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GENETIC IMPROVEMENT OF MUNGBEAN♣

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SUMMARY

Mungbean (*Vigna radiata* (L.) R. Wilczek) is cultivated on more than 6 million hectares in the warmer regions of the world and is one of the most important pulse crops in South and Southeast Asia. The productivity of mungbean is relatively low (average about 400 kg/ha) and similar to other pulse crops. Broadening the genetic base by selecting parents from diverse and interspecific backgrounds is of paramount importance to achieve productivity gains. Development of an open source online mungbean pedigree database system will aid breeders in the choice of parents and avoid duplication in breeding efforts. Development of varieties with resistance to major diseases such as mungbean yellow mosaic disease and pests such as bruchids continues to be a breeding priority. Tolerance to waterlogging and salinity would help to expand this crop further in South Asia. Replacement of longer duration varieties with shorter duration types would contribute to an expansion of the crop in sub-Saharan Africa. Adoption of quality seed and improved agronomic practices are also important to enhance productivity.

Keywords: Mungbean, productivity, breeding

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INTRODUCTION

Mungbean (*Vigna radiata* (L.) R. Wilczek) is one of the most important food legumes in South and Southeast Asia. The grain is consumed as *dhal*, in soup, as bean sprouts, or processed into high value noodles. Mungbean is a cheap source of dietary protein for the poor, with high levels of folate and iron compared with many other legumes (Keatinge *et al*., 2011). Mungbean in rotation with rice improves the physical, chemical and biological properties of the soil, and helps to ameliorate degradation from continuous cereal cropping. A mungbean crop can increase the yield of a subsequent rice crop by up to 8% through the nitrogen it fixes in the soil and by reducing pest and disease problems (Weinberger, 2003).

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The development of mungbean from a relatively marginal crop to one of the most important grain legume crops in Asia was brought about by well-coordinated, collaborative research work led by Asian Vegetable Research and Development Center (AVRDC) – The World Vegetable Center with national partners in mungbean producing countries over a period of about 40 years. This led to the development of short-duration pest- and disease-resistant varieties that can fit into cereal based cropping systems (Shanmugasundaram *et al.,* 2009).

Current status of mungbean: area, production and productivity

Mungbean is cultivated in Asia, Africa and the Americas and covers more than 6 million hectares per annum worldwide. India, with approximately 3 million ha, has the largest mungbean production area followed by China and Myanmar (Figure 1). India has the greatest mungbean production followed by China and Myanmar (Figure 2), while productivity in India is one of the lowest (less than 400 kg/ha; Figure 3) compared with other countries. Indian states with very low productivity (<400 kg/ha) namely, Karnataka, Madhya Pradesh, Maharashtra, Odisha and Tamil Nadu account for about 40% of the cultivated area under mungbean. Very high yield gaps have been observed between experimental plots and farmers' fields. For example, in yield trials in India during the 2010 kharif season (June-July sowing) some promising varieties yielded around 1300 kg/ha compared with the national average of 400 kg/ha in Uttar Pradesh state (IIPR, 2011a). Pest and diseases, non-availability of seed of improved varieties (Bains *et al.,* 2006) and poor crop management practices are the major factors contributing to the yield gap. In Vietnam, a lack of suitable varieties with resistance to pests and diseases was identified as one of the major reasons for low productivity (Singh *et al.,* 2006).

Major biotic and abiotic limitations to yield

Varieties with resistance derived from different sources will be required to combat the emergence or evolution of different strains, species or biotypes of important pests or pathogens. The most important diseases include mungbean yellow mosaic disease, powdery mildew (*Erysiphe polygoni* D.C.), Cercospora leaf spot (*Cercospora canescens* Illis & Martin) and common bacterial blight (*Xanthomonas* spp.). Important pests include bruchids (*Callosobruchus* spp.), pod borer (*Maruca vitrata*), bean flies (*Ophiomyia* spp. and *Melanagromyza* spp.) and thrips (*Megalurothrips* spp.),

Mungbean yellow mosaic disease

Mungbean yellow mosaic disease, caused by at least two different species of begomoviruses (whitefly-transmitted geminiviruses) in South Asia, is the most important viral disease of mungbean in many areas. In India, mungbean yellow mosaic disease severely affects legumes including black gram (*V. mungo* (L.) Hepper) and mungbean. Improved varieties with good resistance are among the top Indian Council of Agricultural Research (ICAR) research priorities for the Eastern Region of India (IIPR, 2011b). Annual yield losses in all legumes due to begomoviruses in India are estimated to be about USD 300 million (Kundagrami *et al.,* 2009). Among begomoviruses infecting legumes in India, *Mungbean yellow mosaic virus* (MYMV) and *Mungbean yellow mosaic India virus* (MYMIV) are probably the most important.

In Bangladesh, diseases caused by MYMIV and *Dolichos yellow mosaic virus* (DoYMV) have been reported (Maruthi *et al.,* 2006). Most of the reported resistance screening to date has been done in north India and Pakistan and it is likely that identified resistance sources are effective against strains of MYMIV (e.g. Akhtar *et al.,* 2011).

AVRDC lines NM 92 and NM 94 are known for their mungbean yellow mosaic disease resistance. NM 94 shows resistance to the disease during the summer season, but is susceptible during the *kharif* (June-July sowing) season. All resistance found in mungbean to date appears to be tolerance (infection with mild symptoms) rather than immunity (Akhtar *et al.,* 2011. Resistance to MYMIV also has been detected in black gram in Kanpur, Uttar Pradesh, but the value of this resistance for variety improvement is unclear (Anjum *et al*., 2010).

New sources of resistance to MYMV (including interspecific sources) have been identified and molecular markers linked to resistance genes are becoming available (Maiti *et al.,* 2011, Chen *et al.,* 2012). These resistant genotypes will be tested to determine whether they are able to provide good protection against the major strains of both MYMV and MYMIV in disease hot spots. Resistance genes from confirmed sources will be stacked or pyramided through marker assisted selection to develop varieties with expanded resistance to the major strains of both MYMV and MYMIV across a wide geographic area and range of seasons.

All begomoviruses are transmitted by whiteflies of the species *Bemisia tabaci* (Hemiptera: Aleyrodidae). *B. tabaci* was believed to be a complex of at least 24 cryptic species, some of which have been referred to as ‘biotypes.’ However, it was recently reported that *B. tabaci* is a complex of 11 well-defined high-level groups containing at least 24 morphologically indistinguishable species (de Barro *et al.,* 2011). The “B” and “Q” biotypes have proven to be particularly invasive, and are efficient virus vectors with a very broad host range. The introduction of more aggressive vector biotypes into South Asia, perhaps as a result of globalization and the increase in international air freight shipment of fresh produce and flowers may be a factor contributing to the re-emergence of mungbean yellow mosaic as a major constraint to mungbean production in recent years.

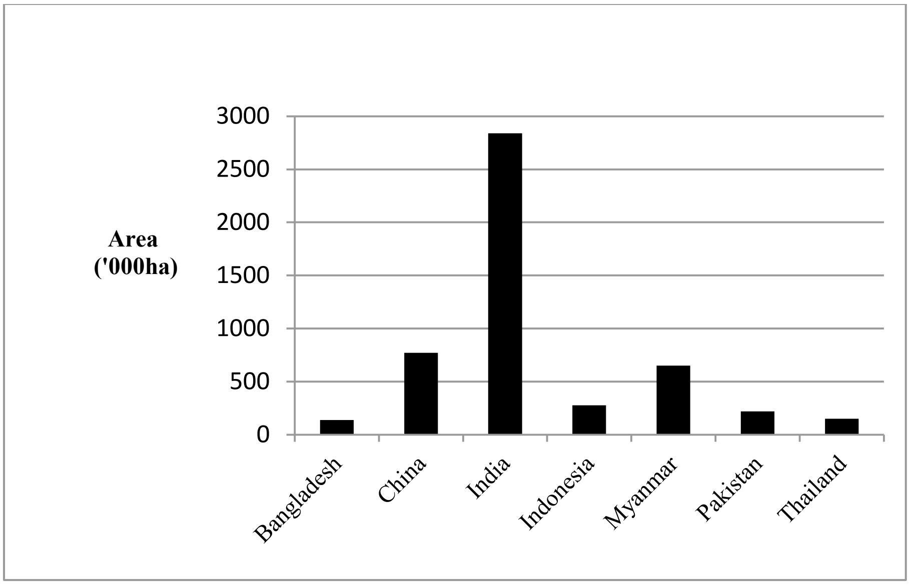

Figure 1. Major countries where mungbean is cultivated (‘000 ha). Latest available year - source: Bangladesh: Bangladesh Department of Agricultural Extension (2012); China: Mogotsi (2006); India: 2007-08 - IIPR (2011); Indonesia: BPS-Statistics Indonesia, RIDS (2011); Myanmar: Weinberger (2003); Pakistan: Ali et al (2010); Thailand: Chaitieng (2002). Downloaded from www.riceindonesia.com, accessed 24April 2012.

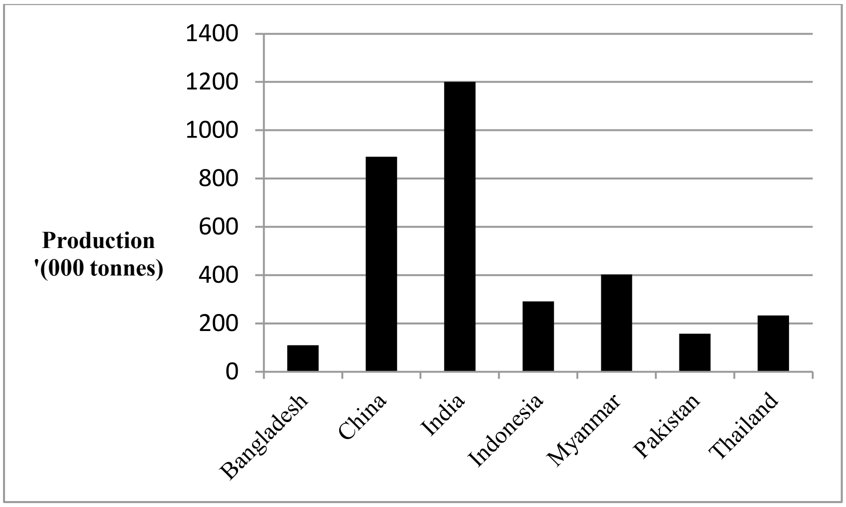

Figure 2. Major mungbean producing countries (in ‘000 t). Latest available year - source: Bangladesh: Bangladesh Department of Agricultural Extension (2012); China: Mogotsi (2006); India: IIPR (2011); Indonesia: BPS-Statistics Indonesia, RIDS (2011); Myanmar: Weinberger (2003); Pakistan: Ali et al (2010); Thailand: Chaitieng (2002). Downloaded from www.riceindonesia.com, accessed 24April 2012.

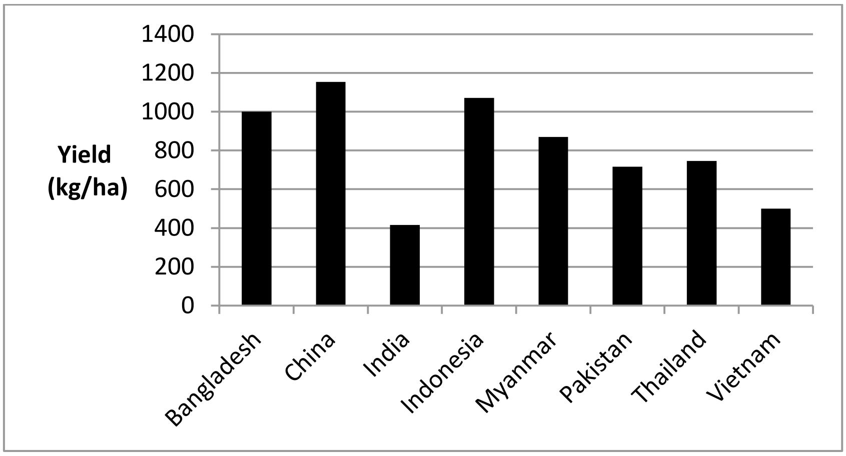

Figure 3. Mungbean productivity in selected countries (kg ha^{-1}). Latest available year - source: Bangladesh: Bangladesh Department of Agricultural Extension (2012); China: Mogotsi (2006); India: IIPR (2011); Indonesia: BPS-Statistics Indonesia, RIDS (2011); Myanmar: Weinberger (2003); Pakistan: Ali et al (2010); Thailand: Chaitieng (2002); Vietnam, Singh et al. (2006). Downloaded from www.riceindonesia.com (accessed 24 April 2012).

Climate uncertainty may be another contributing factor by increasing the number of generations or by extending the geographic range where the vectors and the viruses they carry can thrive. For instance, “B” and “Q” biotypes of *B. tabaci* completed one generation within 17-18 days at 33 °C, whereas it took almost seven weeks to complete its life-cycle at 17 °C (Muniz and Nombela, 2001). In addition, the excessive and inappropriate use of pesticides by farmers attempting to control whitefly-transmitted diseases may exacerbate the situation by selecting for pesticide-resistant strains of the vector. For instance, *B. tabaci* has developed resistance to organochlorines, organophosphates, neonicotinoids and insect growth regulators in India (Jaglan, 2005; Sethi and Dilawari, 2008). It should be noted that the development of resistance in *B. tabaci* to a particular pesticide could lead to the development of cross-resistance to the entire chemical group to which it belongs. For example, development of resistance to imidacloprid led to the development of high levels of cross-resistance to three other neonicotinoids (Wang *et al.,* 2009). Pesticide-induced resurgence of *B. tabaci* is another concern. Use of broad-spectrum synthetic pyrethroids leads to the development of resurgence of *B. tabaci* populations (Mohan and Katiyar, 2000). Synthetic pyrethroids reduce the content of phenols of leaves; phenols are the compounds responsible for resistance against *B. tabaci* in plants. The decrease in phenols leads to the resurgence of the pest (Jeyakumar and Gupta, 2007). Pesticide misuse also destroys natural enemies, and adversely affects the environment and the health of the farmers.

Bruchids

Postharvest damage to mungbean seed by bean weevils or bruchids (*Callosobruchus chinensis* L. and *C. maculatus* F.) is common, causing up to 100% loss (Zhang *et al.,* 2002). Bruchid infestation results in bean weight loss, low germination, and damage, making the seed unfit for human consumption or agricultural or commercial uses (Talekar, 1988). Bruchid infestation starts in the field but most damage occurs in storage, where several cycles of egg laying and adult emergence may lead to complete destruction of the seed lot within 3–4 months (Banto and Sanchez, 1972). The threat of mungbean storage losses forces farmers to sell the grain shortly after harvest when prices are relatively low (Ali *et al.,* 2000). Mungbean varieties resistant to bruchids would allow farmers to store mungbean seed and sell when prices are higher. Current popular mungbean varieties lack bruchid resistance, but AVRDC researchers have identified two black gram accessions (VM 2011, VM2164) that are highly resistant to bruchids (*C. chinensis*) as well as two mungbean accessions (V2802, V 2709) that have been recently confirmed to possess complete resistance to *C. chinensis* and *C. maculatus* (Somta *et al*., 2007). VM 2164 had significantly higher trypsin inhibitor activities than susceptible genotypes. The globulin of VM 2164 adversely affected the bruchid egg deposition (Landerito *et al.,* 1993). The bruchid resistance of V2709 is controlled by one dominant gene, *Br2* (Cheng *et al.,* 2008). Trombay wild black gram (*Vigna mungo* var. *silvestris*) collected from hilly areas around Trombay (a northeastern suburb of Mumbai) was shown to possess resistance to bruchids, and the resistance was found to be mediated by antibiosis (Souframanien and Gopalakrishna, 2007). 'Menaga' and 'Miyazaki,' two varieties of rice bean (*V. umbellata* (Thunb.) Ohwi & Ohashi), also exhibited high resistance to bruchids through antibiosis mechanism (Somta *et al.,* 2006). Hence, transfer of bruchid resistance from resistant *Vigna* genotypes into popular mungbean lines can be accomplished efficiently through interspecific or intraspecific crosses aided by use of molecular markers linked to bruchid resistance genes.

Abiotic stress

Mungbean can cope with drought reasonably well, but it is much less able to cope with waterlogging. Waterlogging is a common problem in locations such as southern Bangladesh, where 60% of national mungbean production is concentrated, and results in significant yield loss (Islam *et al.,* 2007). Development of waterlogging-tolerant varieties will help to reduce damage caused by unseasonal heavy rains during the growing season and increase the versatility of this otherwise hardy crop. In some instances salt stress affects the crop. Win and coworkers (2011) found significant difference in tolerance to salinity (0 to 225 mM NaCl) among *Vigna* genotypes at seedling stage. This calls for screening of mungbean germplasm in the target environment to identify lines suited for salt stress as well as to look at the possibilities of introgression of salt tolerance from related species.

Major quality requirements of mungbean

Grain colour, size and quality

Seed characteristics of mungbean can have a large impact on prices received by farmers, but these vary depending on the market. Seed size (large/medium/small), seed colour (green/yellow) and seed luster (shiny/dull) are traits that vary in importance according to regional preferences and depend on the form in which mungbean is consumed. Medium-sized seeds are preferred for sprout production. Dull-seeded types are preferred for soups, whereas shiny-seeded varieties are preferred for *dhal*. Cooking quality is a trait that sometimes is not given due consideration by breeders, but can make a big impact amongst consumers. For example, some of the yellow-seeded types preferred by consumers in countries such as Sri Lanka and the Philippines require longer cooking time as compared to green-seeded mungbean.

Weather damage due to dew, high humidity and rainfall during the pre-harvest period can lead to poor quality seeds that are discoloured and unsuitable for use in sprouting (Imrie *et al.,* 1988). Pre-harvest sprouting is a serious problem when the crop is subjected to unseasonal rain prior to harvest. Hence it is important to develop varieties with significantly reduced levels of pre-harvest sprouting for regions where this is a common problem.

Short duration types

Use of short-duration varieties to fit into cropping systems and relatively longer duration varieties for regions where cropping duration is not a constraint will help expand mungbean production. There is ample scope for expansion of mungbean cultivation in sub-Saharan Africa. For example, in East African countries such as Kenya and Tanzania, the varieties currently grown by the farmers mature in about 90 days. Replacement of these varieties with higher yielding, drought-tolerant varieties that mature in about 60-65 days would be beneficial for farmers already experiencing unreliable rainfall. Recently Rizvi and others (2012) reported that in Afghanistan, improved mungbean varieties out-yielded the local variety by 70% and resulted in a net benefit of US$575/ha additional income.

Enhanced protein quality

Protein malnutrition remains a major nutrition problem in Asia and affects children most severely (WHO 2000; UNSCN 2010). About 150 million children worldwide are underweight and 182 million are stunted. At least 70% of these children are in Asia. Meat is a good protein source, but is either excluded from vegetarian diets or unaffordable for poor households where protein and micronutrient deficiencies are most prevalent.

Mungbean, with an average protein content of about 26%, provides a significant amount of dietary protein for many South Asians. However, the nutritional value of mungbean protein is limited by its low concentration of sulfuramino acids, including methionine and cysteine. Black gram, a close relative of mungbean, has higher methionine content than mungbean. Improving mungbean protein quality through interspecific breeding with black gram is feasible. Gamma-glutamyl-methionine (γ-Glu-Met) is the major dipeptide in blackgram seeds, whereas gamma-glutamyl-S-methyl-cysteine (γ-Glu-S-metCys) is the dominant dipeptide in mungbean. Both peptides were found in F_2 hybrids between mungbean and black gram. Thus, interspecific breeding has great potential to improve nutritional value of mungbean protein and to help alleviate protein malnutrition in developing countries.

Black gram accession VM2164 possesses seed high methionine content as well as bruchid resistance and is therefore a potential donor parent of both traits. AVRDC has developed a non-destructive method to determine the methionine content in seed, which allows single seed selection for high methionine content in mungbean and black gram hybrids. AVRDC already has made an interspecific cross between VM2164 and NM94. These interspecific crosses will be used to develop a recombinant inbred line (RIL) population for mapping genes involved in high methionine content, molecular marker development, nutritional studies, and for improvement of locally adapted preferred lines for high methionine content through backcrossing.

A narrow genetic base for a global crop

Mungbean is native to tropical regions of Asia such as the Indian subcontinent, Indo-China and Malesia (Indonesia and Papua New Guinea) (USDA-ARS 2012). The greatest genetic diversity of mungbean can be expected in these centres of origin. Mungbean is naturalized in Australia and elsewhere in the paleotropics. The global mungbean crop has an extremely narrow genetic base. The pedigrees of the most popular mungbean lines grown worldwide are based on only a few dozen parental sources (Yang, 1996). Breeders and researchers need access to a broad genetic base of mungbean germplasm to tackle pest and disease problems as well as adapt the crop to new regions. AVRDC is developing an open source online database with pedigree information of released varieties worldwide. This will help breeders in developing new varieties and avoiding duplication of breeding efforts. Future progress in mungbean breeding requires urgent action to identify accessions with favourable agronomic traits and to provide tools to exploit the allelic diversity of mungbean for crop improvement. Worldwide, a total of 43,027 mungbean accessions are held ex situ. Institutes with major collections are: (1) The Institute of Plant Breeding, University of the Philippines, Los Baños, Philippines (6889 accessions); AVRDC – The World Vegetable Center, Taiwan (6358 accessions (AVGRIS 2012a)); the University of Georgia, Griffin, USDA-ARS, USA (3900 accessions); the National Bureau of Plant Genetic Resources (NBPGR), New Delhi, India (3147 accessions); the Regional Station Jodhpur of

NBPGR in Rajasthan, India (2466 accessions); the Field Crops Research Institute of the Department of Agriculture, Bangkhen, Thailand (2250 accessions); and the National Institute of Agrobiological Sciences, Tsukuba-shi, Japan (1579 accessions) (WIEWS 2012). Many of these accessions are still poorly characterized with regard to their genetic and phenotypic diversity, and often characterization data are not publicly available. AVRDC has recently updated its Vegetable Genetic Resources System (AVGRIS) for mungbean and has made characterization data for a total of 9198 accessions available online, covering mungbean, black gram, and rice bean (AVGRIS 2012b). Core collections representing a large part of mungbean diversity have been established and will be available for mining of favourable alleles for breeding.

Strategies for genetic improvement

Conventional breeding methods

Pure line selection, recombination breeding, and mutation breeding have been successfully employed to develop new varieties of mungbean (Fernandez and Shanmugasundaram, 1988; Tickoo *et al.*, 2006). Although crosses with related species (for example, crosses with black gram) have been employed, the number of varieties developed has been relatively few. The use of related species in breeding programs will become increasingly important so as to broaden the genetic base.

Marker assisted selection

Marker-assisted breeding has become a routine tool in crop improvement. Several molecular markers have been developed for important agronomical traits of mungbean, including resistance against bruchids (Chen *et al.,* 2007; Cheng *et al.,* 2008; Sarkar *et al.,* 2011), *Cercospora* (Chankaew *et al*., 2010) and powdery mildew (Kasettranan *et al.,* 2010), and these may be useful for marker assisted selection. Linkage maps based on restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), and simple sequence repeat (SSR) markers are available for interspecific crosses of mungbean and resolve 11 linkage groups (Humphrey *et al.,* 2002; Zhao *et al.,* 2010). However, the polymorphism rates of current marker systems for mungbean are insufficient for molecular breeding n due to the narrow genetic base of the crop. Single nucleotide polymorphism (SNP) markers are highly abundant in the genome and would provide an appropriate marker resource for molecular breeding. The small genome size of mungbean (515 Mb/1C) would make this species highly accessible either for full genome sequencing or a reduced representation library sequencing effort, paving the path to generate a large number of SNP markers (Moe *et al.,* 2011). A marker resource densely covering the mungbean genome would facilitate marker-assisted selection for simple and complex traits in this crop. SNP markers associated with important agronomic traits would enable marker assisted backcrossing and recurrent selection approaches and thus provide a means for quick progress in developing improved mungbean lines.

Feasibility of hybrid production

Heterosis effects of up to 200% have been reported in mungbean for grain yield (Tickoo *et al.,* 2006). However, one of the major barriers to hybrid seed production of mungbean is its cleistogamy. Recently Sorajjapinun and Srinives (2011) reported a chasmogamous flower mutant developed through gamma irradiation, which showed an increase of 9.6% in cross pollination compared with the wild type. Stable male sterile systems will be required to test the feasibility of hybrid mungbean.

CONCLUSION

To improve mungbean productivity breeders must develop varieties with multiple desirable traits. This requires a long-term effort and a multidisciplinary approach. Use of related species such as black gram and rice bean will become increasingly important to tackle pest and disease issues. Emphasis on thermo and photo-period insensitivity will be vital to improve the adaptation of the crop. In countries with established breeding programs the adoption of improved varieties can be significantly improved by providing farmers with better access to quality seed. An increase in adoption rates has been achieved in certain parts of India and Bangladesh; expansion into other areas of the region will benefit farmers. Short-duration mungbean (about 60 days) has the advantage of fitting into more diverse cropping systems. This should be promoted widely in the region and in sub-Saharan Africa to expand mungbean cultivation. Intercropping with cereals such as maize, sorghum or sugarcane is another option that would attract smallholder farmers. The adoption of improved varieties and good agronomic practices including timely weeding and integrated pest management will help to enhance crop productivity and meet the ever-increasing global demand.

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