frontiers in Environmental Science

REVIEW
published: 19 June 2018
doi: 10.3389/fenvs.2018.00053

Perspectives and Challenges for Sustainable Management of Fungal Diseases of Mungbean [*Vigna radiata* (L.) R. Wilczek var. *radiata*]: A Review

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Mungbean (*Vigna radiata* var. *radiata*) is a key legume crop grown predominantly in South and Southeast Asia. Biotic and abiotic stresses cause significant yield reduction in mungbean, and among these, fungal diseases are particularly important. Although disease management practices, including physical, chemical, and biological methods have been researched and described in the literature, few of these are available or have been used by growers. Here we review the economic impact, and sustainable management options for the soil-borne and foliar fungal diseases of mungbean as well as major challenges to manage these diseases. Potential use of all possible components of integrated management practices including host resistance, fungicides, biocontrol agents, natural plant products, and cultural practices etc. are discussed. Major diseases include powdery mildew, anthracnose, Cercospora leaf spot, Fusarium wilt, Rhizoctonia root rot and web blight, Macrophomina charcoal rot/dry root rot and blight. Review of the literature indicated an absence of resistance to Rhizoctonia root rot, little sources of resistance for dry root rot and anthracnose. Major resistant genes (R genes) and quantitative trait loci (QTL) were identified for powdery mildew and Cercospora leaf spot, which may be potentially used in Marker assisted selection (MAS). Although the mechanisms of induced systemic resistance (ISR) by biocontrol agents have been studied with Macrophomina blight, there is little information on the mechanisms and use of systemic acquired resistance (SAR) in managing fungal diseases of mungbean. Several studies targeted exploiting biological control for soil-borne root rot diseases. Botanical products, such as plant extracts, are also found effective to manage root and foliar diseases. However, many of these studies were limited to laboratory and/or green house experiments. Thus, long-term field studies are required for further exploitation of biological methods and commercial applications.

Keywords: mungbean, fungal diseases, quantitative trait loci, host resistance, disease management

OPEN ACCESS

Edited by:
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Specialty section:
This article was submitted to Interdisciplinary Climate Studies, a section of the journal Frontiers in Environmental Science

Received: *20 December 2017*
Accepted: *25 May 2018*
Published: *19 June 2018*

Citation:
Pandey AK, Burlakoti RR, Kenyon L and Nair RM (2018) Perspectives and Challenges for Sustainable Management of Fungal Diseases of Mungbean [Vigna radiata (L.) R. Wilczek var. radiata]: A Review. Front. Environ. Sci. 6:53. doi: 10.3389/fenvs.2018.00053

INTRODUCTION

Mungbean (*Vigna radiata* (L.) R. Wilczek var. *radiata*) is one of the important pulse crops in South and Southeast Asia. About 90% of global production is in South Asia, where India is the largest producer (Nair et al., 2012). India produces about 1.5–2.0 million tons of mungbean annually from about 3–4 million hectares (2014–2015), with an average productivity of 0.5 t ha^{-1} (Jadhav et al., 2016). Mungbean is also grown in China (Zhang et al., 2011), Australia (Clarry, 2016), and United States of America (Fery, 2002). In Australia, acreage of mungbean has increased substantially with 125,000 ha planted in 2015–2016 compared to only 1,000 ha in 1970s (Clarry, 2016). Average yield of mungbean is 0.4 t ha^{-1} in Asia but yields up to 2.5 t ha^{-1} may be attained with selected varieties and good management (AVRDC, 2012). Mungbean seeds is a good source of dietary protein for humans including marginal people, and people who live in areas with less access to meat or where people are mostly vegetarian (AVRDC, 2012). Mungbean sprouts and green pods contain high level of vitamins and minerals (Keatinge et al., 2011; Nair et al., 2015).

Abiotic and biotic stresses caused significant decline in legume yield in South Asia and South East Asia. Among biotic stresses, fungal diseases are responsible for reducing yield up to 40–60% in mungbean (Kaur et al., 2011). Fungal pathogens can infect mungbean plants at different stages, such as during emergence, seedling, vegetative and reproductive stages and cause substantial damage leading to yield loss or complete failure of production. Species of the genera *Fusarium* (wilt), *Rhizoctonia* (wet root rot), and *Macrophomina* (dry root rot) infect mungbean plants during seed/seedlings stages (seed-borne or soil borne), while species of the genera *Colletotrichum* (anthracnose), *Alternaria* and *Cercospora* (leaf spot), *Erysiphe/Podospheara* (*Sphaerotheca*) (powdery mildew) affect plants during vegetative and reproductive stages (**Figure 1**; Ryley et al., 2010). Singh et al. (2013a) reviewed the status of web blight in mungbean and recently, Naimuddin and Singh (2016) published a review on yellow mosaic in mungbean and urdbean from India. However, reviews on fungal diseases of mungbean, their economic impact and major management practices have not been compiled. This manuscript reviews the economic impact of major fungal diseases in the mungbean growing areas of South and Southeast Asia and other areas in world as well as options available for sustainable management of these diseases. The review will also cover efforts in resistant breeding or pre-breeding activities including disease evaluation techniques.

ECONOMIC IMPACT OF MUNGBEAN FUNGAL DISEASES

Mungbean mainly is grown in rain-fed climates and variability in climate such as elevated temperature and CO_2 within the rain-fed ecologies leads to varying intensities of biotic stress (Chakraborty et al., 2000; Sharma et al., 2007) which cause significant loss in production. Foliar and root rot fungal diseases are major production constraints in South Asia and South East Asia. Charcoal rot/dry root rot (**Figures 1a–c**) (*Macrophomina phaseolina)* and Rhizoctonia root rot (**Figure 1d**) (*Rhizoctonia solani)* are economically important soil-borne vascular diseases, causing wilt and root rot complex (Alam et al., 1985; Iqbal and Mukhtar, 2014). Among major soil-borne vascular diseases, dry root rot and wilt is a major concern since the pathogen affects the plant during all growth stages and subsequently causes significant yield loss. Yield loss due to dry root rot was reported to be 11% in Northern India (Kaushik et al., 1987) and up to 44% in Pakistan (Bashir and Malik, 1988). Dry root rot was also reported first time in Shanxi province of China in 2010 (Zhang et al., 2011). Mungbean plants with wilt and root rot symptoms, with incidence of 80–90% in susceptible genotypes, was also reported in 1979 in southwest Ontario (Anderson, 1985).

Anthracnose (*Colletotrichum lindemuthianum* or *C. truncatum* or *C. gloeosporioides)* (**Figure 1f**; Shen et al., 2010), Cercospora leaf spot (**Figure 1g**) (*Cercospora cruenta* or *C. canescens* or *C. kikuchii* or *C. caracallae)* (Joshi et al., 2006), and powdery mildew (**Figure 1h**) (*Erysiphe polygoni* or *Podosphaera fusca)* (Ryley et al., 2010), Macrophomina blight (*M. phaseolina)* and web blight (**Figure 1e**) (*R. solani*) (Alam et al., 1985; Iqbal and Mukhtar, 2014) are the major foliar diseases of mungbean as causing yield loss ranging 20–60% in different continents. A wide range of yield losses (23–96%) due to Cercospora leaf spot was reported from field trials conducted at different states of India (Kaur, 2007; Chand et al., 2012; Bhat et al., 2014) and up to 61% from Pakistan (Iqbal et al., 1995). The impact of powdery mildew on mungbean also was reported from different countries. Yield loss due to powdery mildew was reported up to 21% in the Philippines (Quebral and Cowell, 1978), up to 40% in Australia (Kelly et al., 2017), and from 20 to 100% in different regions of India. Yield losses from powdery mildew was reported 35% from Gujarat, western India (Khunti et al., 2002), 20–40% from Chhattisgarh, central-eastern India (Khare et al., 1998) and 20–40% in Maharashtra, western-central India (Mandhare and Suryawanshi, 2008), and from 9 to 50% in Uttarakhand and Uttar Pradesh of Northern India (Pandey et al., 2009). Reddy et al. (1994b) also reported 100% loss from Maharashtra State, India due to powdery mildew diseases at seedling stage. A wide range of yield losses (24–67%) due to anthracnose disease was estimated from several mungbean growing areas in India (Deeksha and Tripathi, 2002; Kulkarni, 2009; Shukla et al., 2014). Alternaria leaf spot (*Alternaria alternata*) is also reported in South Asia, but economic impact is minor i.e., only 10% loss reported from Jammu and Kashmir, India (Maheshwari and Krishna, 2013). Web blight has been a problem for several decades in Pakistan (Alam et al., 1985) and in India, where it was reported from diverse geographical areas including Kanpur and Uttar Pradesh, northern India (Dwivedi and Saksena, 1974), Punjab, northwest India (Bains et al., 1988), Madhya Pradesh, central India (Tiwari and Khare, 1998), Rajasthan (south India), Bihar, Haryana, and Himanchal Pradesh (northern India) (Anonymous, 2014). About 30–40% of yield loss due to web blight was reported from Rajasthan (Anonymous, 2000) and 20–40% seedling mortality due to *Rhizoctonia* infection was reported from Jabalpur, central India (Tiwari, 1993).

FIGURE 1 | Symptoms of fungal diseases of mungbean at World Vegetable Center, South Asia Hyderabad field, **(a)**. Wilted plant with dry root rot symptom (*Macrophomina phaseolina*), **(b,c)**. Root & stem infected with *M. phaseolina*, **(d)**. Roots showing wet root rot (*Rhizoctonia solani*), **(e)**. Leaf showing web blight (*R. solani*), **(f)**. Leaf showing anthracnose (*Colletotrichum* spp.), **(g)**. Leaf showing *Cercospora* leaf spot (*Cercospora* spp.), **(h)**. Leaves showing powdery mildew.

There is a little information available regarding the dynamics in the prevalence and incidence of diseases in mungbean at temporal and spatial scale. Fusarium wilt caused by *Fusarium oxysporum* and/or *F. solani* was a minor disease of mungbean in Australia. However, the incidence and severity of the disease has increased substantially in recent years and yield losses of up to 80% were reported in the susceptible mungbean cultivars (Kelly, 2017). Outbreaks and spread of diseases were reported in other legume crops, such as soybean (Sconyers et al., 2006) and chickpea (Sharma and Ghosh, 2017). For example, Asian soybean rust (*Phakospora pachyrhizi*) was a problem in Asia and South America, but then spread rapidly across eight states of southeastern United States within a few years of first detection in Louisiana in 2004 (Sconyers et al., 2006). It was speculated that an extreme weather event (hurricane) was responsible for the introduction and spread of the Asian soybean rust. Sharma et al. (2015) also reviewed dry root rot (*Macrophomina phaseolina*) as an emerging disease of chickpea in semiarid tropic region and disease intensity has been increased in a past decade. They further speculated that changes in weather pattern, such as high temperature and drought stress during reproductive stages of the chickpea increased the dry root rot intensity. Climate change could have positive or negative or neutral impact on the dynamics of crop diseases depending on the types of crops, diseases or geographical regions (Luck et al., 2011). Climate change would increase average global temperature, CO_2 level, and cause more extreme rain/drought events (Meehl et al., 2005). Severity of some diseases, such as brown spot of soybean (*Septoria glycines*) and sheath blight of rice (*Rhizoctonia solani*) increased with elevated levels of CO_2 (Kobayashi et al., 2006; Eastburn et al., 2010), whereas variable results were reported for powdery mildew of wheat and barley (Thompson et al., 1993; Hibberd et al., 1996). In South Asia, spot blotch in wheat (*Cochliobolus sativus*) has increased substantially in recent years and it is speculated that elevated night temperatures due to climate change has contributed to this (Sharma et al., 2007). In Australia, root and crown rot of wheat (*Fusarium pseudograminearum*) is expected to increase due to climate change as the disease was high with elevated CO_2, temperature, and drought (Melloy et al., 2010). There is no information available on the impact of climate change on the dynamics of mungbean diseases. However, based on knowledge of similar pathogens/diseases in other crops, we can speculate that the pressure of soil-borne diseases caused by *Fusarium*, *Macrophomina,* and *Rhizoctonia* in mungbean may increase due to climate change. It is difficult to predict the effect of climate change on foliar diseases since they are influenced by the combination of temperature, rainfall and relative humidity, which can't be precisely predicted in most situations of climate change.

PERSPECTIVES FOR SUSTAINABLE DISEASE MANAGEMENT

The options for sustainable management of fungal diseases of mungbean include cultural and physical methods, exploitation of host resistance, use of synthetic fungicides, use of natural products such as botanical extracts, bio-fungicides, and use of

bio-stimulants or defense activators, and these are discussed below.

Cultural and Physical Practices

Use of different cultural practices and physical methods to eliminate seed-borne pathogens were found effective to reduce the foliar and root rot diseases of mungbean in fields. Field sanitation, crop rotation, removal of crop debris and weed hosts in the vicinity of the crop reduced the Cercospora foliar blight in mungbean (as reviewed in Sharma et al., 2011). Removing root rot infected mungbean plants reduced sclerotia loads in the field and delayed sowing and maintaining wider spacing between the plants reduced powdery mildew incidence (as reviewed in Satyagopal et al., 2014). Plastic mulching increased sclerotial mortality of *M. phaseolina* and reduced pathogen infection (Yaqub and Shahzad, 2009). Mungbean seed treatment with gamma rays ($_{60}$Cobalt) for 0–4 min and 90 days of storage had a suppressive effect on root rot fungi (Ikram et al., 2010). Hot water emersion treatments (55–65°C) were effective to eliminate seed-borne infection with *Colletotrichum acutatum* and *C. gloeosporioides* of mungbean (Lee et al., 2007). In South Asia, mungbean is commonly rotated with rice and wheat. It is reported anecdotally that root rot diseases in mungbean have been increased in South Asia and other Asian countries due to continuous rotation with rice. Several soil-borne pathogens, such as *Rhizoctonia*, *Fusarium* etc. are common problem in rice and wheat (Kobayashi et al., 2006; Melloy et al., 2010). These fungal genera also infect mungbean, but more studies are required to determine if the same species and strains also infect mungbean. If it is practical, adding diversity in the crop rotations would help for the sustainable management of these soil-borne diseases in mungbean. Crop diversification and use of diverse cultural practices, such as crop rotation, plant residue management, adjusting the planting dates etc., are recommended as effective strategies for managing crop diseases in conditions of climate change (Juroszek and von Tiedemann, 2011).

Exploitation of Host Resistance

Use of host–resistance is an effective, economical, and eco-friendly method for managing mungbean fungal diseases. In this section, we synthesize the available information regarding the identification of sources of resistance, available methods for efficient and reliable disease reaction phenotyping, identification of molecular markers associated with disease resistance genes and their potential use to improve disease resistance traits in mungbean.

Resistant Sources for Major Fungal Diseases of Mungbean

Reliable and efficient methods are available to screen for reaction to foliar diseases of mungbean including Cercospora leaf spot, powdery mildew, and anthracnose. Screening of these foliar diseases can be successful in natural field conditions where disease pressure is high, or if artificial inoculation with pathogen spores is available (Iqbal et al., 2004; Yadav et al., 2014a,b). For other foliar diseases caused by hemibiotrophic (*Cercospora* spp.) or necrotrophic pathogens, disease can also be evaluated in the greenhouse with artificial inoculation. Several disease rating scales/systems were developed to assess foliar diseases of mungbean (Wongpiyasatid et al., 1999; Khunti et al., 2005; Suryawanshi et al., 2009). Mungbean germplasm accessions can be screened by inoculating with the pathogen in the controlled environments. Reliable and efficient methods were developed for screening mungbean seedlings against powdery mildew in the greenhouse (Wongpiyasatid et al., 1999; Kasettranan et al., 2010); and in the laboratory using a detached leaf assay (Reddy et al., 1987). For the assessment of foliar diseases, both qualitative and quantitative rating scales were used (Reddy et al., 1994b; Wongpiyasatid et al., 1999; Khunti et al., 2005; Marappa, 2008; Suryawanshi et al., 2009). Root rot and wilt diseases are sporadic and highly variables due to genotypes × environment (G × E) interaction, therefore it is very difficult to get consistent results while screening in natural fields. Therefore, host genotypes are usually screened by inoculation at seedling stages in controlled environment for soil-borne diseases (*M. phaseolina*, *R. solani*, and *F. solani*). Different methods such as paper towel (Khan and Shuaib, 2007) and sick pot/field inoculation methods by inoculating the fungus grown in sorghum or maize grains (Dubey et al., 2009; Choudhary et al., 2011) were used for the evaluation of root rot disease.

Sources of resistance against powdery mildew, Cercospora leaf spot, anthracnose, Macrophomina blight and dry root rot have been identified (**Table 1**). The majority of studies targeted resistance to Cercospora leaf spot and powdery mildews and were conducted in the field. There have been fewer studies to identify root rot and anthracnose resistance sources, and these were conducted in both lab/glasshouse and field experiments. Most of the identified resistant materials were derived from cultivars/recombinant lines /breeding lines/land races; however, some were from wild relatives (Marappa, 2008) and mutant lines (Wongpiyasatid et al., 1999). Since screening trials for resistance against Alternaria leaf spot, anthracnose, and root rot diseases are limited, more attention is required on these. These resistant lines from difference sources can be utilized as donors for developing resistant varieties.

Identification of Major Genes and Quantitative Trait Loci (QTL) Linked to Major Diseases

The success of developing varieties resistant to biotic stresses depends on the availability of good sources of resistance materials as well as identification of markers associated with disease resistance major genes or QTL, which can also be used in marker assisted selection (MAS) breeding program to accelerate the resistant screening for large population. In mungbean, exploitation of host resistance and identification of molecular markers associated with major genes or QTL were mainly targeted for powdery mildew and Cercospora leaf spot (Kasettranan et al., 2010), however, no QTL or associated molecular markers were reported for other major fungal diseases including dry root rot and anthracnose. The commercial breeding for powdery mildew and Cercospora leaf spot disease resistance in mungbean mostly utilized major Resistant (R) genes based on the classical gene-for-gene system (Kasettranan et al., 2009). To our knowledge, use of MAS has not been used

TABLE 1 | Resistant genotypes of mungbean against fungal diseases[†].

Diseases	Country where screening conducted	No. of genotypes[‡] evaluated	Resistant genotypes (R, Resistant; HR, highly resistant)
Powdery mildew	Taiwan	4000	R: V2159, V4189, V4207, V4574, V4668, V4990 R/HR: V3912, V4186 HR: V1104, V4631, V4658, V4662, V4717, V4883 (Hartman et al., 1993)
	Thailand	27	R:M5-10 and M5-25 (Wongpiyasatid et al., 1999)
	India	82	R:BPMR-145, Vaibhav, TARM-18, Phule M-2002-13, Phule M-2001-3, Phule M-2003-3, Phule M-2002-17, and Phule M-2001-5 (Mandhare and Suryawanshi, 2008)
	India	12	R:TARM-18 (Sujatha et al., 2011)
	India	60	R:LGG-460 (Yadav et al., 2014a)
	India	374	R:116 resistant lines; HR: BL 849, LM1668, BL 865, AKM 8803, PBM, PMB 63 (Ramakrishnan and Savithramma, 2014)
	India	-	HR: KGS 83, MH 96-1, Pusa 572, GS 33-5, AKM 99-4, GS 21-5, COGG 936, ML 1299, TMB 47, HUM 1, MH 429, MH 429 and MH 530 (Akhtar et al., 2014)
	India	63	HR: KMP-36,39 and 41 R: KMP−2,3,5,19,20,24,30,34,38,42,47,52 and MLGG-8 (Bhaskar, 2017)
	India	146	HR: F4: C1-34-23, F5: C1-15-10, C1-15A-11, C1-21A-17, C1-25-19, C1-28-20, C1-32-22, C1-37-23, C1-38-27, C1-41-28, C1-44-31, C1-175-111, C1-236-152, C1-246-159, C1-275-177 (Kumar et al., 2017)
Cercospora leaf spot (CLS)	Taiwan	4000	R: V1471, V2757, V2773, V4718, V5036 (Hartman et al., 1993)
	Thailand.	27	R: M5-22 and M5-25 (Wongpiyasatid et al., 1999)
	Pakistan	58	R: NCM 255-2, NCM 257-6, ML-267, NCM 251-1, NCM 259-2, NCM 251-13, NCM 257-2, NM-92, NCM 251-12, VC-3960-A88 NCM 257-10, NCM-209, Mung-6 C1/94-4-19, VC 3960-A89 HR: BRM-188, NM-98, C2/94-4-42, 98-cmg-003, NM-2, NM-1, 98cmg-018, Basanti, CO-3, PDM-11, VC3960-88, BARIMung-2 (Iqbal et al., 2004)
	India	696	R: ML5, 443, 453, 515, 610, 611, 613, 682, 688, 713, 728, 735,746, 759 and 769 (Singh et al., 2004)
	India	170	No infection: *Vigna aconitifolia, V. glabrascence, V. sublobata, V. umbellata* and a mutant PBM. R: 90 genotypes including PANT M103, PANT M3, PUSA 105, ML 613, PANT M2, ML 173, ML 347, ML 561, PANT M4, PDM 11 (Marappa, 2008)
	India	65	R: GM-02-08, GM-02-13, GM-03-03 HR: LGG-460 (Yadav et al., 2014b)
	India	113	R: ML-5, ML-4, HUM-9, HUM-4, HUM-1, SM-9-124, LGG-450, and SM-9-107 (Singh and Singh, 2014)
	India	136	R: 52 genotypes HR: 1224-52 and 12404 (Zhimo et al., 2013)
	India	-	R: AKM 9910, IPM 02-5, ML 1299 and SML 668 (Akhtar et al., 2014)
	India	63	MR: KMP-13 (Bhaskar, 2017)
CLS, anthracnose, Macrophomina blight	India	56	R: ML1486, ML1464, ML1194 and ML1349 (Kaur et al., 2011)
Dry root rot	India	25	R: MSJ 118, KM 4-44 and KM 4-59 (Choudhary et al., 2011)
	Pakistan	29	R: 40504, NCM 257-5, 40457, NCM 251-4, 6368-64-72 HR: NCM 252-10 and 40536 (Khan and Shuaib, 2007)

[†] *All the trials were conducted in the field except dry root rot screening work by Khan and Shuaib (2007), which was conducted in the greenhouse.*
[‡] *Genotypes include cultivars, landraces, wild relatives, breeding lines, mutant lines, and germplasms.*

for mungbean breeding programs targeted for fungal disease resistance in developing countries. However, identification of molecular markers associated with disease resistant major genes and QTL shows the potential application of MAS in mungbean disease resistance. Genetic studies using different sources of resistance revealed both monogenic (qualitative) and quantitative modes of inheritance in mungbean for powdery mildew resistance (Reddy et al., 1994a; Kasettranan et al., 2009). Gawande and Patil (2003) reported that both additive and dominant gene actions were important in inheritance of powdery mildew resistance including non-allelic interactions. Several earlier studies reported monogenic inheritance of powdery mildew resistance controlled by single dominant genes and studies were conducted using mungbean varieties ML3 and ML5 (AVRDC, 1979), and breeding lines VC 1560A (AVRDC, 1981), ATF 3640 (Humphry et al., 2003) and RUM (Reddy et al., 1994a). Using restriction fragment length polymorphism (RFLP) markers, Chaitieng et al. (2002) and Humphry et al. (2003) revealed single major locus conferring the resistance against powdery mildew with 65 and 80% R^2, respectively. Khajudparn et al. (2007) found non-allelic dominant gene for powdery mildew in F_2 populations developed from resistant lines V4718, V4758, and V4785 (obtained from World Vegetable Center) and susceptible line CN72. Reddy (2009) studied the inheritance of Pm3 gene (different from earlier identified resistant genes, Pm1 and Pm2), a new gene responsible for powdery mildew by using local mungbean cultivar Mulmarada from Maharashtra (India). He found that F_1, F_2, and F_3 families exhibited complete resistance to powdery mildew is controlled by single dominant gene.

Several researchers reported quantitative mode of inheritance for powdery mildew resistance (Young et al., 1993; Sorajjapinun et al., 2005). Sorajjapinun et al. (2005) reported that additive gene action was found to play a major role in controlling powdery mildew (*E. polygoni*) resistance in the population of crosses developed between moderately resistant KPS 2 and resistant VC 6468-11-1A (sourced from the World Vegetable Center). Using mapping population developed from advanced mungbean breeding line VC3890 (from World Vegetable Center) as a resistance parent, Young et al. (1993) identified three QTL associated with powdery mildew (*E. polygoni*) resistance. These QTL explained 17 to 28 and 58% of phenotypic variation (R^2) individually and together, respectively. Using SSR markers, Kasettranan et al. (2010) identified two major QTL (qPMR-1 and qPMR-2) associated with powdery mildew resistance, which explained R^2 of 20 and 58%, respectively. They used 190 F_7 recombinant inbred line (RIL) population developed from the crosses between a susceptible cultivar, Kamphaeng Saen 1 and a resistant line, VC6468-11-1A (sourced from World Vegetable Center). SSR markers flanking and closely associated with qPMR-1 (CEDG282 and CEDG191) and qPMR-2 (MB-SSR238 and CEDG166) can be useful for MAS powdery mildew resistant breeding program of mungbean. Chankaew et al. (2013) also identified a major QTL associated powdery mildew resistance on linkage group (LG) 9 and two minor QTL on LG4 in V4718 (sourced from World Vegetable Center). They also detected two major QTL on LG6 and LG9 and one minor QTL on LG4 in the mapping populations developed using mungbean genotype RUM5 (Chankaew et al., 2013).

In Cercospora leaf spot, genetic inheritance studies using different resistant sources revealed that the resistance is controlled by either a single dominant gene (Lee, 1980), a single recessive gene (Mishra et al., 1988) or quantitative genes (AVRDC, 1980; Chankaew et al., 2011). Although the above information is useful for breeders in developing the resistant varieties, progress in selecting CLS-resistant genotypes in large breeding programs is still limited. First QTL mapping for resistance to Cercospora leaf spot in mungbean was carried out in Thailand (Chankaew et al., 2011). Using F_2 (CLS susceptible cultivar Kamphaeng Saen1, KPS1 × CLS-resistance mungbean line, V4718) and BC_1F_1 [(KPS1 × V4718) × KPS1] populations, they identified one major QTL (qCLS) on LG3 located between the markers CEDG 117 and VR 393, which explained 66–81% phenotypic variation. Their study further confirmed that SSR markers flanking qCLS will facilitate transfer of CLS resistance allele from V4718 into elite mungbean cultivars.

Protection With Synthetic Fungicides

Applications of fungicides are the most common approach of managing fungal diseases of crops. The traditional ways of disease management in mungbean include use of broad spectrum fungicides as a seed treatment chemicals and foliar spray. Efficacies of different mode of fungicides evaluated to reduce the major fungal diseases of mungbean are summarized in **Table 2**. Fungicides were evaluated mostly in the field trials as seed treatment and/or foliar sprays. Majority of trials were targeted for Cercospora leaf spot, anthracnose and powdery mildew and few trials were on Macrophomina blight, web blight and dry root rot (**Table 2**). Most of these studies assessed fungicide efficacies in reducing disease incidence and/or severity and yield benefit; however missed the economic analyses of the fungicide applications, which is critical component to recommend for farmers. The major group of effective fungicides to control foliar diseases including powdery mildew, Cercospora leaf spot, web blight, and Macrophomina blight were DMI, and MBC. Application of mancozeb (dithocarbmate) was not effective for powdery mildew; however, was effective for Cercospora leaf spot and Macrophomina blight. Dinocap (QiL) and tridemorph (amines groups) were effective for powdery mildew. Carbendazim and benomyl (MBC) were effective for anthracnose. Most of the foliar spray was applied immediately after the appearance of disease symptoms followed by 2nd and 3rd spray after 15–20 days of first spray for anthracnose, powdery mildew and Cercospora leaf spot as given in the **Table 2**. Seed treatment is applied mainly against wet and dry root rot, anthracnose and Alternaria leaf spot diseases before sowing. For dry and wet root rot disease, carbendazim was found to be most effective fungicides (Rathore, 2006). The other effective fungicides for wet root rot were flutolanil and tolclofos-methyl (SDHI), carbendazim (MBC) and pencycllron (Phenylureas) (Kumari et al., 2012).

To our knowledge, disease outbreak due to break down of fungicides has not yet been reported in mungbean. However,

TABLE 2 | Efficacy of fungicides for the control of fungal diseases in mungbean.

Diseases	FRAC code and Fungicide groups†	Effective fungicides	Method and frequency of application	Efficacy Impact (Disease reduction and yield)
FOLIAR DISEASES				
Powdery mildew	***M02-**(inorganic)	Wettable Sulfur (0.4%)	Twice foliar spray	Highest cost benefit ratio (3.3) was noticed (Das and Narain, 1990)
	3-DMI	Hexaconazole 5 EC (0.005%),	First foliar spray when disease appeared, repeated after 15 days	59% with 779 kg/ha yield in treatment, while 395 kg/ha in check (Khunti et al., 2005)
	29-QiI	Dinocap 48 EC (Dinitrophenyl crotonate)		73% with 1425 kg/ha (Suryawanshi et al., 2009)
	5-Amines	Tridemorph (0.05%)	First foliar spray when disease appeared, repeated after 7 days	69% and 532 kg/ha yield, while 326 kg/ha in check (Rakhonde et al., 2011)
	3-DMI	Propiconazole (0.10%),	Single foliar spray after first disease appearance	100% with 908 kg/ha yield, while 746 kg/ha in check (Akhtar et al., 2014)
Cercospora leaf spot	**3-**DMI	Hexaconazole 5 EC (0.005%),	First foliar spray when disease appeared, repeated after 15 days	59 and 779 kg/ha yield, while 395 kg/ha in check (Khunti et al., 2005)
	3-DMI	Difenconazole (25% EC) (0.0125 %)	Foliar spray after disease initiation, repeated twice at 15 DAS	61% (Kapadiya and Dhruj, 1999)
	1-MBC	Carbendazim (0.10%)	First foliar spray when disease appeared, repeated after 15 days	61% and 690 kg/ha yield at 70 DAS (Khan et al., 2005)
	3-DMI	Hexaconazole (0.1%)	Single foliar spray when disease appeared	81% with 752 kg/ha yield, while 525 kg/ha in check (Veena et al., 2013)
	1-MBC	Carbendazim (0.1 %),	Single foliar spray when disease appeared	77% (Singh et al., 2013b)
	4-PA	Metalaxyl (1.2 kg ha^{-1})	Foliar spray after 50 days of sowing before disease appearance	55% (Shahbaz et al., 2014)
	3-DMI	Propiconazole (0.10%),	Foliar spray after first disease appearance	86% with 908 kg/ha yield, while 746 kg/ha in check (Akhtar et al., 2014)
	1-MBC + **3-**DMI	Carbendazim (0.1%) + Difenconazole (0.02 %),	First foliar spray when disease appeared, repeated after 15 DAS	82 and 72% leaf infection and 76 and 96% pod infection with 825 and 808 g/9 m^2 yield during 2009 and 2010, respectively, while in check yields were 691 and 680 g 9 m^{-2} (Bhat et al., 2015)
	1-MBC + **M03**-dithiocarbamates and relatives	Carbendazim (12%) + Mancozeb (63%) 75% WP	First foliar spray when disease appeared, repeated after 15 DAS	70 and 990 kg/ha yield, while decreased in check (570 kg/ha) (Yadav et al., 2014b)
Anthracnose	**1-**MBC	Carbendazim (0.10%),	First foliar spray when disease appeared, repeated after 15 DAS	38% with 690 kg/ha yield at 70 DAS (Khan et al., 2005)
	1-MBC	Carbendazim (0.1%)	First foliar spray when disease appeared, repeated after 15 DAS	65% with increase in grain (1090 kg/ha) and stalk yield (1470 kg/ha) than untreated plots of resistant cultivar (UPM-98) (Shukla et al., 2014)
	1-MBC	Benomyl 50% (WP),	Single foliar spray @ 1.13 kg (a.i.)/ha per 1136 L of water at 10 days interval of disease	79 and 32 % in 6,601 and M-19-19 varieties with 587 and 669 kg/ha yield, respectively, while in untreated plots yields were 327 and 90 kg/ha (Bashir et al., 1985)
Web blight	**3-**DMI	Propiconazole (0.10%),	Foliar spray after first disease appearence	78% with 908 kg/ha yield, while 746 kg/ha in check (Akhtar et al., 2014)
	1-MBC	Carbendazim 50% WP (0.1%)	First foliar spray when disease appeared, repeated after 15 DAS	59% and 620 kg/ha yield, while it was reduced to 360 kg/ha in check (Jhamaria and Sharma, 2002)
Macrophomina blight	**M03**-Dithiocarbamates and relatives	Mancozeb (0.2%)	Single foliar spray after 7 days of pathogen inoculation	80% and 15 g/plant yield (Murugapriya et al., 2011)

(Continued)

TABLE 2 | Continued

Diseases	FRAC code and Fungicide groups†	Effective fungicides	Method and frequency of application	Efficacy Impact (Disease reduction and yield)
	1-MBC, **M03-**dithiocarbamates and relatives	Carbendazim (0.1%), mancozeb (0.2%)	Foliar spray after appearance of disease	94 and 88% due to mancozeb and carbendazim with 14 and 13.5 g yield/plant, while 5 g/plant yield in check (Rana et al., 2014)
Alternaria leaf spot	**3-**DMI	Hexaconazole (0.03)	First spray immediately after disease appearance and 2nd and 3rd spray were done at 10 days of interval	85% and yield 868 kg/ha, while yield decreased in control to 432 kg/ha (Maheshwari and Krishna, 2013)
ROOT ROT DISEASES				
Dry root rot	**1-**MBC	Carbendazim	Seed treatment @ 2 g kg seeds^{-1}	Reduced 54% disease incidence in pre-emergence and 66% at post-emergence (Kumari et al., 2012)
Damping off/wet root rot	**7-**SDHI, **14–**AH, **1** MBC, **20-**Phenylureas	Flutolanil (1 um a.i. ml^{-1}), tolclofos-methyl and carbendazim (5 urn a.i. ml^{-1}), pencycuron (50 urn a.i. ml^{-1})	Seed dressing (2×3 g ai kg^{-1} seed) or as soil drench (200 and 300 p.g ml^{-1}) of all the fungicides	Flutolanil, tolclofos-methyl, carbendazim and pencyclIron were most effective completely (100%) inhibited growth of *R. solani* and also reduced disease incidence (Reddy et al., 1992)

**The bold values indicate the FRAC (Fungicide Resistance Action Committee) code designated to the fungicide group. †DMI, De Methylation Inhibitors; QiI, Quinone inside Inhibitors; MBC, Methyl Benzimidazole Carbamates; PA, Phenyl Amides; SDHI, Succinatedehydrogenase inhibitors; AH, Aromatic Hydrocarbons (Chlorophenyls, nitroanilines); DAS, Day after spray.*

disease management failures in legume crops associated with fungicide resistance have been reported from several countries (Chang et al., 2007; Lonergan et al., 2015; Price et al., 2015). For example, Price et al. (2015) reported that isolates of *C. kikuchii* (Cercospora leaf spot) from soybean fields in Louisiana State, USA were insensitive to thiophanate methyl. Isolates of *Ascochyta rabiei* (ascochyta blight of chickpea) from Canada and USA showed insensitivity with fungicides pyraclostrobin, chlorothalonil, fluxapyroxad, and prothioconazole (Chang et al., 2007; Lonergan et al., 2015). More than 90% mungbean are produced in developing countries where strict regulations for fungicides are lacking and poor extension services to educate farmers to apply fungicides properly. This may lead in future the disease outbreak due to fungicide resistance problems. Therefore, fungicide resistance management strategies, such as rotation of fungicides with different mode of actions, tank mix of broad spectrum and selective fungicides, and integrate the fungicide spray programs with other components of disease management practices, should be implemented at regional and national level as recommended by Fungicide Resistance Action Committee (FRAC). Use of next generation fungicides derived from active constituents of natural products, which are ecologically safe and effective at lower doses, would also be beneficial (Sierotzki and Scalliet, 2013).

Biological Methods

Biological Control Agents

Very limited information is available on the biological methods to manage mungbean foliar diseases including powdery mildews, Cercospora leaf spot, and anthracnose. However, more information is available for the management of root rot pathogens. Most of these studies were conducted in the laboratories to evaluate the effects of bio-control agents (*Trichoderma* species, *Pseudomonas*, *Bacillus* etc.) to inhibit growth of root rot pathogens, *Rhizoctonia* and *Macrophomina*. Few studies were also conducted in the greenhouse to study the impact of seed or soil applications of the biocontrol agents to reduce the root rot; however, only very few studies were conducted in fields.

Sharma et al. (2017) recommended that application of biocontrol agents is more effective to suppress the soil-borne diseases as effective chemical protectants are either not available or not economical. Integrated applications of biocontrol agent with organic amendments were recommended to reduce root of mungbean in fields (Raghuchander et al., 1993; Ehteshamul-Haque et al., 1995). Dubey and Patel (2002) reported that soil application of *T. viride* (8 g/kg) multiplied in pulse bran and saw dust in the greenhouse experiment showed 75% reduction in root rot disease caused by *R. solani* and also promoted plant growth. A 76% reduction in Rhizoctonia root rot was reported when *Gliocladium virens* (*Trichoderma virens*) applied as seed treatment @ 10^6 spores/ml/10 g seeds (Dubey, 2003). Bioproducts Pusa 5SD (*T. viride*) showed 72% root rot reduction and 978 kg ha^{-1}, Pusa 5SD (*T. harzianum*) showed 71% disease reduction and 940 kg ha^{-1} yield in sick field (Dubey et al., 2011). Similarly, *T. harzianum*, and *T. viride* reduced about 54–73% Rhizoctonia root rot incidences (Singh et al., 2008; Maheshwari and Krishna, 2013) in green house and field experiments, respectively.

Seed dressing and soil drenching with bacterial strains of *Pseudomonas aeruginosa* and *Bacillus subtilis* significantly reduced 42% Macrophomina root rot, 39% Fusarium root rot and 70% Rhizocotnia root rot incidences in mungbean (Siddiqui et al., 2001). Bacterial strain TNAU-1 (*Burkholderia* spp.) inhibited mycelial growth of *M. phaseolina* in *in vitro* dual culture and also reduced root rot incidence up to three-fold when applied as a seed treatment and soil application with talc

based formulations (Satya et al., 2011). *Trichoderma viride* and *T. harzianum* were found to be reduced *M. phaseolina* growth (respective 42–33 and 42–25 mm) in dual culture (Ebenezar and Yesuraja, 2000). In the field study, Kumari et al. (2012) found that mixed application of vermicompost (10%) + bavistin (0.1%) + *T. harzianum* (4%) exhibited 100% reduction of Macrophomina root rot. *Bacillus subtilis* and *T. longibrachyatum* against *M. phaseolina* exhibited 64 and 63% antagonistic activity, respectively (Tandel et al., 2014). In greenhouse study, application of 4 g kg^{-1} seeds of *T. harzianum* with 25 g kg^{-1} of phosphate solubilizing bacteria as seed dresser reduced 26% incidence of Macrophomina root rot (Deshmukh et al., 2016).

The compatibility of different bioagents against root rot pathogens has also been studied. Application of plant growth promoting rhizobacteria, *Pseudomonas aeruginosa*, with a medicinal plant *Launaea nudicaulis* @ 0.5% as soil amendment reduced 51% of Macrophomina root rot, while combined application of *L. nudicaulis* (0.1% W/W) + *P. aeruginosa* and *L. nudicaulis* (1.0% w/w) + *P. lilacinus* gave 0% infection reduced of Rhizoctonia and Fusarium root rot, respectively (Mansoor et al., 2007). In the green house and field trials (Thilagavathi et al., 2007), soil application of *Pseudomonas fluorescens* strain Pf1+ *Trichoderma viride* strain Tv1 controlled 86% Macrophomina root rot in pot culture and 59% in field conditions with 833 kg ha^{-1} yield. The authors also found that *T. viride* strain is not compatible with *B. subtilis* (Bs16), but *P. fluorescens* strain is compatible with *B. subtilis* and *T. viride* in the management of dry root rot. Yadav et al. (2017) reported that *T. viride*, *T. harzianum*, and *Pseudomonas fluorescens* were effective to reduce powdery mildew of mungbean (∼80–84% reduction).

Botanical Fungicides and Bio-Stimulants

The plant products, particularly plant extract and essential oils, showed prominent toxicity to the diverse genera of plant pathogenic fungi, bacteria, insects and nematodes (Pandey and Tripathi, 2011). Plants synthesize aromatic secondary metabolites in the form of terpenes, like phenols (carvacrol, eugenol, and thymol), phenolic acids, quinones, flavones, flavonoids, flavonols, tannins and coumarins (Cowan, 1999), these groups of compounds show fungicidal effect and serves as plant defense mechanisms against fungal pathogens (Slusarenko et al., 2008; Das et al., 2010). For mungbean diseases, most of studies were preliminary and different kinds of plant extracts or their products have been evaluated against mungbean fungal pathogens (Javaid and Amin, 2009; Murugapriya et al., 2011). Foliar spray of neem extract (1:4 w/v) was reduced 65% of Cercospora leaf spot and increased 25% yield in mungbean (Uddin et al., 2013). Leaves extracts behada (*Terminali belerica*), tapioca (*Manihot utilissimum*), and sadafuli (*Vinca rosea*) reduced 60–66% of conidial germination of powdery mildew fungus *E. polygoni* (Rakhonde et al., 2011). Similarly, *in vitro* evaluation of leaf extracts of *Adenocalymma alliaceum* and *Allium* spp. reduced about 75–77% mycelia growth of *M. phaseolina*, Macrophomina blight incidences in greenhouse experiments (Murugapriya et al., 2011; Rana et al., 2014). In the greenhouse experiments, combined applications of 10% extract of *Allium* spp., mancozeb (0.2%), and 10% extract of *Allium* spp. with zinc sulfate (0.5%) reduced about 88–94% incidence of Macrophomina root rot (Sundaramoorthy et al., 2013). Javaid and Saddique (2011) found that amendment of dry leaf manure of *Datura metel* (1.5% w/w) in the soil reduced 80% plant mortality caused by *M. phaseolina*. Similarly, soil application of *L. nudicaulis* (1% w/w) extract also reduced dry root rot (62%), wet root rot (75%) and Fusarium wilt (100%) incidences (Mansoor et al., 2007) in glasshouse. Mungbean seeds dressing with 2% concentration of palmarosa (*Cymbopogon martinii*) oil gave complete inhibition of *M. phaseolina* mycelial growth (100%) in poison food testing and also caused 72.33% reduction in dry root rot in the greenhouse trials (Kumari et al., 2012).

Induced systemic resistance (ISR) and systemic acquired resistance (SAR) are both important phenomenon in the interactions of plant-pathosystems. Both ISR and SAR increased productions of proteins (defense enzymes) like peroxidase (PO), pathogenesis related (PR), phenylalanine ammonia lyase (PAL), polyphenol oxidase (PPO), phenols etc. (Jones and Dangl, 2006; Walters et al., 2009), which showed positive associations with resistance for several fungal diseases of vegetable and legume crops (Vallad and Goodman, 2004; Abdel-Kader et al., 2013). In mungbean, limited studies have been conducted to understand the mechanism of ISR and SAR. Similar to other crops, increase production of plant defense enzymes were reported when mungbean plants were treated with bioagents and plant products and also challenged with plant pathogens. Application of 10% aqueous leaf extracts of *Allium alliaceum* and other *Allium* sp. exhibited increase in PO, PPO, PAL and total phenol contents in mungbean plants inoculated with *Macrophomina phaseolina* (Sundaramoorthy et al., 2013). Treatment of *M. phaseolina* pre-inoculated mungbean plants with Pf1 (*Pseudomonas fluorescens*) formulation amended with chitin increased the accumulation of PAL, PO, PPO, chitinase, β-1,3-glucanse and phenolics indicating that the PGPR strains amended with chitin bioformulation induced defense-related enzymes and pathogenesis related (PR) proteins (Saravanakumar et al., 2007). Higher levels of PO and PPO activity was observed in *M. phaseolina* infection treated with the bioformulation combination of plant growth promoting bacteria (*P. fluorescens*) and biocontrol agents (*Trichoderma* or *Bacillus*) than the plants treated with single biocontrol agent (Thilagavathi et al., 2007). Mechanism of SAR were studied for bacterial (Dutta et al., 2005; Farahani and Taghavi, 2016) and viral diseases (Rashid et al., 2004) of mungbean, but study regarding fungal diseases are still meager. Thus, more investigations are required to understand the SAR and ISR mechanisms in the interactions between mungbean and fungal diseases.

CHALLENGES FOR THE SUSTAINBLE DISEASE MANAGEMENT

More than 90% of mungbean are cultivated in the developing countries, where small farmers do not have proper knowledge on integrated pest management and several challenges exist in the implementation of integrated management options. For example, use of gamma rays for seed treatment is a good option to eliminate seed-borne pathogen from seed, but it is

not viable for the small holder farmers since they produce seeds in their farm in a small scale. Several developing countries in south Asia do not have strong national breeding programs in mungbean to exploit host resistance for multiple diseases. Disease resistant genotypes identified in several studies were evaluated in few locations or seasons. Variability in pathogen populations exists among diverse geography; therefore, screening trials should be conducted multi-locations and years while developing breeding lines for disease resistance. Instability and breakdown of disease resistance in mungbean cultivars is a major challenge in breeding programs due to monogenic host resistance and high pathogenic variability (Nair et al., 2017). Integration of disease resistance traits without compromising valuable agronomic traits is a key challenge for mungbean breeders as linkage drags inhibit the proper use of genetic diversity from wild germplasm into the commercial cultivars (Acosta-Gallegos et al., 2008; Keneni et al., 2011). Further, undesired and desired traits co-inheritance may affect on seed quality.

In developing countries including India, fungicides are registered by CIBRC (Central Insecticide Board and Registration Committee) with their effective dose and label claim which provides guideline to the growers. However, where fungicides are not registered, agriculture officers or fungicide retailers provide fungicides spray guidelines to the growers. Several growers do not apply fungicides with appropriate doses and timing, although majority of fungicides used are preventative (broad-spectrum), which require applying prior to pathogen infection or prior to first symptoms appearance. In addition, farmers do not commonly rotate fungicides with different mode of actions due to poor knowledge and extension on IPM. As fungicides resistance is a big concern for legume industry in several countries (Chang et al., 2007; Lonergan et al., 2015; Price et al., 2015), the problem may arise in mungbean industry. Fungicide resistance could be significant challenge for the mungbean farmers in future to manage diseases effectively. Fungicide resistance management strategies recommended by FRAC, which we have described in the section "Protection With Synthetic Fungicide," have not been deployed at regional or national levels in several developing countries.

Additionally, attempts have been made to produce and apply biopesticide commercially in the developing countries. Challenges also exist for the commercial use of biopesticides in mungbean. Most of biopesticides only suppress the diseases and are not effective as chemical fungicides, therefore growers are reluctant to use the products (Flexner and Belnavis, 2000; Felde et al., 2006). Due to poor extension, growers do not apply the biopesticides as a component of integrated approach. In addition, several abiotic and biotic factors make the biopesticides less effective in field (Meyer and Roberts, 2002; Sharma et al., 2017). Sharma et al. (2017) speculated that there could be risk of developing biocontrol agents as crop pests and therefore, careful attentions are required while developing/evaluating biocontrol agents. However, we did not find any reports in the literature showing the evidences of biocontrol agents shifted to crop pathogens. Few researchers suggested that application of biocontrol agent is effective when mixed with other biocontrol agents; however, other investigators reported that such combinations may not be always advantageous as antagonism can occur among biocontrol agents (Viaene and Abawi, 2000). Most of studies to exploit botanicals and other bio-based products were evaluated in laboratory or controlled environments and their efficacy has not been evaluated in fields. This shows future potentiality of these products for the sustainable management of diseases, however, growers do not have current access of these products.

Mungbean farmers in the developing countries are not well educated about the impact of global climate change in the disease management. Global climate change would influence the emergence of new diseases, biology of the plant pathogens, disease development and their management practices in different geographical regions (Chakraborty et al., 2000; Juroszek and von Tiedemann, 2011; Luck et al., 2011). Global rise in temperature and CO_2 due to climate change may modify aggressiveness and fecundity of the plant pathogens, increase host susceptibility, and change host architecture and host-pathogen interaction (Chakraborty et al., 2000; Luck et al., 2011). The mungbean breeding programs in the developing countries does not have enough resources and strategies for developing resistant varieties for biotic and abiotic stresses associated with climate change elevation in temperature, CO_2, and moisture stress due to climate change may also affect the efficacies and the durability of plant protection chemicals and biocontrol agents (reviewed in Juroszek and von Tiedemann, 2011), which could be also key challenge to manage mungbean diseases in future.

CONCLUSIONS AND FUTURE PROSPECTS

The present review identified that root rot complex and wilt caused by soil-borne pathogens and foliar diseases are major fungal diseases impacting mungbean production in South Asia and South East Asia. Fusarium wilt and root rot and powdery mildew are problematic in Australia. For the management of these diseases potential options such as chemical and non-chemical (cultural, physical, host-plant resistance, biological) have been investigated by the researchers. Although several field trials were conducted to evaluate fungicides and other non-chemical management options by researchers from universities and governments, very little information has been transferred to the mungbean growers in South and Southeast Asia due to the poor linkage between research and extension activities. Deployment of Integrated Disease Management (IDM) to manage mungbean diseases in a coordinated approach requires good collaborations among academia, national and international research institutes, national extension agencies and growers.

Use of resistant varieties (if available) in combination with other components of management is a most effective option to combat with these fungal diseases. Described literature

revealed that sources of resistant genotypes have been identified for Cercospora leaf spot, powdery mildew, and anthracnose diseases and few for dry root rot by screening mungbean germplasms in natural field/artificial conditions in few specific locations. The identified sources for resistance in these diseases could be region specific as they were tested in a few specific locations. For example, V4718 mungbean accession from the WorldVeg gene bank has been used as a source of resistance to powdery mildew in Thailand and India. Breeding lines developed from the above source through cross breeding, and selections have been shared to the partners in the ACIAR funded International Mungbean Improvement Network project. Therefore, evaluation of resistant genotypes for these diseases at multi-locations in a coordinated approach would help in deploying host resistance at a larger scale. Compared to foliar diseases, few resistant genotypes of mungbean are available for root rot diseases. This may be due to the less priority given to the screening of these diseases in the past. However, the incidence of dry root rot in mungbean grown as part of rice based farming system in eastern part of India (Odisha state) and in Myanmar has triggered the need for identification of sources of resistance. Sharma and Ghosh (2017) reported that chickpea genotype which showed a good level of resistance to Fusarium wilt at 24°C were susceptible at 27°C. Therefore, breeding programs should consider potential impact of climate change in the new and existing biotic stresses. Attention should be given to develop climate resilient cultivars (such as cultivars can show a good level of resistance at higher temperature) with greater diversity and incorporating traits for multiple disease resistance. Literature evidenced that molecular markers are available for powdery mildew and Cercospora leaf spot, however, there is need to validate them in breeding programs. More attention is required to develop the molecular markers for root rot and anthracnose diseases. Currently, as a part of the network, we are screening 296 mini-core accessions of mungbean (Schafleitner et al., 2015) for resistance to anthracnose, dry root rot, powdery mildew and Cercospora leaf spot diseases. The resistant accessions identified will be shared among the project partners for cultivar development.

Application of synthetic fungicides is a common practice to control fungal diseases of mungbean, and growers also integrate other cultural methods with chemical sprays. Efficacies of several fungicides (**Table 2**) were evaluated in fields and controlled environments at universities and research institutions, however, there is a knowledge gap regarding how much of these evaluated fungicides are currently used by mungbean growers. In addition, additional research are required for fungicide efficacy trials including rotating and tank mixing with different modes of actions, different rates as well as volume of water for spray coverage. Attentions should also be given to develop and evaluate new generation fungicides. Fungicide resistance problem has not yet been reported in mungbean growing areas, which could also be due to research gap to investigate fungicide sensitivity against mungbean pathogens. In literature, baseline sensitivity data are not available for any fungicides and pathogens. Therefore, future research is recommended for *in vitro* fungicide sensitivity test using large numbers of pathogen isolates from diverse areas. Fungicide resistance management strategies (such as integrating chemical fungicides with other management practices, judicial use of fungicides, rotation and tank mix of different groups of fungicides) should be deployed at regional and national level to reduce the risk of developing fungicide resistance fungal population. Future impact of climate change on diseases of other crops such as wheat, soybean, and potatoes etc. were studied (reviewed in Luck et al., 2011). Climate change could make crop disease management more challenging in the developing countries. To our knowledge, no studies have been conducted to understand the effect(s) of climate change on mungbean diseases, and thus future research should address this. Induced resistance due to bio-stimulants has been explored for a few diseases including Macrophomina blight and therefore, additional research is required to exploit induced resistance to manage anthracnose, powdery mildew, Cercospora leaf spot and root rot diseases. Regarding biological control, investigation has been focused for root rot pathogens using strains of *Trichoderma, Pseudomonas*, and *Bacillus* as seed dresser and soil application. Biocontrol agents were more effective in reducing diseases in controlled environments than in fields. Plant-based products as described understory have been extensively researched for the control of seed/soil borne and foliar pathogens, but few have yet reached the market due to lack of their large scale trials at field level. Use of genomics tools has opened avenue to understand the mode of actions of biocontrol agents and genes associated with it (Sharma et al., 2017), however, more research is required in this area. Coordinated approaches from researchers from the universities, private sectors, national and international research centers are required to evaluate promising biocontrol agents, biostimulants, and botanical products in fields at multilocations and commercialize these products. Compatibility between different products including fungicides and these bioagents should be also evaluated. Persistent efforts are required for refinement, validation, transfer and adoption of the integrated disease management modules by the mungbean growers.

AUTHOR CONTRIBUTIONS

AP lead author in reviewing the literature, compiling the information preparing the reveiw draft and revising the manuscript. RB substantial contribution in writing the manuscript from the begining of the manuscript draft. Guided lead author to outline the sections and compile the manuscript. Critically reviewed and revised the manuscript, resturctured the entire manuscript with signifcant contribution to shape the manuscript for the final version. LK crtically reviewed the manuscript and contributed to rewrite and restructure the manuscript. Substanital contribution to revise the all sections of manuscript including abstract, prospects and conclusion. RN guided lead author to compile the manuscript, Significant contribution to revise the manuscript and contributed to write the Host Resistance section of the manuscript.

ACKNOWLEDGMENTS

Funding for this review was provided by core donors to the World Vegetable Center: Republic of China (Taiwan), UK aid, United States Agency for International Development (USAID), Australian Centre for International Agricultural Research (ACIAR) through ACIAR Project on International Mungbean Improvement Network (CIM-2014-079), Germany, Thailand, Philippines, Korea, and Japan.

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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

The reviewer RR and handling editor declared their shared affiliation