Chapter 10
Mung Bean (*Vigna radiata* (L.) R. Wilczek) Breeding

Jungmin Ha and Suk-Ha Lee

Abstract Mung bean (*Vigna radiata* (L.) R. Wilczek) is a fast-growing, warm-season pulse crop that is primarily cultivated in developing countries in Asia. This crop has been showing a steady increase in production worldwide. Mung bean represents a good source of protein and contains higher folate and iron levels than other legumes. Moreover, it has a short lifecycle and can fix atmospheric nitrogen through symbiosis with nitrogen-fixing bacteria, making it ideal for intercropping with other major crops. Despite the importance of mung bean, there has been relatively little effort aimed at developing a breeding system for this crop, and genomic information is lacking compared to other legume species. Since mung bean has a small genome size, a short lifecycle, and is self-pollinating, it could be used as a model organism for studying legume plants. Moreover, the mung bean genome has recently been sequenced. The success of mung bean breeding depends on mining useful alleles from diverse germplasm and identifying markers closely associated with desirable phenotypes. The increasing affordability of high-throughput marker genotyping and the availability of a reference genome sequence will allow researchers and breeders to pinpoint the exact locations of genes and mutations that contribute to target phenotypes. Several research institutes and universities are currently constructing germplasm collections to maintain and secure mung bean genetic resources. Breeding via induced mutations and genetic engineering has helped improve mung bean cultivars, and genomic information from other well-studied legume species has been used to make up for the shortage of genomic information for mung bean. This chapter summarizes the current status of mung bean breeding, as well as genetic and genomic studies of this important crop.

Keywords Mung bean · Biodiversity · Domestication · Developing countries · Translational genomics · Quantitative trait locus · Synteny

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10.1 Introduction

10.1.1 Botanical Classification and Distribution

Mung bean is a fast-growing, warm-season pulse crop belonging to the subgenus *Ceratotropis* of the genus *Vigna* in the papilionoid subfamily of the Fabaceae. This self-pollinating diploid crop has a chromosome number of 2n = 2x = 22 (Arumuganathan and Earle 1991). Mung bean is mainly cultivated in South, East, and Southeast Asia by smallholder farmers. Mung bean grows in frost-free areas within a wide range of latitudes from Asia to Africa, South America, and Australia (Nair et al. 2012). With a cultivation area of approximately 6 million hectares, Asia has the largest mung bean cultivation area, with India, China, Myanmar, Thailand, Sri Lanka, Bangladesh and Indonesia, accounting for ~90% of world production (Lambrides and Godwin 2007). Among the Asian countries, India is the world's largest producer of mung bean, accounting for over 50% of global annual production (Nair et al. 2012).

10.1.2 Importance

Mung bean represents a good source of dietary protein and has higher folate and iron contents than most other legumes (Keatinge et al. 2011). Mung bean roots fix atmospheric nitrogen via symbiosis with nitrogen-fixing rhizobia, leading to improved soil fertility and texture, making this plant valuable both economically and nutritionally (Graham and Vance 2003). Intercropping mung bean in rice-rice and rice-wheat systems increases the yields of subsequently planted cereal crops and reduces pest occurrence, as it improves soil quality and reduces the amount of nitrogen fertilizer required in the soil due to its residual effects (Faria et al. 1989; Yaqub et al. 2010). Mung bean can be consumed in the form of vegetable sprouts or cooked as an ingredient in soups, porridge, pancakes, noodles, ice cream or sweet paste for cake fillings, making it highly versatile for the human diet. In addition, mung bean forage is beneficial in the diet of sheep, without any negative effects, and the haulm is used as livestock feed (Agboola and Fayemi 1972; Garg et al. 2004). Consequently, the global consumption of mung bean increased by 22–66% from 1984 to 2006, and annual production has increased by a large percentage (Shanmugasundaram et al. 2009).

Mung bean is currently regarded as a major cash crop and has therefore attracted interest by the research community worldwide. Thus, efforts are underway to develop an international mung bean network to coordinate research activities among different research groups.

10.1.3 Domestication, Selection, and Early Improvements

Mung beanis believed to have been domesticated in India ~3500 years ago based on domesticated mung bean diversity data, morphological studies, and archeological evidence (Fuller and Harvey 2006; Jain and Mehra 1980; Singh et al. 1975; Vishnu-Mittre 1974). However, the wild form of mung bean, *Vigna radiata* var. *sublobata*, is indigenous to the subtropical and tropical regions of northern and eastern Australia and is widely distributed throughout Africa, Asia, and Australia (Lawn and Cottrell 1988). Based on studies of protein variation and enzyme diversity, mung bean in West Asia exhibits the greatest variation, and mung bean is presumed to have moved to other Asian countries and to Africa (Tomooka et al. 1992a; Dela Vina and Tomooka 1994). Therefore, modern mung bean cultivars have resulted from multiple rounds of domestication, and this plant is currently distributed throughout southern and eastern Asia, Africa, and Austronesia (Lambrides and Godwin 2007).

10.2 Cultivation and Traditional Breeding

10.2.1 Current Cultivation Practices

Mung bean is a short-day, warm-season crop. This crop grows for 90–120 days from planting to maturity during the warm season without frost conditions (Oplinger et al. 1990). The flowering of mung bean responds differentially according to day length. Short days hasten flowering, whereas long days delay flowering (Aggarwal and Poehlman 1977). Mung bean seeds require temperatures of at least 15 °C for planting, and the optimum temperature for growing mung bean is a mean temperature of 20–30 °C during the crop production period. Elevations should not exceed 1800–2000 m (Oplinger et al. 1990). Mung bean is mainly grown in semiarid to subhumid lowland tropics and subtropics with 600–1000 mm of annual rainfall. If water stress occurs during the reproductive stage, it has a negative impact on flower formation, leading to a decrease in total yields (Raza et al. 2012). High humidity and excessive rainfall can result in disease problems and low yields (Oplinger et al. 1990). Mung bean grows well under good drainage conditions in sandy loam rather than clay soil, with a pH of 6.3–7.2 (Oplinger et al. 1990). Mung bean can be sown at various row spacing, from 20 to 100 cm, and narrower rows can have potential yield benefits. In plants grown in narrower rows, the nitrogen fixation rate is 15–30% higher than in those grown in broad rows, and faster ground cover of narrow spacing can help suppress weeds (Taj et al. 2002).

10.2.2 Current Agricultural Problems and Challenges

The harvesting index of mung bean is low due to its indeterminate growth habit, late and nonsynchronous maturity, and losses due to abiotic and biotic stresses (Alam Mondal et al. 2011; Fernandez and Shanmugasundaram 1988). A major problem in mung bean cultivation is synchronicity. Mung bean has an indeterminate growth habit, and flowering and pod maturity do not occur at a uniform time but are typically spread out over a long period (Khattak et al. 2001; Tah and Saxena 2009). If harvesting is performed once at the peak of the early harvest period, a large portion of the yield potential is lost because the harvest accounts for only ~50% of the total yield that could be harvested. However, delaying harvest can also lead to yield loss because mature and dried pods may shatter or fall off, and are more likely to be exposed to pest and pathogen attack at this stage. Preventing yield loss by performing multiple harvests also has its challenges, as it results in additional costs, and each harvest must be performed with care to avoid damaging the plants, which could make the harvesting procedure and the use of mechanical tools inefficient (Iqbal et al. 2015).

Synchronous maturity is a primary objective of mung bean breeding programs, as it could contribute greatly to productivity and cost-effective harvesting. Although early and even pod maturity were shown to have a positive effect on grain yield, the genetic basis of this trait in mung bean is currently unknown (Afzal et al. 2003; Chen et al. 2008).

10.2.3 Traditional Breeding

The objectives of conventional mung bean breeding include high yields, uniform maturity, and resistance to *Cercospora* leaf spot, powdery mildew, mung bean yellow mosaic virus, bruchids, bean flies and mung bean pod borer (Tomooka et al. 2005). In general, wild species serve as sources of useful genes because the currently cultivated germplasm has a limited number of alleles, as many alleles have been lost due to a genetic bottleneck that has occurred during domestication and modern breeding programs (Hyten et al. 2006). Useful alleles from wild relative species have been used to improve modern mung bean cultivars (Doyle 1988; Kumar et al. 2011; Tanksley and McCouch 1997). For example, a bruchid-resistant mung bean cultivar has been developed by importing an allele from a wild mung bean relative, TC1996, which is completely resistant to bruchid beetles, *Callosobruchus chinensis* and *C. maculatus*; these pests result in serious yield losses during mung bean storage (Somta et al. 2008; Talekar 1988; Tomooka et al. 1992b). A yellow mosaic disease-resistant allele from *Vigna mungo*, a wild relative species, was transferred into cultivated mung bean and used to develop yellow mosaic virus-resistant mung bean cultivars (Basak et al. 2005; Gill et al. 1983;

Singh 1980). Genetic maps have been constructed based on cultivated mung bean and wild mung bean accessions or related wild species, providing genetic information about agronomically-important traits such as seed quality, weathering tolerance and pest/disease resistance (Lörz and Wenzel 2007; Isemura et al. 2012; Lambrides et al. 2000; Wang et al. 2016). Since the importance of maintaining germplasms has become increasingly clear, several research institutions and universities are currently constructing germplasm collections to sustain mung bean genetic resources. AVRDC-The World Vegetable Center, Tainan, Taiwan, currently holds the world's largest *Vigna* germplasm collection, consisting of 11,832 accessions (10,673 *Vigna* species, 881 *V. angularis*, 278 *V. unguiculata*), representing important resources for interspecific hybridization for mung bean cultivar improvement.

10.3 Germplasm Biodiversity and Conservation

10.3.1 Germplasm Diversity

The general goal of breeding is to accumulate useful alleles from various parental lines into a new plant variety. The first step in finding superior alleles or the individuals carrying them is to secure a germplasm pool with high genetic diversity. Essentially, breeders have to rely on existing natural DNA variation because DNA modification using genetic engineering is still limited and is even viewed unfavorably by the general public (Priest 2000). Therefore, the availability of natural genetic resources with rich variation is fundamental for successful breeding programs. Therefore, many institutes have been established for various research activities including mung bean germplasm conservation and cultivar improvement.

Mung bean germplasm is maintained at several centers throughout the world, including AVRDC-The World Vegetable Center, Taiwan; National Bureau of Plant Genetic Resources of the Indian Council of Agricultural Research; the Institute of Crop Germplasm Resources of the Chinese Academy of Agricultural Sciences; the Plant Genetic Resources Conservation Unit of the University of Georgia, USA and the University of the Philippines. Additionally, the Rural Development Administration (RDA), Korea, and the University of the Philippines house duplicates of some of the mung bean germplasm found in AVRDC-The World Vegetable Center (Ebert 2013; Kim et al. 2015). Mung bean core collections have also been established in China, India, Korea and the USA to allow breeders and researchers to have easier access to useful germplasm and to enable the efficient use of genetic resources. A core collection consisting of 1481 accessions and a mini-core collection consisting of 296 accessions were constructed by AVRDC-The World Vegetable Center based on phenotypic and molecular characterization using 20 SSR markers, respectively (Shanmugasundaram et al. 2009). Due to the importance of genetic

diversity, molecular markers such as random amplified polymorphic DNA (RAPD), restriction fragment length polymorphism (RFLP), simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) markers have long been used to analyze germplasm and genetic diversity. These techniques have been applied to improve mung bean cultivars with a focus on yield, nutritional improvement, and disease resistance through linkage map construction.

10.3.2 Cultivar Characterization and Phylogeny

Kang et al. (2014) recently sequenced cultivated mung bean *Vigna radiata* var. VC1973A and obtained the transcriptome sequences of 22 *Vigna* accessions from 18 species (Table 10.1). Based on de novo transcriptome assembly, approximate divergence dates were calculated through phylogenetic analysis (Fig. 10.1). This phylogenetic study allowed the relationships of the two homoeologous genomes of the allotetraploid wild species, *V. reflex-pilosa*, to be traced. One genome was found to be closely related to *V. trinervia* (divergence date, 0.09 million years ago), and the other was found to be a sister to seven wild relatives (divergence date, 2.7 million years ago), suggesting that the diploid progenitor lineage has not been sampled or may be extinct. These studies have provided insights into the evolution within *Vigna* species, which may facilitate the improvement of mung bean cultivars.

10.4 Molecular Breeding

10.4.1 Molecular Marker-Assisted Breeding

The use of molecular marker systems has helped breeders identify loci associated with desirable phenotypes. Tracking the inheritance of a DNA segment with known benefits using molecular markers is more precise and efficient than traditional breeding (Collard and Mackill 2008). The recent availability of physical map data and the development of high-throughput marker genotyping based on high-coverage, whole-genome sequencing have facilitated forward genetics studies by increasing the resolution of physical maps and marker density within linkage groups (Huang et al. 2010; Zhou et al. 2015).

Restriction fragment length polymorphism (RFLP) markers were initially used to analyze the genetics of bruchid resistance in mung bean via forward genetics (Young et al. 1992). A total of 153 RFLP markers were grouped into 14 linkage groups covering 1295 centiMorgans (cM), with an average marker interval of 9.3 cM. Quantitative trait loci (QTLs) for seed weight were also identified (Fatokun et al. 1992). The initial linkage map of mung bean, consisting of 11 linkage groups,

Table 10.1 List of *Vigna* species subjected to transcriptome analysis

Scientific name	Common name	Accession or cultivar name	Origin	Number of chromosomes	Estimated genome size (Mbp)
Vigna mungo var. *mungo*	Blackgram	Chai Nat 80	Thailand	2n = 2x = 22	538
Vigna mungo var. *silvestris*	Wild blackgram	TC2210	India	2n = 2x = 22	538
Vigna radiata var. *radiata*	Mung bean	Sunhwanokdu	Korea	2n = 2x = 22	612
Vigna radiata var. *sublobata*	Wild mung bean	TC1966	Madagascar	2n = 2x = 22	465
Vigna angularis var. *angularis*	Adzuki bean	Kyungwonpat	Korea	2n = 2x = 22	539
Vigna umbellata	Rice bean	CIAT34386	Unknown	2n = 2x = 22	562
Vigna umbellata	Wild rice bean	2004 T2	Thailand	2n = 2x = 22	562
Vigna reflexo-pilosa var. *glabra*	Créole bean	V1160	The Philippines	2n = 4x = 44	978
Vigna reflexo-pilosa var. *reflexo-pilosa*	Wild creole bean	AusTRCF100879	Papua New Guinea	2n = 4x = 44	978
Vigna aconitifolia	Moth bean	AusTRCF96939	India	2n = 2x = 22	1100
Vigna trilobata	NA	TVNu-953	India	2n = 2x = 22	513
Vigna stipulacea	NA	ILRI524	India	2n = 2x = 22	NA
Vigna hainiana	NA	AusTRCF85155	India	2n = 2x = 22	1394
Vigna grandiflora	NA	JP108509	Thailand	2n = 2x = 22	NA
Vigna subramaniana	NA	NI1135	India	2n = 2x = 22	NA
Vigna nakashimae	NA	KUV12	Unknown	2n = 2x = 22	NA
Vigna nepalensis	NA	AusTRCF85148	India	2n = 2x = 22	NA
Vigna riukiuensis	NA	96 J028	Japan	2n = 2x = 22	NA
Vigna minima	NA	JP120064	Thailand	2n = 2x = 22	1027
Vigna trinervia var. *trinervia*	NA	AusTRCF319618	Papua New Guinea	2n = 2x = 22	NA
Vigna subterranea var. *subterranea*	Bambara groundnut	TVSu-84	Nigeria	2n = 2x = 22	880
Vigna vexillata var. *macrosperma*	Zombie pea	NI339	Costa Rica	2n = 2x = 22	562

Source: Kang et al. (2014)

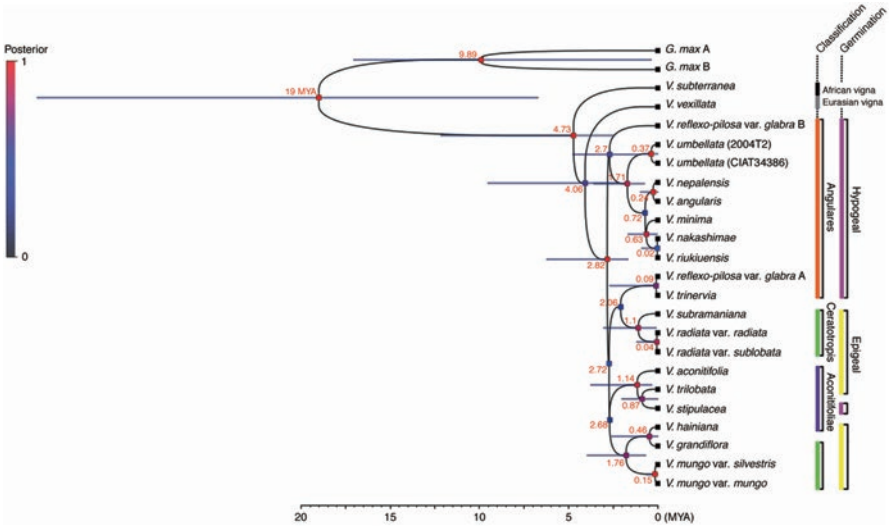

Fig. 10.1 Phylogenetic tree constructed based on de novo transcriptome assemblies from 22 *Vigna* species. (Source: Kang et al. 2014)

was developed using RFLP markers from mung bean and an interspecific hybrid population generated between *Vigna radiata* ssp. *radiata* and *V. radiata* ssp. *sublobata.* The map consisted of 171 markers covering 1570 cM, with an average marker interval of 9 cM. Several important traits were mapped, such as seed size and resistance to powdery mildew and seed bruchids (Menancio-Hautea et al. 1992).

The first random amplified polymorphic DNA (RAPD) study in mung bean was conducted to evaluate the genetic diversity among 23 accessions of wild and cultivated mung bean species including *Vigna angularis*, *V. umbellata*, *V. radiata*, *V. aconitifolia* and *V. mungo* (Kaga et al. 1996). By integrating 52 RFLP and 56 RAPD markers, a genetic map comprising 12 linkage groups was constructed from an F2 mapping population from a cross between *V. radiata* ssp. *radiata* and *V. radiata* ssp. *sublobata* (Lambrides et al. 2000). In addition, a genetic map consisting of 115 markers, covering 691.7 cM, was constructed using a recombinant inbred line derived from the previously examined F2 population. In addition, genes responsible for bruchid resistance were mapped to a linkage map constructed using both RFLP and RAPD markers (Kaga and Ishimoto 1998). A genetic map with higher marker density was subsequently constructed using RFLP markers alone (Humphry et al. 2002). Genetic diversity in mung bean was then assessed using RAPD and inter simple sequence repeat (ISSR) markers (Chattopadhyay et al. 2005).

Simple sequence repeat (SSR) markers are highly informative markers that are codominant, PCR-based, easy to generate and highly polymorphic in terms of repeat-length. The first SSR markers reported in mung bean were generated from 6 SSR sequences with 5 different types of motifs (Yu et al. 1999). Based on the

close phylogenetic relationship between mung bean and adzuki bean, SSR markers from adzuki bean were used to evaluate genetic diversity in 415 cultivated, 189 wild and 11 intermediate mung bean accessions, and higher allelic polymorphisms were successfully detected in wild mung bean (Sangiri et al. 2008). Using partial linkage maps, SSR markers associated with resistance to powdery mildew and *Cercospora* leaf spot were identified (Chankaew et al. 2011; Kasettranan et al. 2010). Using 237 SSR markers from mung bean, cowpea, adzuki bean and common bean, and 193 expressed sequence taq (EST)-SSR markers from soybean, the 11 initial linkage groups were constructed, covering 727.6 cM (Isemura et al. 2012). In total, 105 QTLs and genes related to 38 domestication-related traits were identified. The positions of previously mapped genes and QTLs, such as the bruchid resistance gene, *Br1*, 100-seed weight QTLs and the gene controlling black mottle on the seed coat were corrected on the genetic map (Fatokun et al. 1992; Kaga and Ishimoto 1998; Lambrides et al. 2000).

Before the advent of next generation sequencing (NGS) and high-throughput genotyping, the number of available polymorphic genetic markers represented a bottleneck to quantifying the genetic diversity of a population. The use of a limited number of markers can introduce bias in QTL studies because the sampled sequences may not represent the allelic diversity of the whole genome (Moragues et al. 2010). Due to advancements in NGS, researchers have focused on finding single nucleotide polymorphisms (SNPs) to be used as genetic markers. SNP markers are single base, biallelic, codominant, and ubiquitous over the genome (Brumfield et al. 2003). Two mung bean cultivars, Seonhwanogdu and Jangannogdu, were sequenced using the Illumina 454 sequencing platform to study resistance to stink bug (*Riptortus clavatus*) and adzuki bean weevil (*Callosobruchus chinensis*) (Moe et al. 2011). By comparing de novo assembled contigs from the two cultivars, 1334 and 1630 microsatellite repeat motifs, respectively, were identified, and 2098 single nucleotide variations were detected. A number of markers developed in this study have served as valuable resources for functional genomics studies by increasing the marker density of linkage maps. Cultivars Seonhwanogdu and Gyeonggijaerae5 were sequenced on the Illumina HiSeq2000 platform, and 265,001 homozygous SNPs were found.

These sequence variations identified in several mung bean cultivars can be analyzed in the context of their physical locations in the genome if a reference genome sequence is available. Seonhwanogdu (*VC1973A*), its polyploidy relative *Vigna reflexo-pilosa* var. *glabra* (accession *V1160*), and its wild relative *V. radiata* var. *sublobata* (accession *TC1966*) were sequenced and de novo assembled in 2014, and the reference genome sequence of mung bean was published (Kang et al. 2014). Along with the draft genome assembly, transcriptome assemblies from 22 accessions of 18 *Vigna* species were analyzed, facilitating genomic research in the subgenus *Ceratotropis* and providing insight into the evolution of *Vigna* species. In total, 2748 scaffolds covering 431 Mbp were anchored onto 11 pseudochromosomes using a high-density genetic map. This genetic map was constructed using 1321

SNP markers developed by genotyping-by-sequencing (GBS) from an F6 population of 190 recombinant inbred lines (RILs) derived from a cross between Seonhwanogdu (*VC1973A*) and Gyeonggijaerae5 (V2985). The N50 length is 1.62 Mbp, and ~80% of the estimated genome size (579 Mbp) is covered in this map. In total, 22,427 high-confidence protein-coding genes were annotated. Compared to the previous low-resolution linkage maps and fragmental genomic sequence information, this study represents an important milestone in *Vigna* genomic analysis. In total, 2,922,833 SNPs were revealed between wild and cultivated mung bean varieties across the genome at a frequency of 6.78 per 1 kbp. Among these SNPs, 63,294 are located in protein-coding sequence (CDS) regions, 30,405 of which represent nonsynonymous changes. Also, 55,689 of 342,853 insertions/deletions (InDels) are located around genic regions, resulting in frameshifts in 1057 genes. Microsatellite repeats (200,808 SSRs) were detected, which could possibly be used as SSR markers (Kang et al. 2014).

10.4.2 Functional Genomics

Molecular markers developed from transcriptome data are also highly informative because they are based on variations present in expressed regions of the genome. Since expressed sequence tag (EST) sequences for many crop species have been deposited in databases, data mining is a fast, cost-effective way to develop markers. In recent years, EST-based SSR markers have been developed for functional genomics studies in mung bean. Using 12,596 EST sequences from cv. Jangannogdu, 2299 SSR motifs were identified in 1848 EST sequences from which 97 PCR primer sets were designed and successfully amplified in two mung bean cultivars, TM96-2 and TARM-18 (Moe et al. 2011). Approximately 45% and 55% of the SSR motifs are located in CDS and untranslated regions (UTRs), respectively. Through data mining of the NCBI database for mung bean, EST-SSR markers were identified without incurring additional costs for sequencing (Chavan and Gacche 2014). Wang et al. (2015) used biotin-labeled oligo-probes and streptavidin-coated beads to construct an SSR-enriched library from six mung bean genotypes (ACC41, VC1973A, V2709, C01478, C01558, C01579) and discovered 308,509 SSR motifs. To characterize and validate SSR markers detected from in silico EST-SSR markers, the mung bean transcriptome was sequenced using Illumina paired-end sequencing (Chen et al. 2015). Putative SSR markers were identified by analyzing repetitive sequences in the assembled unigenes, and 13,134 EST-SSRs were detected. Among the primers designed from randomly chosen EST-SSRs, 66 primers were successfully amplified and found to be polymorphic among 31 mung bean accessions. By annotating the unigenes harboring SSRs verified by PCR, the possible effects of EST-SSRs were identified. These recent studies have resulted in the development of a number of SSR markers, thus resulting in advances in linkage map and QTL mapping analysis, which could further facilitate mung bean breeding programs.

10.4.3 Translational Genomics

Genomic information from well-studied species can be used to analyze other species; this concept is referred to as translational genomics (Varshney et al. 2015). By applying genomic information from model species to crops that are poorly understood, translational genomics has helped breeders and researchers improve and study various crops more easily (Stacey and VandenBosch 2005). Genomic sequences are currently available for mung bean, but few QTL studies have been performed. Several studies have been performed to characterize the mung bean genome using translational genomics. Flowering genes in mung bean have been identified using genome-wide comparisons between mung bean and *Arabidopsis* (Kim et al. 2014). In *Arabidopsis*, 207 genes are known to be involved in flowering, 129 of which are homologous to mung bean genes. Some of these genes are located close to SSR markers on a genetic map previously constructed for mung bean (Isemura et al. 2012). In addition, by comparing the mung bean and soybean genomes, five putative flowering-related genes in mung bean were found to be homologous to soybean flowering genes (Kim et al. 2014).

Comparative analysis between mung bean and soybean would facilitate analysis of mung bean, as SoyBase (the USDA-ARS soybean genetic database) lists over 1000 QTLs associated with more than 100 agronomically-important traits, such as seed weight, days to first flowering, seed oil content, plant height and so on. Based on sequence similarity and conserved synteny between soybean and mung bean, 1089 putative mung bean QTLs were identified using marker sequence information associated with QTLs in soybean (Table 10.2; Fig. 10.2) (Kim et al. 2015). For example, synteny blocks in soybean containing QTLs for seed weight and nematode resistance are homologous to synteny blocks in mung bean harboring QTLs for seed size/germination and bruchid resistance (Fig. 10.3) (Kang et al. 2014).

Table 10.2 Putative mung bean QTLs identified through analyzing sequence similarity and conserved synteny between soybean and mung bean

Trait	Soybean QTLs	Mung bean QTLs
First flower	104	54
Leaflet length	66	53
Leaflet width	61	55
Plant height	268	171
Pod maturity	196	142
Pod number	59	40
Seed oil	236	178
Seed oil to protein ratios	16	0
Seed protein	356	140
Seed weight	272	245
Seed weight per plant	16	11

Source: Kim et al. (2015)

Fig. 10.2 Identification of putative QTLs in mung bean using translational genomics. (Source: Kim et al. 2015)

Another synteny analysis identified a candidate gene for QTLs found in mung bean (Fig. 10.4). A mung bean genomic region containing a QTL for both days-to-flowering and days-to-first-flowering has a syntenic relationship with a soybean genomic region containing QTLs for first flowering that mapped to key flowering genes encoding phytochrome A. Through this comparative analysis, a candidate flowering gene was identified in mung bean, as well as QTLs for flowering (Hwang et al. 2017). To date, a few QTL studies involving the identification of putative candidate genes for these QTLs have been conducted in mung bean. With the availability of the mung bean reference genome sequence, translational genomics studies could be performed, which would facilitate molecular studies in mung bean leading to functional characterization of the genes of interest.

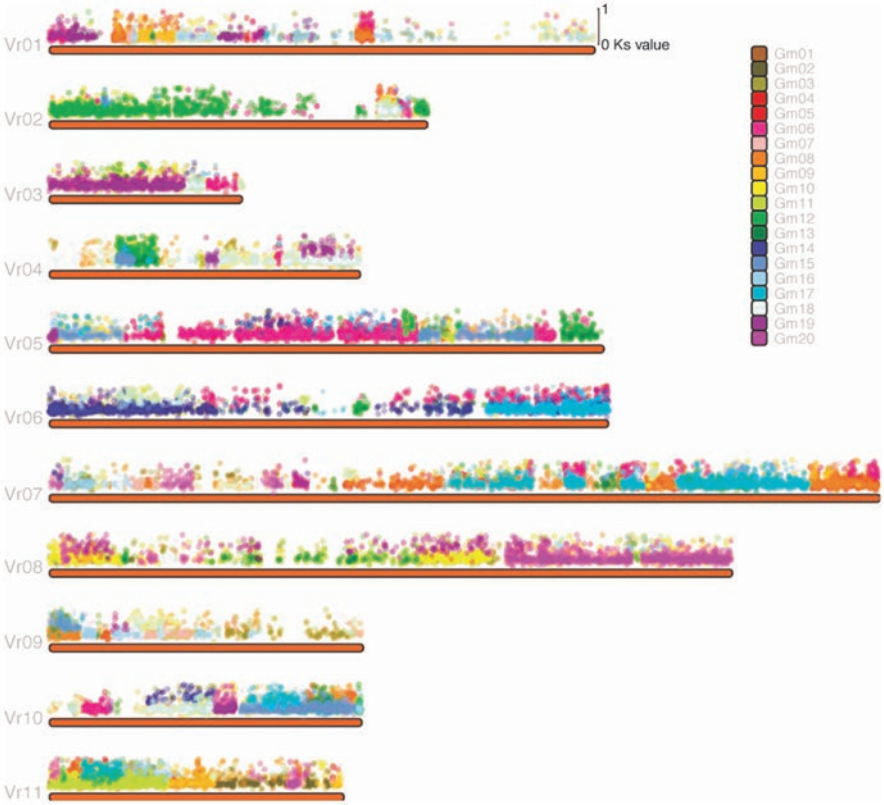

Fig. 10.3 Distribution of synteny blocks between mung bean and soybean on the mung bean chromosomes. (Source: Kang et al. 2014)

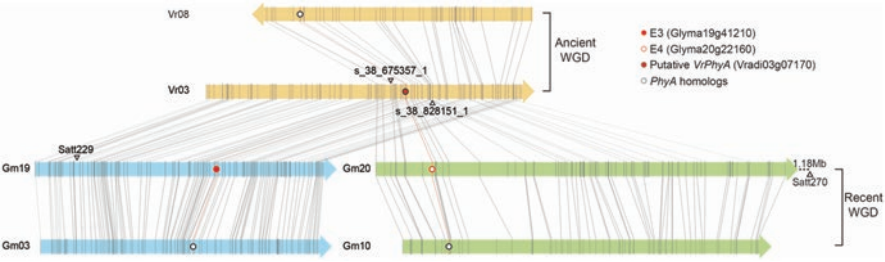

Fig. 10.4 Identification of a candidate gene in a QTL region using translational genomics. (Source: Hwang et al. 2017)

10.5 Genetic Engineering

10.5.1 Limitations of Conventional Breeding

Efforts to develop new mung bean varieties via traditional breeding have achieved limited success due to the narrow genetic variation in this crop, as mung bean is a self-pollinated species, and only a few parental lines have been used repeatedly in breeding programs. In addition to increasing genetic diversity using wild relatives as breeding materials, the use of biotechnological tools for improving mung bean cultivars has emerged as a powerful way to overcome bottlenecks in mung bean breeding, as these tools enable key genes to be introduced into elite plant lines.

10.5.2 Regeneration in Mung Bean

The ability to regenerate whole plants through tissue culture allows genes to be transferred into plant cells, followed by regeneration to produce stably transformed plants (Chandra and Pental 2003). Progress in transgenic research in mung bean has been very slow due to its highly recalcitrant nature in tissue culture and its very low frequency of regeneration, especially after transformation (Dita et al. 2006; Eapen 2008; Varshney et al. 2015). Although several research studies have reported regeneration protocols for mung bean via embryogenesis (Kaviraj et al. 2006; Sivakumar et al. 2010) and organogenesis (Gulati and Jaiwal 1994; Himabindu et al. 2014; Rao et al. 2005), the regeneration efficiency is very low, except for a few reports using cotyledonary node explants (Amutha et al. 2006; Sagare and Mohanty 2015; Vijayan et al. 2006; Yadav et al. 2010). To date, there are only a few reports of the production of stably transformed mung bean where whole transgenic plants have been recovered and transgenes have been stably inherited and passed to subsequent generations (Baloda et al. 2017; Mahalakshmi et al. 2006; Sonia et al. 2007; Vijayan and Kirti 2012; Yadav et al. 2012).

10.5.3 Genetic Transformation

Genetic transformation in mung bean was first conducted using hypocotyls and primary leaves (Jaiwal et al. 2001). A binary vector containing the reporter gene *GUS* and the selection marker *nptII* was successfully transformed into mung bean. Mahalakshmi et al. (2006) developed a genotype-independent, high-frequency plant regeneration protocol for mung bean with a survival rate of ~90% and successfully transformed primary leaf explants. Subsequently, the insecticidal α-amylase inhibitor-1 gene from *Phaseolus vulgaris* and the bialaphos resistance (*bar*) gene were successfully expressed in mung bean using cotyledonary node explants (Sonia et al. 2007). After introducing a pathogenesis-related gene (*BjNPR1*) from mustard into

mung bean, transgenic mung bean plants showed resistance against fungal-related diseases (Vijayan and Kirti 2012). Yadav et al. (2012) transformed the *annexin 1 bj* gene into mung bean and the resulting transgenic plants showed improved drought stress tolerance. Transgenic mung bean plants with increased salt tolerance were obtained by introducing the *codA* gene into mung bean (Baloda et al. 2017).

Despite its recalcitrant nature in tissue culture and its low regeneration frequency, researchers have developed protocols for regenerating and transforming mung bean at high frequency. Although DNA modification of food crops is viewed negatively by consumers, genetic engineering can help save time and labor, thereby overcoming the limitations of traditional breeding. Advances in the development of biotechnological tools, such as clustered regularly interspaced short palindromic repeats (CRISPR) Cas9/dCas9, and their successful application to food crops might help mitigate public concerns while improving mung bean cultivars (Ran et al. 2013).

10.6 Mutation Breeding

10.6.1 Mutagenesis and Genetic Diversity

Conventional breeding methods have limited effects in enhancing yields in mung bean due to their low genetic variability within the existing germplasm. There has been a continuous decline in the genetic diversity of this crop, prompting breeders to induce mutations artificially. Inducing mutations using physical and chemical mutagens can be one of the most effective ways to create genetic variability. This technique has played a key role in modern plant breeding and genetic studies (Raina et al. 2016).

10.6.2 Cultivars Developed by Mutagenesis

Several mutagens have been used in mung bean, including ethyl methane sulfonate (EMS), sodium azide (SA), hydrazine hydrate (HZ) and gamma rays. Significant increases in the number of fertile branches and pods as well as seed yields were detected in mutant mung bean obtained through the use of EMS and HZ (Wani 2006). Several mung bean cultivars were treated with EMS and gamma rays, thereby generating genetic variability and leading to the development of new cultivars with high yields and increased resistance to bean fly infestation (Khan and Goyal 2009; Wani 2006). Mutants with variegated leaves or synchronous pod maturity were obtained through the use of gamma irradiation (Sangsiri et al. 2007; Tah and Saxena 2009). SA, EMS, and gamma rays were used to produce a wide range of viable morphological and physiological mutants (Auti and Apparao 2009). To date, 39 mutant mung bean cultivars have been officially released, including cultivars derived from crossing with mutant varieties (Table 10.3). The availability of these varieties

Table 10.3 List of mutant *Vigna radiata* (L.) Wil. varieties

Variety	Country	Local registration year	Mutagen	Characteristics
Dhauli (TT9E)	India	1979		High yield, early maturity, tolerance or resistance to MYMV
Pant Moong 2	India	1982	Irradiation with gamma rays	Resistance to MYMV, more pods, high yield
Co 4	India	1982	Irradiation of seeds with gamma rays	High yield, early maturity, resistance to drought
ML 26-10-3	India	1983	Irradiation of seeds with gamma rays	Resistance to MYMV, high yield
TAP-7	India	1983	Irradiation of seeds with gamma rays	Early maturity, resistance to mildew and leaf spot, high yield
NIAB Mung-28	Pakistan	1983	Irradiation of seeds with gamma rays	Early and uniform maturity, high yield
NIAB Mung 19-19	Pakistan	1985	Irradiation with gamma rays	Early maturity, determinate type, high yield, tolerance to MYMV
NIAB Mung 121-25	Pakistan	1985	Irradiation of seeds with gamma rays	Early maturity, determinate type, high yield
NIAB Mung 13-1	Pakistan	1986	Irradiation of seeds with gamma rays	Early maturity, shortness, more pods, harvest index, seed size, high yield
NIAB Mung 20-21	Pakistan	1986	Irradiation of seeds with gamma rays	Early maturity, shortness, harvest index, high yield, tolerance to MYMV, resistance to *Cerospora* leaf spot
Camar	Indonesia	1987	Irradiation of seeds with gamma rays	Resistance to *Cerospora* leaf spot, resistance to *Uromyces* sp., resistance to scrab diseases, high yield, tolerance to salinity and acid soil
NIAB Mung 54	Pakistan	1990	Irradiation with gamma rays	Early and synchronous maturity, non-shattering pods, tolerance to MYMV and CLS, large seed size, high yield
NIAB Mung 51	Pakistan	1990	Irradiation with gamma rays	Early and synchronous maturity, non-shattering pods, profuse hairiness, tolerance to MYMV and CLS, large seed size, high yield
Binamoog-1	Bangladesh	1992		

(continued)

Table 10.3 (continued)

Variety	Country	Local registration year	Mutagen	Characteristics
MUM-2	India	1992	Treatment with EMS	High yield, resistance to diseases
BM 4	India	1992		High yield, early maturity, tolerance or resistance to MYMV
NIAB Mung 92	Pakistan	1992	Hybridization with mutant NIAM Mung 36	Resistance to MYMV, early maturity, resistance to grain shattering, large seed size
LGG 450	India	1993		High yield, early maturity, tolerance or resistance to MYMV
LGG-407	India	1993		High yield, early maturity, tolerance or resistance to MYMV
Binamoog-2	Bangladesh	1994	Hybridization with gamma-ray induced mutant MB-55(4)	Large seed size, early and synchronous maturity, high yield, tolerance to leaf MYMV and *Cercospora* leaf spot
TARM-2	India	1994	Hybridization with a mutant RUM 5 obtained by gamma irradiation	High yield, medium late maturity, resistance to powdery mildew disease
TARM-18	India	1996	Hybridization with a mutant variety TARM-2	High yield, resistance to powdery mildew disease
Binamoog-3	Bangladesh	1997	Irradiation of hybrid seeds from cross (Mutant MB55-4 x AURDC line V1560D)	Seed yield, synchronous pod maturity, tolerance to MYMV and *Cercospora* leaf spot
Binamoog-4	Bangladesh	1997	Irradiation of hybrid seeds from cross (Mutant MB55-4 x AURDC line V1560D)	Seed yield, synchronous pod maturity, early maturing, dwarf plant type, tolerance to MYMV and *Cercospora* leaf spot
TARM-1	India	1997	Hybridization with a mutant RUM 5 obtained by gamma irradiation	High yield, resistance to powdery mildew disease, medium maturity
Binamoog-5	Bangladesh	1998	Irradiation of hybrid seeds from cross (Mutant MB55-4 x AURDC line V1560D)	High seed yield, synchronous pod maturity, tolerance to MYMV and *Cercospora* leaf spot

(continued)

Table 10.3 (continued)

Variety	Country	Local registration year	Mutagen	Characteristics
NIAB Mung 98	Pakistan	1998	Hybridization with mutant variety Mung 20-21 obtained by gamma rays	Resistance to MYMV and *Cercospora* leaf spot, high yield, medium seed size
AEM-96	Pakistan	1998		
Chai Nat 72	Thailand	1999	Irradiation with gamma rays	High yield, large grain size, resistance to fungal disease
Binamoog-6	Bangladesh	2005	Gamma irradiation of an advanced mutant line, VC-6173-10	Increased pod, reduced seed size, tolerance to leaf MYMV and *Cercospora* leaf spot
Binamoog-7	Bangladesh	2005	Treatment of seeds from Binamoog-2 with EMS	High seed yield, synchronous pod maturity, tolerance to MYMV and *Cercospora* leaf spot
TMB-37	India	2005		Early maturity, resistance to MYMV, high yield, large seed size,
NIAB MUNG 2006	Pakistan	2006	Hybridization with mutant NIAB Mung 92	Purple hypocotyl and stem, high number of pods and clusters, resistance to diseases
TM-96-2	India	2007	Hybridization with mutant variety TARM-2 obtained by irradiation with gamma rays	Resistance to powdery mildew disease and *Corynespora* leaf spot, early maturity
TJM-3	India	2007	Hybridization with a mutant variety TARM-1 obtained by irradiation with gamma rays	Resistance to MYMV, powdery mildew and *Rhizoctonia* root-rot disease, early maturity, large seeds
TM 2000-2	India	2010		Resistance to powdery mildew
Binamoog-8	Bangladesh		Irradiation of seeds of advanced line MB-149 with gamma rays	Synchronous pod maturity
Binamoog-9	Bangladesh		Irradiation of seeds of BARI Mung-6 with gamma rays	Synchronous pod maturity
Chai Nut 84-1	Thailand			

Source: FAO/IAEA Mutant variety database, 2018 (https://mvd.iaea.org)

increases genetic diversity, and they provide breeding materials for conventional plant breeding, thus contributing to the genetic improvement of mung bean. The mutagens that were used to produce these varieties are not targeted to specific genetic regions, and the casual variations resulting from mutagenesis have not been identified. The availability of the mung bean reference genome combined with recent advances in targeted mutagenesis and sequencing techniques will enable researchers and breeders to identify the casual variations induced by mutagens, thereby facilitating forward genetics analysis to characterize the links between genes and phenotypes (Kang et al. 2014; Ran et al. 2013). Mutation-assisted plant breeding will play a crucial role in the generation of optimized crop cultivars to migrate the threats posed by global climate change and food shortages.

10.7 Diseases in Mung Bean

10.7.1 Impact of Pathogens

Numerous types of pathogens affect mung bean, including viruses, fungi, bacteria and nematodes. Diseases in mung bean can affect various tissues, including but not limited to seeds, leaves, flowers, roots and stems. Pathogens can reduce mung bean yields by affecting nearly all stages of development, including seed germination, shoot development, flower development and so on. These reduced yields can have a detrimental impact on the wellbeing of the many people dependent on mung bean. A complete list of pests that use mung bean as a major and minor host can be found at the Centre for Agriculture and Bioscience International (CABI, https://www.cabi.org/) (Tables 10.4 and 10.5). However, few cultivars have been bred for full resistance against such pathogens, and few studies have focused on the identification and characterization of pathogens of mung bean.

10.7.2 Viral Pathogens

One of the best-studied viruses in mung bean is the geminivirus mung bean yellow mosaic virus (MYMV). This virus is composed of two DNA components, DNA 1 and DNA 2, each comprising roughly 2.7 kb; the full reference genome for MYMV is currently available (Morinaga et al. 1993). The leaves of MYMV-infected plants show yellow discoloration. MYMV is the most devastating virus in mung bean, with yield losses of up to 85% (Karthikeyan et al. 2014). There are currently no fully-resistant cultivars available, and even highly resistant lines show high levels of variation, depending on the geographic location (Nair et al. 2017). MYMV is transmitted by the tobacco whitefly (*Bemisia tabaci* Genn.), a vector of many other geminiviruses as well, including other mung bean viral diseases such as mung bean

Table 10.4 List of pests that use mung bean as a major host (CABI, https://www.cabi.org/)

Pest	Details, common name	Pest	Details, common name
Acherontia styx	Small death's head hawkmoth	*Macrophomina phaseolina*	Charcoal rot of bean/tobacco
Agrius convolvuli	*Convolvulus* hawkmoth	*Maruca amboinalis*	
Alfalfa mosaic virus	Alfalfa yellow spot	*Medythia suturalis*	Striped bean flea beetle
Amrasca		*Megalurothrips distalis*	
Amrasca biguttula	Indian cotton jassid	*Megalurothrips usitatus*	Bean flower thrips
Amsacta moorei	Tiger moth	*Mung bean yellow mosaic virus*	
Aphis craccivora	Groundnut aphid	*Nezara viridula*	Green stink bug
Blackeye cowpea mosaic virus	BICMV	*Ophiomyia phaseoli*	Bean fly
Boeremia exigua var. *exigua*	Leaf spot	*Orgyia postica*	Cocoa tussock moth
Borreria latifolia	Broadleaf buttonweed	*Oxycetonia versicolor*	
Broad bean wilt virus	*Lamium* mild mosaic	*Phyllophaga*	White grubs
Cadophora gregata	Brown stem rot of soybean	*Pratylenchus brachyurus*	Root-lesion nematode
Callosobruchus	Pulse beetle	*Rhizobium radiobacter*	Crown gall
Callosobruchus analis	Weevil (bean)	*Rhizobium rhizogenes*	Gall
Callosobruchus chinensis	Chinese bruchid	*Riptortus*	
Callosobruchus maculatus	Cowpea weevil	*Riptortus clavatus*	Bean bug
Callosobruchus phaseoli		*Riptortus dentipes*	Pod-sucking bug
Chalara elegans	Black root rot	*Riptortus linearis*	
Choanephora cucurbitarum	*Choanephora* fruit rot	*Rottboellia cochinchinensis*	Itch grass
Colletotrichum dematium	Leaf spot	*Scirtothrips dorsalis*	Chilli thrips
Colletotrichum truncatum	Soybean anthracnose	*Sclerotinia sclerotiorum*	Cottony soft rot
Commelina benghalensis	Wandering Jew	*Spodoptera littoralis*	Cotton leafworm
Cowpea severe mosaic virus		*Spodoptera litura*	Taro caterpillar
Cucumber mosaic virus	Cucumber mosaic	*Stegobium paniceum*	Drugstore beetle
Curtobacterium flaccumfaciens pv. *flaccumfaciens*	Bacterial tan spot	*Thanatephorus cucumeris*	Many names depending on host
Erysiphe diffusa	Soybean powdery mildew	Tomato spotted wilt virus	Tomato spotted wilt
Gonocephalum	False wireworm	Urd bean leaf crinkle virus	
Heterodera cajani	Pigeon pea cyst nematode	*Xanthium spinosum*	Bathurst burr
Lampides boeticus	Pea blue butterfly	*Xanthomonas campestris* pv. *vignaeradiatae*	

Table 10.5 List of pests that use mung bean as minor host (CABI, https://www.cabi.org/)

Pest	Common name
Acyrthosiphon pisum	Pea aphid
Aphis gossypii	Cotton aphid
Aproaerema modicella	Groundnut leaf miner
Aspergillus niger	Black mold of onion
Athelia rolfsii	Sclerotium rot
Bean common mosaic necrosis virus	
Bean common mosaic virus	Common mosaic of beans
Cleome rutidosperma	Fringed spiderflower
Cochliobolus lunatus	Head mold of grasses, rice and sorghum
Cochliobolus sativus	Root and foot rot
Colletotrichum capsici	Leaf spot of peppers
Colletotrichum lindemuthianum	Anthracnose of bean
Corcyra cephalonica	Rice meal moth
Cowpea aphid-borne mosaic virus	
Cuscuta campestris	Field dodder
Cyrtozemia dispar	
Dactyloctenium aegyptium	Crowfoot grass
Etiella zinckenella	Pea pod borer
Glomerella cingulata	Anthracnose
Haematonectria haematococca	Dry rot of potato
Heterodera glycines	Soybean cyst nematode
Hilda patruelis	Groundnut hopper
Holotrichia serrata	White grub
Hoplolaimus indicus	Lance nematode
Leveillula taurica	Powdery mildew of cotton
Melanagromyza obtusa	Pod fly
Melanagromyza sojae	Soybean stem miner
Meloidogyne ethiopica	Root-knot nematode
Meloidogyne incognita	Root-knot nematode
Olpidium brassicae	Lettuce big vein
Ophiomyia centrosematis	Stem fly
Peanut stripe virus	Groundnut stripe disease
Phoma pinodella	Leaf spot of pea
Phytoplasma aurantifolia	Lime witches' broom phytoplasma
Podosphaera xanthii	Powdery mildew of cucurbits
Pratylenchus penetrans	Nematode, northern root lesion
Pseudocercospora griseola	Angular bean leaf spot
Pseudomonas savastanoi pv. *phaseolicola*	Halo blight of beans
Pythium debaryanum	Damping-off
Rotylenchulus reniformis	Reniform nematode
Scutellonema bradys	Yam nematode
Scutellonema clathricaudatum	

(continued)

Table 10.5 (continued)

Pest	Common name
Sitophilus oryzae	Lesser grain weevil
Thysanoplusia orichalcea	Slender burnished brass moth
Tribolium castaneum	Red flour beetle
Trichoplusia ni	Cabbage looper
Uromyces appendiculatus	Bean rust
Verticillium dahliae	Verticillium wilt
Xanthomonas axonopodis pv. *phaseoli*	Bean blight

yellow India mosaic virus (MYIMV) (Baker et al. 2013; Markham et al. 1994). Fortunately, as tobacco whitefly is one of the most important crop disease vectors, its occurrence, distribution and transmission mechanisms are well understood, which could potentially help combat the spread of MYMV in mung bean. There is no clear consensus on whether the MYMV resistance genes are monogenic or digenic traits, which in theory could make breeding resistant plants easier; however, variations in pathogen load and other factors could make the breeding process more difficult (Alam et al. 2014).

10.7.3 Fungal Pathogens

Traditionally, fungi are not well-studied. Only recently, owing to rapid improvements in molecular techniques such as polymerase chain reaction (PCR) and NGS, have mycologists been able to grasp the scale of this kingdom and to accurately identify fungal species (Blackwell 2011; Hawksworth and Rossman 1997). This improvement in molecular techniques will indeed lead to better fungal identification and allow for better diagnosis of fungal diseases in mung bean. One of the most important fungal pathogens is *Cercospora canescens* Ellis & G. Martin, which causes the foliar disease known as *Cercospora* leaf spot (CLS) in mung bean and other agriculturally-important plants. *Cercospora canescens* belongs to the Ascomycota phylum, which contains many other important plant and human pathogens. This pathogen also infects other closely-related legume species such as *Vigna unguiculata* (cowpea) and *Phaseolus vulgaris* (common bean) (Dhingra and Asmus 1983; Williams 1975). Even though it can reduce yields by approximately 40%, there is little consensus on the genetic basis for CLS resistance, and whether the resistance gene is monogenic or multigenic is a source of disagreement (Chankaew et al. 2011). What makes breeding CLS-resistant lines or cultivars more difficult is the variation of *C. canescens* among strains, even when isolated from the same region and the same host (mung bean). This pathogen shows variation in terms of

pigmentation and mycelial characteristics, as well as genetic markers such as ITS and RAPD markers (Joshi et al. 2006). Indeed, the natural variation in this species may hinder the development of CLS-resistant lines.

10.7.4 Bacterial Pathogens

Traditionally, isolating and culturing pure microorganisms has been difficult, especially for obligate pathogens, as artificial or natural medium may not be able to replicate the niche of the pathogen due to our limited understanding of a particular organism (Stewart 2012). *Xanthomonas axonopodis* pv. *phaseoli*, previously known as *Xanthomonas phaseoli*, belongs to the class of gammaproteobacteria that causes bacterial leaf blight. Depending on the pathovar, this bacterium can affect a wide range of plant species, from legumes (pv. *phaseoli*) to citrus (pv. *citri*). *Xanthomonas axonopodis* affects a wide range of hosts, including common beans, mung bean, black gram, cowpea and so on. One of the most effective prevention methods for *X. axonopodis* is pretreating seeds since they represent the primary source of this pathogen (Baker and Smith 1966). *Xanthomonas axonopodis* has potentially devastating effects on crop yields and poses one of the major constraints to common bean production in Ethiopia, as it causes common bean blight (Belete and Bastas 2017). However, it is not yet clear whether this is also the case in mung bean.

10.7.5 Nematodes Affecting Mung Bean

Nematodes, belonging to the kingdom Animalia, include various pathogens affecting animals and plants. Although they are often viewed as having harmful impacts on agriculture or human health, some nematodes play important roles in ecology, such as the essential cycling of nutrients and toxins alike (Barker et al. 1994). *Heterodera cajani* Koshy (pigeon pea cyst nematode, also referred to as *Heterodera vigni* Edward & Misra), is a nematode that infects crops such as pigeon pea, mung bean and some *Phaseolus* species. Nematodes can affect both the dry matter content and grain yield of crops. In some cases, up to 86% of grain yield can be lost due to nematodes. Furthermore, to properly control nematodes, a population-monitoring system is required throughout the growth period (Saxena and Reddy 1987). Various methods have been tested for their nematocidal efficiency against *H. cajani*, including using fungi or essential oil derived from herbs (Sangwan et al. 1990; Siddiqui and Mahmood 1996).

10.8 Conclusion and Prospects

As mung bean has become an important crop in many Asian countries due to its high nutritional contents, most studies in mung bean have focused on yield-related traits, such as resistance to yellow mosaic disease (Kitsanachandee et al. 2013), bruchid (Mei et al. 2009), *Cercospora* leaf spot (Chankaew et al. 2011) and other domestication-related traits (Isemura et al. 2012). Since mung bean is mainly cultivated in developing countries, relatively little attention has been paid to this crop, and progress in mung bean breeding has been slow due to the lack of genomic information. In 2014, the reference genome sequence of mung bean was published, allowing breeders and researchers to study the genetic and genomic backgrounds of agronomically-important traits. A number of markers and putative QTLs have been developed based on this genome sequence, along with phenotypic data, represent valuable resources for identifying and locating casual genes for important traits. The use of genomic information from other legume species, especially soybean, will help researchers investigate QTLs and identify candidate genes in mung bean through analysis of sequence similarity and synteny.

A mung bean core collection consisting of 1481 accessions developed by AVRDC-The World Vegetable Center has been used to evaluate various agronomic traits, such as plant height, flowering time, 1000 seed weight and so on (Schafleitner et al. 2015). This collection could be valuable for genome-wide association studies (GWAS) to further detect promising candidate genes.

Collections of wild mung beans from diverse origins grown under different climatic conditions are needed. Analysis of the genetic diversity of these lines would help breeders develop cultivars that can grow in semiarid regions by investigating allelic variations in beneficial traits, especially drought tolerance. As mung bean is a fast-growing crop with a small genome, it represents a good model system for genomic studies of legume species. The recent availability of a mung bean reference genome sequence has facilitated translational genomics studies using the well-studied soybean genome, which could in turn facilitate QTL analysis, GWAS and candidate gene identification in mung bean.

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Appendices

Appendix I: Research Institutes Maintaining Mung Bean Germplasms

Institution	Country	Contact information and website
AVRDC-The world vegetable center	Taiwan	http://avrdc.org
National bureau of plant genetic resources of the Indian council of agricultural research	India	http://www.nbpgr.ernet.in
Institute of crop germplasm resources, Chinese academy of agricultural sciences	China	http://www.cgris.net/cgrisngb.html
Plant genetic resources conservation unit, University of Georgia	USA	https://www.ars.usda.gov/southeast-area/griffin-ga/pgrcu/
University of the Philippines	Philippines	https://www.up.edu.ph/
Rural Development Administration	South Korea	https://www.rda.go.kr

Appendix II: List of Mung Bean Mini Core Collection Provided by AVRDC-The World Vegetable Center

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI000020	4.8	1.9	28	40	53	9	8.8	71.47	Southeast Asia
VI000099	4.1	1.6	22	56	43	8.3	12	32.39	South Asia
VI000105	4.3	1.5	25	42	43	7.2	10.8	35.29	South Asia
VI000164	4.1	1.5	30	34	43	5.6	10.2	29.69	Southwest Asia
VI000170	4.2	1.4	14	33	40	7.5	10	33.71	Southwest Asia
VI000175	4.8	1.8	26	43	43	7.6	10.8	38.67	South Asia
VI000188	4.5	1.5	19	43	40	7.1	11.6	28.88	Southwest Asia
VI000203	4.2	1.5	21	35	43	7.4	11.4	30.98	Southwest Asia
VI000212	4.2	1.6	25	43	43	5.3	9.6	27.34	North America
VI000232	4.9	1.7	20	33	40	8.3	10.6	37.71	Southwest Asia
VI000238	4.4	1.5	21	45	43	6.7	11.4	30.19	Southwest Asia
VI000253	4.2	1.6	19	58	46	8	12.8	31.13	South Asia
VI000316	4.5	1.5	18	34	43	7	9.8	31.21	Southwest Asia
VI000317	4.1	1.4	14	40	43	7.7	12.2	33.87	Southwest Asia
VI000319	4	1.4	17	34	43	6.7	10.8	30.92	Southwest Asia
VI000380	5.8	2.3	23	47	43	9.7	9	70.69	Southeast Asia
VI000461	4.2	1.6	26	54	46	7.8	12.2	32.09	Southeast Asia
VI000470	5	2	19	35	43	8	8.6	66.94	Southwest Asia

(continued)

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI000532	4.4	1.5	19	49	46	7.6	14.4	26.46	South Asia
VI000537	4	1.5	25	47	46	7.1	12.6	25.9	South Asia
VI000542	3.7	1.5	18	28	43	6.5	10.6	25.29	South Asia
VI000551	4.1	1.5	22	41	43	6.7	11.8	28.62	South Asia
VI000554	4.2	1.6	21	43	43	7.1	11.6	30.23	South Asia
VI000559	4.4	1.4	23	43	43	7.1	11.6	29.35	South Asia
VI000578	4.3	1.4	28	63	53	7.1	10.4	26.99	South Asia
VI000589	3.9	1.5	22	39	40	7.1	11.4	33.25	South Asia
VI000616	4.7	1.9	20	50	39	7.6	13.6	32.76	South Asia
VI000618	4	1.5	25	29	40	6.1	8.6	31.83	South Asia
VI000625	3.9	1.6	21	51	43	7.5	11.6	35.66	South Asia
VI000680	5.1	2	23	33	40	7.3	11.4	39.58	North America
VI000723	4.5	1.6	22	29	40	7	10.6	29.85	Southwest Asia
VI000732	4.9	1.9	19	35	43	6.6	9	39.7	South Asia
VI000735	4.6	1.8	21	41	47	6.9	10.6	39.3	South Asia
VI000736	5.4	2	26	60	53	9.9	11.4	60.78	South Asia
VI000749	4.9	1.7	23	51	43	7.7	11	31.98	South Asia
VI000764	4.7	1.7	20	61	43	6.6	10	37.88	South Asia
VI000766	4.4	1.7	23	46	40	7.1	11	34.56	South Asia
VI000805	4.9	2	24	39	43	8.1	11.8	48.38	South Asia
VI000815_1	4	1.5	19	26	53	8.2	9.4	34.74	South Asia
VI000818	5	1.9	22	44	40	7.2	10.6	30.97	South Asia
VI000852	4.3	1.6	17	20	40	7.1	10.8	30.94	South Asia
VI000938	4.3	1.4	16	44	47	7.1	9.8	33.49	South Asia
VI000942	4.4	1.8	17	41	40	8.8	10.8	46.06	South Asia
VI000953	5.1	2.2	24	44	43	8.6	10.8	66.37	South Asia
VI000981	5.1	1.8	20	33	42	7	10.8	38.47	Southeast Asia
VI001023	5.4	2	18	43	43	8.1	12.2	34.71	South Asia
VI001066	4.6	1.9	21	39	53	8.6	11.8	40.68	Oceania/Pacific
VI001096	5.5	2	21	37	43	8	12	52.69	Oceania/Pacific
VI001124	5.6	2.4	28	58	45	7.9	9.6	65.3	Oceania/Pacific
VI001126	4.8	1.8	47	56	53	8.6	13.6	39.77	Oceania/Pacific
VI001162	4.8	1.7	13	47	42	6.4	11	27.34	Oceania/Pacific
VI001191	5	1.9	26	50	46	9.9	13.8	52.93	Southeast Asia
VI001211	5.3	2.1	22	50	46	7.7	9.8	53.68	Southeast Asia
VI001221	5.6	2.2	28	45	44	9.1	10.6	69.72	Southeast Asia
VI001244	5.3	2.4	26	43	44	8.7	7.4	74.78	Southeast Asia
VI001268	5.1	1.8	20	39	46	6.5	10	34.34	South Asia
VI001282	4.9	1.7	21	43	43	7.4	13	31.64	South Asia
VI001284	5	1.7	21	42	43	5.8	8.8	31.7	South Asia
VI001339	5.9	2.3	28	61	46	9.8	10.8	64.42	Southeast Asia
VI001385	4	1.3	27	46	53	6.8	11.4	29.29	South Asia

(continued)

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI001400	4.6	1.6	23	58	46	6.6	10.6	34.27	South Asia
VI001403	4.1	1.6	35	38	53	7.5	13	32.22	South Asia
VI001406_1	3.9	1.5	17	49	43	7	9.8	32.79	South West Asia
VI001408	4	1.5	21	52	43	7.4	11.6	30.18	South Asia
VI001411	4.5	1.5	25	49	43	6.3	10.8	27.38	South Asia
VI001412	4.8	1.8	28	66	47	7.2	11	33.41	South Asia
VI001419	4.4	1.8	21	50	43	6.8	10.6	28.78	South Asia
VI001435	4.6	1.7	18	37	43	6.4	8.2	31.76	North America
VI001448	3.7	1.5	15	58	43	6.9	10.4	21.15	South Asia
VI001471	4.2	1.5	27	43	43	7.1	9.6	33.54	South Asia
VI001482	5.2	1.8	21	45	43	7.8	12.8	31.99	South Asia
VI001490	4.3	1.6	15	43	40	6.6	10.6	29.79	South West Asia
VI001509	4.4	1.6	17	40	43	6.6	12	32.21	South West Asia
VI001514	4.7	1.7	18	48	43	7	11.4	31.03	South Asia
VI001520	4.1	1.4	18	24	40	6.7	11.8	23.85	South Asia
VI001533	4.6	1.6	27	59	53	7.3	12.4	29.89	South Asia
VI001535	4.6	1.7	22	56	45	6.8	11.8	52.82	South Asia
VI001539_1	3.9	1.4	39	71	55	7.6	11	28.62	South Asia
VI001548	4.6	1.7	33	73	53	7.1	11.2	30.45	South Asia
VI001556_1	4.1	1.3	38	72	43	6.6	10	27.98	South Asia
VI001557	4.5	1.6	18	39	47	6	8.4	30.11	North America
VI001562	4.1	1.5	14	36	47	6.9	10.2	29.11	South Asia
VI001576	4.1	1.4	26	52	43	8.6	12.8	28.51	South Asia
VI001579	4.8	1.7	20	48	40	7.1	13	34.95	South Asia
VI001605	4.4	1.7	21	50	43	6.9	11	31.39	South Asia
VI001612	4.7	1.8	22	41	45	6.7	9.4	30.8	unknown
VI001628	4.9	1.8	21	44	43	6.5	11.2	28	South Asia
VI001651	4.2	1.6	18	34	44	6.1	8.6	33.35	South Asia
VI001652	4.3	1.4	17	44	46	6.6	11.6	33	South Asia
VI001654	4.1	1.5	19	48	47	7.1	10.8	31.85	South Asia
VI001678	4.9	1.9	14	23	41	6.7	10.8	36.83	South Asia
VI001692	4.3	1.4	23	29	43	7.1	11.4	27.29	South Asia
VI001698	5.1	2	20	31	42	7.7	13.2	32.92	South Asia
VI001728	4.4	1.7	18	34	43	5.7	10.4	28.18	South Asia
VI001733	5.3	2	18	41	42	6.9	9.2	40.23	South Asia
VI001743	4.3	1.5	14	36	43	6.8	12.2	31.84	South Asia
VI001756	4.6	1.7	19	45	44	7.4	12	34.48	South Asia
VI001762	4.3	1.5	20	48	45	6.6	11.8	31.9	South Asia
VI001806	4.4	1.5	24	42	40	6.3	8.8	28.48	Southwest Asia
VI001806_1	5.6	1.9	20	34	40	8.2	11.4	33.16	Southwest Asia
VI001820	4.2	1.7	20	50	48	7	11	32.08	Europe
VI001859	5.1	1.8	37	46	53	9.4	11	48.89	Southeast Asia

(continued)

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI001974	4.6	1.8	21	33	44	7.2	11.4	36.62	East Asia
VI001993	4.5	1.9	24	42	45	7.7	11.6	37.51	East Asia
VI002009	4.1	1.6	17	25	44	6.9	11	33.63	South Asia
VI002012	4.7	1.8	22	21	46	7.6	8.8	33.21	South Asia
VI002051	4.9	1.7	26	59	46	6.7	10.8	36.36	South Asia
VI002063	5.1	1.9	38	49	46	9.7	13.2	45.67	North America
VI002173	4.6	1.6	20	56	48	7.3	11.4	36.8	South Asia
VI002173_1	4.8	1.8	23	51	48	7.5	12	32	South Asia
VI002176	4.6	1.7	17	37	40	7.7	13.2	31.1	South Asia
VI002176_1	4.4	1.8	18	43	40	7.2	12.2	34.2	South Asia
VI002190	4.3	1.6	19	22	43	6.4	10.6	30.13	South Asia
VI002195	5.4	2.1	29	43	43	8.8	11.2	57.9	Southeast Asia
VI002197	5.3	1.9	20	40	44	7.8	10.6	37.7	East Asia
VI002206	5.2	2.1	27	35	42	8.7	11.8	50.01	Southeast Asia
VI002239	4	1.5	16	25	42	5.2	5.8	34.3	Southwest Asia
VI002274	5.9	2	14	53	43	5.5	6.4	56.2	Southwest Asia
VI002284	3.9	1.5	13	28	41	6.6	11	34.1	Southwest Asia
VI002402	4.6	1.7	24	32	43	8.1	12.6	50.5	Southeast Asia
VI002432	4.8	2	18	27	50	9.1	11	57.4	Southeast Asia
VI002437	4.3	1.6	23	46	46	7.5	12.4	35.6	East Asia
VI002456	5.2	1.7	12	40	43	11.2	13.6	52	East Asia
VI002469	4.4	1.9	23	66	50	8.8	13	51.6	Southeast Asia
VI002487	4.6	1.5	20	51	43	7.5	12.2	31	Southwest Asia
VI002523	5.2	2.2	18	48	60	7.9	11.8	52.5	Southeast Asia
VI002529	5	2	19	63	50	5	7.4	57.1	Southeast Asia
VI002532	4.8	1.9	21	28	44	7.7	8.6	38.2	South Asia
VI002537	4.7	1.9	16	18	44	6.8	10.2	43.3	Southwest Asia
VI002569	5.2	1.8	22	50	50	8.6	11.4	53.5	Africa
VI002587	5.3	1.8	14	26	42	7.8	11.4	54.1	Oceania/Pacific
VI002611	4.5	1.9	19	46	49	8.1	10.4	48.3	Southeast Asia
VI002646	4.5	1.8	19	32	50	7.9	9	56.5	Southeast Asia
VI002647	5.1	2.1	26	36	49	8.9	8.6	69.3	Southeast Asia
VI002672	5	2	22	32	49	8.3	10.4	54.3	Southeast Asia
VI002739	5	1.9	19	24	49	9	9	68.3	Southwest Asia
VI002802	3.7	1.3	17	22	40	6.2	10.4	29.3	Southwest Asia
VI002859	4	1.4	12	29	40	6.5	10.4	33.8	Southwest Asia
VI002860	4	1.5	10	23	39	5.6	8.4	31.3	Southwest Asia
VI002872	4.6	1.7	13	41	41	6.8	12.2	36.2	Southwest Asia
VI002877	5.2	1.8	25	51	44	8.2	12.4	43.9	Southwest Asia
VI002894	4.4	1.7	27	45	49	8.2	13.6	40.4	Southwest Asia
VI002926	4.2	1.5	23	47	45	7.1	11	32.2	South Asia
VI002934	4.6	1.7	30	54	45	7.9	13.4	34.9	South Asia

(continued)

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI002986	4.1	1.3	21	39	47	7	10.6	34.2	South Asia
VI002993	5	1.6	38	66	45	7.5	13	31.1	South Asia
VI002999	4.2	1.5	29	50	45	7.2	11.8	33.1	South Asia
VI003019	4.1	1.7	32	41	43	7.6	11.4	40	unknown
VI003019_1	4.3	1.7	34	49	44	7.3	11.2	42	unknown
VI003034	4.1	1.6	30	48	46	7.4	13.2	30.1	South Asia
VI003035	4.4	1.6	33	56	45	6.8	11.4	31.2	South Asia
VI003057	4	1.4	21	49	45	7.8	11.4	30.9	South Asia
VI003062	4.4	1.6	29	48	45	7.5	10.2	32	South Asia
VI003068	4.2	1.5	25	51	45	7.5	10.8	30.7	South Asia
VI003070	4.6	1.7	30	49	45	7.1	11.8	29.8	South Asia
VI003083	4.4	1.6	27	49	43	7.6	10.8	33.2	South Asia
VI003114	3.8	1.3	31	47	45	6.6	11.6	29.8	South Asia
VI003135	3.9	1.4	34	43	49	6.3	10	24.7	South Asia
VI003159	3.9	1.6	24	66	49	6.5	11.6	26.7	South Asia
VI003172	4.4	1.6	27	52	45	7.1	10.8	33.8	South Asia
VI003181	4.5	1.6	13	30	46	6.8	11.6	36.6	South Asia
VI003183	3.8	1.5	23	51	46	7.9	14.4	36	South Asia
VI003187	4.2	1.8	19	40	46	7.2	12.2	40	South Asia
VI003212	4.1	1.5	13	28	41	6.5	11	32.6	South Asia
VI003220	5.2	1.7	28	52	45	7.3	10.6	42	South Asia
VI003232	4.5	1.8	23	55	47	6.7	12.2	29.7	South Asia
VI003235	4.4	1.7	23	52	48	7.2	11	32.9	South Asia
VI003242	4.7	1.7	25	41	44	7.2	10.4	44.6	South Asia
VI003251	4.8	1.7	25	43	46	6.7	12.2	25.6	South Asia
VI003251_1	4.8	1.8	23	43	46	6.8	11.6	31.4	South Asia
VI003252	4.3	1.5	21	45	46	6.4	12.8	31.7	South Asia
VI003255	4.3	1.7	17	48	48	6.3	11.2	28.6	South Asia
VI003276	5.4	1.6	18	35	48	7.5	13	26.2	South Asia
VI003329	4.5	1.7	30	63	48	7.8	13.4	34.4	South Asia
VI003332	4.7	1.6	27	47	46	6.9	11.6	35.8	South Asia
VI003337	4.5	1.5	28	61	47	7.5	13	33.3	South Asia
VI003364	4.3	1.7	21	37	46	9.1	11.8	50.6	South Asia
VI003379	5.1	1.8	37	60	47	8	12.8	41.9	South Asia
VI003382	4.2	1.6	34	47	48	6.9	11.4	41.2	South Asia
VI003407	3.6	1.3	18	51	48	7.1	9	31.2	South Asia
VI003413_1	4.8	1.6	26	44	45	7.2	11.8	37.5	South Asia
VI003440	4.5	1.6	26	47	45	7	9.8	38.3	South Asia
VI003455	4.7	1.6	23	51	46	7.2	12	39.1	South Asia
VI003456	4.3	1.5	36	52	48	6.5	10	30.3	unknown
VI003465	4.1	1.7	21	48	47	7.4	11.8	33.6	South Asia
VI003470	3.7	1.4	34	52	55	6.9	11	25	South Asia

(continued)

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI003480	4.6	1.8	23	60	47	7.8	10.8	59.9	South Asia
VI003490	4	1.6	19	40	46	6	9.8	31.6	South Asia
VI003493	3.7	1.4	18	39	45	6.6	10.8	31	South Asia
VI003514	4.7	1.5	19	43	44	6.7	10.4	31.1	South Asia
VI003517_1	5.1	1.6	34	58	44	6.7	10.6	29.9	South Asia
VI003534	4.8	1.7	17	44	45	7.2	9	33.8	South Asia
VI003534_1	4.3	1.5	20	56	46	7.8	11.8	37.1	South Asia
VI003548	4.2	1.5	23	53	47	7	11.8	30.6	South Asia
VI003554	4.5	1.5	36	65	49	6.7	10.2	36.1	South Asia
VI003560_1	4.4	1.5	24	55	46	6.3	8.2	32.7	South Asia
VI003563	4.4	1.4	33	65	47	7.1	11.4	36.9	South Asia
VI003577	4.3	1.5	25	50	48	6.8	9.8	34.1	South Asia
VI003602	4.8	1.9	24	57	49	8	10.4	42.1	South Asia
VI003642	4.8	1.5	24	54	46	7.5	12	40.9	South Asia
VI003648	4.5	1.5	30	43	45	7.8	11.6	38.9	South Asia
VI003658	4.3	1.7	27	44	45	7	12	37.8	South Asia
VI003664	4.4	1.6	30	46	46	8.3	12.4	38.8	South Asia
VI003678	4.3	1.5	26	42	46	6.4	11.8	36.8	South Asia
VI003685	4	1.5	29	50	47	7.2	11.2	35.2	South Asia
VI003699	3.6	1.3	15	55	48	5.9	10.8	29.4	South Asia
VI003720	4	1.5	18	37	46	6.9	11.8	28.5	South Asia
VI003725	5.9	2	32	35	45	9.1	11.2	42.2	South Asia
VI003733_1	3.9	1.5	26	49	46	6.5	10.8	32.8	South Asia
VI003734_1	4.8	1.8	26	48	46	7.8	11.6	41.8	South Asia
VI003734_2	4.8	1.8	26	48	46	7.8	11.6	45.8	South Asia
VI003744	4.3	1.8	22	51	50	7.5	12	33.9	South Asia
VI003755	4.7	1.8	22	48	44	7.3	11.6	35.7	South Asia
VI003760	4.4	1.6	25	56	47	7.2	11.8	33.7	South Asia
VI003785	4.2	1.5	25	40	43	8	14.4	36.5	South Asia
VI003795	4.1	1.4	19	47	49	6.9	12.4	40.4	South Asia
VI003801	4.8	1.8	27	41	45	8.1	12.2	48.8	South Asia
VI003882	4.7	1.6	15	35	40	6.6	10	29.03	Southwest Asia
VI003886	4.4	1.5	25	45	43	7.6	10.4	41.47	South Asia
VI003886	4.8	1.8	23	35	43	7.5	9.6	39.04	South Asia
VI003893	4.8	1.7	35	53	53	6.9	11.6	38.08	South Asia
VI003894	4.5	1.6	20	58	43	7.4	12	31.73	South Asia
VI003907	4.2	1.6	19	19	40	7.4	11.8	35.07	Southwest Asia
VI003914	4.6	1.5	23	50	43	6.6	11.4	33.53	South Asia
VI003925	4.5	1.6	19	40	43	7	11.6	26.04	South Asia
VI003927	4.7	1.5	26	53	46	6.5	10.6	30.69	South Asia
VI003929	4.2	1.3	23	35	40	6.1	10.4	27.88	South Asia
VI003942	4.4	1.6	19	32	40	5.7	8.6	31.31	Southwest Asia

(continued)

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI003944	4.6	1.7	17	40	40	7.3	11	41.42	Southwest Asia
VI003947	4.9	2	23	46	40	7.6	11.4	42.72	South Asia
VI003948	4.8	1.9	23	43	40	7.6	12	34.05	South Asia
VI003951–2	4.1	1.6	15	46	40	8.3	14.4	36.95	South Asia
VI003954	4.5	1.7	24	35	40	6.9	11	36.55	South Asia
VI003957	4.5	1.6	28	59	43	6.8	11	32.88	South Asia
VI003958	4.6	1.6	25	41	43	7.5	12	33.92	South Asia
VI003959	4.4	1.6	26	56	43	7.4	11.8	31.55	South Asia
VI004006	4.1	1.4	16	52	43	6.8	13.2	30.76	South Asia
VI004010	4.5	1.5	20	50	43	7.7	10.6	37.28	South Asia
VI004024	5	1.7	19	51	47	8.4	11.4	50.5	Oceania/Pacific
VI004044_1	4.2	1.6	16	38	43	7.1	11.8	30.78	South Asia
VI004045	4.3	1.5	19	40	43	7.6	13.4	27.4	South Asia
VI004048_1	4	1.4	16	33	39	6.6	11.4	25.76	South Asia
VI004069	4.7	1.8	25	50	43	7.7	12.8	38.24	South Asia
VI004096	3.9	1.4	25	53	53	6.9	10.8	30.15	South Asia
VI004096_1	3.7	1.4	30	59	53	7.3	10.8	32.04	South Asia
VI004129	3.7	1.6	19	26	43	5.4	9.4	25.66	unknown
VI004138	4.5	1.5	19	49	40	7.3	11.4	39.96	South Asia
VI004145	4.2	1.5	14	28	40	5.8	10.2	32	Southwest Asia
VI004184	4.8	1.7	28	30	44	7.8	12.6	34.3	Europe
VI004243_2	4.5	1.7	19	24	40	6.6	10.4	37.4	Southwest Asia
VI004244	4.8	1.7	30	24	44	6.2	9.4	34.4	South Asia
VI004297	4.3	1.6	18	25	40	6.1	10.2	37.5	Southwest Asia
VI004302	4.3	1.6	16	25	46	6.3	10.4	38.2	Southwest Asia
VI004307	3.8	1.5	19	23	40	6.4	10.8	37.1	Southwest Asia
VI004312	4.5	1.5	21	27	39	7.2	11.2	38.1	South Asia
VI004347_1	4	1.5	20	22	40	6.1	10.6	36.8	South Asia
VI004351	4.2	1.4	20	18	41	6.5	10	34.3	South Asia
VI004423	4.2	1.5	18	21	40	5.8	9.2	34	Southwest Asia
VI004432	3.8	1.5	20	26	40	6	9	37.1	Southwest Asia
VI004480	4.3	1.6	17	20	41	6.3	9.8	34.4	Southwest Asia
VI004639	4.3	1.5	19	29	39	6.2	8.8	36	Southwest Asia
VI004666	4.3	1.5	15	35	40	7.3	10.8	35.2	Southwest Asia
VI004691	3.7	1.5	19	29	40	6.4	11.2	36.7	Southwest Asia
VI004694	4.5	1.8	19	35	40	6.4	10.2	37.9	Southwest Asia
VI004710	3.4	1.4	19	29	43	6.9	9.8	40.7	Southwest Asia
VI004734	4	1.6	16	20	40	5.3	6.2	38.3	Southwest Asia
VI004743	4.5	1.5	24	59	48	7.1	10	32.5	South Asia
VI004789	4.6	1.5	24	54	47	7.7	11.8	32.7	South Asia
VI004810	4.2	1.3	15	33	46	7.3	10.6	36.8	South Asia
VI004811	4.3	1.4	19	36	47	6.9	11.2	30.4	South Asia

(continued)

AVRDC genebank number	Characteristics[a]								Origin
	PLL	PLW	PHF	PHM	DF	PL	SP	SW	
VI004822	3.7	1.3	22	42	45	7	10.4	29.7	South Asia
VI004838	4.1	1.5	15	48	45	6.6	12.2	33.8	South Asia
VI004842	4.3	1.4	21	47	47	7.4	11.8	34.4	South Asia
VI004853	4.8	1.6	17	46	43	7.1	11.8	34	South Asia
VI004871	3.9	1.4	21	46	48	7	11	36.8	South Asia
VI004877	4	1.4	21	48	48	7.9	12	35.7	South Asia
VI004915	4.3	1.4	16	42	45	6.8	11.4	42.7	South Asia
VI004931	4.4	1.4	21	46	46	7.4	10.4	36.4	Southwest Asia
VI004933	5	1.7	22	60	46	7.9	11.4	36.6	Southwest Asia
VI004934	4.8	1.5	21	56	46	6.8	10.8	36.1	Southwest Asia
VI004937	4.3	1.5	25	59	46	7.3	11	35.4	Southwest Asia
VI004942	5.1	1.8	21	47	46	7.6	11	41.8	Southwest Asia
VI004954	5.2	1.8	25	49	44	7.7	11.8	47.1	Southwest Asia
VI004956	4.6	1.6	19	54	46	7.8	11.6	36.2	Southwest Asia
VI004957	4.6	1.5	21	53	47	7.5	11	35.5	Southwest Asia
VI004958	4.4	1.5	18	49	47	7.8	11.6	41.1	Southwest Asia
VI004965	4.7	1.5	23	46	45	7.6	10.8	32.1	Southwest Asia
VI004968	5	1.7	20	51	45	6.7	10	33.8	Southwest Asia
VI004969	4.6	1.6	23	52	45	6.7	10.6	34.8	Southwest Asia
VI004973	4.3	1.5	21	57	47	7.3	10	30.9	South Asia
VI005022	4.2	1.5	16	57	46	6.2	8.8	33.3	South Asia
VI005024	4.5	2.1	19	78	48	5.6	7.6	48.1	East Asia
VI005030	4.3	1.7	66	90	60	7.9	10.6	36.1	Central America
VI005041	5.8	1.8	20	39	46	8.8	9.8	64.6	unknown
VI005066	4.1	1.4	14	34	46	7.7	10.4	34.9	South Asia
VI014178	3.7	1.3	67	94	64	8.3	11.8	33	Africa

Source: AVRDC-The World Vegetable Center, http://avrdc.org/the-avrdc-the-world-vegetable-center-mungbean-vigna-radiata-core-and-mini-core-collections/

[a]Abbreviations: *PLL* primary leaf length (cm), *PLW* primary leaf width (cm), *PHF* plant height at flowering (cm), *PHM* plant height at maturity (cm), *DF* days to 50% flowering, *PL* pod length (cm), *SP* seeds per pod, *SW* 1000 seed weight (g)

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