

Production of Mungbeans: Biotic Limitations—Genetic Advancement

Shreya Tiwari¹, Puja Kumari², Deepali Pegwar², Kalam Khan³ and
Dubbaka Sriharshini³

¹ Assistant Professor, School of Science, SAM Global University, Raisen

² School of Science, SAM Global University, Raisen

³ Department of Agriculture Sciences, IES University, Bhopal

³ School of Agriculture, Oriental University, Indore

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The mungbean, or *Vigna radiata* (L.) R. Wilczek var. *radiata*, is a significant food and economic crop in Asia. The introduction of short-duration variants has allowed the mungbean to spread into new areas, including South America and Sub-Saharan Africa. Both biotic and abiotic variables limit the production of mungbean. The main insect pests are bruchoids, whiteflies, thrips, stem flies, aphids, and pod borers. Yellow mosaic, anthracnose, powdery mildew, *Cercospora* leaf spot, halo blight, bacterial leaf spot, and tan spot are the main diseases that affect mungbeans. Drought, waterlogging, salt, and heat stress are important abiotic factors that have an impact on mungbean productivity. Mungbean breeding has been essential in creating varieties with resistance to biotic and abiotic causes, but there are still many challenges to overcome, including the exact and accurate identification of resistance source(s) for some characteristics and the phenotypes given by multigenes. The most recent advancements in phenotyping, genomes, proteomics, and metabolomics may be of tremendous assistance in understanding insect/pathogen-plant, plant-environment interactions, as well as the essential elements contributing to resistance to biotic and abiotic stressors. This review talks about the difficulties in genetic improvement as well as the existing biotic and abiotic limits on mungbean production.

Keywords: Breeding, mungbean, stresses, Insect-pests, diseases, marker-assisted selection

Introduction

Vigna radiata (L.) R. Wilczek var. *radiata*, also known as mungbean, is a short-duration grain legume that is grown on more than 7 million hectares mostly in Asia but is also quickly gaining popularity in other areas of the world. Mungbean seeds are a good source of fiber, antioxidants, phytonutrients, and proteins (24% of which is readily digested).

(Itoh et al, 2006). Mungbean is considered as whole or split seeds, flour, or sprouts, making it a significant nutritional source of protein. High concentrations of thiamine, niacin, and ascorbic acid may be found in mungbean sprouts. The mungbean has a potential yield of 2.5 to 3.0 t/ha, but its typical productivity is a shockingly low 0.5 t/ha. Poor crop management techniques, abiotic and biotic restrictions, and the lack of high-quality seeds of better kinds for farmers all contribute to the low yield. (Chauhan et al., 2010; Pratap et al., 2019a) Diseases include yellow mosaic, anthracnose, powdery mildew, Cercospora leaf spot (CLS), dry root rot, halo blight, and tan spot, as well as insect pests include bruchids, whiteflies, thrips, aphids, and pod borers, are among the main biotic factors. (Lal, 1987; Singh et al., 2000; War et al., 2017; Pandey et al., 2018).

As breeding efforts were based on a small number of parental lines, there is a lack of genetic variety in farmed mungbeans, necessitating the need to enlarge their constrained genetic basis. Short-duration cultivars have made it possible for mungbean to be grown in various parts of the world, such as Sub-Saharan Africa and South America, and in a variety of cropping systems (including intercropping with rice, wheat, and maize). (Shanmugasundaram, 2007; Moghadam et al., 2011). Identification of the sources for tolerance characteristics exhibited at the appropriate stage depends on breeding knowledge of the biotic and abiotic stressors in mungbean as well as the impact of environmental stresses at distinct plant development stages. The genetic foundation of plant interactions with pests, pathogens, and the environment may be analysed using cutting-edge technologies like phenotyping, genomics, proteomics, and metabolomics to develop efficient crop enhancement techniques. In this context, we explain about mungbean's biotic and abiotic restrictions and the breeding work being done to enhance this short-duration crop.

Biotic Stress in Mungbean

Major Diseases and Their Economic Effects

Mungbean yellow mosaic disease (MYMD) is an important viral disease of mungbean. (Taylor et al., 1996; Singh et al., 2000; Raguchander et al., 2005; Mbeyagala et al., 2017; Pandey et al., 2018). Numerous begomoviruses, which are spread by the whitefly *Bemisia tabaci* (Gennadius), are the cause of MYMD (Hemiptera: Aleyrodidae). Cercospora leaf spot (CLS) [*Cercospora canescens* Ellis & G. Martin], powdery mildew [*Podosphaera fusca* (Fr.) U. Braun & Shishkoff, *Erysiphe polygoni* (Vaha) Weltzien], and anthracnose

[*Colletotrichum acutatum* (J.H. Simmonds), *C. truncatum* (Schwein.) Andrus An emerging condition affecting mungbeans is dry root rot (*Macrophomina phaseolina* (Tassi) Goid). Web blight (*Rhizoctonia solani* Kuhn), Fusarium wilt (*Fusarium solani* (Mart.) Sacc), and Alternaria leaf spot (*Alternaria alternata* (Fr.) Keissl) are the less severe ones. (Ryley and Tatnell, 2011; Pandey et al., 2018).

The effectiveness of bactericides, fungicides, bio-fungicides, and botanicals in seed treatment and foliar spray, as well as the influence of cultural, practices to prevent mungbean infections, have all been the subject of studies. The most efficient and long-lasting approach to integrated disease control is the use of cultivars with genetic resistance.

Breeding for the ability to resist viral diseases

Researchers reported that in mungbean, the genetic resistance against MYMD is governed by a single recessive gene (Reddy, 2009a), a dominant gene (Sandhu et al., 1985), two recessive genes and complementary recessive genes (Kulkarni, 2009; Shukla et al., 2014). Due to a single recessive gene, the mungbean cultivar NM 92 exhibited resistance to MYMD. As per Dhole and Reddy (2012), two recessive genes controlled the segregation ratio in the F₂ population in six crosses between resistant and susceptible genotypes.

However, F₂ and F₃ populations obtained via intraspecific [KMG 189 VBN (Gg)] and interspecific [TNAU RED VRM (Gg) 1] crosses showed the significance of a single recessive gene in MYMD resistance. In their study with F₂ populations derived from crosses between two local lines (NM-92 and NM-93-resistant to MYMD) and four exotic lines (VC-1973A, VC-2254A, VC-2771A, and VC-3726A-susceptible to MYMD), Saleem et al. (1998) discovered that susceptibility and resistance were controlled by a single genetic factor and that susceptibility was dominant over resistance (Maheshwari and Krishna, 2013). Plant breeders can use linked marker-assisted genotyping to do recurrent genotyping throughout the growing season even in the absence of disease incidence. Due to the complicated, time-consuming, and laborious nature of phenotyping against begomoviruses, this method will facilitate the introduction of MYMD-resistance by molecular breeding. Through interspecific origins, fresh donors of MYMD resistance have also been found.

TABLE 1 | Resistant sources of mungbean against mungbean yellow mosaic disease.

Genotype(S)	Resistant level*	Country
NM-10-12-01	R	Thailand
NM-2, VC-3960 (A-88), 98-CMH-016, VC-3960 (A-89), BRM-195 014043, 014133, 014249, 014250 08	R R R MR	Pakistan Pakistan
ML 1265, ML 1229	R	India
SML 1815, MH 421	R	India
BPMR-145, Vaibhav, Phule M-2003-3, TARM-18, Phule M-2002-13, Phule M-2001-3, Phule M-2002-17, Phule M-2001	R	India
EC300072, K141	R	India
LGG424B, LM108B	I	
VC-6960-88, VC-6773 (B-G), VC-3960-89, ACC-12840014, VC-1089 A	R	Bangladesh
NCM-15-11, AZRI-1, AZRI-06, NCM-21, 14063, NCM-11-8 NM 94	R T- Odisha and Andhra Pradesh MR- Tirunelveli	Pakistan India
ML1628	T	
VRMG(g)1, LM 235 (GY), K 851, T 44, Nelambur, Sona Moong, AVRDC 1785/5, LM 150, Madura moong, TNAU 26, WBM 202 (GY), KM 2, TARM 22, HUM 1, LGG 429/1, TARM2/2, TARM2/1, NM 94, Bari mung 2	R	India
ML267, LGG407	R	India
ML-5, ML 405, ML 408, ML 337, MUM 2, VGG3 45, Pusa 8773	R	India
ML-818	R	India
ML-9	MR	
GG-89 and GG-39, R: TM-98-50, TM-97-55, Co-5	I	India
IPM 2-14, PDM139	R	
HUM 1, HUM 12, DMS 03-17-2, Pant Mung 4, Pusa 9531, HUM 16, Meha, RMG 62, TMB 37	MR	India
ML-881, UPM-98,	HR	
Ganga-14, HUM-I, PDM-262, HUM-8	R	India

Breeding for the ability to resist fungal diseases

Useful breeding for fungi requires readily accessible resistant genetic material, markers related to important genes or QTL areas, and marker-assisted selection (MAS). There are molecular markers for *Cercospora* leaf spot and powdery mildew in mungbean that may be used in breeding programs. Therefore no research has been done on QTLs or molecular markers for anthracnose and dry root rot. For resistance to powdery mildew, both qualitative and quantitative pathways of inheritance have been identified. Powdery mildew resistance was linked to SSR marker-based QTLs like qPMR-1 and qPMR-2. Mungbean line V4718 had one significant QTL on linkage group 9 and two minor QTLs on linkage group 4. (Chankaew et al., 2013). The discovery of effective markers would be reliable fine mapping using populations created from crossings between parents that were extremely vulnerable and highly resistant.

TABLE 2 | Resistant genotypes of mungbean against fungal diseases.

Diseases	Genotype(s)	Resistant level*	Country
Anthracnose	ML1464, ML1486, ML1194 and ML1349	R	India
Cercospora leaf spot (CLS)	V1471, V2773, V2757, V5036 and V4718	R	Taiwan
	M5-22 and M5-25	R	Thailand
	BRM-188, C2/94-4-42, NM-98, 98-cmg-003, NM-1, NM-2, 98cmg-018, Basanti, PDM-11, CO-3, BARIMung-2 and VC3960-88	HR	Pakistan
	ML5, 453, 443, 515, 611, 610, 613, 682, 713, 688, 735, 728, 746, 759 and 769	R	India
	PANT M103, PUSA 105, PANT M3, PANT M2, ML 613, ML 173, ML 561, ML 347, PDM 11 and PANT M4	R	India
	ML1464, ML1486, ML1194 and ML1349	R	India
	GM-02-08, GM-03-03 and GM-02-13	R	India
	LGG-460	HR	
	ML-5, HUM-9, ML-4, HUM-4, SM-9-124, HUM-1, LGG-450, and SM-9-107	R	India
	1224-52 and 12404	HR	India
	AKM 9910, ML 1299, IPM 02-5, and SML 668	R	India
	KMP-13	MR	India
Powdery mildew	V4189, V2159, V4207, V4668, V4990 and V4574	R	Taiwan
	V3912 and V4186	R/HR	
	V1104, V4658, V4631, V4717, V4662, and V4883	HR	
	M5-10 and M5-25	R	Thailand
	BPMR-145, TARIM-18, Vaibhav, Phule M-2002-13, Phule M-2003-3, Phule M-2001-3, Phule M-2001-5 and Phule M-2002-17	R	India
	TARM-18	R	India
	LGG-460	R	India
	BL 849, BL 865, LM1668, PMB 63 and AKM 8803	HR	India
	KGS 83, Pusa 572, MH 96-1, GS 33-5, GS 21-5, AKM 99-4, COGG 936, TMB 47, ML 1299, MH 429, HUM 1, MH 429 and MH 530	HR	India
	C1-34-23, C1-32-22, C1-37-23, C1-28-20, C1-38-27, C1-44-31, C1-175-111, C1-41-28, C1-246-159, C1-236-152, C1-275-177	HR	India
	KMP-36, KMP39 and KMP41	HR	India
Macrophomina blight	ML1464, ML1486, ML1194 and ML1349	R	India
Dry root rot (DRR)	MSJ 118, KM 4-59 and KM 4-44	R	India
	40504, 40457, NCM 257-5, 6368-64-72 and NCM 251-4	R	Pakistan
	NCM 252-10 and 40536	HR	

Breeding for the ability to resist bacterial diseases

Bacterial diseases can grow in agricultural waste and are spread through seeds. The cornerstone of integrated disease management is acknowledged to be genotypic resistance. Identifying genetic markers linked to bacterial illnesses in mungbean and screening mungbean genotypes for resistance to those diseases have received little attention. Jalgaon 781, P 646, P 475, and PLM 501 mungbean genotypes were shown to be resistant to bacterial leaf spot (*X. phaseoli*) in an evaluation of 2160 mungbean genotypes from India. In field

tests, 8 out of 100 mungbean genotypes from Pakistan were shown to be resistant to bacterial leaf spot disease (Noble et al., 2019).

The inheritance of resistance to bacterial leaf blight (BLB), which is controlled by a single dominant gene, was found to be monogenic dominant in the mungbean genotypes Jalgaon 781, P 646, P 475, and PLM 501. There is no information on the QTLs of mungbean against bacterial disease, even though that QTLs for the bacterial leaf blight disease have been found in other crops like chickpea. The creation of resistant commercial cultivars will be accelerated by the discovery of genetic markers/QTLs linked to halo blight, tan spot, and bacterial leaf spot disease resistance in mungbean. Genome-wide association studies may be used to establish these markers utilizing large, variable mungbean mapping populations that are representative of global germplasm. (Schafleitner et al., 2015; Noble et al., 2019).

Major insect-pests and economic impacts

Crop protection against insect pests heavily relies on host plant resilience. Breeders have opportunities to breed for insect pest resistance as a result of the discovery of new sources for insect resistance. Insect resistance might be one of several qualities derived from the core gene pool of diversity that breeders have access to. To find sources of insect resistance in mungbean, extensive screening tests have been conducted in both controlled and uncontrolled environment. There haven't been many investigations done to identify resistance sources in mungbean for stem fly. The World Vegetable Center and The International Center for Tropical Agriculture (CIAT) have discovered certain genotypes that are resistant to stem flies and have been used as possible sources in breeding stem flies. Several of the sources of resistance in mungbean have been discovered through breeding against the spotted pod borer. (Swaminathan et al., 2012, Chiang et al., 1980)

Breeding for insect resistance

As resistance is introduced into cultivars through breeding, it is crucial to identify the origins of such resistance. The main gene pool is the breeder's initial choice for a source of resistance. The crop can integrate additional options for variety from the secondary and tertiary gene pools.

The absence of homogeneous insect infection across seasons and regions in some major pests, whose rearing and multiplication are difficult on artificial diets, makes it difficult

to screen plants against insect pests even if a variety of screening techniques have been devised.

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