Mungbean Genetic Resources and Utilization

2

Gayacharan, Sunil Archak, Kavita Gupta, Veena Gupta, Vandana Tyagi and Kuldeep Singh

Abstract

Mungbean also known as green gram is an important food legume crop. It is the most widely grown crop among five cultivated Asiatic Vignas, viz. mungbean, urdbean, mothbean, adzukibean, and ricebean. The crop is expanding to non-traditional growing areas mainly due to its short duration of life cycle, high nutritional value, low input requirement, soil ameliorating properties, and high global demand. The crop fits well in cereal crop-based cropping systems in warm humid regions of South, East, and Southeast Asia. Mungbean cultivation covers over six million ha of land worldwide with annual production of around three million tons of grains. Narrow genetic base, disease pest proneness, and photo–thermo-sensitivity are the major problems resulting in the poor yield of the crop. The utilization of very few parental genotypes in mungbean breeding programs has led to the narrowed genetic base of the mungbean varieties. This has posed a serious threat to the mungbean cultivation amid newly emerging pests and pathogens of the crop. Worldwide over 43,000 mungbean germplasm are conserved ex situ which are playing crucial role in enhancing yield as well as resilience to the crop against biotic and abiotic stresses. Recent evaluation and characterization of ex situ collections of mungbean germplasm revealed substantial amount of useful variability in mungbean. Transboundary movement of germplasm has also helped in the development and release of varieties in several countries. Enhanced and efficient utilization of ex situ conserved mungbean and related wild species germplasm in breeding programs with the help of modern genomics tools would help in the development of desired genotypes with higher yield potential. In this chapter, we have discussed the collection, conservation, and utilization of mungbean and wild Vigna species germplasm.

2.1 Introduction

Mungbean is native of Indo-Burma region of Asia where it was first probably domesticated, believed to have originated in the Indian gene center (Jain and Mehra 1978). The wild progenitor species of munglocan has been designated as *V. radiata* var. *sublobata* and are of Indian origin (Chandel et al. 1984). The wild *V. radiata* var. *sublobata* occurs in Tarai region, sub-Himalayan tract, and sporadically in western and eastern peninsular tracts of India (Arora and Nayar 1984). India is also the primary center of diversity for mungbean (Arora 1988). Mungbean diversity is well dispersed throughout the continent from Himalayas in north

Gayacharan · S. Archak · K. Gupta · V. Gupta · V. Tyagi · K. Singh (✉)
ICAR-National Bureau of Plant Genetic Resources, New Delhi, India
e-mail: kuldeep.singh4@icar.gov.in; director.nbpgr@icar.gov.in

R. M. Nair et al. (eds.), *The Mungbean Genome*, Compendium of Plant Genomes,
https://doi.org/10.1007/978-3-030-20008-4_2

to southern peninsular and northeastern region. The Indo-gangetic plains are considered as secondary center of diversity for mungbean (Bisht et al. 1998a). In early days, mungbean seed was carried by emigrants and traders from Asia to the Middle East, East Africa, Latin America, parts of South America and Australia (Poehlman 1991). It is the most widely distributed among the Asiatic *Vigna* species, and its production is steadily increasing (Kim et al. 2015). Currently, the crop is cultivated throughout the South and Southeast Asia, including India, Pakistan, Bangladesh, Sri Lanka, Myanmar, Thailand, Philippines, Laos, Cambodia, Vietnam, Indonesia, Malaysia, South China, and Taiwan. In the USA, it was grown as early as 1835 as the Chickasaw pea. It is also grown to a lesser extent in many parts of Africa and USA (Oklahoma) and reintroduced in many parts of Australia. However, it did not become a major commercial crop in these countries. In India, the crop is mainly grown in states of Rajasthan, Maharashtra, Gujarat, Odisha, Bihar, Andhra Pradesh, and Madhya Pradesh.

Vigna species including wild relatives flourish in hot humid weather of subtropical to tropical regions. Mungbean is fast-growing crop and completes its life cycle from 50 to 90 days. It requires rainfall of 600–1000 mm/year. Optimal temperature required for vegetative growth ranges from 28 to 30 °C, however, some related wild *Vigna* species like *V. umbellata*, *V. angularis*, *V. trilobata*, etc. can sustain temperature few degrees cooler than the mungbean. The available breeders' varieties or landraces cannot sustain below 15 or above 45 °C of temperature. The crop is highly sensitive to waterlogging conditions and tolerant to saline soils to some extent. The crop can be grown in well-drained loamy to sandy loamy soils with a pH range of 5–8.

2.1.1 Taxonomic Classification

Mungbean belongs to the family Fabaceae, subgenus *Ceratotropis* in the genus *Vigna* Savi. Earlier mungbean was known as *Phaseolus aureus* before many species of the genus moved to a new genus *Vigna* (Lambrides and Godwin 2007). The genus *Vigna* consists of large group of cultivated crops and wild relatives distributed in Asia and Africa. It comprised of around seven subgenera and 19 sections with around hundred species (Maxted et al. 2004; Singh et al. 2006; Takahashi et al. 2016) out of which seven (She et al. 2015) species are most commonly cultivated around the world. The two species are African originated (*Vigna unguiculata* L. and *Vigna subterranea* L.) and other five species are from Asiatic group known to be originated in Indian subcontinent (*V. radiata* L., *V. mungo* L., and *V. aconitifolia* Jacq.) and in the Far East Asia (*V. angularis* Willd. and *V. umbellata* (Vavilov 1926; Smartt 1985). The species *V. radiata* has four direct subspecies, i.e., *V. radiata* subsp. *radiata, V. radiata* subsp. *sublobata* (L.) R. Wilczek, *V. radiata* var. *radiata* (L.) R. Wilczek, and *Vigna radiata* var. *setulosa* (Dalzell) Ohwi & H. Ohashi.

2.1.2 Mungbean Gene Pool

Cross compatibility among *Vigna* species is not so well defined, and so their gene pool, but in general there is no cross compatibility barrier between domesticated forms and their closest relatives (Tomooka et al. 2014). There are few studies on such wide hybridization for widening genetic base of *Vigna radiata* using *Vigna mungo* (Gosal and Bajaj 1983), *Vigna umbellata* (Pandian et al. 2008), *V. trilobata* (Pandiyan et al. 2012), and interspecific barriers could be easily overcome. Though interspecific crosses of *Vigna radiata* with other *Vigna* species like *V. mungo, V. radiata* var. *sublobata, V. radiata* var. *setulosa, V. trilobata, V. trinervia, V. hainiana, V. dalzelliana* are possible, cross-barrier problems particularly due to incompatibility in chromosomal pairing also have been observed in some cases (Pandian et al. 2008). Tomooka et al. (2011) have classified gene pool of mungbean as *V. radiata* as *V. radiata* var. *radiata* and its closest wild relative, i.e., *V. radiata* var. *sublobata* in gene pool 1 (GP-1). *V. mungo, V. subramaniana, V. grandiflora, V. stipulacea, V. tenuicaulis, V. trinervia,* and *V. umbellata* in GP-2, and other species in sections *V. aconitifolia* and *V.*

angularis in GP-3. However, some research groups have deviations from this gene pool classification like *V. radiata* var. *setulosa* which is a wild form placed in GP-1, *V. aconitifolia* in GP-2, and *V. umbellata* in GP-3 (Pratap et al. 2014a). From recent hybridization work, it is observed that *V. glabrescens* gives fertile progenies when crossed with *V. radiata* without any crossing barriers, though the species is grouped in GP-3. This indicates that there is a need to revisit *Vigna* gene pool classification and molecular tools along with conventional crossing-based studies will give robust grouping of *Vigna* species.

2.2 Mungbean Germplasm Collections and Introductions

2.2.1 Collections

Ex situ conservation of plant genetic resources (PGRs), harboring a wide range of diversity, is important to develop new varieties to face the challenges posed by adverse effects of climate change and to meet the food security aspects of increasing population worldwide. Grain legumes are among the topmost crops, which can help in addressing both these issues effectively. Importance of conservation of plant genetic resources for food and agriculture (PGRFA) was realized since the Neolithic era when human started practicing farming, seed selection, and seed storage. However, the systemic explorations, collections, and conservation of crop germplasm started in 1916 by renowned Russian geneticist N. I. Vavilov, and today over 7.4 million accessions are conserved ex situ worldwide (https://cdn.croptrust.org). The N. I. Vavilov Research Institute of Plant Industry (VIR), St. Petersburg, Russia, is one of the largest genebanks which holds over 230,000 accessions of various crops including 863 accessions of mungbean. These mungbean collections are the oldest collections, and most of them were collected between the years 1910 and 1927.

In India, mungbean germplasm collections started way back in 1925 to collect mungbean landraces from all over India and Burma (Bose 1932). During that period, mungbean germplasm collection efforts were made in several states of the country, but there was no coordination or exchange of the germplasm among them (Bisht et al. 1998b). Extensive and organized explorations were taken up throughout the Indian sub-continent only after the establishment of ICAR-National Bureau of Plant Genetic Resources (NBPGR) in 1976 (Rana et al. 2016). NBPGR is a nodal agency for germplasm introductions, collections, and conservation in India. The National Genebank at ICAR-NBPGR has documented more than 11,000 accessions of mungbean including 7,453 indigenous accessions and 3,588 exotic accessions (Figs. 2.1 and 2.2). Of these at present 3,927 accessions comprising of 3,392 indigenous collections from 28 states of India and 535 exotic collections from 12 countries across the world are conserved in long-term storage conditions (−20 °C). Maximum of the diversity collected and conserved is from Rajasthan and Gujarat, whereas diversity from northeastern states is least explored (Fig. 2.3). Fifty-six out of 108 mungbean breeders' varieties developed through various crop improvement programs on mungbean are also part of this collection (Fig. 2.4). To give due credit to breeders' germplasm other than the varietal genotypes, ICAR-NBPGR is also providing soft protection through Plant Germplasm Registration Committee (PGRC) under the aegis of ICAR. Till date, thirteen germplasm have been registered in PGRC (Fig. 2.4, Table 2.1) with novel unique traits.

The importance of mungbean as a crop was also realized worldwide and AVRDC-The World Vegetable Center, Taiwan, took the lead in collection, conservation, exchange, and varietal improvement programs at international level. The center maintains the second largest mungbean germplasm collections (6,700 accessions, Schafleitner et al. 2015). The Southern Regional Plant Introduction Station, University of Georgia, under USDA's National Plant Germplasm System conserves around 3,928 accessions of mungbean (https://www.ars-grin.gov/). 2,250 accessions are ex situ conserved by Field Crops Research Center, Department of Agriculture, Bang Khen, Thailand (www.fao.org/docrep/013/i1500e/Thailand.pdf). 1,076 accessions are ex

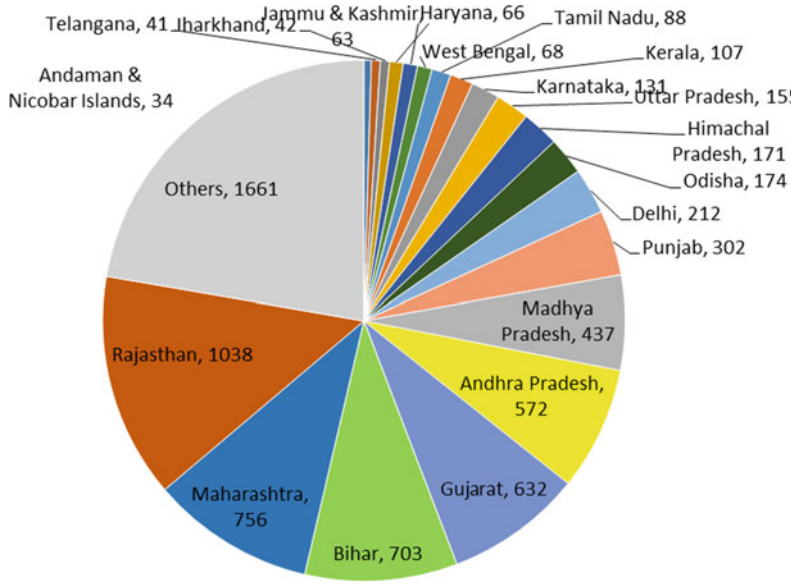

Fig. 2.1 State-wise distribution of indigenous collections documented at National Genebank, ICAR-NBPGR

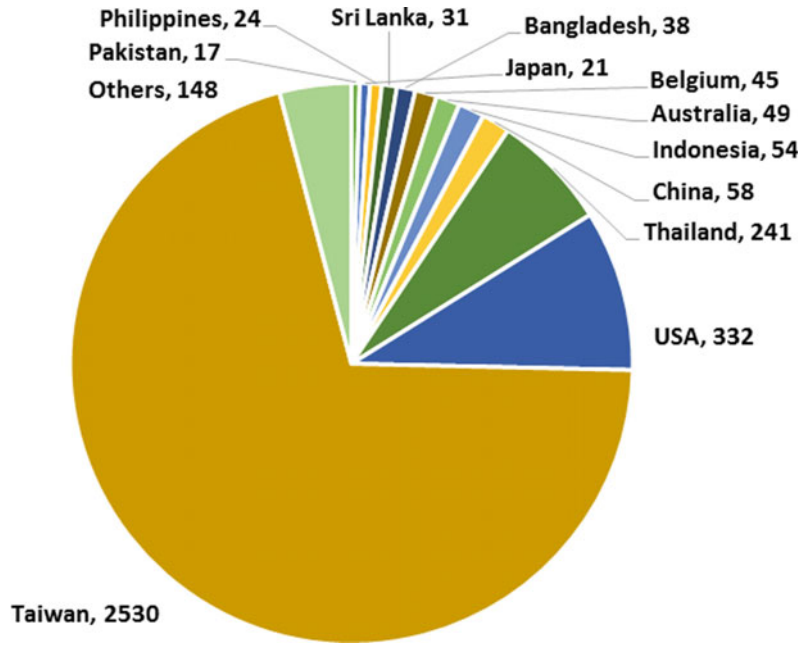

Fig. 2.2 Country-wise distribution of exotic collections documented at National Genebank, ICAR-NBPGR

situ conserved by The Genetic Resources Center, NARO, Tsukuba, Japan (https://www.gene.affrc.go.jp/databases-plant_search_en.php). Around 1,006 accessions of mungbean are conserved in the genebank of Department for Plant Genetic Resources, Austrian Agency for Health and Food Safety (AGES), Austria (https://www.genbank.at/en/ecpgr-vigna.html). The Australian Grains Genebank (AGG), Horsham, Victoria, conserves 1,385 accessions of mungbean germplasm. The national genebank managed by Institute of Crop Germplasm Resources of the Chinese Academy of Agricultural Sciences (CAAS) is another major custodian of mungbean germplasm.

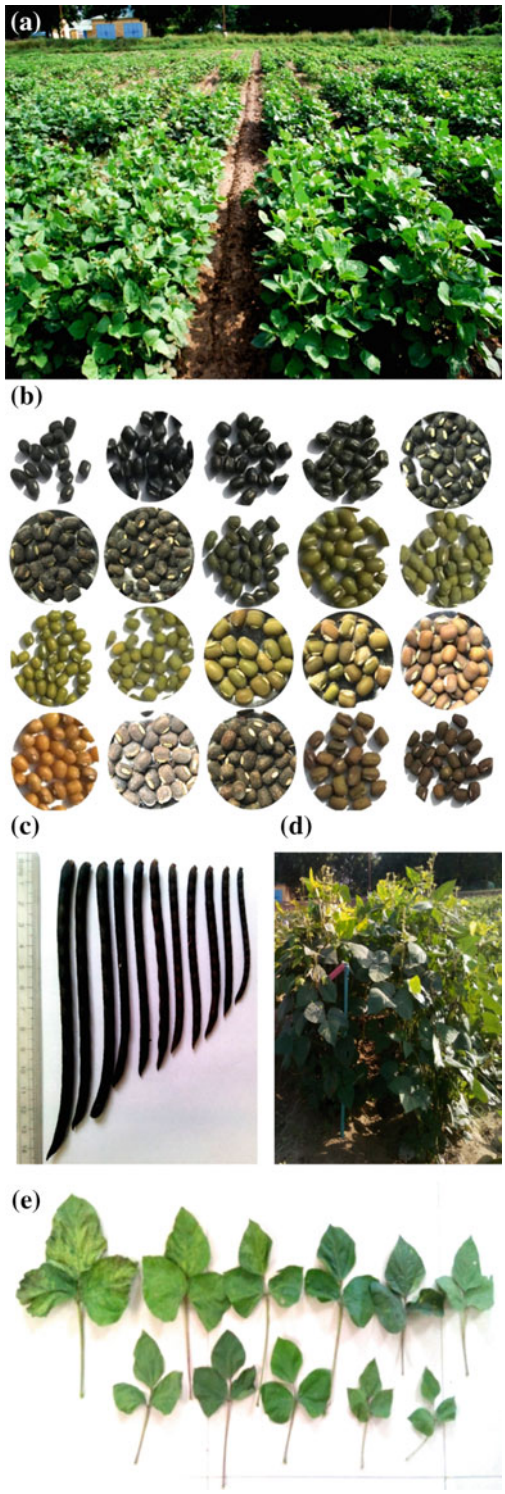

Fig. 2.3 Highlights of phenotypic variation present in mungbean gene pool. **a**. Field view, **b**. seed coat color variability, **c**. variability for pod length and pod thickness (each pod contains 14–15 seeds), **d**. a lodging resistant and around 120 cm tall accession (IC553601), **e**. leaf size variation

Worldwide over 43,000 mungbean germplasm are conserved ex situ (Nair et al. 2013). Over 9,000 mungbean seed samples are kept under black box system in Svalbard Global Seed Vault as safety duplicates by thirteen different national and international genebanks (https://www.nordgen.org/sgsv/index.php?).

2.2.2 Introductions

In India, there is a single-window system for the exchange of small samples of plant germplasm (including genetically modified crops) meant for research, and ICAR-NBPGR is the authorized nodal institution. It regulates the import of seeds/planting material for research under the provisions of Plant Quarantine (Regulation of Import into India) Order, 2003, of the Destructive Insects and Pests (DIP) Act of 1914. The plant introductions include germplasm, elite strains, improved varieties, genetic stocks, and related species from various parts of the world.

Introductions are done time to time based on the breeders or researchers' requirement. Nearly four thousand diverse accessions of mungbean were introduced in India from various countries like Australia, Bangladesh, Bhutan, Brazil, Canada, China, Czech Republic, Ghana, Germany, Ethiopia, Indonesia, Italy, Japan, Madagascar, Malaysia, Nepal, Netherlands, Philippines, Russia, Sri Lanka, Surinam, Sweden, Taiwan, Thailand, Uruguay, USA, and Uzbekistan since 1976. Some of the important introductions having highly desirable traits for the crop improvement are mentioned here. EC118889, EC118894, EC118895, and EC118898 were procured for traits like high grain yield potential, wide adaptability, synchronous and early maturity, large seeded and having resistance to *Tobacco mosaic virus*, lodging. Mungbean germplasm lines, viz. EC318985 to 319057, EC390990–EC390993, were introduced from AVRDC, Taiwan, having useful traits like resistance to charcoal rot, leaf crinkle virus, tolerance to drought and flood and photo-insensitive. Four accessions EC393407–EC393410 were introduced from Bangladesh having important traits like long pods with large, shiny green seed, and synchronous maturity. There

Fig. 2.4 Few representative accessions of mungbean showing seed size and seed coat luster variability

were several other mungbean introductions like six accessions viz. EC391170–EC391175 from Indonesia for high grain yield trait. Similarly, other notable introductions made are EC396424–EC396425, EC718740–EC718745 for important traits like early maturity, resistant to mungbean yellow mosaic disease (MYMD), *pea yellow mosaic virus* and bold seed. Preferred traits for introduction in mungbean are short duration, bold seed (>6 g), photo–thermo-insensitivity, bruchids resistance, pre-harvest sprouting tolerance, resistance against powdery mildew, and *Cercospora* leaf spot disease. Many of the introductions were further utilized in mungbean varietal development programs, few of which are mentioned in Table 2.2.

Table 2.1 Trait-specific germplasm identified in mungbean

Trait	Accessions ID
Cercospora leaf spot resistance	EC118895, EC124083A, EC124084A, EC124089A, EC245968
Powdery mildew resistance	EC118898, EC155745, EC155747, EC318985, V4718
Mottle virus resistance	EC124098, EC124104, EC124111, EC245968
Root rot disease resistance	EC124105
Charcoal rot resistance	EC245968, EC319008
Leaf crinkle virus resistance	EC319011
Mungbean yellow mosaic disease (MYMD) resistance	IC118998, K-1, EC397139, IC305286, IC305291, IC305284, IC472115, IC364130, EC319013, EC501570, EC565626, NM-92, NM-94, **IC573451, IC573453, IC573454, IC573455, IC573456**
Nematode resistance	IC212049
Bruchid (*Callosobruchus chinensis* and *C. maculatus*) resistance	EC0398897 (V2802), EC0398896 (V2709)
Extra early flowering (25–27 days)	EC398944, IC073537, IC507478, EC398883, EC398880, EC398890, IC076477, IC507476_2, IC314609_2, EC398953, IC073392, EC396129, EC396423, IC076422, IC119106, EC398890, IC39335, IC39332
Early maturity (48–50 days)	IC008822-3B, IC314302, IC076422, IC119106, IC314609_1, IC447908, EC398944, EC592177, IC314562, EC398901, EC398955, EC501566, **IC0589309, IC0589310**
Synchronous flowering and maturity (5–8 days of flowering period)	EC396115, IC076414, EC397140_2, IC488968, IC076422, IC507389, IC488582, IC118970, EC398923, IC076601_1, EC397138, IC314437, IC076378, EC398915, IC076417_1, EC397141, IC314691, IC076463, EC396143, IC076370, IC507524_1
High pod length (12–16 cm)	EC398937, EC398904, EC398887, EC398935, EC398902, EC398936, IC418452, IC148442, VI003370
Pentafoliate leaf small leaflets	**IC296679**
Trilobed leaflets	IC76451
Purple stem, petiole and leaf veins	IC19420, EC9129
High number of seeds per pod ($\geq$ 14.5–17.1)	IC507314, IC418452, IC507342_2, IC548274, IC488554_1, IC148415, IC252010_1, IC076388, IC076460, IC507337, VI004979, VI002090
100 seed weight (7.5–7.89 g)	EC398923, EC398903, EC398884, EC396413, EC396116, EC398919, EC396154, IC507459, EC398882, **IC0418452** (9.43), **IC296771** (6.2 g), VI005034, VI001244, VI000946
Lodging resistance and plant height	IC553601 ($\sim$120 cm), VI014178, VI005030
High protein content	EC251557, PLM-350, **IC296771** (27.8%), **IC573456** (25.8%)
High iron content (mg/100 g)	**IC573449** (9.18), **IC573450** (11.7), **IC573451** (11.8), **IC573454** (10.59), **IC573455** (11.35), **IC573456** (8.29)
High zinc content (mg/100 g)	**IC573453** (3.56), **IC573456** (4.19)
Photosensitive nature	**IC0546478**

Note Accessions in bold are registered germplasm at ICAR-NBPGR, New Delhi; prefix EC means exotic collection and IC means indigenous collection. Accessions starting with prefix 'V' or 'VI' belong to World Vegetable Center collections

Table 2.2 Utilization of exotic germplasm for pulse improvement

Accession	Country of origin/source	Varieties released in India
China moong	China	Shining Moong 1, Sunaiana, RMG62, Jalgaon 781, DGGV-2
NM9473	Pakistan/AVRDC, Taiwan	Pusa 9531
NM92	Pakistan/AVRDC, Taiwan	Pusa Vishal
NM94	Pakistan/AVRDC, Taiwan	SML688
V2164	AVRDC, Taiwan	SML134
V3484	AVRDC, Taiwan	Pusa101, WGG2
VC1137-213 (M 178)	AVRDC, Taiwan	Pusa105
CES44	Philippines	AAU34
MG50-10	Philippines	Co5, Co6
VC6368 (ML 26)	AVRDC, Taiwan	Pant mung 2, Pant mung 5
VC6367(44-55-2)	Thailand	IPM 410-3 (Shikha)
Iranian germplasm	Iran	PS 16
VC 6368 (46-40-4)	AVRDC, Taiwan	UPM 98
VC 6370 (30-65)	AVRDC, Taiwan	UPM 98-1

2.3 Process to Access Genetic Resources

Plant germplasm exchange process and related regulatory mechanisms are the same for each crop. Exchange of plant germplasm in India is regulated by Biological Diversity Act (BDA), 2002, in conjuncture with Plant Quarantine Order 2003 (PQO-2003). BDA defines that who and how any non-Indian can access the germplasm from India while Plant Quarantine Order ensures that the exchanged germplasm is free of pest, pathogen, and weed (of quarantine importance). The import/introduction of plant germplasm into India is governed by the PQO-2003 (Regulation of Import into India). Director, ICAR-NBPGR, has been authorized to issue import permit for import of germplasm, transgenic or genetically modified organisms for research purposes for further distribution to the researchers in the country. For commercial and bulk import, permission is granted based on the recommendations of EXIM Committee of Department of Agriculture, Cooperation and Farmers Welfare, Government of India.

BDA, 2002, was enacted in compliance to Convention on Biological Diversity (CBD). As per the provisions of the Act, a non-Indian can access any biological resource occurring in India with the prior approval of National Biodiversity Authority (NBA). Section 2.3 (2) of the BDA, 2002, defines the non-Indian entity. However, access under Collaborative Research Project which is compliant to the International Collaborative Guidelines issued by the Ministry of Environment, Forest and Climate Change (MoEFCC), is exempted (provisions in Sect. 2.5). For accessing germplasm resources which are not covered under any collaborative research project, the indentor can apply online at http://absefiling.nic.in/NBA/login/auth.

The germplasm exchange (import/export) is being carried out with about thirty countries and international agricultural research centers for augmenting diverse genetic resources and making them available to researchers/breeders/users for utilization in various research programs.

ICAR-NBPGR carries out this important activity under an established procedure.

2.4 Mungbean Germplasm Characterization and Evaluation

Characterization and evaluation are the first and foremost important activity for the utilization of germplasm in crop improvement programs. Characterization is the description and establishment of diagnostic characters of a plant germplasm. Generally, characterization traits are highly inheritable and qualitative in nature. Evaluation is the description of plant germplasm expression in optimum or adverse environmental conditions to reveal its potential useful variability available within the germplasm. Evaluation traits are quantitative in nature but are highly important for crop improvement. Major objective of the evaluation is to identify trait-specific germplasm of breeders/researchers' importance. In general, characterization and preliminary evaluation (for yield and yield-attributing traits) are done simultaneously while evaluation for biotic and abiotic stresses is done separately.

Like in any other genebank, characterization and evaluation are the main activity of NBPGR. Total 1,532 accessions were well characterized using 19 qualitative and 19 quantitative traits during 1993 (Kawalkar et al. 1996). During 2016–18, further another around 1,500 indigenous and exotic collections were characterized and evaluated for 27 agro-morphological traits and biotic and abiotic stresses like MYMD disease and heat stress. Based on these morphological observations and statistical analyses, it was found that cultivated mungbean gene pool harbors very good amount of variation for various economically important traits like seed weight, flowering period, pod length, number of seeds/pod, and seed size (Table 2.3, Fig. 2.4). For qualitative traits, very good level of phenotypic variations is observed. Range of variation for phenotypic traits reported in mungbean germplasm in national and international studies is highlighted in Table 2.3. Recently, World Vegetable Centre has characterized global mungbean collections of 5,234 accessions for eight agro-morphological traits; viz. primary leaf length, primary leaf width, plant height at flowering, plant height at maturity, days to 50% flowering, pod length, seeds per pod, and 1,000 seed weight were characterized (Schafleitner et al. 2015). It was observed that good amount of phenotypic variability is present for certain traits in global mungbean collections in terms of Shanon's diversity index which was 0.82 (average of all traits). Overall, variability for root nodulation, petiole length, number of primary branches, number of pod bearing peduncles, flowering period, plant height and seed weight, seed coat color, and flowering period was observed comparatively higher than the rest of the traits studied (Bisht et al. 1998a; Schafleitner et al. 2015).

Several other research groups also have characterized mungbean germplasm for understanding genetic variability, genetic divergence, and trait association (Abna et al. 2012; Bisht et al. 1998b; Chattopadhyay et al. 2008; Hakim 2016; Rahim et al. 2010; Sangiri et al. 2008; Singh et al. 2014; Tantasawat et al. 2010; Yimram et al. 2009). Simultaneously, mungbean germplasm has also been evaluated against important biotic and abiotic stresses like bruchids (Somta et al. 2007; Somta et al. 2008), nematodes (Mukhtar et al. 2017), MYMD (Akhtar et al. 2011; Ghafoor et al. 1992; Iqbal et al. 2011; Jalaluddin and Shaikh 1981; Shad et al. 2006; Sudha et al. 2013a, b), *Cercospora* leaf spot, and powdery mildew (Chankaew et al. 2011; Raje and Rao 2002; Reddy et al. 1987).

The characterization and evaluation studies done in mungbean have resulted in the identification of several trait-specific mungbean germplasm, some of which are listed in Table 2.1.

2.5 Development of Mungbean Core and Mini-Core

Core and mini-core are the output of characterization and evaluation of a large set of ex situ collections of any crop germplasm. The core

Table 2.3 Phenotypic variation available in cultivated mungbean gene pool

Trait	Range	Phenotypic CV (%)
Primary leaf length (cm) #	3.3–6.4	10.64
Primary leaf width (cm) #	1.1–2.8	13.38
Terminal leaf length (cm)	5.0–13.6	20.9
Terminal leaf width (cm)	1.5–12.9	21.06
Petiole length (cm)	1.0–25.0	38.34
No. of primary branches	1.0–9.0	34.37
Nodulation	0.0–98	76.39
First pod bearing node	2.0–8.0	7.62
No. of pod bearing peduncle	2.0–36.0	52.61
Plant height at flowering (cm) #	9.0–68.0	28.21
Plant height at maturity (cm) #	12.0–94.0	30.14
Days to initial flowering	24.0–80.0	15.01
Days to 50% flowering #	39.0–73.0	8.79
Days to 50% flowering	25.0–90.0	14.50
Flowering period	5.00–50.00	32.92
Days to initial maturity	37.0–90.0	11.13
Days to 80% maturity	48.0–110.0	11.16
Pod length (cm)	5.0–16.0	14.95
Pod length (cm) #	5.0–17.1	13.75
Number of seeds per pod	5.0–17.0	13.12
Number of seeds per pod #	5.8–15.4	11.29
100 seed weight (g)	1.58–7.89	30.18
100 seed weight (g) #	2.027–7.58	24.6

Source Catalogs of NBPGR and recently mungbean characterization unpublished data #Mungbean characterization data from AVRDC-The World Vegetable Centre (Schafleitner et al. 2015)

concept was first given by Frankel (1984) with the objective of enhancing germplasm utilization efficiency particularly in crops with large number of ex situ collections where the selection of suitable germplasm for breeding and research becomes a difficult task. Till date, two cores have been developed in mungbean. First mungbean core was developed by NBPGR utilizing its 1,532 ex situ collections available by that time in National Genebank (Bisht et al. 1998a). A subset of 152 accessions was developed based on 38 agro-morphological descriptors. AVRDC-The World Vegetable Center, Taiwan, has developed another mungbean core of 1,481 accessions from 5,234 global mungbean collections conserved in its genebank (Schafleitmer et al. 2015). This core was developed by random selection of 20% of the accessions after geographical stratification and cluster analysis of eight phenotypic traits. Further to bring down this number to a more workable size, entire 1,481 core accessions were genotyped using 20 simple sequence repeats (SSRs) and a mini-core set of 296 accessions was developed.

2.6 Mungbean Varietal Development Programs

Germplasm evaluation and characterization have significantly contributed to the crop improvement and varietal release through direct selection or as donor in biparental crossing programs. At the inception of mungbean varietal development

programs, mungbean varieties were mainly released by selection and purification of landraces (Singh et al. 2016). However, Indian National Agricultural Research System (NARS) lead by All India Coordinated Research Project (AICRP) took systematic efforts and several varieties were developed through extensive nationwide crossing programs. This resulted in significant yield enhancement despite the spread of several devastating diseases like MYMD, leaf crinkle, powdery mildew, etc. As a result, till 2018 total 108 mungbean varieties have been released in India among which 52 are released by Central Variety Release Committee (CVRC) and 56 are released by State Variety Release Committees (SVRCs) (Project Coordinator, AICRP on MULLaRP report, 2018). Parallel to Indian mungbean improvement programs, there are other countries like Australia, Bangladesh, Myanmar, Pakistan, Philippines, Taiwan, China, Thailand, etc., where significant work has been done in mungbean. AVRDC-The World Vegetable Centre, Taiwan, is heading international mungbean improvement programs. Several varieties have been released worldwide from national programs or through International Mungbean Improvement Network program of AVRDC (Shanmugasundaram et al. 2009).

Traditional mungbean cultivars have multiple drawbacks like seed shattering, indeterminate growth habit, small seed, highly prone to diseases like mungbean yellow mosaic virus disease (MYMD), and long maturity period of usually 90–110 days (Shanmugasundaram et al. 2009). Due to these constraints, mungbean yield in traditional farming systems could not reach beyond 400 kg/ha. However, diverse germplasm utilization in breeding programs has led to the development of several mungbean varieties having yield potential over 2.0 tones/ha with other desirable traits. AICRP on MULLaRP has been very instrumental in improving this Indian origin crop in the country. Mungbean varieties for several traits like early and synchronous maturity, pod length, MYMD resistance, bold seed, storage quality, summer season and regional environment specific as well as varieties of wider adaptability, etc., have been released and are in process of development. Recently, a mungbean variety Virat (IPM 205-7) developed, from a cross between IPM2-1 and EC398889, matures within 52–55 days and gives average yield of 1–1.2 tones/ha. Similarly, there are other varieties like Shikha (IPM410-3), Kanika (IPM 302-2), and Varsha (IPM 2K14-9) which yield 1.2–1.4 tons/ha and have wider adaptability.

2.7 Mungbean Crop Wild Relatives (CWRs) and Their Utilization

Mungbean crop wild relatives are distributed throughout the Asian countries (Fig. 2.5). Indian gene center harbors several *Vigna* wild species like *V. radiata* var. *sublobata, V. umbellata, V. vexillata, V. aconitifolia, V. trilobata, V. stipulacea, V. dalzelliana, V. trinervia* var. *bourneae, V. mungo var. sylvestris, V. khandalensis, V. hainiana, V. pilosa, V. grandis, V. marina, V. capensis, V. angularis var. nipponensis,* etc. Over 2,000 collections of wild *Vigna* species are conserved ex situ in Indian National Genebank at ICAR-NBPGR, New Delhi (Table 2.4). Few of the *Vigna* species like *V. aconitifolia* and *V. umbellata* are found both as wild and cultivated forms and are under active cultivation in many Indian states. Apart from being a genetic resource, *Vigna* CWRs play other important roles; they are used for various purposes like food grain (*V. marina, V. umbellata, V. stipulacea, V. trilobata*), green pods (*V. umbellata, V. minima, V. subterranea*), forage (*V. luteola*), green manure (*V. hosei, V. parkeri, V. stipulacea*), tubers (*V. adenatha, V. vexillata, V. ambacensis, V. angivensis, V. fischeri, V. monophylla, V. reticulata*), cover crop (*Vigna trinervia*), ornamental (*V. caracalla*), etc., and many times these have multiple uses (Tomooka et al. 2011).

Vigna wild relatives inhabit extreme and diverse environments like dry harsh (*V. aconitifolia* and *V. aridicola*), sandy saline seashore (*V. marina*), swampy marshland habitat (*V. luteola* and *V. adenantha*), limestone outcrops (*V. exilis*), high altitudes (*V. angularis* var. *nipponensis* and *Vigna nakashimae*) which shows that *Vigna* CWRs are goldmines for adaptive traits to

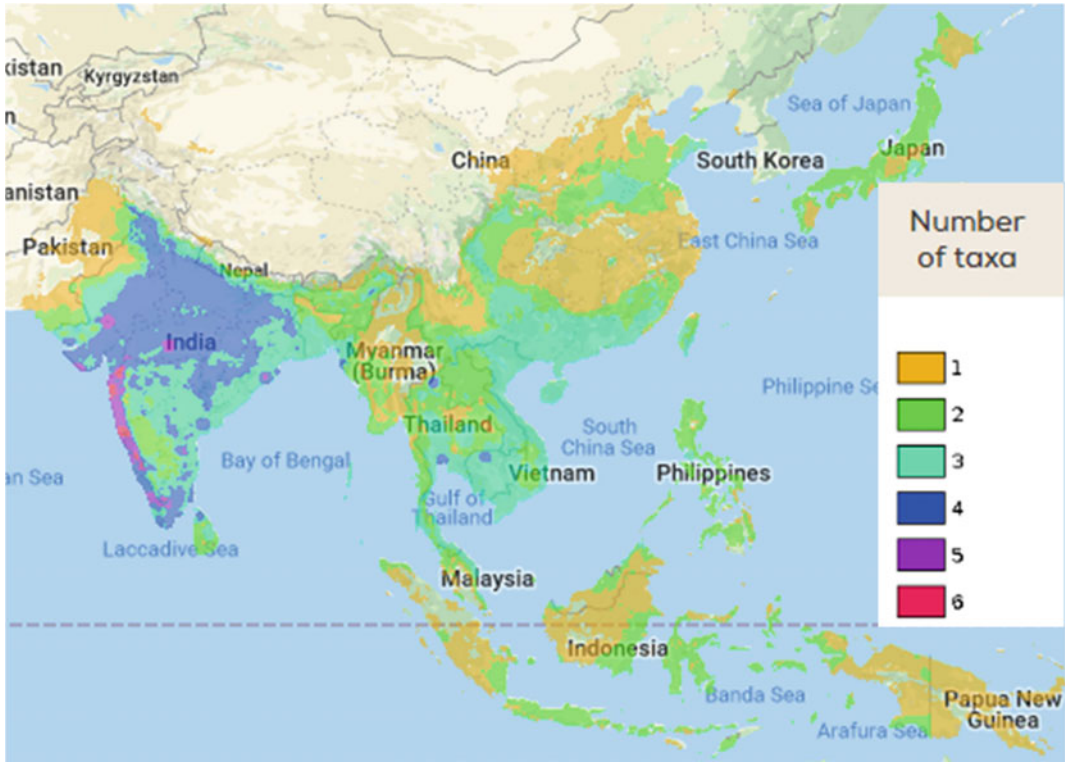

Fig. 2.5 Taxon richness of CWRs of *V. radiata*. *Source* https://www.cwrdiversity.org/

improve cultivated *Vigna* species against all major abiotic stresses. *Vigna* CWRs are also rich source of resistance for several biotic stresses like *V. umbellata,* and *V. radiata* var. *sublobata* used for breeding MYMD-resistant mungbean varieties (Pandiyan et al. 2008; Sudha et al. 2013a, b; Sudha et al. 2015; Pratap et al. 2014a). *V. vexillata* possess resistance for cowpea mottle carmovirus (Ogundiwin et al. 2002) and legume pod borer *Maruca vitrata* (Jackai et al. 1996). Powdery mildew resistance is available in *V. stipulacea* (Tomooka et al. 2006). Storage insect pest is a major factor for postharvest losses in pulses, and mungbean is highly susceptible to storage pests. However, mungbean CWRs like *V. umbellata, V. minima, V. vexillata, V. reticulata, V. oblongifolia, V. luteola, V. reflexo-pilosa, V. umbellata, V. minima,* and *V. radiata var. sublobata* are identified as resistant for major storage pests like cowpea weevil (*Callosobruchus maculatus*), adzuki bean weevil (*C. chinensis*), and storage weevil (*Callosobruchus analis*) (Fujii and Miyazaki 1987; Tomooka et al. 1992; Tomooka et al. 2000; Kashiwaba et al. 2003). *V. umbellata* and *V. glabrescens* are reported to possess photo-thermo–insensitivity (Pratap et al. 2014b) a very much important trait for expanding mungbean cultivation in non-traditional areas and crop rotations.

Recently, it was realized that mungbean varietal genetic base is very narrow as very limited variability is used in mungbean varietal development programs. The pedigree information of most of the breeders' varieties released indicate that varieties are being bred using breeders' varieties, and only few of them are released using new sources of germplasm. Evaluation of entire collections of mungbean germplasm at ICAR-NBPGR including global mungbean mini-core developed by World Vegetable Center (unpublished data) during *kharif* 2016 and 2018 indicated that only a few of the accessions were resistant to MYMD (the most devastating disease of mungbean) within cultivated gene pool of mungbean.

Table 2.4 *Vigna* species and their distribution in Indian subcontinent

Species	Indian collections	Distribution (Indian states)
V. aconitifolia	2,629	Rajasthan, Gujarat, Odisha, Haryana, Maharashtra
V. adenantha	1	Coastal areas along the banks of backwaters, Kerala
V. angularis var. nipponensis	9	Arunachal Pradesh, Mizoram, Nagaland
V. capensis	11	Eastern and Western Himalaya
V. dalzelliana	65	Karnataka, Kerala
V. hainiana	16	Madhya Pradesh, Himachal Pradesh, Maharashtra
V. indica	–	Gujarat, Karnataka, Madhya Pradesh, Maharashtra, and Rajasthan
V. khandalensis	12	Maharashtra
V. konkanensis	–	Maharashtra
V. marina	3	Andaman and Nicobar islands, Kerala
V. minima	6	Andhra Pradesh, Goa, Gujarat, Rajasthan
V. mungo var. silvestris	20	Goa, Karnataka, Kerala, Madhya Pradesh, Maharashtra, Odisha, Rajasthan, Tamil Nadu
V. nepalensis	3	Nagaland
V. pilosa	18	Kerala, Karnataka
V. radiata var. setulosa	11	Kerala, Maharashtra, West Bengal
V. radiata var. *sublobata*	282	Andhra Pradesh, Goa, Himachal Pradesh, Karnataka, Kerala, Madhya Pradesh, Maharashtra, Odisha, Rajasthan, Tamil Nadu
V. sahyadriana	–	Northern Western Ghats (Maharashtra)
V. stipulacea	6	Tamil Nadu, Kerala, Madhya Pradesh, Chhattisgarh, Maharashtra, Odisha, Rajasthan, Tamil Nadu
V. subramaniana	–	Himachal Pradesh, Kerala, Punjab
V. trilobata	182	Andhra Pradesh, Karnataka, Kerala, Rajasthan, Tamil Nadu
V. trinervia	5	Odisha
V. trinervia var. bourneae	30	Goa, Karnataka, Tamil Nadu
V. umbellata	2,933	Arunachal Pradesh, Karnataka, Assam, Meghalaya, Nagaland, Himachal Pradesh, Uttarakhand, Jharkhand, West Bengal
V. vexillata	115	Andhra Pradesh, Goa, Himachal Pradesh, Kerala, Maharashtra
V. wightii	4	Kerala

Information not available in National Genebank portal (http://pgrportal.nbpgr.ernet.in)

However, recent developments in mungbean genomics and use of wild *Vigna* CWRs in pre-breeding programs are good sign for the crop. Mungbean varieties are being bred utilizing cross-compatible *Vigna* CWRs. HUM 1, Pant Moong 4, IPM99-125, IPM 205–7, and IPM 4094 are few recently released varieties which were developed from *Vigna radiata* × *Vigna mungo* crosses (Pratap et al. 2014a). There are some other *Vigna* species like *V. umbellata*, *V. glabrescens*, *V. trilobata*, *V. radiata* var. *sublobata*, *V. mungo* var. *sylvestris*, etc., which are currently being used in mungbean varietal development programs, but till now only limited success could be achieved.

2.8 Mungbean Genomic Resources and Their Importance

Genomics tools and genomic resources have become very essential part of crop improvement and genetic resources management programs. Since the last decade, there has been tremendous development in genomics technologies and these tools are helping in identifications of genes/QTLs for all kind of traits, introgression of traits, shortening of breeding cycles, development of new and ideal plant types, development of new variations through utilizing alien species or through mutational approaches, etc. Similarly, the genomics is playing great role in plant germplasm management. For example, DNA fingerprinting and bar coding of varieties and other novel germplasm are using set of molecular markers which helps in avoiding misuse of breeders' and farmers' material. Genotyping of conserved genebank material helps in identifying duplicates and saves waste of resources in germplasm maintenance. Diversity analysis of on-farm germplasm across the regions or globes and comparison with the conserved genebank collections helps in making strategy for future collections. There are several such applications of genomics where it is playing complementary roles in crop improvement and germplasm management.

In addition to nutritional qualities, certain traits of mungbean like small genome size, short life cycle, self-pollinating, and close genetic relationship with many other legume species make it a suitable model organism for genetic studies (Kim et al. 2015). Complete de novo genome sequencing of cultivated mungbean (*V. radiata* var. *radiata, VC1973A*) (Kang et al. 2014) and its wild relative (*V. radiata* var. *sublobata* TC1966) and de novo assembly of RNA-seq data of 22 accessions of other 18 *Vigna* species which was completed during 2014 itself highlights the importance of the mungbean crop. Not only the genomic DNA information but cytoplasmic genomes of mungbean were also decoded. Sequencing of chloroplast genome was done by Tangphatsornruang et al. (2009) while mitochondrial genome was sequenced by Lin et al. (2016). Once the whole genome sequencing (WGS) and transcriptome sequence data are available, genetic and genomic studies become easier. The genomic sequence information becomes the raw material for several studies like genome annotations, genome-wide association mapping (GWAS), development of genome-wide DNA markers, development of saturated linkage map, gene tagging, identification of other genomic information like small RNAs, microRNAs, transposons, etc. WGS of other related *Vigna* species like *V. unguiculata* (Cowpea Modern Breeding Consortium) and *V. angularis* (Kang et al. 2015) can further fasten comparative genomics studies in mungbean. Annotation of transcriptome sequences for functional genes has been carried out in mungbean (Moe et al. 2011; Gupta et al. 2014; Chen et al. 2015), and DNA sequence-based markers like SNPs and EST-SSRs were developed. Earlier to advancement in genome sequencing technologies, several DNA-based molecular markers were also developed (Kaga et al. 2000; Barkley et al. 2008), and they are still being used particularly which are linked to a trait of interest (Schafleitner et al. 2016). These markers were also used in making linkage mapping, and markers were linked to loci governing important traits like seed weight, seed coat color, resistance for powdery mildew, YMV, bruchids, *Cercospora* leaf spot (Kim et al. 2015). Recent update on *Vigna radiata* in NCBI database indicates that there are three assemblies for three genotypes viz. VC1973A, RIL59, and Kamphaeng Saen 1; however, only one (VC1973A) assembly was converted to discrete linkage groups of the mungbean genome. There are total 30,060 annotated genes, 49,192 identified proteins, and 135,798 SNPs available in the database.

2.9 Future Prospects and Challenges

Mungbean is one of the highest priced pulse crops. The cultivation area is consistently increasing across the globe. However, potential yield of the crop could not be realized due to its

highly prone nature toward several devastating diseases, insect pests, and abiotic stresses like waterlogging, low moisture, and terminal heat in summer mung. Thermo- and photo-sensitivity is another major concern. Several superior varieties have been bred, but the process of breeding has narrowed the genetic base of the cultivated mungbean gene pool. Present germplasm screening studies show that resistance sources for disease like MYMD are not available in entire mungbean germplasm. Now broadening the genetic base along with continuing traditional breeding programs has become a challenge for mungbean crop improvement programs. The rich genetic resources of mungbean crop wild relatives like *V. umbellata, V. trilobata, V. glabrascens, V. radiata* var. *sublobata, V. mungo* var. *sylvestris, V. aconitifolia, V. marina,* etc., can play a very important role in the crop improvement. Conserved diversity, genomic resources, and advanced genomic tools are of immense importance in achieving the potential yield. Focus is on targeted germplasm collection based on gap analysis, geo-referencing of all the indigenous germplasm/superimposing it with soil and climate maps and generation of robust cores based on high-throughput genomic resources and phenotypic traits.

References

Abna F, Golam F, Bhassu S (2012) Estimation of genetic diversity of mungbean (*Vigna radiata* L. Wilczek) in Malaysian tropical environment. Afr J Microbiol Res 6:1770–1775

Akhtar KP, Sarwar G, Abbas G, Asghar MJ, Sarwar N, Shah TM (2011) Screening of mungbean germplasm against *Mungbean yellow mosaic virus* and its vector *Bemisia tabaci*. Crop Prot 30:1202–1209

Arora RK (1988) The Indian gene centre. Priorities and prospects for collection. In: Paroda RS, Arora RK, Chandel KPS (eds) Plant genetic resources: Indian perspectives. NBPGR, New Delhi, p 545

Barkley NA, Wang ML, Gillaspie AG, Dean RE, Pederson GA, Jenkins TM (2008). Discovering and verifying DNA polymorphisms in a mung bean [*V. radiata* (L.) R. Wilczek] collection by EcoTILLING and sequencing. BMC Res Notes 1:28

Bisht IS, Mahajan RK, Patel DP (1998a) The use of characterization data to establish the Indian mungbean core collection and assessment of genetic diversity. Genet Res Crop Ev 127–133

Bisht IS, Mahajan RK, Kawalkar TG (1998b) Diversity in greengram (*Vigna radiata* (L.) Wilczek) germplasm collection and its potential use in crop improvement. Ann Appl Biol 132:301–312

Bose RD (1932) Studies in Indian pulses. IV Mung or green gram (*Phaseolus aureus* Roxb). Indian J Agric Sci 2:607–624

Chandel KPS, Lester RN, Starling RJ (1984) The wild ancestors of urid and mung beans (*Vigna mungo* (L.) Hepper and *V. radiata* (L.) Wilczek). J Linn Soc 89(1):85–96

Chankaew S, Somta P, Sorajjapinun W, Srinives P (2011) Quantitative trait loci mapping of Cercospora leaf spot resistance in mungbean, *Vigna radiata* (L.) Wilczek. Mol Breed 28(2):255–264

Chattopadhyay K, Bhattacharya S, Mandal N, Sarkar HK (2008) PCR-based characterization of mung bean (*Vigna radiata*) genotypes from Indian subcontinent at intra-and inter-specific level. J Plant Biochem Biot 17:141–148

Chen H, Wang L, Wang S, Liu C, Blair MW, Cheng X (2015) Transcriptome sequencing of mung bean (*Vigna radiata* L.) genes and the identification of EST-SSR markers. PLOS One 10:e0120273

Frankel OH (1984) Genetic perspectives of germplasm conservation. In: Arber WK, Llimensee K, Peacock WJ, Starlinger P (eds) Genetic manipulation: impact on man and society. Cambridge University Press, Cambridge, pp 161–170

Fujii K, Miyazaki S (1987) Infestation resistance of wild legumes (*Vigna sublobata*) to azuki bean weevil, *Callosobruchus chinensis* (L.) (Coleoptera: Bruchidae) and its relationship with cytogenetic classification. Appl Entomol Zool 22:229–230

Ghafoor A, Zubair M, Malik BA, Iqbal SM (1992) Evaluation of selected germplasm of mungbean (*Vigna radiata* (L.) Wilczek). Pak J Bot 24:112–118

Gosal SS, Bajaj YPS (1983) Interspecific hybridization between *Vigna mungo* and *Vigna radiata* through embryo culture. Euphytica 32:129–137

Gupta SK, Bansal R, Gopalakrishna T (2014) Development and characterization of genic SSR markers for mungbean (*Vigna radiata* (L.) Wilczek). Euphytica 195:245–258

Hakim L (2016) Variability and correlation of agronomic characters of mungbean germplasm and their utilization for variety improvement program lukman hakim. Indones J Agri Sci 9:24–28

Iqbal U, Iqbal SM, Afzal R, Jamal A, Farooq MA, Zahid A (2011) Screening of mungbean germplasm against *Mungbean yellow mosaic virus* (MYMV) under field conditions. Pak J Phytopathol 23:48–51

Jackai LEN, Padulosi S, Ng Q (1996) Resistance to the legume pod borer, *Maruca vitrata* Fabricius, and the probable modalities involved in wild *Vigna*. Crop Prot 15:753–761

Jalaluddin M, Shaikh MAQ (1981) Evaluation of mungbean (*Vigna radiata* (L.) Wilczek) germplasm for

resistance to *Mungbean yellow mosaic virus*. SABRAO J 13:61–68

Kaga A, Ishii T, Tsukimoto K, Tokoro E, Kamijima O (2000) Comparative molecular mapping in *Ceratotropis* species using an interspecific cross between azuki bean (*Vigna angularis*) and rice bean (*V. umbellata*). Theor Appl Genet 100:207–213

Kang YJ, Kim SK, Kim MY, Lestari P, Kim KH, Ha BK, Shim S et al (2014) Genome sequence of mungbean and insights into evolution within *Vigna* species. Nature Commun 5:6443

Kang YJ, Satyawan D, Shim S et al (2015) Draft genome sequence of adzuki bean (*vigna angularis*). Sci Rep 5:8069

Kashiwaba K, Tomooka N, Kaga A, Han OK, Vaughan DA (2003) Characterization of resistance to three bruchid species (*Callosobruchus* spp., Coleoptera, Bruchidae) in cultivated rice bean (*Vigna umbellata*). J Econ Entomol 96:207–213

Kawalkar TG, Bisht IS, Mahajan RK, Patel DP, Gupta PN, Chandel KPS (1996) Catalogue on greengram (*Vigna radiata* L. Wilczek) germplasm. NBPGR, New Delhi, pp 130

Kim SK, Nair RM, Lee J, Lee SH (2015) Genomic resources in mungbean for future breeding programs. Front Plant Sci 6:626

Lambrides CJ, Godwin I (2007) "Mungbean." In: Kole C (ed) Genome mapping and molecular breeding in plants pulses, sugar and tuber crops, vol 3. Springer, Berlin, pp 69–90

Lin CP, Lo HF, Chen CY, Chen LFO (2016) The complete mitochondrial genome of mungbean (*Vigna radiata* var. *radiata,* NM92) and a phylogenetic analysis of crops in angiosperms. Mitochondrial DNA Part A 27:3731–3732

Maxted N, Mabuza-Dlamini P, Moss H, Padulosi S, Jarvis A, Guarino L (2004) An ecogeographic survey: African Vigna. In: Systematic and ecogeographic studies of crop genepools, vol 10. International Plant Genetic Resources Institute, Rome, Italy

Moe KT, Chung JW, Cho YI, Moon JK, Ku JH, Jung JK, Park YJ (2011) Sequence information on simple sequence repeats and single nucleotide polymorphisms through transcriptome analysis of mungbean. J Integr Plant Biol 53:63–73

Mukhtar T, Arooj M, Ashfaq M, Gulzar A (2017) Resistance evaluation and host status of selected green gram germplasm against *Meloidogyne incognita*. Crop Prot 92:198–202

Nair RM, Schafleitner R, Kenyon L, Srinivasan R, Easdown W, Ebert AW, Hanson P (2013) Genetic improvement of mungbean. SABRAO J Breed Genet 44:177–190

Ogundiwin EA, Thottappilly G, AkenOva ME, Ekpo EJA, Fatokun CA (2002) Resistance to cowpea mottle carmovirus in *Vigna vexillata*. Plant Breed 121:517–520

Pandiyan M, Ramamoorthi N, Ganesh SK, Jebaraj S, Pgarajan P, Balasubramanian P (2008) Broadening the genetic base and introgression of MYMV resistance and yield improvement through unexplored genes from wild relatives in mungbean. Plant Mut Rep 2: 33–43

Pandiyan M, Senthil N, Suersh R, Chakravarthy N, Packiaraj D, Jagadeesh S (2012) Interspecific hybridization of *Vigna radiata* × *Vigna trilobata*. Euphytica 35:1017–1022

Poehlman JM (1991) The Mungbean. Oxford and IBH publishers, New Delhi

Pratap A, Malviya N, Tomar R et al (2014) *Vigna.* In: Pratap A, Kumar J (eds) Alien gene transfer in crop plants, achievements and impacts, vol 2. Springer, New York, pp 163–189. https://doi.org/10.1007/978-1-4614-9572-7_8

Pratap A, Basu PS, Gupta S, Malviya N, Rajan N, Tomar R, Singh NP (2014b) Identification and characterization of sources for photo- and thermo-insensitivity in Vigna species. Plant Breed 133:756–764

Rahim MA, Mia AA, Mahmud F, Zeba N, Afrin KS (2010) Genetic variability, character ASSOCIATION and genetic divergence in mungbean (*Vigna radiate L.* Wilczek). Plant Omics 3:1

Raje RS, Rao SK (2002) Screening of mungbean (*Vigna radiata* L. wilczek) germplasm for yellow mosaic virus, Cercospora leaf spot and powdery mildew. Legume Res 25:99–104

Rana JC, Gautam NK, Gayacharan Singh M, Yadav R, Tripathi K, Yadav SK, Bhardwaj R (2016) Genetic resources of pulse crops in India: an overview. Indian J Genet Pl Br 76:420–436

Reddy KS, Pawar SE, Bhatia CR (1987) Screening for powdery mildew (*Erysiphae polygoni* DC.) resistance in mungbean (*Vigna radiata* (L.) Wilczek) using excised leaves. Proc Plant Sci 97:365–369

Sangiri C, Kaga A, Tomooka N, Vaughan D, Srinives P (2008) Genetic diversity of the mungbean (*Vigna radiata*, Leguminosae) genepool on the basis of microsatellite analysis. Aust J Bot 55:837–847

Schafleitner R, Nair R, Rathore A, Wang YW, Lin CY, Chu SH, Lin PY, Chang JC, Ebert AW (2015) The AVRDC—The World Vegetable Center mungbean (*Vigna radiata*) core and mini core collections. BMC Genom 16:344

Schafleitner R, Huang SM, Chu SH, Yen JY, Lin CY, Yan MR, Long-fang OC et al (2016) Identification of single nucleotide polymorphism markers associated with resistance to bruchids (*Callosobruchus* spp.) in wild mungbean (*Vigna radiata* var. *sublobata*) and cultivated *V. radiata* through genotyping by sequencing and quantitative trait locus analysis. BMC Plant Biol 16:159

Shad N, Mughal SM, Farooq K, Bashir M (2006) Evaluation of mungbean germplasm for resistance against *Mungbean yellow mosaic begomovirus*. Pak J Bot 38:449

Shanmugasundaram S, Keatinge JDH, Hughes J (2009). Counting on beans: mungbean improvement in Asia. In: Spielman DJ, Pandya-Lorch R (eds) Millions fed: proven successes in agricultural development.

International Food Policy Research Institute, Washington, DC, pp 103–108

She CW, Jiang XH, Ou LJ, Lui J, Long KL, Zhang LH, Duan WT, Zhao W, Hu JC (2015) Molecular cytogenetic characterization and phylogenetic analysis of the seven cultivated *Vigna* species (Fabaceae). Plant Biol 17:268–280

Singh CM, Mishra SB, Anil P, Madhuri A (2014) Morphological characterization and discriminant function analysis in mungbean [*Vigna radiata* (L.) Wilczek] germplasm. Electron J Plant Breed 5:87–96

Singh M, Bisht IS, Sardana S, Gautam NK, Hussain Z, Gupta S, Singh BB, Dwivedi NK (2006) Asiatic *Vigna*. In: Dhillon BS, Saxena S, Agrawal A, Tyagi RK (eds) Plant genetic resources: foodgrain crops. Narosa Publishing House, ISPGR, ICAR-NBPGR, New Delhi, pp 275–301

Singh DP, Singh BB, Pratap A (2016) Genetic improvement of mungbean and urdbean and their role in enhancing pulse production in India. Indian J Genet Plant Breed 76:550–567

Smartt J (1985) Evolution of grain legumes III. Pulses in the genus *Vigna*. Exp Agric 21:87–100

Somta C, Somta P, Tomooka N, Ooi PC, Vaughan DA, Srinives P (2008) Characterization of new sources of mungbean (*Vigna radiata* (L.) Wilczek) resistance to bruchids, *Callosobruchus* spp. (Coleoptera: Bruchidae). J Stored Prods Res 44:316–321

Somta P, Ammaranan C, Ooi PAC, Srinives P (2007) Inheritance of seed resistance to bruchids in cultivated mungbean (*Vigna radiata*, L. Wilczek). Euphytica 155:47–55

Sudha M, Karthikeyan A, Nagarajan P, P Raveendran M, Senthil N, Pandiyan M, Angappan K, Ramalingam J, Bharathi M, Rabindran R, Veluthambi K, Balasubramanian P (2013) Screening of mungbean (*Vigna radiata*) germplasm for resistance to *Mungbean yellow mosaic virus* using agroinoculation. Can J Plant Pathol 35:424–430

Sudha M, Anusuya P, Mahadev NG, Karthikeyan A, Nagarajan P, Raveendran M, Balasubramanian P (2013b) Molecular studies on mungbean (*Vigna radiata* (L.) Wilczek) and ricebean (*Vigna umbellata* (Thunb.)) interspecific hybridisation for *Mungbean yellow mosaic* virus resistance and development of species-specific SCAR marker for ricebean. Arch Phytopath Plant Prot 46:503–517

Sudha M, Karthikeyan A, Shobhana VG, Nagarajan P, Raveendran M, Senthil N, Bharathi M (2015) Search for Vigna species conferring resistance to *Mungbean yellow mosaic virus* in mungbean. Plant Genet Res 13:162–167

Takahashi Y, Somta P, Muto C, Iseki K, Naito K, Pandiyan M et al (2016) Novel genetic resources in the genus *Vigna* unveiled from gene bank accessions. PLOS One 11:e0147568. https://doi.org/10.1371/journal.pone.0147568

Tangphatsornruang S, Sangsrakru D, Chanprasert J, Uthaipaisanwong P, Yoocha T, Jomchai N, Tragoonrung S (2009) The chloroplast genome sequence of mungbean (*Vigna radiata*) determined by high-throughput pyrosequencing: structural organization and phylogenetic relationships. DNA Res 17:11–22

Tantasawat P, Trongchuen J, Prajongjai T, Thongpae T, Petkhum C, Seehalak W, Machikowa T (2010) Variety identification and genetic relationships of mungbean and blackgram in Thailand based on morphological characters and ISSR analysis. Afr J Biotech 9:4452–4464

Tomooka NT, Isemura et al (2014) *Vigna* species. Broadening the genetic base of grain legumes. Springer, pp 175–208

Tomooka N, Kaga A, Isemura T, Vaughan DA (2011) *Vigna*. In: Kole C (ed) Wild crop relatives: genomic and breeding resources. Legume crops and forages, chapter 15, pp 291–311

Tomooka N, Kaga A, Vaughan DA (2006) The Asian *Vigna* (*Vigna* subgenus *Ceratotropis*) biodiversity and evolution. In: Sharma AK, Sharma A (eds) Plant genome: biodiversity and evolution. Part C: phanerogams (angiosperms–dicotyledons), vol 1. Science Publisher, Enfield, New Jersey, pp 87–126

Tomooka N, Kashiwaba K, Vaughan DA, Ishimoto M, Egawa Y (2000) The effectiveness of evaluating wild species: searching for sources of resistance to bruchid beetles in the genus *Vigna* subgenus Ceratotropis. Euphytica 115:27–41

Tomooka N, Lairungreang C, Nakeeraks P, Egawa Y, Thavarasook C (1992) Development of bruchid-resistant mungbean line using wild mungbean germplasm in Thailand. Plant Breed 109:60–66

Vavilov NI (1926) Studies on the origin of cultivated plants. Bull Appl Botany Genet Plant Breed (Leningrad) 16:1–248 (In Russian English summary pp 139–248)

Yimram T, Somta P, Srinivas P (2009) Genetic variation in cultivated mungbean germplasm and its implication in breeding for high yield. Field Crops Res 112: 260–266