Germplasm Diversity and Breeding Approaches for Genetic Improvement of Mungbean

Rafiul Amin Laskar, Bhaskar Dowarah, and Nilofer Sheikh

Abstract In Asia, the mungbean [*Vigna radiata* (L.) R. Wilczek var. radiata] has been known to be an excellent source of nutritious food and income for the people. Mungbean growth in other locations, including Africa proper and South America, has been aided by the development of short-duration variants. Mungbean cultivation and production are limited by both biotic and abiotic causes. The main insect pests include aphids, bruchids, *Helicoverpa*, leafhopper, mirid, pod borers, stem fly, thrips, and whitefly. Halo blight, anthracnose, tan spot, yellow mosaic, and powdery mildew bacterial leaf spot and tan spot are the most common mungbean diseases. Drought, waterlogging, salt, and heat stress are among abiotic factors that impact mungbean productivity. Mungbean improvement through breeding techniques has indeed been crucial in generating resistant varieties against biotic and abiotic stressors. There are still numerous challenges to overcome, including the detection of consistent and reliable sources of resistance for specific features and qualities imparted by several genes. Understanding interactions of plants with the insect, pathogen, environment, and the essential factors conferring resistance to biotic and abiotic stressors might be greatly aided by the recent advancements in genetic improvement technologies. In this chapter, the present biotic and abiotic restrictions in cultivation and production of mungbean, as well as barriers to its genetic modification, and potential breeding approaches are examined.

Keywords Mungbean · Breeding · Environmental stresses · Insect-pests · Molecular approaches · Biotechnological tools

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1 Introduction

1.1 Taxonomic Classification and Geographic Distribution

Mungbean, commonly called green gram or simply gram, is a dicotyledonous angiosperm belonging to the family Fabaceae. The cultivated mungbean was given the name *Phaseolus radiatus* L. by Carl Linnaeus (1753), and the wild mungbean was given the name *Phaseolus sublobatus* Roxb. by William Roxburgh (1832). Hara (1955) accepted the name for domesticated mungbean, but he called *P. radiatus* var. setulosus (Dalz.) Hara comb. nov. as a new combination to taxonomic biology aimed at the wild mungbean variety, keeping *P. sublobatus* Roxb. nom. nud. as synonym for the same in his publication. Ohwi and Ohashi (1969) designated *Vigna radiata* (L.) Wilczek var. setulosa (Dalz.) Ohwi et Ohashi comb. nov. by citing *P. sublobatus* in Roxburgh (1832) and *P. setulosus* Roxb. as its synonyms. Later, in 1970, Verdcourt described *V. radiata* (L.) Wilczek var. sublobata (Roxb.) Verdc. comb. & stat. nov. as a new combination with a new taxonomic rank based on *P. sublobatus* Roxb. This naming of Verdcourt was accepted by Takahashi et al. (2018). However, most taxonomists have recently had difficulties separating wild mungbean from *V. grandiflora* and/or *V. trinervia*, which Bairiganjan et al. (1985) considered being separate species. Therefore, Takahashi et al. (2018) in their description considered it appropriate to distinguish domesticated and wild mungbean as varieties. Because of these factors, *V. radiata* (L.) Wilczek var. radiata and *V. radiata* (L.) Wilczek var. sublobata (Roxb.) Verdc are the accepted nomenclature for domesticated and wild mungbean, respectively.

Mungbean is considered to have first evolved in India and has been developed from the variety sublobata, which grows wild in India and Burma (Purseglove, 1977). Afterwards, it is thought to have spread to various regions across Asia, Africa, the West Indies, and the USA. Mungbean is a type of low-altitude, short-term grain legume that typically thrives as a dryland crop at around 2000 meters above sea level (Akpapunam, 1996). Mungbean is cultivated across the globe, spanning over 7 million hectares, with a primary focus on Asia, though it's also grown in other regions (Nair et al. 2019). Its popularity stems from its ability to withstand drought conditions, its minimal prerequisites, and its fast-growing cycle. As a result, mungbean is widely cultivated across many Asian countries, as well as in dry parts of southern Europe and warmer regions of Canada and the United States (Hou et al., 2019).

1.2 History, Origin, and Domestication

Archaeological evidence and domesticated mungbean diversity data are suggestive of the fact that the domestication of mungbean has started in its origin in India, approximately 3500 years ago (Fuller & Harvey, 2006). Crop domestication and

improvement, according to Dempewolf et al. (2017), is a process of multiple rounds of selection that leads to the separation of genetic diversity important to agriculture from progenitor wild species. During the early stages of domestication, the cultivation practice of mungbean migrated from its origin to other regions of Asia and gradually to the countries of African continent. The mungbean we cultivate today is the result of multiple rounds of domestication and have undergone many selections. The wild relative of the cultivated mungbean, i.e., *V. radiata* var. sublobata, is considered the putative progenitor. This putative progenitor is native to northern and eastern Australia's subtropical and tropical areas (Lawn & Cottrell, 1988). This weedy plant can be found in the wild. Luckily, the wild relatives of a domesticated plant are a source of beneficial genes, which is of no difference in the case of mungbean also. These useful genes get lost from the domesticated cultivars due to selection pressure and the domestication bottleneck effect. In recent decades, significant advancements have been achieved in integrating characteristics from wild plants into cultivated crops, primarily aimed at addressing biotic stress factors. Plant breeders have been successful in making use of the useful genes present in the wild relatives of domesticated mungbean in the breeding programs. The mungbean cultivar TC1966, for example, is entirely immune to two bruchid beetle species, *Callosobruchus chinensis* (adzuki bean weevil) and *Callosobruchus maculatus* (cowpea weevil), that otherwise prove to be detrimental to the mungbean in stores (Somta et al., 2007; Talekar, 1988). Plant breeders have taken advantage of this for developing mungbean varieties resistant towards bruchid (Tomooka et al., 1992). Apart from just breeding success, genetic linkage map construction using wild and domesticated mungbean accessions have provided valuable information regarding commercially important traits (Lambrides et al., 2000). So, one cannot deny the fact that the germplasm of the wild relatives of domesticated mungbean will be needed in the future to improve productivity.

1.3 Cytogenetics

Mungbean is a diploid plant with $2n = 22$ somatic chromosomes. Bhatnagar (1974) devised the karyotype formula for mungbean as "4Lsm + 4 Msm + 3Mm" "[L = long (2.7–3.5 μm), M = medium (1.9–2.6 μm, sm = sub median centromere and m = median centromere)]."

1.4 Nutritional Values and Importance

Many health organizations have suggested increasing plant-based food intake to enhance chronic disease prevention and general human health, leading to the inclusion of a range of plant-based foods in healthcare programs. Among such crops exhibiting tremendous health benefits is the mungbean. Studies of the biochemical

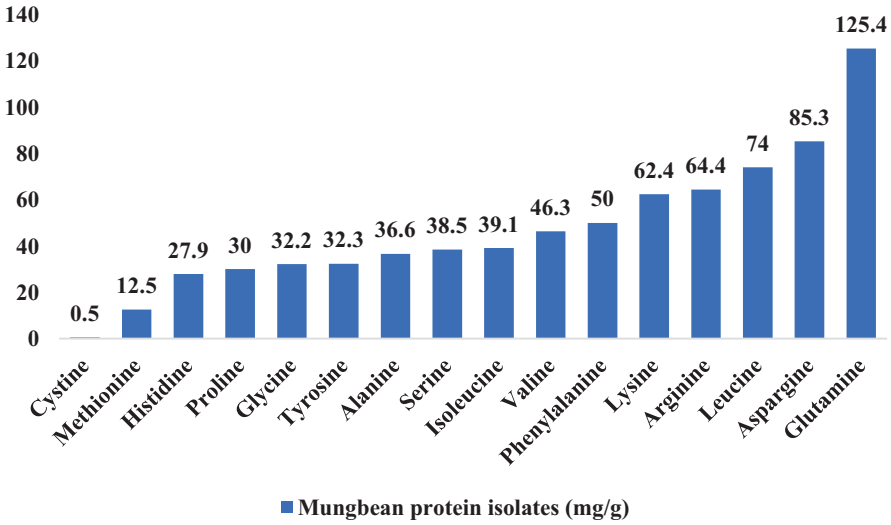

Fig. 1 Amino acid compositions of mungbean seed protein isolates

composition of mungbean have shown that it is a plentiful source of protein, dietary fiber, vitamins, and various other nutrients. Due to its high nutrient-rich seeds, mungbean has been cultivated as an important food and feed crop for humans and animals for centuries. Compared to soy and kidney beans, mungbean seeds have a significantly higher protein content ranging from 20.97% to 31.32%, which is approximately twice as much as that found in maize, a cereal seed (Anwar et al., 2007). The proteins and peptides of mungbean have been shown to have antibacterial and angiotensin-converting enzyme (ACE)-inhibiting properties (Tang et al., 2014). According to FAO/WHO, mungbean is a decent protein and amino acid source except for sulfur-containing amino acids, methionine, and cysteine. But with the help of genetic engineering techniques, 8S globulin was being inserted with methionine and cysteine sequences (Yi-Shen et al., 2018). Proximate compositions of amino acids in mungbean protein isolates are given in Fig. 1. Total amino acid content of mungbean is 800.2 mg/g, where the total essential amino acids share is 348.2 mg/g, the total aromatic amino acid is 96.7 mg/g, and the total sulfur amino acids is 13 mg/g (Kudre et al., 2013). Apart from its nutritional value, mungbean improves the yield of other crops by minimizing the need for synthetic nitrogen fertilizers in the soil (Fernandez et al., 1988).

1.5 Adaptation and Cultivation

Mungbean is an excellent food legume crop widely grown in South, East, and Southeast Asia, accounting for 90% of global output. Mungbean is a drought-tolerant, low-input crop that can offer both green manure and animal feed, making

it a popular choice among smallholder farmers. Mungbean thrives in a variety of agroclimatic environments. According to the World Vegetable Center, a warmer and humid climate with temperatures ranging from 250 °C to 350 °C and 400–550 mm of rainfall evenly dispersed throughout a growth period of 60 to 90 days is ideal for production. Mungbean exhibits drought tolerance to a reasonable extent but it is susceptible to waterlogging or overwater stress (Mehandi et al., 2019). Mungbean has the ability to be grown in different soil types, but it thrives the most in well-drained loamy to sandy loam soils. To ensure effective atmospheric nitrogen fixation by the bacteria living in the root nodules during the growing stage, proper drainage and adequate aeration in the field are necessary. Soil is readied for sowing by preparing ridges and furrows in the field. Pretreatment of the soil with well-decomposed farmyard manure enhances the quality of the soil. NPK fertilizers are applied as per soil nutrient status. Moreover, the application of the biofungicide *Trichoderma viride* along with farmyard manure before sowing can protect the mungbean plants from several fungal pathogens. Seeds can be pretreated with antifungal captan, thiram, and symbiotic diazotroph *Rhizobium*. Weed removal during the growing period is necessary for better grain yield. Mungbean cultivation needs attention for a wide range of diseases and pests such as seed and seedling rot, yellow mosaic, *Cercospora* leaf spot, powdery mildew, tobacco caterpillar, whitefly, bean pod borer, thrips, cowpea aphid, etc. When the pods are ripe and dried but not yet breaking, they are harvested using both manual and mechanized techniques.

2 Production Statistics

Mungbean is considerably an underused legume that is not individually classified by the Food and Agriculture Organization's (FAO) statistics database but is known as a "future smart food" for Asia (FAO, 2018). Mungbean is often used to make bean sprouts, translucent noodles, and mungbean paste in Eastern and Southeastern Asia, whereas in Eastern Africa, it is most typically served as a bean stew (Nair & Schreinemachers, 2020). Because there are no commercial hybrids and farmers can easily preserve their own seed, the private seed market is uninterested in the crop. As a result, the public sector is heavily involved in variety creation and scaling. The Asian mungbean research nations cultivated mungbean on around 10 lakh hectares, yielding roughly 0.77 megaton of dry grain, or around 16% of world mungbean production (Nair & Schreinemachers, 2020). Myanmar, India, Bangladesh, and Pakistan (Schreinemachers et al., 2019), which account for 66% of the world output, were the subjects of a previous research. According to secondary statistics, mungbean cultivation in Southeast Asia decreased by 100,000 hectares (18%) between 2008 and 2017. The majority of this drop was due to Indonesia, whose mungbean acreage declined by nearly 25% (Agriculture Mo, 2018). One possible cause is that mungbean yields are lower than those of other crops. In East Africa, on the other hand, the area under mungbean appears to be expanding, despite the fact that the available statistics indicate a large year-to-year variance. In Asia, the typical

mungbean farmer planted 0.5–1.0 ha, with Thailand (6.2 ha/farmer) having a greater average area and Vietnam (0.2 ha/farmer) having a smaller average area. The average area per producer in East Africa is 0.4–1.4 hectares.

Although mungbean has a yield potential of 2.5-3.0 t/ha, its actual average yield is significantly lower at 0.5 t/ha. This low production is attributed to various factors, including abiotic and biotic stresses, inadequate crop management techniques, and the absence of high-quality seeds of superior varieties (Chauhan et al., 2010; Pratap et al., 2019). Some of the most significant biotic factors affecting mungbean production include yellow mosaic, anthracnose, powdery mildew, Cercospora leaf spot (CLS), dry root rot, halo blight, and tan spot, as well as insect pests such as bruchids, whitefly, thrips, aphids, and pod borers (War et al., 2017; Pandey et al., 2018). Drought, waterlogging, heat, and salinity stress are all abiotic factors that impact mungbean productivity (HanumanthaRao et al., 2016). Owing to breeding attempts that were confined to only a handful of inbred lines, genetic diversity in cultivated mungbeans is limited, necessitating the broadening of the genetic basis of mungbeans under cultivations. Mungbean has been expanded to multiple intercropping systems with rice, wheat, and maize for production worldwide, including South America and Sub-Saharan Africa, thanks to the development of short-duration variants (Moghadam et al., 2011). To improve crop yield and stabilize agricultural output, it is important to develop varieties that can withstand both biotic and abiotic stress factors. Identifying the sources of tolerance traits displayed at the relevant growth stages requires crucial breeding information on stressors affecting mungbean, as well as the influence of environmental pressures on plant growth. The genetic foundation of symbioses with pests, pathogens, and the environment may be analyzed using advanced breeding approaches to build efficient crop improvement techniques.

3 Biotic and Abiotic Stress

In South Asia, Southeast Asia, and Sub-Saharan Africa, viral, bacterial, and fungal infections are economically significant (Mbeyagala et al., 2017; Pandey et al., 2018). Mungbean yellow mosaic disease (MYMD) is a serious viral mungbean disease (Noble et al., 2019). The whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) transmits numerous begomoviruses that cause MYMD (Nair et al., 2017). MYMD-related economic losses in India amount to an 85% drop in yield (Karthikeyan et al., 2014). In India and Pakistan, dry root rot caused output losses of 10–44% in mungbean production (Bashir & Malik, 1988). According to Singh et al., (2013), crop losses ranging from 33% to 44% were attributed to Rhizoctonia root rot in India. Additionally, Shukla et al., (2014) reported that anthracnose caused crop losses ranging from 30% to 70%. CLS caused 97% of yield losses in Pakistan and other Indian states (Bhat et al., 2014), whereas powdery mildew caused 40% of yield losses (Khajudparn et al., 2007). Fusarium wilt caused 20% production loss (Anderson, 1985), while *Alternaria* leaf spot caused 10% yield loss among minor

fungal infections (Maheshwari & Krishna, 2013). Between 2009 and 2014, a survey of mungbean farms across China found average output decreases of 30–50% caused by halo blight-led cropping disaster (Sun et al., 2017). Halo blight is a newly identified disease in China (Sun et al., 2017) and Australia (Noble et al., 2019). Pandey et al. (2018) investigated the influence of cultural practices on mungbean infections and assessed the efficacy of bactericides, fungicides, bio-fungicides, and botanicals for seed treatment and foliar spray. The most efficient and long-lasting technique for integrated disease control is to deploy genetically resistant cultivars.

Insect pests attack mungbean throughout the agricultural cycle, from seeding to storage, wreaking havoc on output. Some insect pests cause direct harm to crops, while others serve as disease carriers. Mungbean is susceptible to several pests, with the stem fly (bean fly), *Ophiomyia phaseoli*, being one of the most severe. Additionally, *Melanagromyza sojae* and *Ophiomyia centrosematis* are two other stem fly species that can attack mungbean crops (Talekar, 1990). The stem fly infests the crop within a week of germination, and under epidemic conditions, it can lead to complete crop loss (Chiang & Talekar, 1980). Another widespread mungbean pest is *B. tabaci*, which feeds on the plant's phloem sap, excreting honeydew or indirectly spreading MYMD, which causes black sooty mould on the plant. In addition to pests, abiotic stressors pose a significant threat to mungbean crops' growth and yield, resulting in significant agricultural losses worldwide (Ye et al., 2017). Crop production reduction owing to environmental variables has progressively grown throughout the decades (Boyer et al., 2013). Crops develop by using resources from their surrounding environment (light, water, carbon, and mineral nutrients). The growth and development of crops are influenced by both the microenvironment and the management practices used in cultivation. Due to climate change, the interactions between plants and their environment are becoming increasingly complex (Goyary, 2009). To understand how these factors impact crop growth and development, researchers use eco-physiological features and comprehensive phenotyping-based insights into crop physiology and external signals (Biswas et al., 2018). This information can help predict harvests and develop measures to control growth. When plants experience abiotic stress, such as changes in temperature or water availability, they often undergo molecular, biochemical, physiological, and morphological changes that affect their productivity (Ahmad & Prasad, 2012). Some crop production models predict a decrease in key agricultural crop yields due to changing climatic conditions, which can create unfavorable conditions for crop development due to abiotic factors (Rosenzweig et al., 2014). Such attempts in mungbean are uncommon and need extra care. Environmental pressures constitute a threat to global agriculture in the contemporary period and provide production consistency across geographies and crop seasons. New methods are being developed to better understand probable stress tolerance processes and to identify stress tolerance characteristics in order to promote sustainable agriculture (Fiorani & Schurr, 2013). The activation of several stress-regulated genes is required for basic tolerance mechanisms to be put into action, as they work together through coordinated cellular and molecular responses (Latif et al., 2016). Many factors that contribute to stress tolerance are neglected when breeding lines are phenotyped for plainly apparent

qualities such as growth and yield components. This might be owing to the ease with which these features can be measured precisely and quickly. As a result, modern plant phenotyping platforms include picture capture and automation in contemporary phenotyping technologies. These latest initiatives are projected to improve efforts to transform the fundamental physiology of agricultural plants for outputs with real-world standards to help breeding programs in severe settings (such as salinity, soil moisture, high temperatures, and so on).

4 Breeding Strategies and Constraints

It is crucial to identify sources of resistance for introducing resistance into cultivars through breeding. The primary gene pool is the initial choice for resistance sources, while the secondary and tertiary gene pools offer additional options for incorporating variation into the crop. To effectively breed for fungal stressors, easily accessible resistant germplasm and markers linked to QTL regions or critical genes are necessary for marker-assisted selection (MAS). In mungbean, molecular markers for *Cercospora* leaf spot and powdery mildew have been identified for use in breeding efforts. Both qualitative and quantitative inheritance routes have been observed for powdery mildew resistance (Kasettranan et al., 2009). Seeds can carry bacterial diseases that are capable of surviving in agricultural waste. Integrated disease management often involves varietal resistance, which has been recognized as a crucial element (Noble et al., 2019). However, little attention has been paid to the screening of mungbean genotypes for bacterial infections or the detection of genetic markers linked to bacterial illnesses. Identifying genetic markers/QTLs associated with resistance to bacterial leaf spot, halo blight, and tan spot in mungbean can accelerate the development of resistant commercial cultivars. Genome-wide association analysis of large and diverse mungbean mapping populations representative of global germplasm can be used to identify these markers (Noble et al., 2019). Additionally, the effectiveness of breeding programs that confer MYMD resistance has been improved by investigating genotypic diversity, identifying linked markers for the R gene, and constructing QTL maps using molecular markers (Sudha et al., 2013).

A marker related to resistance against yellow mosaic virus in mungbean, called "VMYR1," was identified by Basak et al. (2004). Linked marker-assisted genotyping can be used by plant breeders to perform repeat genotyping when disease incidence is absent during the growing season, as phenotyping for begomoviruses is challenging and requires significant labor. Interspecific sources have also been discovered as new MYMD resistance donors (Nair et al., 2017). Although various screening technologies have been developed, screening plants for insect resistance remains a particularly challenging task. This is due to the non-uniform insect infection patterns observed across seasons and locations for certain key pests, which also face difficulties in rearing and reproducing on feedstuffs. To achieve success in insect resistance breeding, it is essential to comprehend the nature of the pest, the infestation stage, and the bio-molecular aspects of the plant-insect relationship. It is

crucial to have the ideal population of insect pests at their most susceptible stage of the crop. This enables the identification of resistant genotypes against insects and prevents or eradicates escapes through uniform infestation during relevant phases of plant growth (Maxwell & Jennings, 1980). One of the most important strategies in insect resistance breeding involves identifying resistance coding genes from wild/cultivated species and transferring them into improved lines through recombination, hybridization, and selection. Conventional plant breeding, despite its limitations, has resulted in significant progress in mungbean output as well as disease and insect resistance (Fernandez & Shanmugasundaram, 1988). Physical and chemical mutagens have been utilized to develop insect and disease-resistant mungbean cultivars, as well as other desirable characteristics (Watanasit et al., 2001). Details of 39 mungbean varieties improved through induced mutagenesis are recorded in Table 1. One of the conditions for crop improvement is genetic heterogeneity (Laskar & Khan, 2017). There is a limited ability to select improved genotypes in mungbean due to insufficient diversity. To rapidly increase genetic diversity, induced mutagenesis has proven to be the most effective technique and has been utilized in several crops such as cowpea (Raina et al., 2018a, 2020a, 2022a, b; Rasik et al., 2022),

Table 1 Details of mutant cultivars of mungbean released

Variety name	Country	Registration year	Mutagen type	Mutant development type	Characters improved
AEM-96	Pakistan	1998	Physical	Direct use of an induced mutant CV.6601 with 200 Gy	1246–1298 kg/ha grain yield, short stature combined with short duration and synchrony in maturity
Binamoog-1	Bangladesh	1992	–	–	Resistance to powdery mildew and suitable for rice fallows
Binamoog-2	Bangladesh	1994	Physical	Crossing with one mutant Mutant MB-55(4) × D-2773	Larger seed size, early and synchronous maturity (7–10 days earlier), high yield (16%), tolerant to leaf MYMV and *Cercospora* leaf spot
Binamoog-3	Bangladesh	1997	Physical	Mutagenic treatment of breeding material (F1, F2, seeds, etc.) (mutant MB55-4 × AURDC line V1560D) with 200 Gy	Seed yield, synchronous pod maturity, tolerant to yellow mosaic virus and *Cercospora* leaf spot

(continued)

Table 1 (continued)

Variety name	Country	Registration year	Mutagen type	Mutant development type	Characters improved
Binamoog-4	Bangladesh	1997	Physical	Mutagenic treatment of breeding material (F1, F2, seeds, etc.) (mutant MB55-4 × AURDC line V1560D) with 200 Gy	Seed yield, synchronous pod maturity, early maturing, dwarf plant type, tolerant to yellow mosaic virus and *Cercospora* leaf spot
Binamoog-5	Bangladesh	1998	Physical	Mutagenic treatment of breeding material (F1, F2, seeds, etc.) (mutant MB55-4 × AURDC line V1560D) with 200 Gy	Higher seed yield, synchronize pod maturity, tolerance to leaf MYMV and *Cercospora* leaf spot
Binamoog-6	Bangladesh	2005	Physical	Direct use of an induced mutant VC-6173-10 with 400 Gy	Purple hypocotyl and stem, high number of pods and clusters, resistance to diseases
Binamoog-7	Bangladesh	2005	Chemical	Direct use of an induced mutant Binamoog-2 with 0.75% EMS	Increased pod, reduced seed size, increased seed, tolerant to MYMV and *Cercospora* leaf spot
Binamoog-8	Bangladesh	2010	Physical	Direct use of an induced mutant MB-149 with 400 Gy	Medium plant height (35–40 cm), early maturing (64–67 days), deep green leaf color, shiny green seed coat color, 22–23% protein content, average seed yield of 1.80 tons ha^{-1}, and tolerant to MYMV

(continued)

Table 1 (continued)

Variety name	Country	Registration year	Mutagen type	Mutant development type	Characters improved
Binamoog-9	Bangladesh	2017	Physical	Direct use of an induced mutant BARI Mung-6 with 400 Gy	The distinct features of the selected mutant MBM-07 (Binamoog-8) are medium plant height (35–40 cm), early maturing (64–67 days), deep green leaf color, shiny green seed coat color, 22–23% protein content, average seed yield of 1.74 t/ha and potential 1.95 t/ha, and tolerant to MYMV
BM 4	India	1992	Chemical	Direct use of an induced mutant T-44 with 0.15% EMS	Resistant to *Macrophomina* blight and tolerant to MYMV
Camar	Indonesia	1991	Physical	Direct use of an induced mutant Manyar with 100 Gy	Resistance to *Cercospora* leaf spot, resistance to *Uromyces* sp., medium resistance to scrab diseases, high yield, and tolerance to salinity and acid soil
Chai Nat 72	Thailand	1999	Physical	Direct use of an induced mutant Kamphangsaen 2 with 600Gy	High yield, larger grain size, and resistance to fungal diseases
Chai Nut 84-1	Thailand	2012	Physical	Direct use of an induced mutant Chai Nut 36 with 500Gy	High yield and starch, large seeds
Co 4	India	1982	Physical	Direct use of an induced mutant Co 1 with 200Gy	High yield, early maturity and resistance to drought

(continued)

Table 1 (continued)

Variety name	Country	Registration year	Mutagen type	Mutant development type	Characters improved
Dhauli (TT9E)	India	1979	–	Crossing with one mutant T-51 × local type	High yield, early maturity with tolerance or resistance to MYMV
LGG 450	India	1993	Physical	Direct use of an induced mutant Pant Mung-2 with 40 kR gamma rays	High yield, early maturity with tolerance or resistance to MYMV
LGG-407	India	1993	Physical	Direct use of an induced mutant Pant Mung-2 with 40 kR gamma rays	High yield, early maturity with tolerance or resistance to MYMV
ML 26-10-3	India	1983	Physical	Direct use of an induced mutant ML-26 with gamma rays	Resistance to MYMV and high yield
MUM-2	India	1992	Chemical	Direct use of an induced mutant K-851 with 0.2% EMS	High yield and resistance to diseases
NIAB Mung 121-25	Pakistan	1985	Physical	Direct use of an induced mutant RC 71-27 with 200 Gy	Early maturity (60–65 days), determinate type, high yield (44%), recommended as spring and summer crop
NIAB Mung 13-1	Pakistan	1986	Physical	Direct use of an induced mutant 6601 with 100 Gy	Early maturity, shortness, more pods, harvest index (28%), TGW (40.5 g), and higher yield (44%)
NIAB Mung 19-19	Pakistan	1985	Physical	Direct use of an induced mutant Pak 22 with 400 Gy	Early maturity (60–65 days), determinate type, high yield (35%), recommended as spring and summer crop, high tolerance to mungbean yellow mosaic virus

(continued)

Table 1 (continued)

Variety name	Country	Registration year	Mutagen type	Mutant development type	Characters improved
NIAB MUNG 2006	Pakistan	2006	–	Crossing with one mutant variety NIAB Mung 92 × VC-1560D	Yellow mosaic virus resistance, resistance to powdery mildew, *Rhizoctonia* root-rot disease resistance, early maturity, and large seeds
NIAB Mung 20-21	Pakistan	1986	Physical	Direct use of an induced mutant Pak 22 with 400 Gy	Early maturity, shortness, harvest index (31%), high yield (65%), tolerance to yellow mosaic virus, resistance to *Cercospora* leaf spot, suitable as catch crop
NIAB Mung 51	Pakistan	1990	Physical	Mutagenic treatment of breeding material (F1, F2, seeds, etc.) (6601x1973A) with 100 Gy	Early and synchronous maturity, non-shattering pods, profuse hairiness, tolerant to MYMV and CLS diseases, larger seed size, higher yield potential, crop vegetation: Summer (66 days) and spring (67 days)
NIAB Mung 54	Pakistan	1990	Physical	Mutagenic treatment of breeding material (F1, F2, seeds, etc.) (6601x1973A) with 100 Gy	Early and synchronous maturity, non-shattering pods, tolerant to MYMV and CLS diseases, larger seed size, higher yield potential, crop vegetation: summer (71 days) and spring (73 days)

(continued)

Table 1 (continued)

Variety name	Country	Registration year	Mutagen type	Mutant development type	Characters improved
NIAB Mung 92	Pakistan	1992	–	Crossing with one mutant NIAB Mung 36 × VC 2768B	Resistance to MYMV, early maturity, resistance to grain shattering, and large seed size
NIAB Mung 98	Pakistan	1998	Physical	Crossing with one mutant NIAB Mung 20–21 × VC 1482E	Resistance to diseases (yellow mosaic virus and *Cercospora* leaf spot), high yield, and medium seed size
NIAB Mung-28	Pakistan	1983	Physical	Direct use of an induced mutant Pak 17 with 200 Gy	Early and uniform maturity and high yield
Pant Moong 2	India	1982	Physical	Direct use of an induced mutant ML-26 with 100 Gy	Resistance to MYMV, more pods, and high yield
TAP-7	India	1983	Physical	Direct use of an induced mutant S-8 with 30 kR gamma rays	Early maturity (5–7 days), resistance to mildew and leaf spot, higher yield (23%)
TARM-1	India	1997	Physical	Direct use of an induced mutant RUM 5 with 30 kR gamma rays	High yield, resistance to powdery mildew disease, and medium maturity
TARM-18	India	1996	Physical	Crossing with one mutant TARM-2 × PDM-54	High yield and resistance to powdery mildew disease
TARM-2	India	1994	Physical	Direct use of an induced mutant RUM 5 with 30 kR gamma rays	High yield, medium–late maturity, and resistance to powdery mildew disease
TJM-3	India	2007	Physical	Crossing with one mutant TARM-1 × Kopargaon	Early maturity, large seeds, and resistance to powdery mildew, *Rhizoctonia* root-rot disease

(continued)

Table 1 (continued)

Variety name	Country	Registration year	Mutagen type	Mutant development type	Characters improved
TM 2000-2	India	2010	Physical	Crossing with one mutant TARM-1 × JL-781	Higher seed yield and synchronous pod maturity, tolerance to leaf MYMV and *Cercospora* leaf spot
TM-96-2	India	2007	Physical	Crossing with one mutant TARM-2 × Kopargaon	Resistance to powdery mildew and *Corynespora* leaf spot
TMB-37	India	2005	Physical	Crossing with one mutant TARM-2 × Kopargaon	High yield, early maturity with tolerance or resistance to MYMV

Source: The Joint FAO/IAEA Mutant Variety Database (https://mvd.iaea.org)

lentil (Laskar et al., 2018a, b, 2019; Wani et al., 2021), faba bean (Khursheed et al., 2015, 2016, 2018a, b, c, 2019), fenugreek (Hasan et al., 2018), mungbean (Wani et al., 2017), urdbean (Goyal et al., 2019a, b, 2020a, b, 2021a, b), chickpea (Laskar et al., 2015; Raina et al., 2017, 2019), black cumin (Tantray et al., 2017; Amin et al., 2020), and finger millet (Sellapillaibanumathi et al., 2022). Because natural mutations occur sporadically, artificial mutations are generated, and genetic gain is best achieved by using mutagens (Raina & Khan, 2020; Raina et al., 2016, 2018b, 2020b, 2021, 2022c). Auti (2012) stressed that mutation breeding or induced mutation has a lot of promise for improving mungbean. Traditional breeding methods for producing pest-resistant cultivars include pure line, mass, and recurrent selection (Burton & Widstorm, 2001). Insect resistance and enhanced agronomic features are being developed in mungbean using techniques such as pedigree, backcross, and bulk selection breeding.

Sehgal et al. (2018) reported on various successful projects related to mungbean, aimed at screening and developing cultivars that are resistant to high temperature, salt, waterlogging, and water stress. These projects considered the physiological, biochemical, and molecular aspects of the crop. To facilitate future crop development with specific traits, a panel of donor resources would consist of breeding lines that have been identified and chosen for the aforementioned circumstances. By selecting a few genotypes that are well-suited to the region in the initial stages of mungbean breeding, certain genotypes were identified as being particularly resistant to biotic stresses and high yield. Indirect selection was made for yield, plant type, and adaptation-related features, though no direct selection was done for abiotic stress tolerance. The selection of improved cultivars with increased resilience to

drought has been proven successful. Fernandez and Kuo (1993) used a stress tolerance measure to choose genotypes with high resilience to temperature and water shocks and yield in mungbean (STI). Singh (1997) reported mungbean plant types suitable for Kharif (rainy) and dry (spring/summer) seasons. Pratap et al. (2013) recommended the development of short-duration cultivars for Spring/Summer farming to minimize heat and drought stress toward the end of the growing season. Cultivars that are well adapted to the summer season have a crop cycle of 60–65 days, a determinate growth habit, a high harvest index, reduced photoperiod sensitivity, quick initial development, longer pods with more than 10 seeds per pod, and large seeds. In light of this, numerous early maturing mungbean lines have been selected and released as commercial cultivars.

Whenever wild resources are used as donors for disease or pest-resistant cultivars, linkage drag becomes a significant concern. In resistance breeding, the use of wild germplasm is a dominant contributor to resistance introgression into commercial cultivars, but unwanted hereditary linkages frequently hamper this process (Keneni et al., 2011). Undesirable traits such as leaf area index, seed structure, and color can be passed along with beneficial traits due to low dominance multigenic disease and insect resistance. To overcome linkage drag, crossing over between homologous chromosomes during meiosis is critical for transferring genes that govern desirable characteristics (Edwards & Singh, 2006). However, the inheritance of undesirable and desirable traits together can impact seed quality, germination, and other traits. Generating a high number of F2 populations is necessary to increase the recovery of novel recombinants due to crossing-over. The emergence and dissemination of whitefly-transmitted viruses are influenced by factors such as the evolution of viral strains, the creation of aggressive biotypes, and a rise in the whitefly population (Chiel et al., 2007). Insect biotypes reflect the genetic variety of a pest population, and although they may appear identical, their biological characteristics differ. Breeding for disease resistance is hindered by the creation of multiple strains by a pathogen, as well as biotypic variety in insect pests, as plant varieties resistant through one disease strain or pest biotype could be sensitive to a different pathogen or insect biotype of the same pathogen.

Although there were multiple ongoing efforts to develop plant cultivars for a particular biotic and abiotic stress on a wider level, achievements were limited due to the cumulative effect of many stresses and unforeseen increases in pest and pathogen episodes throughout the plant's growth stages, resulting in only a few calculable achievements in legumes. A comprehensive examination is necessary for various stages of the breeding process, including seed germination, early growth, vegetative phase, flowering, early pod development, as well as the reproductive and final maturity stages. With such a diverse range of developing phases, pinpointing a precise phase inducing a characteristic for breeding appears to be difficult; however, many approaches have focused on the flowering and reproductive phases in order to develop progenies that can sustain stress and result in better pod and seed yields.

5 Conclusion

The objective of high-yielding mungbean varieties is conceivable by utilizing a wider range of genetic diversity. Mungbean has typically been farmed in less productive vulnerable areas' minimal resources because of which the selection pressure has been focused on stress adaptability rather than yield. Thus, improving the genetics of such crops in order to increase output necessitates genetic restoration in order to generate diverse genotypes. Induced mutations can aid in the regeneration and restoration of diversity that has been vanished over time as a result of adaptation to various stressors. Although disease resistance genotypes were established for powdery mildew, yellow mosaic, and CLS, to accelerate the establishment of resistant breeding lines, molecular markers for anthracnose and dry root rot further required to be developed and identified markers must be employed in the breeding effort. Introduction of undesirable characteristics into the cultivars from insect-resistant origins for bruchids and whiteflies is challenging. To achieve stable resistance against diseases and insects in mungbeans, a combination of conventional breeding methods and molecular techniques is required. The identification of molecular markers has facilitated the evaluation of pest and disease resistance, minimizing our dependence on time-consuming phenotypic data, particularly in extensive trials. Insect resistance can also be transferred from related legumes like black gram to green gram using molecular markers. However, identifying and combining numerous resistance genes into the same cultivar are critical. In order to generate mungbean with disease and insect pest resistance while avoiding strain/biotype formation, breeders should focus on gene pyramiding. In order to understand the ways in which herbivores and pathogens function, it is important to explore the mechanisms of disease and insect resistance, as well as the specific signal molecules involved in these processes. In addition, RNAi technology could be employed to increase mungbean stress tolerance against biological factors. Though, Large-scale field experiments are necessary to prove the effectiveness of RNAi as a potential pest control method in plant breeding.

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