Breeding Progress and Future Challenges: Biotic Stresses

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Abstract

Mungbean is a short-duration legume crop cultivated in South Asia, Southeast Asia and Australasia. Its cultivation is rapidly spreading to other parts of the world. Insect pests and diseases are the major constraints in increasing the productivity of mungbean crop. The important diseases in mungbean include mungbean yellow mosaic, anthracnose, powdery mildew, Cercospora leaf spot, dry root rot, halo blight, bacterial leaf spot and tan spot. The major insect-pests of mungbean are stem fly, thrips, aphids, whitefly, pod borers and bruchids. Development of host plant resistance to insect pests and diseases in mungbean by breeding for resistance is an alternative, economical and environment-friendly approach. Though breeding for resistance to insect pests and diseases has been extensively studied in mungbean, the success rate in stabilizing the resistance has been less due to the development of insect biotypes, new strains in pathogens and the environmental interactions. This chapter covers the insect and disease resistance sources in mungbean, resistant traits, the genetic basis of resistance and different breeding methods involved in breeding for insect and disease resistance.

5.1 Introduction

The Asiatic *Vigna* species belong to the subgenus *Ceratotropis* of which 4 species are globally recognized for their high agronomic importance. These include *V. radiata* (L.) Wilczek (green gram or mungbean); *V. mungo* (L.) Hepper (black gram or urdbean); *V. angularis* (W) Ohwi and Ohashi (adzuki bean); and *V. aconitifolia* (Jacq.) (moth bean) (Pratap et al. 2015); besides, *V. umbellata* (Thumb.) Ohwi and Ohashi (rice-bean) and *V. glabrescens* Marechal, Mascherpa and Stainier (tua pea) are of little importance. Among these, mungbean, also known as green gram, is economically the most important as indicated by its area, production and consumption at the global level (Kumar et al. 2006; Tomooka et al. 2007; Nair et al. 2013). Mungbean is a warm season, short-day plant that has been grown in India since ancient times. Besides India, it is widely grown in South Asia and Southeast Asia and also in Africa, South America and Australia and serves as a major source of

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dietary protein for the vast majority of vegetarian people (AVRDC 2012; Clarry 2016). As of now, mungbean is grown over an area of 6.0 million ha globally with the production of 3.5 million tonnes. However, despite an average yield potential of >1.2 t/ha for most of the released mungbean varieties, the average productivity is still <0.7 t/ha in India and <1.0 t/ha in several other mungbean-growing countries (Pratap et al. 2019). Several factors such as biotic and abiotic stresses, environmental fluctuations and high genotype × environment interaction affect the yield of mungbean. Among the biotic stresses, diseases alone can lead to a yield reduction of 10–100%, while weeds may cause 50–90 and insect pests up to 20–55% yield loss (Rana et al. 2016), depending upon the stage of the crop, the severity of the stress and prevailing environmental factors. To stabilize the mungbean production and improve its productivity, it is important to develop the cultivars that are either resistant to and/or withstand the insect and disease pressure. Advanced technologies such as genomics, proteomics and metabolomics have paved way for the in-depth studies in the genetic basis of insect–plant and pathogen–plant interactions, which in turn can be applied to design effective crop improvement strategies.

5.2 Major Biotic Stresses

Among the biological constraints, diseases impart the most serious constraints, which may limit its productivity besides affecting the physical quality of seeds, leading them unusable. Mungbean is prone to several viral, fungal and bacterial diseases (Khattak et al. 2000; Pandey et al. 2018; Noble et al. 2019) (Table 5.1). Among the viral diseases, mungbean yellow mosaic disease (MYMD) is the most important disease of mungbean (Singh and De 2006; Kitsanachandee et al. 2013), caused by Begomovirus and transmitted by whitefly. The MYMD (Fig. 5.1a) on *Vigna* species was first time reported by Mclean (1941) from western India in the late 1940s in lima bean and later in mungbean from the Indian Agricultural Research Institute, New Delhi (Naraini 1960), followed by Pakistan (Ahmad and Harwood 1973). From India, 32–78% yield reduction in mungbean grains has been reported (Khattak et al. 2000). However, yield reduction was higher (100%) at early growth stages (Kitsanachandee et al. 2013). Urdbean leaf crinkle disease caused by urdbean leaf crinkle virus (ULCV) is an emerging viral disease of mungbean in South Asia and Southeast Asia (Singh et al. 1988).

Although 35 fungal diseases are reported to affect mungbean globally, only very few of them are widespread and economically important. Fungal diseases (Fig. 5.1b–e) of common occurrence are Cercospora leaf spot (CLS) [*Cercospora* spp.], powdery mildew (*Erysiphe polygoni* DC, *Podosphaera fusca* (Fr.) U. Braun and Shishkoff), dry root rot and Macrophomina blight [*Macrophomina phaseolina* (Tassi) Goid], anthracnose (*Colletotrichum* sp.), Rhizoctonia root rot and web blight (*Rhizoctonia solani* Kuhn) (Singh et al. 2011; Pandey et al. 2018). Bacterial diseases such as halo blight (*Pseudomonas savastanoi* pv. *phaseolicola*) and tan spot (*Curtobacterium flaccumfaciens* pv. *flaccumfaciens*) (Fig. 5.1f, g) are economically the most significant diseases of mungbean in Australia (Ryley and Tatnell 2011). Bacterial leaf spot caused by *Xanthomonas campestris* pv. *Vigna radiata* is prevalent in India (Thakur et al. 1977). All the diseases together can cause significant yield losses of up to 10–100% (Rana et al. 2016). All bacterial pathogens are seed-borne and can persist in stubbles, and varietal resistance is recognized as the cornerstone of integrated disease management (Noble et al. 2019). Previously thought to be restricted to Australia, recent reports indicate that their distribution may be more widespread (Sun et al. 2017).

Insect pests are one of the major constraints in mungbean production and take a heavy toll on the yield. Insect pests attack different parts of the mungbean plant including roots, shoots, flowers and pods at different growth stages. The damage by insect pests is either direct, where damage is caused by direct feeding by the insects such as pod borers, thrips, aphids and/or indirect, where insects act as vectors of some serious diseases

Table 5.1 Characteristic symptoms and distribution of common fungal and bacterial diseases of mungbean

Disease	Causal pathogen(s)	Characteristic symptoms	Distribution
Fungal diseases			
Cercospora leaf spot	*Cercospora cruenta* Sacc. (*Mycosphaerella cruenta* Latham), *C. canescens* Ell. and Martin, C. kikuchii Matsumato and Tomoyasum *(M. phaseoli) C. dolichi* Ell. and Evr *C. caracallae* (Speg.) Greene	Small leaf spots (1–5 mm) with brown to greyish centres and reddish border	Taiwan (Hartman et al. 1993), Thailand (Wongpiyasatid et al. 1999), India (Zhimo et al. 2013), Pakistan (Iqbal et al. 2004)
Powdery mildew	*Erysiphe polygoni* DC., *Podosphaera fusca*	White powdery coating on leaves, stems and pods	Australia (Ryley and Tatnell 2011), Taiwan (Hartman et al. 1993), Thailand (Kasettranan et al. 2010), India (Mandhare and Suryawanshi 2008)
Anthracnose	*Colletotrichum lindemuthianum* (Sacc. and Magn.) Bri. and Cav. (*Glomerella lindemuthianum* (Sacc. and Magn.) Shear) *C. Capsici* (Syd.) Butler and Bisby, *C. dematinum* (Pers. ex Fr.) *Grov., C. truncatum* (schw.) Andrus and Moore, *C. graminicola (*Ces.) Wilson	Circular, brown, sunken spots with dark centres and bright red orange margin leaves	India (Kaur et al. 2011), Pakistan (Bashir et al. 1985)
Dry root rot and macrophomina blight	*Macrophomina phaseolina* (Tassi) Goid (*Rhizoctonia bataticola* (Taub) Butler)	Dark brown patch on stem with black dot-like sclerotia and brown pycnidia	India (Choudhary et al. 2011), Pakistan (Khan and Shuaib 2007)
Rhizoctonia root rot and web blight	*Thanatephorus cucumeris* (Frank) *Donk.* (*Rhizoctonia solani* Kuhn.)	Necrotic small circular brown spots, fungal hyphae are seen spreading like spider web on the affected leaves with sclerotia	India (Reddy et al. 1992; Jhamaria and Sharma 2002)
Alternaria leaf spot	*Alternaria alternata* (Fr.) Keissler	Leaf spots with concentric rings leading to 'shot holes'	India (Maheshwari and Krishna 2013)
Rust	*Uromyces appendiculatus* (Pers.) *Unger. Phakopsora pachyrhizi* Syd	Reddish brown pin head uredo pustules surrounded by yellow	India (Satyagopal et al. 2014)
Bacterial diseases			
Bacterial leaf spot	*Xanthomonas campestris* pv. *Vigna radiata* Dye, mungbean strain	Brown raised spots on both surfaces which later become necrotic, water-soaked or with translucent border	India (Thakur et al. 1977)
Halo blight	*Pseudomonas syringae pv. phaseolicola* (Burk.) Young Dye and Wilkie	Water-soaked spots surrounded by a greenish yellow halo	Australia (Noble et al. 2019), China (Sun et al. 2017), India (Patel and Jindal 1972)
Tan spot	*Curtobacterium flaccumfaciens* pv. *flaccumfaciens*	Papery brown lesions originating on the leaf margins and spreading inwardly	Australia (Diatloff and Imrie 2000)

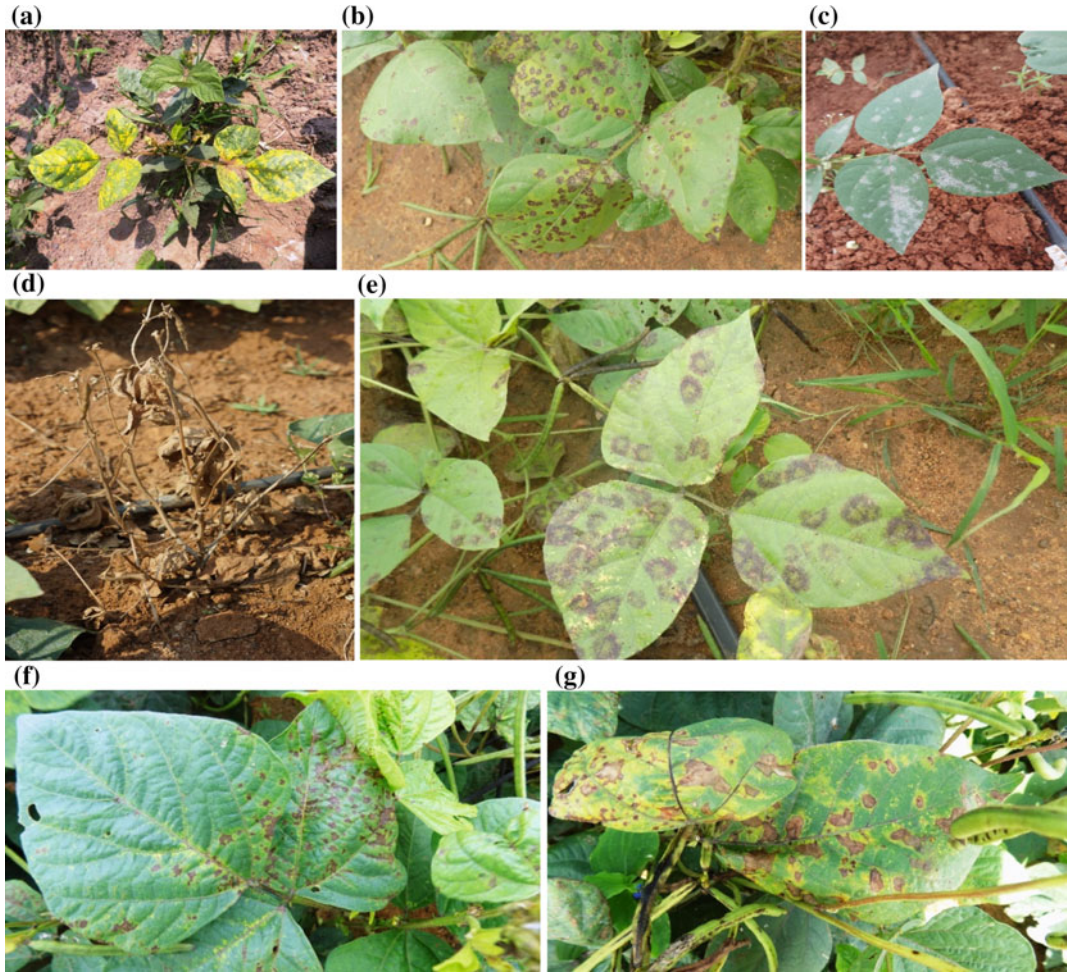

Fig. 5.1 **a**–**g** Symptoms of major diseases in mungbean. **a** mungbean yellow mosaic disease, **b** cercospora leaf spot, **c** powdery mildew, **d** dry root rot, **e** anthracnose, **f** halo blight and **g** tan spot. (from Pandey et al. 2018)

such as *mungbean yellow mosaic virus* (MYMV), *bean common mosaic virus* (BCMV) and *peanut bud necrosis virus* (PBNV). The common insect pests of mungbean along with the country of distribution are given in Table 5.2; Kooner and Chhabra (1980) enlisted 12 potential species of defoliators, pod borers, leafhoppers, aphids and stem borers which commonly affect mungbean in India. However, the major pests are stem fly, thrips, aphids, pod borers, whitefly and bruchids (Chiang and Talekar 1980; Kooner et al. 2006; Gentry 2010; Mbeyagala et al. 2017; Fig. 5.2a–e).

5.3 Plant Genetic Resources

Genetic resources in crop plants have evolved over thousands of years surviving all odds against nature and therefore provide a reservoir of useful genes for various survival traits. The wild and weedy relatives of crop plants grow in harsh environments and therefore provide an important source of adaptation-related traits and resistance to biotic and abiotic stresses. Therefore, their collection, evaluation, characterization, documentation and utilization in crop improvement are of

Table 5.2 Key insect pests of mungbean

Scientific name	Common name	Distribution and references
Madurasia obscurella Jacoby	Galerucid beetle	Australia (Gentry 2010), India (Kooner et al. 2006), Uganda (Mbeyagala et al. 2017)
Ophiomyia phaseoli (Tryon) *Melanagromyza sojae* (Zehntner)	Bean fly/Stem fly	Australia (Gentry 2010), Bangladesh (Islam et al. 1984; Rahman et al. 1981), India (Sahoo and Patnaik 1994; Kooner et al. 2006), Indonesia (Indiati et al. 2017), Pakistan (Khattak et al. 2004), South Africa (DAFF 2010), Taiwan (Chiang and Talekar 1980), Thailand (Srinives 1991), Uganda (Mbeyagala et al. 2017) India (Singh 1982), South Africa (DAFF 2010), Taiwan (Chiang and Talekar 1980), Thailand (Srinives 1991)
Bemisia tabaci (Gennadius)	Whitefly	Australia (Gentry 2010), Bangladesh (Rahman et al. 1981), India (Ganapathy and Durairaj 1995; Yadav and Singh 2006; Kooner et al. 2006), Indonesia (Indiati et al. 2017), Nigeria (Asawalam and Constance 2018), Pakistan (Khattak et al. 2004), Taiwan (AVRDC 1998), Thailand (Srinives 1991), Uganda (Mbeyagala et al. 2017)
Empoasca spp.	Green jassid	Australia (Gentry 2010), Bangladesh (Hossain et al. 2004), India (Sahoo and Patnaik 1994; Yadav and Singh 2006), Nigeria (Asawalam and Constance 2018), Taiwan (AVRDC 1998), Pakistan (Khattak et al. 2004), Thailand (Srinives 1991), Uganda (Mbeyagala et al. 2017), Indonesia (Indiati et al. 2017)
Polyphagotarsonemus latus (Banks)	Bean mite	India (Kooner et al. 2006; Duraimurugan and Tyagi 2014)
Aphis craccivora Koch	Black aphid	India (Sahoo and Patnaik 1994; Yadav and Singh 2006; Kooner et al. 2006; Swaminathan et al. 2012), Australia (Gentry 2010), Uganda (Mbeyagala et al. 2017), Thailand (Srinives 1991), Bangladesh (Hossain et al. 2004), South Africa (DAFF 2010), Ethiopia (Abate et al. 1982)
Acherontia styx (Westwood)	Til hawk moth	India (Das 1999; Kooner et al. 2006)
Spilosoma obliqua Walker	Bihar hairy caterpillar	India (Kooner et al. 2006), Bangladesh (Islam et al. 1984), Pakistan (Khattak et al. 2004), Uganda (Mbeyagala et al. 2017), Ethiopia (Abate et al. 1982)
Spodoptera litura (Fabricius)	Tobacco caterpillar	India (Kooner et al. 2006; Swaminathan et al. 2012), Bangladesh (Islam et al. 1984), Pakistan (Khattak et al. 2004), Indonesia (Marwoto 2008; Indiati et al. 2017)
Maruca testulalis (Geyer)	Spotted caterpillar	India (Kooner et al. 2006; Swaminathan et al. 2012), Australia (Gentry 2010), Uganda (Mbeyagala et al. 2017), Bangladesh (Rahman et al. 1981; Hossain et al. 2004), Thailand (Srinives 1991), Indonesia (Indiati et al. 2017), Ethiopia (Abate et al. 1982)
Moorei (Butler)	Red hairy caterpillar	India (Chhabra and Kooner 1998; Kooner et al. 2006; Swaminathan et al. 2012)
Anomis flava (Fab.)	Green semilooper	India (Swaminathan et al. 2012), Australia (Gentry 2010)
Ootheca bennigsen Weise *Ootheca mutabilis* (Sch.)	Bean foliage beetles	Uganda (Mbeyagala et al. 2017), Ethiopia (Abate et al. 1982)
Helicoverpa armigera (Hubner)	Gram pod borer	India (Kooner et al. 2006), Australia (Gentry 2010), Uganda (Mbeyagala et al. 2017), Bangladesh (Rahman et al. 1981; Hossain et al. 2004), Thailand (Srinives 1991), Ethiopia (Abate et al. 1982)

(continued)

Table 5.2 (continued)

Scientific name	Common name	Distribution and references
Megalurothrips spp. *Caliothrips indicus* (Bagnall)	Thrips	India (Duraimurugan and Tyagi 2014), Australia (Gentry 2010), Uganda (Mbeyagala et al. 2017), Pakistan (Khattak et al. 2004), Bangladesh (Rahman et al. 1981; Hossain et al. 2004), Taiwan (Chiang and Talekar 1980), Thailand (Srinives 1991), Indonesia (Indiati 2015; Indiati et al. 2017), India (Yadav and Singh 2006), Pakistan (Afzal et al. 2002)
Clavigralla gibbosa Spinola	Pod bug	India (Kooner et al. 2006; Swaminathan et al. 2012), Uganda (Mbeyagala et al. 2017), Thailand (Srinives 1991), Ethiopia (Abate et al. 1982)
Mylabris pustulata (Thunberg)	Blister beetle	India (Kooner et al. 2006; Swaminathan et al. 2012; Duraimurugan and Tyagi 2014), Uganda (Mbeyagala et al. 2017), Ethiopia (Abate et al. 1982)
Lampides boeticus Linnaeus	Blue butterfly	India (Swaminathan et al. 2012)
Nezara viridula (Lin.)	Green vegetable stink bug	India (Swaminathan et al. 2012), Australia, Uganda (Mbeyagala et al. 2017), Indonesia (Indiati et al. 2017), South Africa (DAFF 2010), Ethiopia (Abate et al. 1982)
Anoplocnemis spp.	Giant coreid bug	Australia (Gentry 2010), Uganda (Mbeyagala et al. 2017), Ethiopia (Abate et al. 1982)
Riptortus spp.	Brown bean bug	India (Swaminathan et al. 2012), Australia (Gentry 2010), Uganda (Mbeyagala et al. 2017), Indonesia (Indiati et al. 2017)
Creontiades pacificus (Stål)	Brown mirid	Uganda (Mbeyagala et al. 2017), Australia (Gentry 2010),
Megacopta cribraria (Fab.)	Kudzu bug	Indonesia (Indiati et al. 2017)
Callosobruchus maculatus (Fab.) *Callosobruchus chinensis* L.	Stored pests—bruchids	India (Swaminathan et al. 2012), Uganda (Mbeyagala et al. 2017), Australia (Gentry 2010), South Africa (DAFF 2010), Ethiopia (Abate et al. 1982), Taiwan (Fernandez and Talekar 1990)

utmost importance. Globally, the mungbean germplasm collections are maintained at different places including Indian Council of Agricultural Research (ICAR)-NBPGR; the University of the Philippines; The World Vegetable Center (erstwhile Asian Vegetable Research and Development Center, AVRDC), Taiwan; the Institute of Crop Germplasm Resources of the Chinese Academy of Agricultural Sciences; and the Plant Genetic Resources Conservation Unit of the University of Georgia, USA (Ebert et al. 2013). The current global holdings of mungbean include 24918 accessions among which 4104 accessions are maintained at ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR) (Singh et al. 2017). Simultaneously, >1800 accessions including 193 wild accessions are also maintained in medium-term storage facility of ICAR-Indian Institute of Pulses Research, Kanpur. Several collections of other *Vigna* species are also maintained at ICAR-NBPGR which can be useful genetic resources for mungbean improvement programme through distant hybridization. Table 5.3 provides the details of such germplasm resources available at ICAR-NBPGR genebank.

5.4 Sources of Resistance to Diseases

A number of reports are available which have identified sources of resistance against MYMD of mungbean (Manivannan et al. 2001; Pathak and Jhamaria 2004; Kumar et al. 2006; Kaur et al.

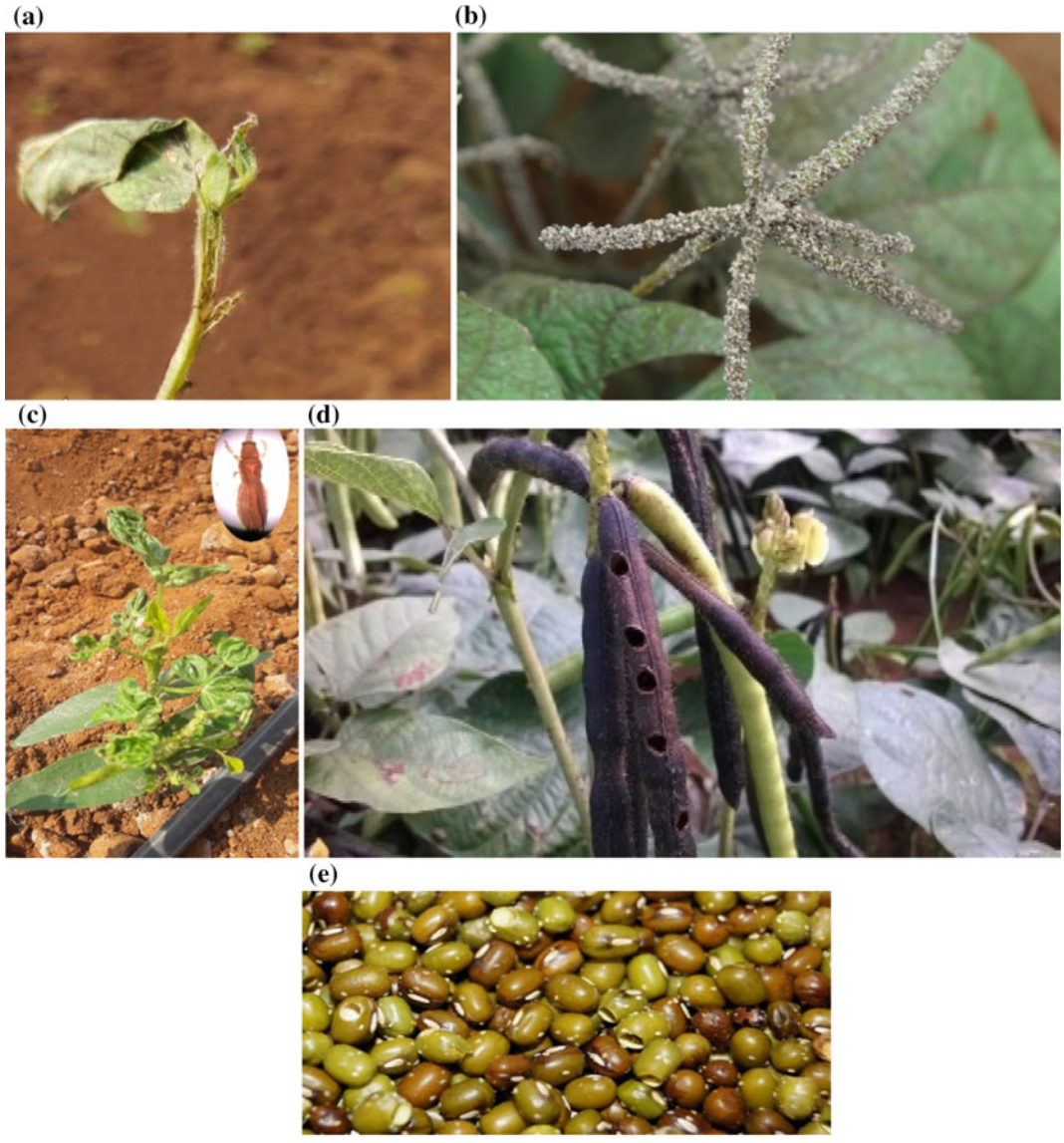

Fig. 5.2 **a**–**e** Damage by major insect pests in mungbean. **a** stem fly, **b** cowpea aphid, **c** seedling thrips, **d** pod borer and **e** bruchids

2007; Yadav and Brar 2010; Iqbal et al. 2011; Zhimo et al. 2013; Suman 2015). Mungbean lines ML 109, ML 111, ML 161, LM 214 were initially reported as resistant to MYMD (Sandhu 1978). Later, Singh (1982) reported that out of 777 lines screened, 22 were highly resistant to this disease. Rajarathinam et al. (1990) also reported Vamban 1 as highly resistant to this disease. Under the All India Coordinated Research Project on MULLaRP (AICRP on MULLaRP) crops, a large number of lines were screened against MYMD and several lines including Pant Mung 3, Pant Mung 2, MN 303, DPU 88-31, PDM 54 and DU 3 were reported as resistant (Singh et al. 2002). Sharma and Dubey (1984) screened a large number of mungbean lines against ULCV and reported D 215, HPM 1, Madana 1, M 58, ML 12 and T44 as immune to this disease. Singh

Table 5.3 Plant genetic resources maintained in the genebank of ICAR-NBPGR

S. no.	Common name	Species	Indigenous collection (IC)	Exotic collection (EC)
1	Adzuki bean	*Vigna angularis*	89	98
2	Beach pea	*Vigna marina*	2	0
3	Black gram	*Vigna mungo*	2091	7
4	Black gram	*Vigna mungo* var. *mungo*	4	0
5	Cowpea	*Vigna catjang*	0	2
6	Cowpea	*Vigna sesquipedalis*	0	1
7	Cowpea	*Vigna sinensis*	0	19
8	Cowpea	*Vigna unguiculata*	2556	1062
9	Cowpea	*Vigna unguiculata* subsp. *cylindrical*	0	4
10	Cowpea	*Vigna unguiculata* subsp. *unguiculata*	4	0
11	Green gram	*Vigna radiata* var. *setulosa*	2	0
12	Moth bean	*Vigna aconitifolia*	1474	37
13	Mungbean	*Vigna radiata*	3387	534
14	Ricebean	*Vigna umbellata*	1883	144
15	Vigna	*Vigna* sp.	12	0
16	Wild black gram	*Vigna mungo* var. *silvestris*	16	0
17	Wild Vigna	*Vigna angularis* var. *nipponensis*	9	0
18	Wild Vigna	*Vigna bourneae*	4	0
19	Wild Vigna	*Vigna dalzelliana*	28	0
20	Wild Vigna	*Vigna hainiana*	6	0
21	Wild Vigna	*Vigna khandalensis*	1	0
22	Wild Vigna	*Vigna minima*	1	0
23	Wild Vigna	*Vigna nepalensis*	3	0
24	Wild Vigna	*Vigna pilosa*	3	0
25	Wild Vigna	*Vigna radiata* var. *sublobata*	227	0
26	Wild Vigna	*Vigna stipulacea*	6	0
27	Wild Vigna	*Vigna sylvestris*	1	0
28	Wild Vigna	*Vigna trilobata*	141	0
29	Wild Vigna	*Vigna trinervia*	2	0
30	Wild Vigna	*Vigna trinervia* var. *bourneae*	11	0
31	Wild Vigna	*Vigna vexillata*	107	1
32	Yard long bean	*Vigna unguiculata* subsp. *sesquipedalis*	88	1

Source www.genebank.nbpgr.ernet.in (accessed on 31.01.2019)

Table 5.4 Sources of resistance to major diseases in mungbean

Genotype/accession number	Country	References
Yellow mosaic disease		
IW 3390, EC 398897, TM-11-07, TM-11-34, PDM-139, IPM-02-03, IPM-02-14, Pusa-0672, Pusa-0871, CO-7 and MH-521	India	Reddy and Singh (1995); Mohan et al. (2014)
Powdery mildew		
LGG-460, Vaibhav, BPMR-145, TARM-18, Phule M-2003-3, Phule M- 2002-13, Phule M-2002-17, Phule M- 2001-3 and Phule M-2001-5	India	Mandhare and Suryawanshi (2008)
V2159, V4189, V4207, V4574, V4668, V4990 (resistant), R/HR: V3912, V4186 (resistant/highly resistant) V1104, V4631, V4658, V4662, V4717, V4883 (highly resistant)	Taiwan	Hartman et al. (1993)
R:M5-10 and M5-25	Thailand	Wongpiyasatid et al. (1999)
Cercospora leaf spot		
LGG-460, GM-02-08, GM-02-13 and GM-03-03, NM-98, 98-cmg-003, C2/94-4-42, NM-1, NM-2, 98cmg-018, BRM-188, CO-3, Basanti, PDM-11, BARI Mung-2 and VC3960-88	India	Haque et al. (1997)
V1471, V2757, V2773, V4718, V5036	Taiwan	Hartman et al. (1993)
M5-22 and M5-25	Thailand	Wongpiyasatid et al. (1999)
NCM 255-2, NCM 257-6, ML-267, NCM 251-1, NCM 259-2, NCM 251-13, NCM 257-2, NM-92, NCM 251-12, VC-3960-A88, NCM 257-10, NCM-209, Mung-6 C1/94-4-19, VC 3960-A89 (resistant) BRM-188, NM-98, C2/94-4-42, 98-cmg-003, NM-2, NM-1, 98cmg-018, Basanti, CO-3, PDM-11, VC3960-88, BARI Mung-2 (highly resistant)	Pakistan	Iqbal et al. (2004)
Urdbean leaf crinkle virus		
D 215, HPM 1, Madana 1, M 58, ML 12, T44, V 2182 and V 2294	India	Singh and Dubey (1982)
Dry root rot		
40504, NCM 257-5, 40457, NCM 251-4, 6368-64-72 (resistant) HR: NCM 252-10 and 40536 (highly resistant)	Pakistan	Khan and Shuaib (2007)

et al. (1988) reported AVRDC lines V 2182 and V 2294 as resistant to ULCV. Mungbean lines BPMR 1 and BPMR 115 were reported as resistant to powdery mildew by Singh and Gurha (2005). Mandhare and Suryawanshi (2008) identified resistance sources for powdery mildew, viz. Vaibhav, BPMR-145, TARM-18, Phule M-2003-3, Phule M-2002-13, Phule M-2002-17, Phule M-2001-3 and Phule M-2001-5. Hegde (1999) reported that four genotypes, viz. DHMC 9601, DHMC 9602, DHMC 9603 and DHMC 9604, were highly resistant to powdery mildew under natural epiphytotic conditions.

For other diseases, Yadav et al. (2014) reported mungbean genotype LGG-460 as highly resistant against CLS under disease epiphytotic conditions while GM-02-08, GM-02-13 and GM-03-03 were categorized as resistant. Haque et al. (1997) identified 12 genotypes, viz. NM-98, 98-cmg-003, C2/94-4-42, NM-1, NM-2, 98cmg-018, BRM-188, CO-3, Basanti, PDM-11, BARI Mung-2 and VC3960-88, that were highly resistant to Cercospora leaf spot. Table 5.4 describes the promising resistant lines of mungbean which can be used for transferring disease resistance.

5.5 Sources of Resistance to Insect Pests

Whitefly is the vector of MYMV in mungbean and causes indirect losses of 80–100% (Kitsanachandee et al. 2013; Nair et al. 2017). In addition to transmitting the MYMD, the direct

yield losses by whitefly in mungbean range between 17 and 71% (Chhabra and Kooner 1998; Mansoor-Ul-Hassan et al. 1998). In mungbean, various insect-resistant sources have been identified through a series of screening methods. Khattak et al. (2004) reported NM 92 as resistant to whiteflies. In another study, Yadav and Dahiya (2000) reported ML 803, ML 839, PDM 91-249 and PBM 5 as resistant sources against whitefly. Likewise, Kooner and Cheema (2007) identified ML 1265 and ML 1229 as highly resistant to this pest, and these lines have been extensively used as resistant sources in mungbean breeding programmes in India. The other genotypes reported as resistant to whitefly are TMB 36 and RMG 1004 (Singh and Singh 2014) and ML 1774 and ML 1779 (Cheema et al. 2015). These could contribute as important sources for mungbean breeding to whitefly resistance. Nymphs and adults of bean blossom thrips or flower thrips [*Megalurothrips distalis* (Karny)] cause heavy yield reduction of the crop by feeding on the pedicles and stigma of flowers (Chhabra and Kooner 1985a, b). Malik (1990) observed that summer mungbean genotypes SML 77, UPM 82-4 and Pusa 107 were resistant to *M. distalis* under natural as well as artificial screen house conditions. The cultivars Co 3, Co 4 and Co 5 were also reported to be less susceptible to thrips (Lal 1987). Chhabra (2001) reported mungbean genotypes PIMS 2, PIMS 3, CO 3, ML 5 and ML 337 as resistant to thrips. NM-92 has also been reported to be resistant to thrips in India and Pakistan (Khattak et al. 2004; Kooner et al. 2005). MH 3153 recorded the lowest number of thrips per leaf among eight advanced mungbean genotypes/cultivars in Pakistan (Nadeem et al. 2014).

For stem fly, *Ophiomyia* sp., Talekar (1990) reported 3 mungbean cultivars, viz. V2396, V3495 and V4281, as resistant. CIAT accessions such as G05253, G05776, G02005 and G02472 are highly resistant to bean fly and are recommended as the potential sources resistant to this pest (Abate 1990). For sweet potato whitefly, *Bemisia tabaci* (Gennadius), 43 accessions of mungbean were identified as resistant out of >2000 genotypes (Chhabra et al. 1980, 1988; Kooner 1998; Kooner and Cheema 2007; Kooner et al. 1977). In other studies, Kooner et al. (1997) reported the mungbean lines, viz. ML 1, ML 6, ML 7, P 290, P 292, P 131, P 293, P 325, P 364 and 11,148, as least susceptible to *B. tabaci* and MYMV.

Chhabra et al. (1988) reported ML 337, ML 423 and ML 438 cultivars as least susceptible to Jassids. For cowpea aphid, *Aphis craccivora* Koch JRUM 1, JRUM 11, JRUM 33, DPI 703, LAM 14-2, UPM 83-6 and UPM 83-10, Pusa 115, PDM 116 and ML 353 have been reported as resistant (Sahoo and Hota 1991). The cultivars J1, LM 11, P526 and Co3 are less susceptible to the pod borer, *Helicoverpa armigera* (Hub.) (Lal 1987). Further, Chhabra et al. (1988) reported that genotypes ML 337, ML 423 and ML 428 are resistant to this pest. Swarnalatha (2007) reported that LGG 505, ML 267, LGG 502, LGG 407, LGG 460 and LGG 485 were resistant to the legume pod borer, *M. testulalis*. Genotypes MGG 364, MGG 365 and MGG 363 have been reported as tolerant to Maruca pod borer damage (Choragudi et al. 2012).

Among the stored grain pests, bruchids, *Callosobruchus maculatus* (Fab.) and *C. chinensis* (L.) cause extensive damage to mungbean if not properly stored (Cheema et al. 2017). Initially, a wild mungbean accession TC1966 (*V. radiata* var. *sublobata* (Roxb.) Verdc.) was identified as a potential source of resistance to *C. maculatus* and *C. chinensis* (Fujii and Miyazaki 1987; Fujii et al. 1989; Lambrides and Imrie 2000; Kashiwaba et al. 2003). TC1966 was extensively used in breeding programmes for developing bruchid-resistant mungbean. More recently, two of the accessions (V2802 and V2709) were confirmed to possess complete resistance to *C. chinensis* and *C. maculatus* (Somta et al. 2007). Reduced survival and prolonged developmental period (30.5–31.5 days) of *C. chinensis* were recorded on four moderately resistant mungbean accessions, LM131, V1123, LM 371 and STY 2633 (Duraimurugan et al. 2014). In another study, the accessions KM-12-5 and P-S-16 were also reported as relatively resistant against *C. analis* (Soumia et al. 2017). Presently, a few mungbean accessions, viz. TC 1966, ACC41,

V2709, V2802, V1128, V2817, are the only known sources of bruchid resistance in mungbean (Sarkar et al. 2011; War et al. 2017). Resistance to bruchid has also been reported in wild black gram, *V. nepalensis*, and ricebean, *V. umbellata*, genotypes (Tomooka et al. 2000). After extensive research in breeding for insect resistance in mungbean, World Vegetable Center has been successful in developing improved mungbean lines with high levels of resistance to *C. maculatus* and *C. chinensis* (Nair et al. 2015).

5.6 Genetic Basis of Resistance

Besides studying the inheritance of resistance to various biotic and abiotic stresses, investigations have been carried out to understand the genetics of quantitative and qualitative traits in mungbean (Table 5.5). Kumar et al. (2006) thoroughly discussed the inheritance pattern of various economically important traits in this crop. The first report on genetic studies in mungbean was made by Bose (1932), who reported that the colour of

Table 5.5 Inheritance pattern, resistance genes/loci and associated markers of major mungbean diseases and storage pest

Disease	Resistant accessions	Resistant genes/alleles/locus	Linkage group	Associated marker	Inheritance pattern
Yellow mosaic disease	NM-6-68-2 KMG189, BM6, TM-99-37, BARI Mung-6, NM-12-1, VC6372 (45-8-1)	qYMIV1 and qYMIV2 qYMIV3, qYMIV4 and qYMIV5 qYMIV7	LG2, LG3 LG4, LG7 LG9A	CM9, CM815, MYMVR-683 (SCAR), CEDG180 cp02662, DMB-SSR158	Independent major recessive genes with additive effects (Akbar et al. 2018; Aski et al. 2014; Chen et al. 2015; Kitsanachandee et al. 2013; Alam et al. 2014). Monogenic inheritance of single recessive genes (Khattak et al. 2000; Sai et al. 2017)
Powdery mildew	V4718, RUM5, VC121OA VC6468-11-1A, V4758, V4785, VC3980A	Qpmr-1 Qpmr-2 Pm1, Pm2	LG2, LG4, LG9	CEDG282, CEDG191, CEDG166, MB-SSR238 (SSR)	Additive and dominant gene action of >2 major and minor genes (Kasettranan et al. 2010; Chankaew et al. 2013; Humphry et al. 2003)
Cercospora leaf spot	VC6372 (45-8-1), v4781, HUM-1, ML-1194, ML-1229, ML 820, EC-27087, EC26271-3, BARI Mung-2	qCLS	LG3	Between CEDG117 and VR393	Monogenic inheritance of single dominant gene (Singh et al. 2017; Chauhan and Gupta 2004; Thakur et al. 1977) Quantitative inheritance of multiple genes (Chankew et al. 2013)
Bruchid	V2709, V2802 TC1966, ACC41, VC1973A, Jangan Mung	VrPG1P1, VrPG1P2, Br1	LG5, LG9	MB87, SSR017 SSR037, OPC-06, DMB-SSR-158 (SSR), STSbr1/SMJ44, STSbr2/SMJ64 (STS)	Monogenic inheritance of few dominant major genes with some modifiers (Bhatacharya 2014; Kaewwongwal et al. 2017; Schafleitner et al. 2016) Single dominant gene (Hong et al. 2015; Mahato et al. 2015; Sun et al. 2008)

unripe pod is due to the same gene responsible for flower colour. Later, numerous studies were conducted on the inheritance pattern of morphological traits, viz. plant type, plant colour, leaf type, flower colour, inflorescence type, pod pubescence, shape and colour, shattering habit, seed coat colour and surface, hard-seededness, resistance/tolerance to biotic and abiotic stresses (Singh 1982).

There are many reports on the inheritance of resistance to MYMD in mungbean; however, most of these reports are contradictory. The discordance in the nature of inheritance of MYMD could be ascribed to species non-specificity as most of these are silent on the exact species of MYMD-causing virus. In most of the reports, the allelic relationships have been studied in MYMD, which suggest that the resistance is controlled by a single recessive gene (Malik et al. 1986; Saleem et al. 1998; Reddy and Singh 1995; Sudha et al. 2013), dominant gene (Sandhu et al. 1985), two recessive genes (Pal et al. 1991; Ammavasai et al. 2004) and complementary recessive genes (Shukla and Pandya 1985). Thus, a more extensive study is needed to finalize the mode of inheritance of the resistance of MYMD in mungbean. The studies on the genetic basis of resistance to MYMV in F_1, F_2 and F_3 progenies indicated that a single recessive gene is responsible for its resistance, and the expression of the major gene responsible for MYMD resistance/susceptibility is affected by modifying genes (Khattak et al. 2000). These modifying genes caused variation in the degree of MYMD resistance/susceptibility in the progenies derived from a single cross. It has been further reported that the inheritance of MYMV resistance occurs through a major recessive gene without any maternal effect (Khan et al. 2007). Though MYMD resistance has been suggested to be monogenic (Pal et al. 1991; Gupta et al. 2013), some reports consider this resistance as digenic (Singh 1980; Verma and Brar 1996; Shukla and Pandya 1985; Ammavasai et al. 2004). Its control has also been reported due to digenic inhibitory gene interaction (Verma and Singh 1986; Solanki et al. 1982). In addition to complex inheritance mechanisms of this disease, non-uniform and fluctuating distributions of whitefly populations in the field always reduce the accuracy in evaluating the resistance and lead to errors in the selection of resistant genotypes. Developing MYMD-resistant varieties through conventional approaches remains difficult due to the explosion of new isolates and complex mechanisms of MYMD resistance (Selvi et al. 2006). In this situation, molecular marker technology can increase the efficiency of breeding through marker-assisted selection (MAS), in which phenotypic selection is carried out using DNA markers associated with the trait of interest. The marker–trait association and gene tagging have shown that single dominant gene is involved in governing MYMIV in black gram (Gupta et al. 2013) and soya bean, whereas five QTLs were identified till date in mungbean for MYMIV (Kitsanachandee et al. 2013). Among other diseases, powdery mildew was reported to be quantitatively inherited with high heritability and predominantly additive gene action (Kasettranan et al. 2010).

Resistance to bruchids has been reported to be controlled by a single gene (Kitamura et al. 1988; Young et al. 1992; Srinives 1996; Miyagi et al. 2004; Lawn and Rebetzke 2006). Sun et al. (2008) reported that the bruchid resistance of resistant mungbean cultivar V2709 was controlled by a single dominant locus named *Br2*. Sarkar et al. (2011) reported that bruchid resistance in Indian *V. sublobata* accession is controlled by a major dominant gene but might have varying degrees of expressivity. Some reports have suggested that resistance to *C. chinensis* in mungbean is dominant and governed by a few major genes (probably two) with some modifiers (Sarkar and Bhattacharyya 2015). The F_1 and F_2 seeds in mungbean showed that the resistance to *C. chinensis* and *Riptortus clavatus* Thunberg is controlled by a single dominant gene (Hong et al. 2015). However, the segregation pattern of reciprocal reaction to each insect in F_2 seeds showed that seeds were susceptible to both the insects.

5.7 Breeding Methods and Strategies

The last 3 decades have seen improvement in mungbean breeding with the focus on the development of short duration, widely adaptable, synchronous and photo- and thermo-period-tolerant varieties. Of late, the major emphasis is on development of mungbean varieties having resistance to multiple diseases as well as insect pests. Germplasm resources and improved mungbean lines are being deployed to develop more stable and resilient varieties. To develop high yielding and biotic stress-resistant cultivars in mungbean, the common methods that have been deployed are the introduction, selection, hybridization and mutation breeding (Pratap et al. 2012).

5.7.1 Selection

Selection from indigenous and exotic germplasm as well as landraces has always been an important tool in the development of superior cultivars. For a successful hybridization programme, selection of diverse parents with useful traits is the prime requisite as the breeding materials developed from genetically divergent parents are likely to produce more heterotic effects and also lead to the recovery of better segregants in the subsequent segregating generations. Selection from indigenous and exotic germplasm as well as landraces has played an important role in the development of superior cultivars of pulse crops. Before 1950, virtually all the mungbean varieties were developed by a selection of superior genotypes from the collected samples of local cultivars. Some of the varieties were also developed from the exotic materials. The desirable plants were selected, and the superior pure lines were established after their progeny testing (Pratap et al. 2012, 2013; Nair et al. 2013). The pure lines were evaluated for yield, yield traits and reaction to diseases, and the best pure line was released for cultivation (Pratap et al. 2012; Nair et al. 2013).

The earliest efforts to collect landraces were made from all over India and Burma as early as 1925 (Bose 1932). These collections were utilized to isolate pure lines from the stocks, and selections were made on the basis of colour of the stem, flowers, ripe pods, seed colour and texture and other morphological features. As a result, a few varieties were developed. However, most of the early selections such as Jalgaon Local, China Mung 1/49, Kopargaon, Krishna II, Gwalior 3, Khachrod 5, Bhilsa Green 16, BR 5, BR 6, BR 7 were susceptible to MYMD and powdery mildew although better in a few other traits such as uniformity, bold seeds and longer pods. Later, a few selections such as KM 1, Co2, R 288-8, T 150, Utkal 2, selections 196, 697, 855, 932, 946, T 1630 and T 2105 which were either tolerant or moderately resistant to MYMD were carried out. Most of these selections were taken before the 1960s, and a few of them such as T 44, Sona mung, Kopargaon, Co 1 and Co 2 are still cultivated in small pockets in interiors of India. Large-seeded varieties of mungbean, Pusa Vishal, Pant moong 5 and SML 668 were developed from the selection of AVRDC material, and these became highly popular among the farmers.

5.7.2 Hybridization

Most of the biotic stress-resistant varieties of mungbean, especially in the last 4 decades, have been developed through hybridization. Resistance sources have been utilized to combine good agronomic base and disease/pest resistance to develop such varieties.

5.7.3 Intraspecific Hybridization

Studies have been carried out on the development of short duration, photo- and thermo-period-insensitive varieties of mungbean coupled with resistance to major biotic stresses, viz. MYMD and powdery mildew (Pratap et al.

2014a, 2015; Singh et al. 2017). In most of the varieties developed through hybridization, the pedigree method of breeding has been followed. Until now, >100 varieties have been developed in India through intraspecific hybridization.

With the development of varieties such as HUM 6, HUM 12, Meha (IPM 99-125), HUM 16 and MH 2-15, the mungbean production and productivity witnessed a big boost in India. ML 1265, a whitefly-resistant variety, was released as a commercial cultivar in India (Cheema et al. 2017). The variety PKV AKM 4 developed from a cross between BM4 X PS 16 was recommended for two zones, viz. central zone and south zone of India. In more recent times, IPM 02-3, currently the most popular variety of mungbean in India, was developed using IPM 99-125 and Pusa Bold 2 and recommended for both *spring* and *kharif* seasons. This variety is highly resistant to MYMD as well as to other major diseases of mungbean and has high yield potential, medium–large, shining and green seed and wider adaptability. However, this variety recorded high (82.52%) pre-harvest sprouting value (Lamichhane et al. 2017) making it prone to pre-harvest sprouting during the rainy season. Another highly popular variety, MH 421, developed from the cross Muskan X BDYR 2 is also highly resistant to MYMD and has a share of about 15–18% in breeder seed indent. Recently, the ICAR-Indian Institute of Pulses Research, Kanpur, released IPM 410-3 (Shikha) variety for entire northern, western and central India and covers the majority of the mungbean area in the country. This variety is also highly resistant to MYMD and powdery mildew, and moderately resistant to CLS. IPM 205-7 is an early duration mungbean variety that matures in <55 days and is suitable for summer cultivation (Pratap et al. 2013). Developed from the cross IPM 02-1 X EC 398889, this variety is most suitable to be grown as a catch crop after the harvest of *rabi* crops and before the onset of monsoon and best utilizes the short-season window of 60–70 days available during the summer season. This variety is also highly resistant to MYMD and powdery mildew and moderately resistant to CLS. IPM 2-14 was released for spring cultivation in south zone of the country and is gaining popularity. The varieties DGGV-2 developed from the cross between China mung x TM-98-50 and Pusa 0672 developed from the cross between 11/395 x ML 267 were released for south zone of India. The varieties such as KM 2241, HUM 16, MH 2-15 and TMB 37 were developed through intraspecific hybridization and became very popular among the farmers in short time. Table 5.6 illustrates the popular mungbean varieties developed in India in the last 10 years. Mungbean genotypes/improved lines developed in countries other than India are shown in Table 5.7.

5.7.4 Interspecific Hybridization

Planned utilization of exotic and wild genetic resources of mungbean can result in yield improvement, plant type and several other characters, such as resistance to biotic and abiotic stresses (Pratap et al. 2015). Wild relatives of cultivated *Vigna* species offer new sources of variability for a number of traits, viz. resistance to biotic stresses such as powdery mildew (Tomooka et al. 2006), MYMV (Pandiyan et al. 2008), bruchids (Tomooka et al. 1992; Somta et al. 2006) (Table 5.8), abiotic stresses such as photo- and thermo-insensitivity (Pratap et al. 2014a; Basu et al. 2019) and agronomic traits (Tomooka et al. 2001), which are hitherto not found in the cultivated species and therefore provide additional avenues of selection for agronomic traits (Pratap et al. 2014a, b). While mungbean has erect growth habit, a large number of seeds/pod, early maturity and desired quality traits, to further improve its branching, synchronous maturity, non-shattering pods and durable resistance to CLS, urdbean can be utilized as a donor (Singh 1990). Likewise, traits such as the number of clusters/plants, longer pods with a large number of seeds, durable resistance to MYMV, CLS, powdery mildew and bruchids may be transferred from ricebean.

Crossability barriers create complications for making successful inter-species gene transfer in mungbean (Pratap et al. 2018). These barriers

Table 5.6 List of mungbean varieties identified/released by all India Coordinated Research Project on MULLaRP (Project Coordinators Report 2018)

Name of variety	Pedigree	Year of release	Average yield (q/ha)	Reaction to major disease
KM 2241	Samrat X PDM 54	2008	10–11	Resistant to MYMD
IPM 02-3	IPM99-125 X Pusa Bold 2	2009	11.0	Resistant to MYMD
PKV AKM 4	BM4 X PS16	2009	10.0	Resistant to MYMD
Pusa 0672	11/395 X ML 267	2009	10.0	Resistant to MYMD
IPM 02-14	IPM99-125 X Pusa Bold 2	2010	11.0	Resistant to MYMD
MGG 347	K-851 X PDM-54	2009	13–15	Tolerant to thrips, stem fly, MYMD, CLS
VBN (Gg)3	K 1 X Vellore Local	2009	9.75	Moderately resistance to MYMD
Basanti	Asha X PDM 90-1	2010	12–15	Resistance to MYMD
Pairymung	TARM 1 X J 781	2010	12	Tolerant to MYMD and resistance to PM
TM-2000-2	JL-781 X TARM-2	2010	10.9	Resistant to PM
SML 832	SML 302 X Pusa Bold 1	2010	11.6	Tolerant to MYMD and thrips
DGGV-2	China Mung X TM-98-50.	2012	11–14	Moderately resistant to PM, tolerant to apion beetle
Shalimar moong-2	PS-7 X Larkipora Local	2013	10.0	Resistant to CLS, moderately resistant to aphid
CO (Gg) 8	COGG923 X VC 6040	2013	–	Resistance to MYMD
MH 421	Muskan X BDYR 2	2014	10–12	Resistant to MYMD
IPM 410-3 (Shikha)	IPM 03-1 X NM 1	2016	11–12	Resistant to MYMD
IPM 205-7 (Virat)	IPM 02-1 X EC 398889	2016	10–11	Resistant to MYMD
SML 1115	SML 134 X SML 715	2016	11–12	Moderately resistant to MYMD
MH 318	CCS HAU, Hisar	2016	12–14	Resistance to MYMD
Pant Mung 8 (PM 09-6)	PM 3 X NDM 99-3	2016	10–11	Resistant to MYMD, CLS and PM
MSJ 118	Mutant of K 851	2016	7–8	Moderately resistant to MYMD
RMG 975	ML 613 X ML 1189	2016	8–9	Moderately resistant to MYMD and tolerant to root knot nematode
KM 2328	KM 2241 X HUM 16	2018	10–12	Resistant to MYMD, CLS, WB, MB and anthracnose

(continued)

Table 5.6 (continued)

Name of variety	Pedigree	Year of release	Average yield (q/ha)	Reaction to major disease
Pusa 1431	Pusa 9531 X IPM 02-19	2018	12–14	Resistant to MYMD, CLS, anthracnose, web blight and ULCV
Kanika	Pant Mung 4 X EC398897	2018	12–13	Highly resistant to MYMD and CLS and resistant to leaf crinkle and leaf curl
Varsha	EC398885 X PDM 139	2018	12–13	Highly resistant to MYMD and PM and moderately resistant to CLS

Table 5.7 List of mungbean varieties/advanced breeding lines developed in different countries

Genotype/improved lines	Pedigree	Specific feature	Country	References
Improved BC_3F_3 lines	CN60 x TC1966	Resistant against bruchid damage (*Callosobruchus chinensis, C. maculatus*)	Thailand	Tomooka et al. (1992)
Improved F_{12} RILS	TC1966 X NM92	Tolerant to bruchid damage	Taiwan	Schafleitner et al. (2016)
Improved F_7 RILS and subsequent advanced generation	V2802 X NM94	Resistant to bruchid damage	Taiwan	Schafleitner et al. (2016)

Table 5.8 Successful transfer of resistance to biotic stresses through distant hybridization

Useful traits	Interspecific crosses	References
MYMD	*Vigna radiata* × *Vigna mungo*	Lekhi et al. (2018)
	Vigna radiata ×13 wild *Vigna* species	Pandiyan et al. (2010)
	V. radiata × *V. sublobata* and *V. mungo*	Pal et al. (2000)
	V. radiata × *V. umbellata*	Bhanu et al. (2018), Bharathi et al. (2006)
MYMD and CLS	VC1482E × NM 20-21 10-43 (NM89) and 10-12 (NM88) (Pakistan)	Ali et al. (1997)
Pest resistance	*V. glabrescens* × *V. radiata*	Chen et al. (1989)
Bruchid beetles	Chainat 60' ('CN60'), *Vigna radiata* × *V. radiata* var. *sublobata* (Thailand)	Tomooka et al. (2006)

may express through reduced fertilization, reduction in the number of hybrid seeds or development of abnormal—shrivelled, small or non-viable seeds, retarded development of hybrid endosperm leading to embryo death or hybrid sterility (Pratap et al. 2015). Several measures have been suggested such as the deployment of embryo rescue, hormonal manipulations and use of mentor pollen, for increasing the success of interspecific crosses. By using sequential embryo rescue, the reciprocal hybrids between *V. mungo* and *V. radiata* are successfully obtained (Gosal and Bajaj 1983; Verma and Singh 1986). *V. mungo* has also been reported to cross successfully with *V. glabrescens* (Dana 1968; Krishnan and De 1968), *V. trilobata* (Dana 1966), and *V. dalzelliana* (Chavan et al. 1966). Similarly, *V. radiata* × *V. umbellata* crosses were generated

to transfer resistance to MYMV and other desirable traits into mungbean (Verma and Brar 1996). Derivatives from mungbean × urdbean crosses have been reported to exhibit a higher level of MYMD resistance caused by MYMV (Gill et al. 1983; Lekhi 2017). Useful disease-resistant genes were also identified from amphidiploids of mungbean x ricebean crosses (Dar et al. 1991). Similarly, progenies from mungbean x ricebean and mungbean × *V. radiata* var. *sublobata* crosses were also recovered which exhibited a high degree of resistance to MYMV (Verma and Brar 1996). Singh et al. (2003) produced successful hybrids between *V. radiata* and *V. umbellata*, and the hybrids possessed intermediate morphology with MYMV resistance. One accession of wild mungbean (*Vigna radiata* var. *sublobata*) exhibited complete resistance to adzuki bean weevils and cowpea weevils (Fujii et al. 1989), which was successfully used in a breeding programme (Tomooka et al. 1992).

Despite numerous attempts of hybridization between cultivated mungbean genotypes and wild genetic resources, the actual release of new cultivars from distant crosses has remained limited. Three mungbean cultivars, viz. HUM 1, Pant Moong 4 and IPM 99-125, have been developed from mungbean x urdbean crosses in India. All these have been highly popular among the farmers and possess improved plant types in addition to high levels of MYMD resistance. There are a few reports of the development of advanced breeding lines and genetic resources utilizing the wild genetic resources indirectly. For example, using IPM 99-125 as one of the parents, genotypes IPM 02-1 and IPM 03-1 were developed at ICAR-IIPR, Kanpur, which were further used in the development of two extra early mungbean genotypes, IPM 205-7 and IPM 409-4 that mature in 50–55 days (Pratap et al. 2013). Currently, a few advanced lines derived from interspecific crosses are under multilocation evaluation in AICRP for their possible release as a cultivar.

5.7.5 Mutation Breeding

Induced mutation using physical and chemical mutagens is one of the many ways to develop new cultivars with improved traits and better characteristics. While most of the mutants usually have one or a few traits improved, such characters may be incorporated in other cultivated varieties through backcross breeding, besides releasing the developed material directly as a variety. Mutation breeding has been used successfully to develop improved cultivars in mungbean possessing resistance to a few biotic stresses (Table 5.9). Mutations were induced in two mungbean varieties, K-851 and PS-16, using EMS and gamma rays. Selection studies were conducted to improve the yield and to generate genetic variability in different quantitative traits, viz. fertile branches per plant, pods per plant and seed yield per plant (Khan and Goyal 2009). Other varieties developed through mutation breeding include Pant Mung 2, Co 4, TMB 37, Dhauli, BM4 and MUM 2. In Pakistan also, the popular varieties NM 51 and NM 54 were developed which were large-seeded varieties resistant to MYMD. These varieties were developed by hybridization and irradiation of F_1 seeds. Bean fly, *O. phaseoli*, is a key pest of mungbean in Thailand (Srinives 1991). To control bean fly, apart from insecticide spraying, the induced mutation was used to improve the resistance of mungbean variety Khampang Saen 2 (KPS2) (Ngampongsai et al. 2009) and an insect tolerant selection Chai Nat 72 (CN 72) was isolated.

5.8 Impact of Resistance Breeding

Besides the development of more than 100 improved varieties in mungbean, remarkable progress was also made in collection, evaluation, characterization and documentation of germplasm resources. There has also been a notable success in transferring disease and insect resistance alleles from wild *Vigna* relatives to

Table 5.9 Varieties/advanced breeding materials developed through mutation breeding

Variety name	Resistance to disease	Radiation used	Area/season of cultivation	References
TARM-2	PM	X-rays, gamma rays, ethyl methyl sulphonate	Southern and central zone, summer season, rice fallow	D'souza et al. (2009)
TARM-18	PM			
TM-96-2	PM			
TMB-37	PM, YMV			
TJM-3	PM, YMV, Rhizoctonia root-rot disease			
NIAB Mung 2006	CLS, MYMV	Induced mutation and hybridization	Pakistan	Haq (2009)
M4-2	CLS (moderately resistant), PM (moderately resistant), bean fly (tolerance)	500 Gy (gamma rays and treated with 1% EMS	Thailand	Ngampongsai et al. (2004)
M5-1				
M5-5				
CN 36				
KPS 32				
Mutant SML-668	YMV	600 Gy gamma rays (M1 generation) 500 Gy gamma rays (M3 generation)	Summer season, India	Reddy (2009)

PM=Powdery mildew, YMV: Yellow Mosaic Virus, CLS: Cercospora leaf spot

cultivated mungbean backgrounds. The impact of biotic stress-resistant varieties has been realized well in production as well as in productivity of mungbean, which showed continuous increase despite fluctuations in its area. The area, production and productivity of mungbean in India have seen a consistent upward trend since the 1960s, and the production increased from 0.60 million tonnes in 1964–65 to about 2.17 million tonnes in 2016–17 (PC Report, 2018, AICRP on MULLaRP). During the corresponding period, productivity also increased from about 280 to >500 kg/ha. While increased irrigation facilities, better inputs and crop management had a role in increasing productivity, deploying biotic stress-resistant cultivars for cultivation had a definite role to play in enhancing productivity. Significant growth in mungbean area and production was witnessed in non-traditional niches, especially in summer, spring and rice fallow cultivation during the last decade (Gupta and Pratap 2016; Singh et al. 2017). It is noteworthy that about 80% of the mungbean breeder seed indent is shared by top ten varieties in India including IPM 02-3, MH 421, GM 4, HUM 16, SML 668, IPM 2-14, Samrat, Pant Moong 5 and Meha (Singh et al. 2017). Among these, IPM 02-3 alone contributes to about 25% of breeder seed indent. Most of these varieties are highly resistant to major diseases and insect pests of mungbean.

5.9 Future Outlook

Mungbean has a distinct advantage of being a short duration and widely adaptable crop that can fit well in several cropping systems. The reduced maturity duration and synchronous maturity in new cultivars have made it an attractive option as a catch crop in short-season windows between two crops and also as a non-competing intercrop in cash crops like sugar cane. Therefore, it has a tremendous scope of vertical as well as horizontal expansion in all major mungbean-growing ecologies of the world. Mungbean plays an important

role in food and nutritional security of several countries including India, Pakistan, Bangladesh, Myanmar and several African countries. In India, it has been projected as one of the major crops for vertical and horizontal expansion to achieve self-sufficiency in pulses in policy documents (Vision 2030, ICAR-IIPR). Therefore, there is a need of a major research boost to this crop to make it a key component of pulse revolution. Biotic stresses are the major constraints in realizing the actual yield potential of a cultivar and ultimately affect the productivity and quality of mungbean to a great extent. Therefore, a major thrust is required on combining pre-harvest sprouting and bruchid resistance and pyramiding genes for resistance to major insect pests (thrips, Jassids and pod borer) and diseases (MYMD, powdery mildew and CLS) utilizing resistance sources in cultivated and wild germplasm.

While several improved cultivars have been developed with enhanced resistances to yellow mosaic, powdery mildew, CLS and a few more diseases, only those problems for which resistance sources are known have been addressed till date. Stem fly and bruchids are serious pests worldwide, and the resistance sources are either limited or genes difficult to utilize for breeding resistance to these pests. Such traits remain untouched and need major attention of breeders. Marker-assisted breeding has been successfully deployed in other pulses such as chickpea (Varshney et al. 2014; Pratap et al. 2017; Mannur et al. 2019), and this technology needs to be put to use for breeding for complex traits in mungbean as well. Molecular markers are now available for powdery mildew and CLS, which require to be utilized in breeding programmes. Root rot and anthracnose are other important diseases, and more attention is required towards the development of molecular markers for these stresses. There is a strong need for generating additional genomic resources to fully utilize the potential of marker technology. One such mission has been recently launched by the Department of Biotechnology (DBT), Government of India, in minor legumes including mungbean urdbean, moth bean, cowpea and horse gram, where numerous genomic and genetic resources will be developed for various biotic stresses. A fine map on the distribution of MYMD-causing viruses will be developed covering all mungbean-growing ecologies of India besides preparing a differential set of mungbean genotypes to identify the prevalence of MYMD-causing species of viruses.

Germplasm has played an important role in the development of many cultivars in mungbean and collection, evaluation and characterization of trait-specific germplasm need a systematic investment of time and money so that potential germplasm can be deployed to best use in filling the gaps related to traits of interest. Mungbean minicore collection (Schafleitner et al. 2015) has been made available to partner countries of the Australian Centre for International Agricultural Research (ACIAR)-funded International Mungbean Improvement Network (IMIN). This germplasm needs to be thoroughly screened for a host of biotic stresses and deployed to introgression breeding for developing biotic stress-resistant cultivars. Breeding materials have already been developed at ICAR-Indian Institute of Pulses Research (IIPR), Kanpur; Department of Agricultural Research (DAR), Myanmar; and Bangladesh Agricultural Research Institute (BARI), Bangladesh, besides World Vegetable Center, Hyderabad, utilizing promising mungbean minicore accessions. While the development of biotic stress-resistant cultivars is important, capacity building of mungbean farmers is also equally significant. Cultivating only resistant cultivars, adopting good practices of crop management and raising a clean crop need to be taught to the poor and marginal farmers as to make mungbean a mainstream pulse crop towards providing a vegetarian solution to global protein and calorie malnutrition.

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