18256, EC000372, EC187898

physiological functions in adzuki bean (Somta et al. 2008; Yang et al. 2015); genetic diversity and population structure, phenloic compounds (Yang 2015). Mega evaluation program at ICRISAT identified promising sources of resistance for wilt (108 accessions), sterility mosaic disease (410), phytophthora blight (152), stem canker (26), alternaria blight (25), pod borer (27), pod fly (21), nematodes (19), drought (7), water logging (62) and salinity (56) (Upadhyaya et al. 2016).

Germplasm registration

Detailed evaluation of germplasm helps in the identification of superior genetic donors for specific traits. These donors greatly enhance the use of germplasm in plant breeding. Nevertheless, it is important to have some kind of right and recognition to the developer of such donors. ICAR-NBPGR is a nodal institute for registering the unique/useful germplasm in India. So far 121 accessions of various pulse crops have been registered as unique/potential donors and some of them are mentioned in Table 3 while detailed information can be obtained from NBPGR Web Page.

Development of core and mini cores

The large variability stored in the genebank in the absence of proper characterization and evaluation creates the problem of plenty. Frankel (1984) proposed that the collections could be pruned to a manageable sample or core collection. The core subset should be designed to minimize repetitiveness within collection and it should represent the rich genetic diversity of crop. The core collection should serve as a working collection and should be extensively examined, and the accessions, which are not included in the core collection, would be designated as reserve collection. Core sets have been developed in mungbean (Bisht et al. 1998; Schafleitmer et al. 2015), chickpea (Upadhyaya et al. 2001; Hanan et al. 1994; Archak et al. 2016), pigeonpea (Upadhyaya et al. 2006; Reddy et al. 2005), lentil (Tullu et al. 2001; Singh et al. 2014), common bean (Logozzo et al. 2007; Pérez-Vega et al. 2009; McClean et al. 2012; Rana et al. 2015), adzuki bean (Wang et al. 2001; Xu et al. 2008), cowpea (Mahalakshmi et al. 2007), chickpea (Upadhyaya 2001; Upadhyaya et al. 2006), mothbean (Meghwal et al. 2015) and Pea (L, Xu-Xiao et al. 2008).

Pre-breeding and utilization

The genetic base of pulses is quite narrow and the real challenge, therefore, is to convert the collected PGR through pre-breeding into parental lines, which will be more acceptable and user friendly to the plant breeders. The existing variability in germplasm has

Table 3. Trait specific registered germplasm of pulse crops at NBPGR

Accessions	Traits	Accessions	Traits	Accessions	Traits
Black gram					
IC0144901	MYMV resistance	IC557433	Shining yellow seeds	IC573438	100-seed weight 4.65g
IC0570262	High iron, MYMV resistance	IC0570264	High iron and MYMV resistance	IC0570265	High zinc, iron and MYMV resistance
IC0570267 IC0570268 IC0570269	High protein, MYMV resistance	IC426765	Photosensitivity	IC0594172	Male sterile mutant
IC296878 habit	Dwarf, ground pod pod bearing habit	IC553269	Brown pod and	IC0594173	Sympodial bearing
Chickpea					
IC296691	Salinity tolerance	IC296738	Multipinnate leaf, shorter internodes	IC0595521	*Ascochyta* blight and wilt resistance
IC0589349	Drought tolerance	IC0598237	Wilt resistance	IC395465	Fasciated broadened stem mutant
IC395466	Outwardly broad leaflets	IC0595522	*Ascochyta* blight and wilt resistance	IC0594480	Wilt resistance
Cowpea					
IC299972	Black seed coat colour	IC202803	Bold seed	IC519745	Black eye cowpea mosaic virus resistance
Green gram					
IC0546478	Photosensitive	IC573449 IC573450	High iron, MYMV resistance	IC573454	High iron, higher pods/cluster, MYMV resistance
IC573451 IC573455	High iron, MYMV resistance	IC573453	High zinc, MYMV resistance	IC573456	High iron, zinc, protein, MYMV resistance
IC296771	High seed weight, long pod, high protein	IC0589309 IC0589310	Very early maturing	IC0418452	High seed weight
Horse gram					
IC0587786	Anthracnose tolerance	IC0587788	Higher fodder yield	IC212722	High protein
Lentil					
IC296884	Bright dark green leaves	IC296883	Multiple disease resistance	IC567650	Rust resistance
IC0595543	Aluminium toxicity tolerance	IC0616579	High iron and zinc		
Pea					
IC296677 IC296678	Leafletless, powdery mildew resistance	IC296737	Male sterile line	IC279125	Bold seeded
IC395309	Tendril type, powdery mildew resistance	IC397028	Yellow wrinkled seeds, powdery mildew resistance	IC0616051	Resistance to pea rust
IC0218988 IC208366 IC208378 IC0598280	Resistance to powdery mildew	IC0610501	Triple poded at every node	IC0598281	Resistance to downy mildew and rust

Pigeonpea					
IC555904 IC555909 IC555911 IC555916 IC555918	Stable CGMS line, creamy white bold seeds, NDT type, 175 days maturity	IC555899	Fertility restoration NDT, type, 135 days maturity	IC557427	CMS (stable male sterility, 145 days maturity
IC557428 IC557429 IC557430	Stable CMS resistance for *Fusarium* wilt and sterility mosaic	IC0588674	Resistance for wilt & strility mosaic	IC0594374	*Fusarium* wilt resistance
IC565837 IC565838 IC565839 IC565840 IC565841	Fertility restoration	IC0574574 IC0574575 IC0574576 IC0574578	Resistance to *Fusarium* wilt and sterility mosaic disease	IC0574577	Resistance to *Fusarium* wilt
IC0573418	Open flower	IC0573419 &IC0573420	CMS having open flower and obcordate leaves	IC537352	Extra early, dwarf, Indeterminate
IC548343	Thermo-insensitive CMS	IC555902 IC0587712	Stable CGMS	IC0587711	Early maturity (133 days)

been exploited to reach to a desirable level of productivity. However, to attain further breakthrough in increasing yield and improving stability in future cultivars, new sources of genes/alleles needs to be identify and incorporated into the background of cultivated varieties. Wild relatives of pulses are known as valuable sources for resistance to several biotic and abiotic stresses beside yield and quality traits. The wild relative of *Cicer,* namely, *C. judaicum* has been reported to be resistant to Botrytis grey mould (Meeta and Bedi 1987), fusarium wilt (Nene and Haware 1980) and has high methionine content; where *C. pinnatifidum* resistant to Botrytis grey mould, has high tryptophan content. Sharma et al. (1993) screened a large number of wild relatives of *Cajanus* and identified sources of resistance for cyst nematode. The identification of lines with the genetic male sterility gene has facilitated the production of hybrids. Some of the sources of male sterile lines, MS 3A, found in ICP 1555, and MS 4A, in ICP 1596, are the field collections from India (Reddy et al. 1978). Efforts have been to transfer resistance to *Helicoverpa armigera* from *C. scarabaeoides*, *C. acutifolius* and *C. platycarpus* to cultivated pigeon pea. Several accessions of *Vigna vexillata* and *V. oblongifolia*, which are incompatible with cowpea, have good levels of resistance to post-flowering insect-pests that devastate cowpea. High level of resistance to bruchids (*Zabrotes subfasciatus Boheman*) and to common bacterial blight was introgressed and pyramided from wild *Phaseolus acutifolius* into common bean (Singh 2004).

At ICRISAT, several cytoplasmic nuclear male sterile lines have been developed from wild *Cajanus* species and have been used for pigeon pea improvement (Saxena et al. 2010). The global collection of wild annual Lens (*L. orientalis, L. odemensis, L. tomentosus, L. nigricans, L. ervoides* and *Cicer* (*C. reticulatum, C. echinospermum, C. judaicum, C. pinnatifidum, C. bijugum*) has been screened and several gene sources have been identified (Singh et al. 2014). In wild annual *Cicer*, important agro-morphological traits, viz. high biomass score, high pods/plant, earliness, and multiple resistance against botrytis gray mold, ascochyta blight and root knot nematode was recorded (Singh et al. 2014) while in wild annual *Lens*, useful gene sources were identified for important traits *viz*., short internode, high pods/plant, multiple resistance against wilt, rust and powdery mildew. As far as introgression of wild gene pool is concerned, traits like, earliness, shorter internode, high pods/plant and resistance against major biotic stresses have been transferred from *C. reticulatum* and *C. echinospermum* (Singh et al. 2015) whereas high pods/plant, earliness, and resistance against rust and powdery mildew have been introgressed from *L. orientalis,* and *L. nigricans* in lentil (Singh et al. 2013). The genetically enhanced stable progenies of these crosses are being evaluated for desired traits under multi-location environments.

Further molecular characterization of wild *Cicer* species for understanding the genetic structure and linkage disequilibrium (LD) pattern by large-scale genotyping of informative microsatellite and single nucleotide polymorphism (SNP) markers was assessed to facilitate chickpea improvement (Saxena et al. 2014). They have also identified 82489 high-quality genome-wide SNPs from 93 wild and cultivated *Cicer* accessions through integrated reference genome- and *de novo*-based GBS assays. High intra- and inter-specific polymorphic potential (66–85%) and broader natural allelic diversity (6–64%) detected by genome wide SNPs among accessions signify their efficacy for monitoring introgression and transferring target trait-regulating genomic (gene) regions/allelic variants from wild to cultivated *Cicer* gene pools for further chickpea genetic improvement (Bajaj et al. 2015).

Genomic resources

Genome sequencing of crops has initiated a detailed gene hunt. Advancements in high throughput sequencing technologies *viz*., sequencing whole genome (Kang et al. 2014) chloroplast (Tangphatsornruang et al. 2009) and mitochondrial genomes (Lin et al. 2016) of mungbean has revealed the information packed in DNA. Likewise whole Genome Sequencing of *Cicer arietinum* (Jain et al 2013; Varshney et al 2013; Parween et al. 2015), *Cajanus cajan* (Singh et al. 2013; Varshney et al. 2012), *V. unguiculata* (Cowpea Modern Breeding Consortium), *V. angularis* (Yang et al. 2015) and *Phaseolus vulgaris* (Guo et al. 2007; Vlasova et al. 2016) can further fasten comparative genomics studies and genomic assisted breeding (Varshney et al. 2005). Based on high-quality, annotated genome sequence of the adzuki bean, cowpea a genome server VigGS has been designed for better utilization of the genomic information (Sakai, Naito et al. 2015). Annotation of transcriptome sequences for functional genes has been carried out in mungbean (Gupta et al. 2014; Chen et al. 2015; Ganguli et al. 2016; Liu et al. 2016), urdbean (Souframanien and Reddy 2015), adzuki bean (Chen et al. 2015), rice bean (Chen et al. 2016), common bean (Martin et al. 2016), lentil (Verma et al. 2013) and pigeon pea (Dutta et al. 2011; Kudapa et al. 2012) for the development of genic marker, differential gene expression studies, etc. In chickpea including wild *Cicer* species extensive transcriptome analysis has been done for studying gene expression under biotic stresses (Jain et al. 2015), abiotic stress (Garg et al. 2016), tissue specific gene expression (Garg et al. 2011; Singh et al. 2013; Pradhan et al. 2014; Kant et al. 2016) and for gene discovery and marker development (Garg et al. 2011; Agarwal et al. 2012; Jhanwar et al. 2012). A Chickpea Transcriptome Database (CTDB) also has been developed for utilizing functional genome information (Verma et al. 2015). The ESTs and genomic data of closely related legumes and also advance high throughput markers such as SSRs and SNPs, these resources have the potential to accelerate gene discovery, mapping and assist molecular breeding in these crops. Currently there are 55,046 genomic survey sequences (GSS), 236,536 DNA or RNA sequences, 204,190 ESTs, 58,339 information about genic loci, 120 unigenes and 208,538 protein sequences under the *Vigna* genus alone in NCBI database.

Ex situ conservation

The *ex situ* seed genebank at NBPGR comprises 12 long-term modules maintained at –20°C for housing the base collections while the active collections are conserved in 22 medium-term modules maintained at 4°C across the country at NBPGR Regional Stations and National Active Germplasm Sites. At present, the genebank holds 64,744 accessions of pulses belonging to 20 genera and 61 species as the base collections (Table 4). Besides, 10,235 duplicate safety samples of pigeonpea and lentil received from ICARDA, Syria and ICRISAT, 554 released varieties of 18 crops have also been conserved in the base collection. A total of 632 accessions of 12 pulse crops belonging *Cajanus* (7), *Cicer* (9), *Cyamopsis* (1), *Lens* (1), *Macrotyloma* (2), *Pisum* (1), *Phaseolus* (1), *Rhynchosia* (7), *Vicia* (1) *and Vigna* (27) have been cryo-stored and one accessions of *Cicer microphyllum* has been conserved through *in vitro* culture.

Germplasm exchange and quarantine

NBPGR undertakes germplasm exchange and its quarantine processing. The exchange of germplasm for crop improvement programmes has the inherent risk of introducing new pests or their virulent races/ biotypes into the country. There are several examples of inadvertent introduction of pets (insects, mites, nematodes, fungi, bacteria, viruses and weeds) world over. Globally there are several examples of movement of pests along with the planting material, which have caused enormous economic losses. There are 85 bruchids of quarantine significance associated with 39 grain legumes species and their wild relatives. Several bruchid species have been intercepted in grain legumes germplasm at NBPGR (Wadhi, 1980; Mathur and Lal, 1996; Khetarpal et al. 2001; Bhalla et al. 2001;

Table 4. Germplasm conservation in the base collection at NBPGR, New Delhi

Crop group	Indigenous	Exotic	Total	Crop group	Indigenous	Exotic	Total
Atylosia species	14	0	14	Jack bean (*Canavalia ensiformis*)	61	1	62
Chickpea (*Cicer arietinum*)	11508	3012	14520	*Canavalia* species	15	3	18
Wild *Cicer species*	26	52	78	Lablab bean (*Lablab purpureus*)	1638	5	1643
Lentil (*Lens culinaris*)	2083	572	2655	*Lablab purpureus var. lignosus*	19	0	19
Lens culinaris ssp. *odemensis*	0	18	18	*Lablab purpureus var. typicus*	4	0	4
Lens ervoides	0	48	48	Lathyrus (*Lathyrus sativus*)	2553	91	2644
Lens species	0	22	22	Yellow Vetch (*Lathyrus aphaca*)	1	0	1
Clusterbean (*Cyamopsis tetragonolobus*)	4275	37	4312	*Rhynchosia* species	6	0	6
Lima bean (*Phaseolus lunatus*)	44	2	46	Sword bean (*Canavalia gladiata*)	34	0	34
Mucuna species	8	0	8	*Canavalia cathartica*	14	0	14
Parkia (*Parkia biglandulosa*)	3	0	3	*Canavalia obtusifolia*	2	0	2
Pea (*Pisum sativum*)	2869	1047	3916	Tree bean (*Parkia roxburghii*)	2	0	2
Pisum sativum ssp. *hortense*	7	0	7	Mung bean (*Vigna radiata*)	3595	537	4132
Pisum sativum var. *arvense*	226	19	245	Black gram (*Vigna mungo*)	3148	6	3154
Pigeonpea (*Cajanus cajan*)	10887	309	11196	*Vigna mungo* var. *silvestris*)	13	0	13
Wild *Cajanus species*	12	0	12	*Vigna dalzelliana*	21	0	21
Pueraria (*Pueraria tuberosa*)	1	0	1	*Vigna vexillata*	115	0	115
Snoutbean	9	0	9	*Vigna radiata* var. *sublobata*	223	0	223
Rhynchosia minima	3	0	3	*Vigna trilobata*	136	0	136
Winged bean (*Psophocarpus tetragonolobus*)	78	143	221	*Vigna* species	19	0	19
Yam bean (*Pachyrhizus* species)	2	0	2	Rice bean (*Vigna umbellata*)	1889	178	2067
Faba bean (*Vicia faba*)	507	377	884	Cowpea (*Vigna unguiculata*)	2671	1093	3764
Flemingia macrophylla	1	0	1	*Vigna unguiculata* ssp. *sesquipedalis*	13	0	13
French bean (*Phaseolus vulgaris*)	2150	1540	3690	*Vigna unguiculata* ssp. *unguiculata*	3	0	3
Scarlet runner (*Phaseolus coccineus*)	10	0	10	Adzuki bean (*Vigna angularis*)	75	100	175
Horse gram (*Macrotyloma uniflorum*)	3013	11	3024	Moth bean (*Vigna aconitifolia*)	1456	33	1489
Dolichos species	8	0	8	Wild Horse gram (*Macrotyloma sargharwalensis*)	1	0	1
Total					**55471**	**9256**	**64727**

Bhalla et al. 2003 and Gutpa et al. 2005a). Among the several interceptions of exotic bruchids on grain legumes, some of them are not yet reported from India include *Acanthoscelides obtectus in Phaseolus vulgaris* from Colombia, Italy, Mexico, The Netherlands, Peru, Slovakia and USA; *Bruchidius atrolineatus* in cowpea from Nigeria, *Bruchus dentipes* in faba bean from ICARDA (Syria); *B. ervi* in lentil from ICARDA (Syria) and in *Lathyrus latifolius, Lens culinaris, L. esculenta, Ulex europaeus, Vicia ervilia, V. sativa* from Egypt, France, Germany, Hungary, Israel, Italy, Reunion Island, Russia, Syria and Turkey, *B.pisorum* in *Pisum sativum* from Bulgaria and Eritrea; *B. lentis* in *L. culinaris* from Syria. *C. analis,* in cowpea from Nigeria; *C. chinensis in* faba bean and cowpea from Eritrea and Nigeria respectively, and *C. maculatus* in cowpea from Nigeria.

Seeds contaminated with nematodes *viz.*, *A. tritici, A. arachidis, A. besseyi, D. dipsaci* and several species of cyst nematodes have been intercepted (Rajan and Lal, 2006). A large number of pathogenic fungi were intercepted from various countries (Lambat et al. 1985; Majumdar et al. 1991; Agarwal et al. 2004; Khetarpal et al. 2006; Singh et al. 2007). It has been reported that 165 fungi are seed-borne in grain legumes (CABI, 2007). Of these 31 fungi are listed as quarantine pests for India and 28 are not reported from India. There are 43 bacterial pests are present world over in grain legumes (CABI, 2007) and 13 bacterial pests are of quarantine significance to India. A large number of viruses are found to affect grain legumes crops. A total of 21 seed-transmitted viruses are yet not reported from India, four viruses are present in India on other crops but not known to occur on grain legume crops, one virus is present in India with a restricted distribution exclusively in Faizabad (Uttar Pradesh) and one virus reported exclusively from Palampur (Himachal Pradesh) on rose but not on grain legumes, hence 27 viruses of grain legumes are of quarantine significance for India (Chalam et al. 2005; 2008a,b; 2009; 2012). The details of pest of quarantine significance can be obtained from NBPGR.

Future challenges and opportunities

Although India is the leading producer of pulses but at the same time it is the foremost consumer and the largest importer of pulses. The declining per capita availability and rising prices have forced us to realize that India need a pulses revolution. To achieve self sufficiency in pulse we have to go along way and make effective and judicious use of all resources, genetic resources and advanced technologies. Advances in genomic platforms and availability of resources have enhanced capacity of researchers to investigate PGR and harness their full potential for improving crop productivity and quality. It is assumed that genomics is bound to play a significant role in management of *ex situ* collections, germplasm characterization, screening phenotyped germplasm to identify superior alleles at key loci. Exploiting the new paradigm set by next generation sequencing (NGS) and bioinformatics to deliver an exhaustive, accurate characterization of DNA variation at high throughput and at a low cost (cost of sequencing has already fallen dramatically and keeps dropping, thus allowing for the direct analysis of large sets of accessions at a fraction of the cost of such an operation just a few short years ago). Other approaches such as focused germplasm collections including wild relatives, precise phenotyping, enhanced PGR exchange, molecular detection and diagnosis of pests, public-private partnership, institutional linkages to characterize and evaluate germplasm expeditiously and on priority at different locations are also need to be strengthened. Joining the loose ends of phenotyping and genotyping with the help of high throughput systems provides opportunities for the efficient use of multi-disciplinary (Agronomy, Biochemistry and Molecular biology) expertise.

Declaration

The authors declare no conflict of interest.

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