MUNGBEAN VARIETAL IMPROVEMENT

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Mungbean, *Vigna radiata (L.)* Wilczek, is a short duration legume crop cultivated primarily for their dry seeds. While the areas for cereals and other pulses have decreased, that for mungbean has doubled in the last two decades with an annual rate of 2.5%. This growth may very likely continue since inungbean's short-growth duration (60 days) makes it suitable for the various cropping systems. Annual mungbean production worldwide is around 2.5 to 3.0 million metric tons harvested from about 5.0 million ha (Poehlman, 1991). Around 45% of the total world mungbean production is in India. In China, mungbean is grown in about.0.5 million ha per year with an average of 2 t/ha yield. In Thailand and the Philippines, mungbean is the most important grain legume; in Sri Lanka it ranks second, while in India, Burma, Bangladesh and Indonesia it is the third most important grain legume.

In India, mungbean is used as a pulse in the preparation of "dahl", a soup porridge eaten with a cereal or other traditional cuisines, and is a main protein source for the vegetarian diet. In other Asian countries, mungbean is used for bean sprouts, starch noodles, mungbean soup, and deep fried patties of different kinds. Mungbean is known for its easy digestibility and low flatus production compared to other pulses. The green pods and seeds may be used as vegetables.

Since mungbean matures in about 60 to 70 days after sowing, it is an excellent crop for rotation in different cropping systems. Mungbean may also be sown as an intercrop or as a green manure or cover crop.

Botany

Mungbean belongs to the order Leguminosae and Papilionoideae family and is botanically recognized as *Vigna radiata (L.)* Wilczek syn. *Phaseolus radiatus* L., P. aureus Roxb (Wilczek, 1954, Verdcourt, 1970). The taxonomic status of the species is given in Table 1. The genus *Vigna* has been broadened to include about 150 species; twenty-two species are native to India and sixteen to Southeast Asia, but the largest number of species are found in Africa (Polhill and van der Maesen, 1985). A few closely related Asian species of *Vigna* and their common names are listed in Table 2.

Table 1. Taxonomic status of mungbean.[a]

Taxonomic Status	
Kingdom:	Plant kingdom
Division:	Spermatophyta
Sub division:	Angiospermae
Class:	Dicotyledoneae
Order:	Leguminosae
Family:	Papilionoideae
Tribe:	Phaseoleae
Genus:	*Vigna*
Subgenus:	Ceratotropis
Species:	*radiata*
Variety:	*radiata*

[a]Rachie and Roberts (1974), Jain and Mehra (1980).

Table 2. Some wild and cultivated species of *Vigna* in Asia.

Species	Common names
Vigna aconitifolia (Jacq.) Marechal	Moth bean, mat bean
Vigna angularis (Willd.) Ohwi and Ohashi	Adzuki bean, red bean
Vigna mango (L.) Hepper	Urd, mash, blackgram, mungo bean
Vigna radiata (L.) Wilczek	Mungbean, moong, greengram, golden gram
Vigna trilobata (L.) Verdc.	Phillipesare bean, jungli bean
Vigna umbellata (Thunb.) Ohwi and Ohashi	Rice bean, red bean
Vigna radiata var. sublobata (Roxb.) Verde. .	Wild progenitor of mungbean

A key to identify four Asiatic *Vigna* species is given below:

A. Geiinination epigeal and petiole of primary leaves short
   a. Hilum not concave — *V. radiata* (mungbean)
   b. Hilum concave — *V. mungo* (blackgram)

B. Germination hypogeal and petiole of primary leaves long
   a. Hilum not concave — *V. angularis* (adzukibean)
   b. Hilum concave — *V. umbellata* (ricebean)

Mungbean is an annual, 0.3 to 1.5 m tall, erect or suberect plant, sometimes slightly twining at the tips. It is deep-rooted, much branched with long petioles. The leaves are alternate, trifoliolate, and dark or light green, the leaflets ovate and vary from 5 to 12 cm wide and 2 to 10 cm long. The inflorescence is an axillary raceme with a peduncle 2 to 13 cm long. The flower is yellow and the keel petal is spirally coiled with a horn-like appendage (Rachie and Roberts, 1974). Pods are 6 to 10 cm long, slender, short and hairy. Seeds are globose, weight 15 to 85 mg, mostly green but sometimes yellow, tawny brown, black or mottled. The white, flat hilum is not concave; germination is epigeal (Bailey, 1970).

Origin

Mungbean probably originated in India (De Candole, 1886; Zhukovsky, 1950; Bailey, 1970) or the Indo-Burmese region (Vavilov, 1951; H.B. Singh et al., 1970; Jain and Mehra, 1980). The primary gene center of diversity for mungbean was suggested to be the central Asian region (Vavilov, 1951) with India as the gene center and probable center of domestication (Smartt, 1985). Lukoki et al. (1980) proposed that *V. radiata* var. *sublobata* (Roxb.) Verde. that occurs wild in India and crosses easily with *V. radiata* var. *radiata* is the wild ancestor of mungbean.

Genetics, Qualitative Characters

Literature on genetic studies of mungbean largely comes from India where a vast array of researchers work on the crop. With mungbean, genetic studies are sparse compared to crops like soybean, due to lesser economic importance of the crop and less funding for research.

Early genetic studies of mungbean were conducted in India by Bose (1939). Before 1.980, 45 different qualitative characters were identified. Recognizing that there were no rules for gene nomenclature for *Vigna,* Fery (1980) suggested that a set of rules proposed for Curcurbitaceae be adopted for *Vigna.* Thus far no one has responsibility for maintenance of a genetic type collection of mungbean although there is a need for this activity. Fery (1980) developed a detailed review of the genetics of *Vigna* including V. *radiata* var. *radiata.* Poehlman (1991) extended the review to include genes identified after 1980.

Disease and Insect Reaction

Mungbean is attacked by many pathogens. These include fungi, bacteria, viruses, and nematodes. For reviews of the genetics of disease resistance see Rachie and Roberts, 1974; D.P. Singh, 1981, 1982, 1986; Fery, 1980; Poehlman, 1991. Many studies report on screening of accessions for resistance but few studies report on inheritance of resistance.

Leaf Spots: Resistance to bacterial leaf spot (BLS), a disease incited by *Xanthomonas phaseoli* (Smith) Dowson, and Cercospora leaf spot (CLS), caused by *Cercospora canescens* Ellis and Martin, are each conditioned by single dominant genes according to D. Singh and Patel (1977), Thakur et al. (1977a, b, c), and AVRDC (1981a, b). However, Yadav et al. (1981) reports resistance to BLS to be governed by a single recessive gene. It was shown that peroxidase polymorphism may be used as a selection index for CLS resistance (Menancio and Ramirez, 1977). Resistance to angular black leaf spot disease caused by *Protomycopsis phaseoli* in the variety LGG 450 (immune) is governed by a single dominant gene (Cheralu and Satyanarayana, 1993)

Powdery Mildew: Resistance to powdery mildew, caused by *Erysiphe polygoni* DC. ext. St. Arnans, is controlled by a single dominant gene (AVRDC, 1979), although it has also been reported to be governed by genes with additive action (Yohe and Poehlman, 1975), and recessive polygenes (AVRDC, 1981a, b). RFLP study also showed that the quantitative genes are controlling powdery mildew resistance (Young et al., 1994).

Viruses: Tolerance or resistance to the mungbean yellow mosaic virus (MYMV) is conferred by a single recessive gene (D. Singh and Patel, 1977; Thakur et al., 1977b; Malik et al., 1988); complementary recessive genes (Shukla and Pandya, 1985); and a dominant gene and complementary recessive genes (Sandhu et al., 1985). RFLP study also indicated a single recessive gene, see Poehlman (1991) for review. Resistance to MYMV was identified in *Vigna radiata var. sublobata* Roxb. Verde., progenitor of mungbean, and genes for resistance have been transferred to commercial mungbean types (B.V. Singh and Ahuja, 1977). Sittiyos et al. (1979) identified a dominant gene conferring resistance to a mungbean strain of cucumber mosaic virus.

Thakur et al. (1977a) studied the relationship of genes governing resistance to bacterial leaf spot and Cercospora leaf spot and tolerance to MYMV. They concluded that the genes were independently inherited and that traditional breeding methods could be utilized to develop multiple disease resistant mungbean.

Green et al (1996) have given a thorough review of MYMV related references in Bangladesh, India, Pakistan and Sri Lanka. They also reported mungbean geimplasm which are reported to have resistance to MYMV and/or vectors (Appendix 1).

From a multilocational testing of selected entries (tested in Bangladesh, India and Pakistan), it was found that NM 20-21 was either moderately resistant or resistant in all three locations. ML-267 was resistant in India and Pakistan but was susceptible in Bangladesh suggesting that there may be different isolates of the virus or the environmental difference influence disease expression. MYMV resistance is governed by three recessive genes with no maternal influence (Mishra and Asthana, 1996)

Bruchid: Resistance to storage insect pest, bruchid is controlled by a single dominant gene in *Vigna radiata* var. *sublobata* (Kitamura et al., 1988). RFLP study has also confirmed it (Young et al., 1992).

Morphological Characters

Growth Habit: Twining growth was reported to be dominant to erect habit (Sen and Ghosh, 1959). Pathak and Singh (1963) determined that the twining growth habit is due to a single recessive gene and that semispreading growth habit is dominant to erect habit.

Leaf Types: Lobed leaflet is governed by a single dominant gene (D. Singh and Mehta, 1953; D.P. Singh, 1980). Sen and Ghosh (1959) reported that the heterozygous genotypes have intermediately lobed leaflets. A dominant gene governs the incised leaflet while its allele produces ovate leaflet (Pokle, 1972). A mutant with four or five leaflets is probably dominant over normal three leaflets (Veeraswamy and Kunjamma, 1958). Mutation induced unifoliate and multifoliate leaflets were governed by independent recessive genes over the nonnal trifoliate leaflets (Santos, 1969). A crinkled lanceolate mutant governed by a single semidoininant gene, lethal in homozygous condition, was described by D. Singh and Saxena (1959). Two trilobate mutants were each found to have a dominant gene over normal monolobate trait. When crossed, an F_2 of 15:1 was obtained (Sareen, 1985). A small leaflet mutant has been reported to be due to a single recessive gene (Singh and Singh, 1995).

Pubescence: Dense plant pubescence is due to a single dominant gene, the recessive allele has medium-dense pubescence (Murty and Patel, 1973).

Pigmentation

Genes governing the pigmentation of various plant parts were reviewed by Fery (1980) and gene designations revised to conform to the new nomenclature. (Also, see Poehlman, 1991).

Seed Coat: Inheritance of seed coat color was studied initially by Bose (1939) who suggested two genes for green seed coat color. Variations in seed coat colors were found to be due to sap-soluble pigments and to the color and number of chloroplasts (Sen and Ghosh, 1959). They reported blue sap color was due to a single dominant gene while buff sap color was due to a recessive gene. Van Rheenen (1965) identified dominant genes conditioning green and spotted seed coat colors. Black spot on the seed coat was due to a single dominant gene (K.B. Singh and Singh, 1970). Murty and Patel (1972) described a four-gene model to explain seven different seed coat colors. A three-gene model was proposed by M.K. Singh (1973) to describe bottle-green and yellowish-green seed coat colors. Green and spotted seed color traits are each governed by a single dominant gene (D. Singh and Patel, 1977b).

Flower: Light-yellowish olive flower color is partially dominant to olive yellow flower color. The genes governing hypocotyl-epicotyl color also govern the olive yellow, and palm-leaf yellow flower colors. An allelic series of three genes were reported to govern pale-green yellow, bryta yellow, and naphthalene yellow flower colors, respectively, in that order of dominance (Murty and Patel, 1973).

Pod: The genes for flower color are known to affect the unripe pod color (Bose, 1939). Purple pigmentation in the vertical suture of unripe pods is due to a single dominant gene. Two independent recessive genes govern light popcorn and almond biscuit color, presence of the two dominant alleles produces black pod color. Black pods are probably due to a single dominant gene over light brown pods (Pathak and Singh, 1963).

Pubescence: Brown pubescence is recessive to colorless, with two dominant alleles required to produce colorless pubescence (Sen and Ghosh, 1959).

Cotyledon, Hypocotyl, Epicotyl, Stem, and Leaf Rachis: Purple hypocotyl is dominant to green hypocotyl and is governed by a single gene. A multiple allelic series with three alleles was suggested to govern the pigmentation of hypocotyl, epicotyl, stem and leaf rachis. A number of papers reported that the pigmentation in hypocotyl, epicotyl, stern, petiole and peduncle is due to single dominant genes (see Fery, 1980, for a list of references).

Red color of cotyledon, hypocotyl and top of the leaf stalk is due to a dominant gene that is suspected to be the same as the multiple allelic series identified by Sen and Ghosh (1959) and van Rheenen (1965). A dominant gene was shown to govern purple hypocotyl by Swindell and Poehlman (1978). A mutant with anthocyanin pigmentation in the hypocotyl, stem, petiole and peduncle was suspected to be due to a recessive gene (Appa Rao and Jana, 1973).

Chlorophyll: Albino seedling is due to a recessive gene with a recessive inhibitor gene (Sen and Ghosh, 1960c). Induced xantha and variegata characters are inherited as monogenic recessives, while a greenish-yellow chlorina behaved as a monogenic recessive in some lines but appeared to be due to two recessive genes in others (Santos, 1969).

Inflorescence, Photoperiod Response and Sterility

Inflorescence: Two dominant genes produce a simple inflorescence; in the absence of one or both of these genes a compound inflorescence arises (Sen and Ghosh, 1959). Single cluster of flowers is dominant to three or more clusters (T.P. Singh and Singh, 1970).

Photoperiod Response: Photoperiod insensitivity is dominant over photoperiod sensitivity (Verma, 1971; Tiwari and Ramanujam, 1976b). A dominant or partially dominant gene governs the sensitivity to photoperiod in P.I. 180311. The gene is expressed in 14 to 16 h photoperiods but not in 12 h photoperiods (Swindell and Poehlman, 1978). Early flowering and early maturity is either dominant or partially dominant and probably governed by two genes (Tiwari and Ramanujam, 1976b).

Sterility: Successful induction of male- and female-sterile mutants through various methods have been reported. In all instances sterility appears to be monogenic recessive (Ganguli, 1972, 1973; V.P. Singh and Chaturvedi, 1981).

Pods and Seed

Seed Shattering: Seed shattering at maturity is due to a single dominant gene (Verma and Krishi, 1969).

Pod Tip: Sen and Ghosh (1959) reported that a dominant gene controlled the swollen pod tip over tapering pod tip.

Seed Size: Small seed size is dominant to large seed size (Sen and Murthy, 1960).

Seed Coat Surface: Bose (1959), Sen and Ghose (1959), and van Rheenen (1965) reported dull, rough seed surface is a monogenic dominant over glossy, smooth seed surface. Sen and Ghosh (1959) identified a second dominant gene that governs dull, rough seed coat. Dull seeds are covered by an inner pod membrane that renders the seed dull; when this membrane is removed the seed coat underneath is shiny (Watt et al., 1977). The pod membrane may contain brown or black pigment through which the seed coat color may not be apparent. Based on this infounation, inheritance of pigmentation in the seed coat that may have been reported earlier for seeds covered with the membrane needs to be reevaluated. With a translucid membrane the seed coat color is visible through the membrane layer (see Poehlman, 1991, for discussion).

Genetics, Quantitative Characters

Many traits of economic importance are inherited in a quantitative fashion and their expression may be affected by both genetic and environmental influences. The extent of the genetic variability of a quantitatively inherited trait and the manner of its inheritance deternines its usefulness in plant improvement.

Genetic Variability

In mungbean the range of genetic variability for characters of economic importance has been studied for large collections of accessions by Banks (1958), Bhargava et al. (1966), K.B. Singh and Malhotra (1970a), Yohe and Poehlman (1972), Virmani et al. (1983), Paroda and Thomas (1988), He et al. (1988), and Sandhu et. al. (1988). In general, the. variability is reported to be sufficiently extensive for progress in mungbean breeding programs.

Relationship of Plant Characters and Yield

A knowledge of the relationship among plant characters is useful when selecting traits to combine for yield improvement. Correlation coefficients of yield vs. some major yield associated characters are summarized in Table 3. The yield component with the largest and most consistent correlation coefficient in a wide array of experiments is pods-per-plant, a close positive relationship to yield being reported in all experiments. Although a larger number of seeds-per-pod and higher 100-seed weight can compensate for low pod number, the association of seeds-per-pod or 100-seed weight with yield is inconsistent in different environments and has low reliability as a selection criteria for yield.

Table 3.Estimates of phenotypic and genotypic (in parenthesis) correlation coefficients for yield vs. specific traits in mungbean.

Pods-per plant	Seeds-per pod	Seed weight	Days-to-flower	Pod length	Reference
0.711 (0.689)	0.073 (0.196)	0.509 (0.720)	-0.131 (-0.158)	0.363 (0.537)	Gupta and Singh, 1969
0.90 (0.950)	0.35 (0.980)	0.0004 (-0.2100)	0.70 (0.80)		Joshi and Kabaria, 1973
0.8512 (0.7095)	0.4438 (0.4516)	0.1600 (0.3300)	0.0323 (0.0967)	0.4026 (0.2676)	K.B. Singh and Malhotra, 1970b
0.9512 (0.9772)	0.6903 (0.9077)	-0.4861 (-0.6506)	0.6140 (0.8220)	0.1631 (0.1421)	Malhotra et al., 1974a
0.503 (0.565)	0.282 (0.3J9)	0.159 (0.468)			Malik et al., 1983
0.847 (0.902)	0.433 (0.455)	-0.010 (-0.008)		0.198 0.204	Gupta et al., 1982

Heritability, Combining Ability, **and Gene Action of Yield and Associated Characters**

Grain yield in mungbean, as in other crops, is a complex character and is influenced by both genetic and environmental factors. Thus the phenotypic variance of yield or a yield associated character is composed of genetic and environmental components and genotype x environment interactions. The proportion of phenotypic variance of a character due to genetic component determines the heritability for that character. If calculated from the total genetic component it is referred to as broad sense heritability, whereas, if only the additive proportion of the genetic component is utilized in the calculation, the heritability is known as narrow sense. Genetic improvement by selection largely depends on an additive gene action component. Most heritability estimates reported for mungbean characters are broad sense heritabilities and provide a less accurate prediction of response to selection than would be provided by narrow sense heritability estimates. A particular heritability estimate is specific only for that population and the environment in which the population was grown. Estimates of broad sense heritability for yield and some yield parameters as reported by different workers are summarized in Table 4. Heritability for 100-seed weight was highest and most consistent among the yield components, followed by days-to-flowering and plant height. Heritability of seed yield varied in different experiments.

Yield: Heritability estimates for seed yield varied from 8.6 to 84.2%. Similarly, for pod number, the yield component with the highest correlation to yield (Table 4), heritability ranged from 21.7 to 90.4%. The range in heritability estimates may be attributed to variations in environments in which the studies were conducted, variations in gene action in the different cultivars studied, variations in specific gene combinations present in the varieties used, and/or the genotype x environment interactions.

The inheritance of yield and its components in mungbean has been studied for combining ability and type of gene action through the use of diallel crosses (K.B. Singh and Jain, 1971a,b; T.P. Singh and Singh, 1971, 1972, 1974a; Yohe and Poehiman, 1975; Ramanujam, 1978; Reddy and Sreeramulu, 1982; Ahuja and Chowdhury, 1984). General combining ability (gca) values for yield and yield components were generally greater than specific combining ability (sca) values, therefore it may be inferred that yield and the yield components were largely governed by additive gene effects.

Table 4. Broad sense heritability estimates for seed yield and some yield related characters in mungbean.

Days to flower-ing	Days to maturi ty	Plant height	Branch es per plant	Pod numbe r	Pod length	Seeds per pod	100-seed weight	Seed yield	Referen ce[a]
		96.8	66.0	87.9	66.0	41.3	85.3	69.9	1
94.9		87.3	34.5	53.8	88.6	39.0	98.6	56.9	2
62.0	71.2	27.0		24.6	-	10.0	51.2	8.6	3
99.0	-	96.9		77.0	89.7	70.2	97.0	79.1	4
39.5	-		50.9	47.8	89.9	58.7	92.9	51.6	5
88.8	81.5	7.9	-	90.4	-	12.3	-	84.2	6
69.0	-	75.0	57.0	78.0	74.0	78.0	-	75.0	7
		96.3	85.2	21.7	95.0	68.3	95.3	59.0	8
65.1	61.4			30.9	33.9	30.5	88.9	27.5	9
-	-	83.0	31.0	43.0	31.0	26.0	97.0	38.0	10

[a] References: 1) Bhargava et al., 1966; 2) Chowdhury et al., 1971; 3) Empig et al., 1970; 4) Giriraj, 1973; 5) Gupta and Singh, 1969; 6) Joshi and Kabari, 1973; 7) Murty et al., 1976; 8) Pokle and Nomulwar, 1975; 9) K.B. Singh and Malhotra, 1979b; 10) Toinar et al., 1972.

Plant Development: Broad sense heritability for plant height (Table 4) varied from 7.9 to 96.9% and that of branches per plant ranged from 31.0 to 85.2%. Significant gca and sca were observed for plant height by Swindell and Poehlman (1976). Tiwari and. Ramanujam (1974) found a large proportion of variance due. to gca for plant habit, number of leaf axils per plant, number of effective leaf axils per plant, and number of branches per plant. Similarly, gca was preponderant in Yohe and Poehlman's (1975) study on the variability in plant height and branch length. For plant height and number of branches, a dominance x dominance gene action was demonstrated (Murty et al., 1976), although Godhani et al. (1978) implicated additive gene action for branch number, and additive, dominance and epistatic gene actions for plant height. Since plant height has high heritability and high genetic advance, it was suggested that additive gene action is predominant (Bhargava et al., 1966; Chowdhury et al., 1971; Giriraji, 1973; Veeraswamy et al., 1973). Pokle and Nomulwar (1975) reported that genetic advance for plant height is low, even though it is highly heritable, and therefore is governed by nonadditive gene action. Reddy and Sreeramulu (1982) also reported

nonadditive gene action for height.

Flowering: Broad sense heritability estimates for days to flowering ranged from 39.5 to 99% (Table 4). Based on the results of several studies, it was suggested that earliness is governed by additive gene action (Chowdhury et al., 1977a; Giriraj, 1973; Godhani et al., 1978; T.P. Singh and Singh 1974a; Swindell and Poehlman, 1976; Tiwari and Ramanujam, 1974; Yohe and Poehlman, 1975). Dominance x dominance gene action for days to flowering was reported by Murty et al. (1976) and Swindell and Poehlman (1978).

Pod Length: Heritability of pod length was fairly high in most environments (Table 4), although reports conflicted on type of gene action (Chowdhury et al., 1971; Pokle and Nomulwar, 1975; T.P. Singh and Singh, 1971; Murty et al., 1976; Godhani et al., 1978). Such reports show the complexity of the inheritance and the environmental response of this character and, therefore, the selection for this trait will encounter difficulty.

Seeds Per Pod: The range in heritability for number of seeds per pod varied from 10.0 to 78.0% (Table 4). Additive and nonadditive gene action was implicated for number of seeds per pod (K.B. Singh and Jain, 1971a; Tiwari and Ramanujam, 1974). Murty et al. (1976) reported that dominance x dominance gene action was important.

Seed Weight: Heritability of seed weight is high, ranging from 51.2 to 98.6% (Table 4). Several workers reported high heritability estimates and high genetic advance indicating that additive gene action is apparent in the inheritance of seed size.

Protein Content: T.P. Singh and Singh (1973b) and T.P. Singh (1974) demonstrated both additive and nonadditive gene action for the inheritance of protein content in mungbean. Tiwari and Ramanujam (1976a) observed predominant additive gene action.

Path Coefficient Analysis of Yield and Its Components

Because yield is a complex trait and its expression is governed by many factors, it is logical to expect that a number of plant traits jointly contribute to enhance yield. A knowledge then of the interrelationships and contributions of various yield components, such as pods-per-plant, seeds-per-pod, pod length, leaf size, or 100-seed weight, to yield would be useful if selection for simultaneous improvement of these traits is to be most effective. To establish such relationships, a "path coefficient" analyses of correlation in a system of related variables may be utilized. Path coefficient analyses in mungbean are reported by K.B. Singh and Malhotra (1970b), T.P. Singh. and Singh (1973a), Chandel et al. (1973), Giriraj and Vijayakumar (1974), Malhotra et al. (1974b), Pokle and Patil (1975), Bhaumik and Jha (1976), Ko and Choe (1976), Sandhu et al. (1980), Abilay and Lantican (1982) and Vidyadhar et al. (1984). The direct and indirect effect of specific yield components to yield were shown in the above reports. The character making major contributions directly to yield was pods-per-plant, with indirect

contributions being made through seeds-per-pod and seed weight. Plant height and number of branches contributed indirectly to yield through pods-per-plant. Pods-per-plant also had a significant relationship to yield as measured by correlation analyses. These results point to the importance of selecting for higher pods-per-plant to improve yield. Uniform spacing of plants is required for valid comparisons of pods-per-plant among mungbean lines.

Genetic Divergence

Mahalanobis' D^2 statistics were used to study the yield and yield components of different strains in mungbean (Gupta and Singh, 1970; Thulasidass, 1984). Seed weight and pod length were found to be important characters contributing toward genetic divergence. Malhotra et al. (1974b) reported that geographic diversity had no direct association with genetic diversity. Thulasidass (1984), in a study of 30 genotypes of different origins, showed an association of genetic diversity with geographic diversity. In the latter study, days to maturity made the greatest contribution toward genetic divergence. Ramanujam et al. (1974) studied genetic divergence in 10 parent and 25 F_1 populations using D^2 and canonical analysis. He reported genetic divergence contributed by flowering time, maturity, seed density and 100-seed weight. Canonical analysis supported the results of the D^2 analysis.

Heterosis

Heterosis in mungbean was reported for yield and the yield components, days to flowering, plant height, leaf size, and branch number (Bhatnagar and Singh, 1964; Misra et al., 1970; Ramanujam et al., 1974; K.B. Singh and Jain, 1970; T.P. Singh and Singh 1974a,b; Swindell and Poehlman, 1976). Overall, yield increase of the Fl over mid-parent yield varied from 17 to 208% and the increase in yield from the F_1 over the high parent varied from 1 to 188%. In a recent study Reddi et al (1994) reported a heterosis of 75.9% and 50.3% over the mid parent and the better parent respectively for yield. The yield components also showed heterosis. The high yield increases reported above may not be realistic in experiments where heterosis was measured from spaced plants as spaced plants are notoriously variable in growth. In 58 crosses, the F_1 was significantly superior to the midparent in only 23 crosses, and in 33 crosses, the F_1 was superior to the high parent in only 6 crosses.

Heterosis for yield and pods per plant was attributed to overdominance and nonfixable genic interactions (T.P. Singh and Singh, 1974a,b). Evidence of significant inbreeding depression was observed for yield in F_2 and F_3. Presence of genes with oppositional dominance was reported to be responsible for lack of heterosis for protein content (T.P. Singh and Singh, 1973b; Tiwari and Ramanujam, 1976a). In 25 crosses, three showed significant heterosis over midparent for methionine content (Tiwari and Ramanujam, 1976a). Due to the low frequency of crosses with significant heterosis and the closed pollination system in mungbean the exploitation of hybrid vigor per se as a breeding procedure is not feasible.

Induced Mutations and Mutants

Many studies have been made of induced mutations in mungbean, especially in India, Pakistan, and Bangladesh. The mutagenic agent used most frequently has been ^{60}Co gamma radiation, but X-rays, neutrons, and chemical mutagens such as EMS and DMSO have been used also. The mutagenic agents cause varying kinds of undesirable mutations in addition to the desirable ones. More point mutations and fewer chromosomal aberrations are obtained with EMS or DMSO than with radiations. With gamma radiation, a dose of 30 to 40 KR ^{60}Co radiation was found to be most effective in producing desirable mutants (D.P. Singh et al., 1979), although the sensitivity dosage of the mutagenic agent may vary with the genotype used (Murray and Newcombe, 1970; Rajput, 1973; Yahya et al., 1975; Khan and Hashim, 1978; Rangaswamy et al., *1973;* V.P. Singh and Chaturvedi, 1981).

A list of induced mutations identified have been reviewed by Gupta (1996). He also lists the mungbean mutants released officially as varieties in different countries.

Mutants commonly reported have been characterized by the following traits: shorter plants, earlier and synchronous maturity, more branches-per-plant, more pod clusters, greater pod set, MYMV resistance, higher 100-seed weight, and higher protein content (Santos, 1969; Bhatt et al., 1972; Dahiya, 1973, 1978; Rajput, 1974; Tikoo and Jain, 1974; Prasad, 1976; Shakoor, 1977; Subramanian, 1980; V.P. Singh and Chaturvedi, 1981; Shaikh et al., 1982). Four mungbean cultivars have been released from mutation breeding programs, 'Pant Mung 2', 'TAP-7', and 'Co4' from India and 'NIAB Mung 2B' from Pakistan (Shanmugasundaram, 1988). The cultivar, 'Pant Moong 2', released in 1982 is reported to be moderately resistant to MYMV, and 'TAP-7', also released in 1982, is reported to be tolerant to powdery mildew and a leaf spot disease.

Cytology and Cytogenetics

Cytological and cytogenetic studies with mungbean have been relatively few due to the small size of the mungbean chromosomes and the difficulty of working with them. The diploid chromosome number of mungbean is 2n=-2x $^{=}$22 (Karpechenko, 1926; Kumar, 1945; Krishan and De, 1965). A pachytene chromosome analysis disclosed that the chromosomes varied in length from 28.1 to 73.3 μ with two bivalents associated with the nucleolus at pachytene (Krishnan and De, 1965). The nuclear chromosomes varied in length and the position of secondary constrictions at pachytene and somatic metaphase stages also varied. The karyotypes of three wild types had shorter somatic chromosomes than two cultivated varieties (Shrivastava et al., 1973). By comparing the chromosome complements of several related species, Bhatnagar et al. (1974) proposed the following karyotype formula for mungbean: $4L^{s}+4M^{t}+3M^{m}$ where L = long (2.7 to 3.5 μ), M = medium (1.9 to 2.6 μ), sm = submedian, and m = median centromere. An idiogram of prometaphase chromosomes was presented by Joseph and Boukamp (1978). Since mungbean has long metacentric and submetacentric chromosomes, it is considered to be more primitive than blackgram (De and

Krishnan, 1966a,b; Sarbhoy, 1980).

Polyploids

Autotetraploids have been induced following colchicine treatment by Kumar and Abraham, 1942a,b; Kumar, 1945; Sen and Ghosh, 1960a; Mitra, 1967; and Kabi and Bhaduri, 1978. Generally, the autotetraploids had gigas floral parts, slow germination, late maturity, high sterility, poor seed set, and larger seed stomata. Autotetraploidy per se is not expected to make a significant impact in the development of new mungbean cultivars. No natural amphidiploids have been identified with a genome homologous to *V. radiata.*

Interspecific Crosses

Several closely related species (see Table 2) have the same chromosome number as mungbean, 2n=2x=22. Based on cytogenetic studies, Dana (1966a,b) proposed the genome designation of AA for V. *radiata* and *V. mungo* and A_1A_1 for *A. umbellata.* Blackgram, rice bean, and adzuki bean have genes for disease resistance and nutritional quality, factors that would be useful in mungbean. So far, not much success has been accomplished in transferring genes for useful characters from related species to mungbean. Reviews of interspecific crosses with mungbean have been made by Yadav et al. (1986) and Poehlinan (1991).

Crosses of mungbean x blackgram were attempted by Sen and Ghosh, 1960b; Dana, 1966a; De and Krishnan, 1966b; Chowdhury and Chowdhury, 1974; Verma, 1977; Ahn and Hartmann, 1978a,b,c; AVRDC, 1979; Chen et al., 1983; Yadav et al., 1986. Generally crosses have been successful only when mungbean is used as the female parent. Success of the crosses, as measured by viability of the crossed seeds and F_1 plant survival, varied with the parent genotype in the cross (AVRDC, 1979). Ahn and Hartmann (1978c) found that compatibility was improved if a mungbean F_1 was used as the female in crosses with blackgram but germination of F_2 seeds was still erratic. Generally, the hybrids are sterile although their amphidiploids have normal meiosis and up to 80% fertility. The amphidiploids are vigorous, but shy in pod production and pod-filling, unstable, and tend to revert back to parental forms by gradual elimination of chromosomes (Yadav et al., 1986). Selection for recombinant types can be made among the derivatives. Amphidiploid-derived lines appear to be superior in yield, tryptophan and methionine content, and protein digestibility, which is attributed to gene introgression between mungbean and blackgram (Yadav et al., 1986).

Attempts have been made to cross mungbean x ricebean *(V. umbellata)* which has resistance to Cercospora leaf spot and powdery mildew pathogens. The sterility of the F_1 was partially overcome by doubling the chromosomes to produce an amphidiploid (Dana, 1966b, Sawa, 1974; Ahn and Hartmann, 1978c; AVRDC, 1979; Chen et al., 1983).

The cross between mungbean and adzuki bean *(Vigna angularis)* produces a few seeds that abort prematurely (Ahn and Hartmann, 1978b,c). A few hybrid plants grown through embryo culture reached maturity without producing seeds. Chromosome pairing in the hybrid was low suggesting that the two species are distantly related.

A cross of mungbean with *V. radiata* var. *sublobata,* the wild progenitor of mungbean, was successful when mungbean was used as the female (Ahuja and Singh, 1977). A wide range of segregation was observed up to the F_4 generation. Successful reciprocal crosses were obtained at AVRDC (AVRDC, 1979). The F_1 plants from a cross between mungbean and *V. trilobata* were sterile, but if the chromosomes were doubled the amphidiploids were fertile (Dana, 1966c,d).

Vigna glabrescens is a natural tetraploid (2n = 44) and its cross with *Vigna radiata* is not possible. Chen and Mok produced F_1 plants by the embryo rescue culture (Chen et al., 1989). The F_1 plants were highly sterile upon selfing, but backcrossing to mungbean parent yielded viable seeds.

Genetic Engineering and Biotechnology

Cell cultures, protoplast fusion, and genetic transformation of cells through vectors form part of a new generation of genetic engineering and biotechnology research. The novel approach involves the potential transfer of genes between species and even genera at the cellular level. For biotechnology to be successful the ability to regenerate whole plants from isolated single cells in a consistent reproducible manner is essential. Until recently most of the legume species have been considered recalcitrant (Bhojwani and Muklopadhyay, 1986). Plant Regeneration varies among species and genotypes within species. In addition to choice of the right genotype, choice of the medium and its constitutients is required. Before biotechnology becomes a useful tool for transfer of valuable genes by the mungbean breeder, stable regeneration and transfer procedures must be developed. Genetic materials evolved through these procedures must then be carefully integrated into traditional plant breeding programs to develop improved cultivars.

Whole plants were regenerated from shoot tips in mungbean, and calli were initiated from mungbean root hypocotyl and shoot explants (R.P. Singh et al., 1986). Root regeneration was obtained with low_ levels of auxin but shoot regeneration appears to be difficult. Recently at AVRDC explants from cotyledons developed multiple shoots on MS or modified medium with 5 mg/1 of cytokinin. All regenerated shoots were able to develop root after subculturing in MS media which lays the foundation for biotechnology research in mungbean. Useful genes for disease and stress resistance are reported to be present in *Vigna* species (Chen et al., 1983) but appropriate technology for transfer to mungbean is necessary. Because biotechnology is an inordinately expensive area of research, major early developments will be in crops with higher economic value.

RFLP Mapping and Its Application in Breeding

A new molecular tool, restriction fragment length polymorphism (RFLP), is used to construct the molecular genetic map for most major crop plants and these maps provide a more direct method for selecting desirable genes via their linkage to easily detectable RFLP markers. N.D. Young has constructed a saturated RFLP map of mungbean in collaboration with AVRDC (Young et al., 1992). The latest RFLP map is given in Fig. 1 (Young et al. unpublished).

Breeding

Until 1971, major mungbean breeding programs operated primarily in India, the Philippines and the U.S.A. In 1972, an International Mungbean Nursery (IMN) was developed by the University of Missouri, Columbia, Missouri, U.S.A., an activity that stimulated international cooperation in mungbean breeding (Poehlman et al., 1976; Poehlman, 1978). With the establishment of the Asian Vegetable Research and Development Center (AVRDC) in 1971/72, the mungbean was selected as a mandate crop and an integrated, interdisciplinary approach to mungbean improvement has since been developed. Since 1976, the IMN has been coordinated through AVRDC (Aim et al., 1985).

Problems of Mungbean Production and Breeding

Relatively minor research attention has been given to mungbean breeding compared to the cereals or soybeans. Yield potential of most present day cultivars is low as the world average yield for mungbean is less than 500 kg/ha. Yield is unstable over locations and seasons due to the susceptibility of mungbean cultivars to environmental stress and disease. This has led to mungbean being grown on marginal lands with a minimum of management inputs. Natural selection under such situations has favored types that can survive under unfavorable environments and culture. Mungbean is less responsive to management inputs than the cereal crops. Although resistance to certain diseases are present in varying degrees in some cultivars, diseases like powdery mildew and Cercospora leaf spot are still major risks in growing mungbean in some production areas. Mungbean yellow mosaic virus (MYMV) is a serious threat for mungbean production in certain seasons in the Indian subcontinent. Insect pests like beanflies and pod borers can cause considerable loss in addition. In countries where labor is becoming expensive, the nonsynchronous pod maturity that necessitates multiple harvesting by hand is yet another problem.

Breeding Objectives

High and stable yield is the primary breeding objectives. Since yields are commonly reduced by disease and insect injury, resistance to Cercospora leaf spot, powdery mildew, MYMV, beanfly, pod borer, bruchids and other regional pests are specific objectives where yield losses from these pests occur. Reduced sensitivity to photoperiod and temperature, early and synchronous flowering, tolerance to lodging and drought, reduced weather damage to seeds, and less pod shattering are common general objectives.

Germplasm Resources

A knowledge of where genetic variability for specific traits is available, and information on its inheritance, breeding behavior and response in varying environments is highly valuable for utilization of germplasm resources in breeding programs. Many accessions of *V. radiata* are being maintained in different countries, but there is a considerable amount of duplication of the accessions among the collections. The major collections of mungbean germplasm are being maintained at AVRDC, Shanhua, Taiwan; University of the Philippines, Los Ban os; U.S. Department of Agriculture, Experiment, Georgia; and Indian Agricultural Research Institute, New Delhi (Anishetty and Moss, 1988; Poehlman, 1991).

AVRDC has been designated by the International Board for Plant Genetic Resources (IBPGR) as the base collection center for mungbean. A set of descriptors was prepared for mungbean so that a uniform system of classification could be used by all agencies maintaining mungbean germplasm collections (IBPGR, 1985). The AVRDC collection contains more than 5,000 accessions and has been systematically catalogued for various morphological, agronomical, and biochemical traits and for disease and insect resistance (Shanmugasundaram and Tschanz, 1985). At AVRDC, the mungbean geilnplasm has been evaluated for 35 characters using the IBPGR descriptors and a few additional traits. The variability in 29 characters among 68 promising cultivars at AVRDC is reported in Table 5. These data suggest a wide range of variability for all characters examined. In a similar screening of the AVRDC mungbean collection at the Malang Institute for Food Crops (Malang, Indonesia), the variability among accessions was larger than at AVRDC. Thulasidass (1984), using multiple regression and classificatory analysis, grouped 30 accessions from AVRDC into seven clusters. Cultivars identified with desirable characters for crossing are V-3388 (U.S.A.), high yield and pods-per-plant; V-3404 (Thailand), pod length and 100-seed weight; V-1789 (India) and V-2184 (Philippines), short duration; and V-1948 (Philippines) and V-3092 (India), number of seeds-per-pod.

Table 5. Genetic variability in 29 characters of 68 promising mungbean cultivars.[a]

Character	**Mean** + SE	**Range**
Yield (kg/ha)	866 ± 19	339 - 1,222
Pods/plant	26+0.8	11 -47
Seeds/pod	11+0.1	9 - 14
1,000 seed weight (gr)	46 + 1.2	23 - 89
Pod length (mm)	88+1	65 - 139
Pod thickness (mm)	5+0.1	4-7
No. of clusters	8+0.2	4 - 16
No. of clusters on main stem	5 :LOA	3-9
No. of pods on main stem	20 ± 0.5	11 - 37
Ave. no. of pods/cluster	3 ± 0.04	2-5
Position of 1st pod (node)	7± 0.06	5-9
Length of peduncle (cm)	16+0.2	9-21
Plant height (cm)	52 ± 0.9	23 - 74
No. of nodes on main stem	12+ 0.1	9-15
Average length of internode (cm)	4+0.1	2.5 - 5.8
Protein (%)	21.8 ±	19-25
Days to flowering (DAP)	41 + 0.3	34 - 52
Days to first pod maturity (DAP)	63 ± 0.4	55 - 76
Mean maturity (DAP)	89 ± 0.2	86 - 96
Photoperiod response[b]	19 ± 0.9	3 - 43
Hairiness (1-5)	0.0419 ± 0.9	0.8 - 3.1
Stem diameter (mm)	0.119 ± 0.9	3.6 - 9.3
Total no. of branches	0.0519 ± 0.9	1.8 - 4.6
Longest branch length (cm)	0.819 ± 0.9	4.4 - 45.7
No. of branches with pods	0.0619 ± 0.9	0.2 - 2.9
Width of middle leaflet (cm)	0.1319 ± 0.9	6.4 - 13.3
Length of middle leaflet (cm)	0.1119 ± 0.9	8.1 - 13.5
Leaf shape (27/26)	0.0119 ± 0.9	0.98 - 1.27
Petiole length (cm)	0.219 ± 0.9	9.6 - 21.7

[a] Planted at AVRDC on Sept. 8, 1977, 4 rows 6 m in length, 50 cm apart, with 3 replications (H.G. Park, AVRDC, unpublished).

[b] Difference in days to flowering between September and December plantings (12 hr and 16 hr photoperiods).

Crossing Methods

The mungbean plant flowers in phases with axillary or terminal racemes containing a cluster of 10 to 20 cleistogamous flowers. Pollination occurs from 9 to 10 pm until midnight (Bose, 1939). Flower shedding is common, averaging about 60%. Outcrossing averages around 2 to 5% (van Rheenen, 1964; Bhadra and Shill, 1986), but varies with the cultivar and the season. A crossing technique was outlined by Boling et al. (1961). For emasculation, the standard and wing petals

are separated with a dissecting needle and the keel petals and anthers are carefully removed. For pollination, a stigma covered wtih fresh pollen from dehisced anthers is rubbed across the stigma of the emasculated flower and the standard and wing petals returned into place. Emasculation in the evening and pollination the following morning gives maximum seeds set. From 20 to 60% pod set has been reported with this procedure (T.P. Singh and Malhotra, 1975; Park and Yang, 1978).

An improved technique was described by Cupka and Edwards (1986) in which the tip of the bud is opened with fine tipped forceps to expose the style and the stigma, and the anthers are slowly dislodged. After pollinating the emasculated bud, a cellophane tape is placed over the opening to seal the bud and reduce humidity and temperature fluctuations within the floret. Emasculation and pollination can be accomplished in one minute with 60% success.

Breeding Methods

Mungbean is a self-pollinated crop and the breeding methods are those commonly used with self-pollinated species. These are:

1. Collection of local cultivars, or introduction of promising cultivars or breeding lines.

2. Pure line selection: Isolation of a superior pure line from a mixed seed lot is a rapid and efficient procedure for obtaining a new cultivar.

3. Selection from hybrid progenies: Pedigree selection is generally practiced in segregating generations following hybridization since individual plants are easily identified and evaluated.

4. Multiple-parent crosses; Multiple-crosses are generally designed to combine two or more useful genes from undesirable parents simultaneously into an adapted germplasm.

5. Backcrosses; A desirable gene may be added to an adapted variety by a succession of crosses using the adapted parent as the recurrent parent, or by making each backcross to a different recurrent parent, a procedure termed "modified backcrossing".

6. Repetitive intercrossing: Intermating for one or two cycles before starting selection (Dahiya and Singh, 1985). As mungbean is a self-pollinating crop, this is a labor-intensive procedure. Most early varieties were developed by pure line selection from native germplasm. Currently, hybridization is the most important breeding procedure. See discussion in Poehlman (1991).

Varietal Improvement Programs

India

A varietal improvement program was initiated under a "Pulse Scheme" in Uttar Pradesh in 1943. 'Mung Type 1' had been developed in 1936 but large scale multiplication started only after 1948 (Mehta and Sahai, 1955). "Co 1" was selected and released in Tamil Nadu (former Madras State) in 1953 (Premsekar and Srinivasan, 1961). Systematic breeding really started after organization of the All-India Coordinated Pulse Improvement Program in 1967. Breeding programs are now conducted in the different states and the Indian Agricultural Research Institute, Delhi. These involve the testing of traditional breeding lines over a series of environments, biometrical studies of the relationships of yield components to yield, and physiological studies of source-sink relationships. A list of mungbean cultivars released in India has been reported by Shanmugasundaram (1988) and Poehlman (1991).

Varietal improvement in India has concentrated on increasing yield and disease resistance. To improve yield potential, a "plant type" concept was proposed, that focused on short, compact plants; high harvest-index; reduced photoperiod sensitivity; early maturity; and more determinate growth habit (Jain, 1971, 1975). Consideration has been given to suitability for planting in a multiple cropping system (L. singh, 1975). The compact plant/early maturity concept is based on obtaining maximum yield-per-hectare-per-day, a desirable feature in a short season, multiple cropping system. Ramanujam (1975) and Thulasidass (1984) have generated information suggesting that more crosses should be made to develop cultivars for specific seasons and locations.

A major mungbean improvement program at the Punjab Agricultural University, Ludhiana, has led to the development of many disease and insect resistant cultivars and breeding lines, beginning with release of the cultivar ML 1 in 1974 (K.B. Singh et al., 1974). The new ML (Mung Ludhiana) and LM (Ludhiana Mung) cultivars have resistance, singly or combined, to disease pathogens inciting MYMV, Cercospora leaf spot *(Cercospora canescens E.* and M.) bacterial leaf spot *(Xanthomonas phaseoli* (Smith) Dowson), root knot nematode *(Meloidogyne incognita* (Kofold and White) Chitwood, and insect pests, whitefly *(Bemisia tabaci* Genn.), leafhoppers or jassids *(Empoasca* spp.), and pod borers *(Lampides boeticus L., Maruca testulalis (Gey.).* (See reviews by G. Singh et al., 1988; Chhabra et al., 1988; Shanmugasundaram, 1988, and Poehlman, 1991). Many other universities across the country also have the breeding programs and produced many cultivars. These cultivars are tested through all India Coordinated Pulses Improvement Program.

A total of 69 improved varieties have been released in India since 1948 (Verma and Brar, 1996). Varieties resistant to different diseases, specifically MYMV has been listed by Singh (1996). Tickoo et al (1996) proposed a plant type with thick stem, with two to 3 erect branches, short internodes, bearing clusters of pod in the top 60 to 75% of the nodes, having small and thick leaves, with long, thick pods with 12 to 18 bold seeds per pod, as ideal to obtain high yield.

Physiologically the yield increase has to come from large seed size and more number of pods since the seed number per pod is fixed.

Philippines

As early as 1916, San Miguel (1916) emphasized that mungbean be improved in productivity, evenness in maturity, total growth, adaptability to seasons, and resistance to disease. In 1956, a varietal improvement program was initiated by the Bureau of Plant Industry (BPI) Economic Garden, Los Banos, with pure lines selected from local varieties (Ballon et al., 1978). Hybridization and selection resulted in the release of'MG-50-10A', 'MD15-2', 'Glabrous No. 3', and 'MG-50-10A-Y'. The University of the Philippines, Los Banos, released 'CES-14', 'CES 55', and several 'PAGASA' lines (Lantican and Catedral, 1977; Catedral and Lantican, 1978). Since 1975, the AVRDC/Philippine Outreach Program has been located at the BPI Economic Garden where AVRDC mungbean breeding lines are evaluated. Cooperatively, the BPI Economic Garden and AVRDC released 'BPI Mg 2' in 1984 and 'BPI Mg 4' in 1986 (Catipon et al., 1988). BPI Mg 7 and 9 are released in 1989 and the latter one has been promoted nationwide as "Taiwan Green". Punto and Lantican (1982), in a study of ten mungbean genotypes over nine locations for two years, found 'PAGASA 1' to be the most stable genotype studied.

Indonesia

Varietal improvement of mungbean was started in 1935 by collection of local varieties (Somaatmadja, 1976; Somaatmadja and Sutaunan, 1978). In 1965, variety 'Jala', introduced from Sri Lanka, was distributed to fanners. During recent years, the Sukamandi Research Institute for Food Crops (SURIF), BORIF and MARIF cooperated with AVRDC in evaluation of AVRDC breeding lines. 'Manyar' and 'Nuri' were released in 1983, 'Walet' and 'Gelatik' in 1986, 'Merpati' in 1991 and 'Sriti' in 1992 (Shanmugasundaram, 1988).

Thailand

Native cultivars with varied seed characters such as dull or shiny seed coats and golden or black seed color were originally grown by farmers (Bhumiratna, 1978). An introduced "Philippine-type" was released as 'Uthong 1' (Nalampang, 1978). Chainat Field Crop Research Center of the Thailand Department of Agriculture and its associated Phitsanulok Field Crop Experiment Station, Kasetsart University and Prince of Songkhla University cooperate with AVRDC in evaluating breeding lines and segregating populations. The AVRDC-Asian Regional Center is located at Kasetsart University, Bangkok.

All the recommended cultivars in Thailand except 'U-thong 1' were introduced from AVRDC such as Kamphaeng Saen 1 (KPS 1), Kamphaeng Saen 2 (KPS 2), Chainat 60 (CN 60), Chainat 36 (CN 36), and Prince of Songkhla University 1 (PSU 1). These cultivars account for over 90% of the total planted area (0.4 million ha) in 1992 (Jansen et al., 1993).

U.S.A.

Mungbean breeding is conducted at the Oklahoma Agricultural Experiment Station, Stillwater. A large-seeded, pure line selection was developed from 'Jumbo'; an introduction from China, was named 'Berken'; and a medium-sized cultivar, 'Kiloga', and a small seeded cultivar, 'Oklahoma 12' were selected from introductions from China (Matlock and Oswalt, 1963). Mungbean genotype/biological nitrogen-fixation studies are conducted at the Texas A&M University, College Station. These universities evaluate the AVRDC breeding lines almost every year and Texas A&M University released 'Texsprout' in 1988.

Australia

A multidisciplinary research program is sponsored by the CSIRO Division of Tropical Crops and Pastures (Lawn and Alm, 1985). Three cultivars, 'Berken' from Oklahoma, 'Celera' (Kingston, 1975), and 'King', an AVRDC breeding line that was released in 1982, account for almost the entire area planted to mungbean. Recently, MYMV resistant lines have been introduced from AVRDC and evaluated.

Bangladesh

Bangladesh Agricultural Research Institute (BARI) has been conducting research on mungbean since 1976. A MYMV tolerant cultivar 'Mubarik' was developed and released by BARI in 1982 for March/April sowing and 'Kanti' in 1987 for August/September sowing. Bangladesh Institute for Nuclear Agriculture (BINA) has been working on mutation breeding using gamma radiation and released BINA Mung-I.

Since 1993, many lines have been introduced from AVRDC and evaluated by BARI and Institute of Postgraduate Studies in Agriculture (IPSA). Among them NM-92, NM 94, VC 6144, VC 6146 have been selected for high yield, MYMV resistance, early (60-65 days) and uniform maturity (Malik et al., in press; Sarker et al., in press).

Pakistan

Mungbean breeding improvement in Pakistan has been mainly confined with the collection and evaluation of local and exotic germplasm until 1970s. The only approved mungbean variety was '6601' until 1983 (Bashir et al., 1988). Five mungbean cultivars, namely, M-28, NM 20 and 21, NM 121 to 25, NM 13-1 and NM 19-19 were developed through mutation breeding by the Nuclear Institute of Agriculture and Biology (NIAB) and released in 1980s. AVRDC breeding materials were introduced and the National Agricultural Research Center (NARC) and NIAB have started the hybridiation program, from which NIAB has developed and released NM-51, NM-54 (Malik, 1991). Recently NIAB has intensified the collaboration with AVRDC by the shuttle breeding and developed several lines with MYMV resistance, high yield, large seed size, and early and uniform maturity.

Sri Lanka

Mungbean breeding is conducted at the Mahaillupallama Agricultural Experiment Station in the dry zone. Cultivars, 'ML 1' 'ML 2', and 'ML 3' were introduced from India. A large seeded cultivar 'M 4' that matures in 75 days and 'Type 51', a small-seeded cultivar that matures in 60 days are grown (Vignarajah, 1978). In cooperation with AVRDC, 'Type 77' was released to farmers in 1982.

A list of varieties released by different countries since 1986 are given in Appendix 2.

Asian Vegetable Research and Development Center

AVRDC is the only international agricultural research center with a mandate on mungbean and has played an important role in mungbean improvement since 1971/72. It was designated as the world mungbean collection center by IBPGR. Its germplasm bank has more than six thousand accessions and most o them have been characterized. The objective of mungbean improvement at AVRDC is to develop early and uniform maturing genotypes with high and stable yield, reduced sensitivity to photoerpiod and temperature and resistance/tolerance to major biotic and abiotic stresses. AVRDC-improved lines carry moderate resistance to Cercospora leaf spot and powdery mildew diseases, reduced photothermal sensitivity, increased 1000-seed weight (70 g) and improved plant type with pods above the canopy. Yield as high as 3 t/ha can be obtained in experimental plots. Each year the selected AVRDC's elite lines and superior accessions from different countries are evaluated in the International Mungbean Nursery (IMN) for adaptability in many countries. Fifty-four cultivars have been officially released from AVRDC breeding lines in 19 countries by national partners. AVRDC's elite lines have been extensively grown in all the countries except in South Asia due to MYMV.

The initial step was to identify germplasm desirable in these characteristics. Accessions from the Philippines had high yield, earliness and uniform maturity. From the germplasm collection, accessions were identified, mostly from India, with insensitivity to photoperiod and temperature; resistance to Cercospora leaf spot and powdery mildew; and resistance or tolerance for beanflies, bruchids and pod borers (1979; 1981a,b). Crosses between the Philippine and Indian germplasm has generated a new group of breeding lines. A combination of bulk, modified bulk, pedigree, single-seed-descent and backcross methods of breeding were used in their development.

At AVRDC, powdery mildew is prevalent in spring and autumn season crops when the weather is cool and dry, and Cercospora leaf spot is prevalent during summer when the weather is hot and humid. The segregating generations are subjected alternatively to these diseases in order to select for combined resistance (Shanmugasundaram and Tschanz, 1985). Photoperiod and temperature variations during these seasons permit selection for these environmental stresses. The IMN provides an opportunity to evaluate superior genotypes over a range of

environments.

Imrie et al. (1981) used the cluster analysis to determine the genotypic and environmental responses and stability of genotypes, and Imrie and Shanmugasundaram (1987) analyzed the 7th and 8th, and the 9th and 10th IMN trials. They found 70 to 80% of the variation was due to environmental causes with 17 to 27% due to genotype x environmental interaction, and less than 3% due to variation among genotypes. A segmented regression analysis was used by Fernandez and Shanmugasundaram (1988) to detect genotypes which are high yielding, less sensitive to environmental fluctuation in unfavorable environments but have the capacity to yield well in favorable environments.

The AVRDC ideotype for mungbean is a monocrop with yield of 3 to 4 t/ha at maturity of 70 days (57.1 kg/ha/day) under optimum environmental and cultural conditions. This assumes having 20 pods-per-plant, 10 seeds-per-pod, and seed weight of 6 gm-per-100 seed in a plant population of 250,000 to 400,000 plants-per-ha. To provide sufficient "source", a rapid and vigorous vegetative growth is needed. The characters visualized to attain this goal are rapid seedling growth, dark green lanceolate leaflets, no branching, a strong erect stem, vigorous root system, abundant nodulation, extended photosynthesis, a vegetative/reproductive ratio of 4:3, high and efficient photosynthesis, and efficient translocation of the photosynthates. To obtain better distribution of the "sink" would require a high harvest-index with a large number of nodes and short internodes, multiple peduncles at each node with abundant pods per cluster, synchronized flowering and ripening, nonshattering pods, with pods above the seed canopy, large number of seeds-per-pod, and large seeds. For yield stability, resistance to diseases and insects, tolerance to temperature and moisture stresses, and resistance to seed weathering is needed.

Employing a multidisciplinary breeding approach, mungbean yield potential has been more than doubled in breeding lines at AVRDC. Plant architecture is being altered to provide for more pods exposed above the canopy and more synchronous maturity. Progress is being made in combining less sensitivity to photoperiod and temperature and resistance to multiple diseases.

Breeding lines from AVRDC have been released in many countries (Costa Rica, China, Ecuador, Fiji, India, Indonesia, Kenya, Republic of Korea, Pakistan, Philippines, Sri Lanka, Taiwan, Tanzania, Thailand, U.S.A., Vietnam. See Shanmugasundaram, 1988). Combining the disease and pest resistance and high yield of AVRDC breeding lines with resistance to local stress factors from native cultivars, poses a major challenge to country breeding programs.

AVRDC's objectives for the 1990s are to increase and stabilize yield, improve early and uniform maturity, maintain resistance to Cercospora leaf spot and photothermal insensitivity, increase resistance to powdery mildew, and incorporate resistance genes for MYMV, bruchid, beanfly and pod borer into the advanced breeding lines.

Bruchid is a very serious pest of mungbean during storage. A wild mungbean accession, *Vigna radiata* ssp. *sublobata (TC* 1966), and two mungbean accessions (V 2709 and V 2802) are highly resistant to bruchid, *Callosobruchus chinensis (L.),* and only TC 1966 is resistant to C. *maculatus (F.).* The bruchid resistant elite lines developed at AVRDC will be distributed to the national partners in the very near future.

AVRDC is committed to strengthening its upstream research activities, particularly in biotechnology. RFLP mapping is a new and powerful tool that can assist breeding programs, improve management of germplasm collections by DNA fingerprinting and provide the basis for cloning genes. AVRDC has constructed a saturated genetic map of mungbean using RFLP markers in collaboration with the University of Minnesota. About 200 RFLP markers using a cross between mungbean and its wild progenitor, *Vigna radiata* ssp: *sublobata,* has been constructed (Young et al., 1992). RFLP markers linked to the genes for powdery mildew and bruchid resistance, seed weight (Fatokun et. al 1992), pod length and days to maturity have already been identified. Recombinant inbred lines is being developed to provide a permanent mapping source that can be distributed worldwide to map markers in a single genetic population. The genes controlling Cercospora leaf spot and MYMV were mapped using different mungbean populations. These genes will be the first targets of RFLP marker-assisted breeding.

RFLP markers were used to accelerate backcross breeding for bruchid resistance. With ony two backcross generations using RFLP-based selection provided the bruchid resistant lines while more than six backcross generations were necessary with the conventional backcross breeding. MYMV is the most serious constraint in mungbean production in South Asia. The first international MYMV nursery, including 17 resistant lines originated from India, Pakistan and Sri Lanka, were sent to more than 20 collaborators in South Asia and neighboring countries.

MYMV ratings in New Delhi, India and Faisalabad, Pakistan were very similar, indicating probably no difference in race between the two regions. However, only four Pakistan and one Sri Lanka originated lines were resistant in Bangladesh. It may be due to high pressure of virus or different races in Bangladesh. A DNA probe specific for MYMV in India has been developed in collaboration with the University of Wisconsin.

AVRDC and NIAB in Pakistan have been collaborating through the shuttle breeding. After AVRDC breeding lines were crossed with MYMV resistant lines, F_2 and F_3 seeds were sent to NIAB in Pakistan and selected for MYMV resistance since MYMV is not present either in Taiwan or in Thailand. The selected materials were sent back to AVRDC in Thailand and selected for CLS resistance and other traits. After one more year of shuttle breeding, the seeds were multiplied in Thailand for yield trials. These selected lines have resistance to MYMV and CLS, high yield, large seed size, and early and uniform maturity. These lines are being distributed to the national programs for trial.

With the establishment of the South Asian Vegetable Research network (SAVERNET), the MYMV network was informally organized after the international MYMV Expert Consultation Workshop in 1991 in Bangkok. The AVRDC/USAID/BARI Project in Bangladesh is ensuring in-country and AVRDC-Bangladesh collaboration. Furthermore, the mungbean session during the International Symposium on Pulses Research in 1994 in New Delhi has reassured the collaborative spirit for mungbean in this region. AVRDC is currently preparing a formal mungbean research network.

Problems and Future Prospects

Dramatic yield improvements have been made in mungbean from hybridization of new pathogen and pest resistant cultivars from India with early maturing,high yielding cultivars from the Philippines and elsewhere. Traidtionally, mungbean is grown in a low yield environment, with little attention to the yield inputs routinely given to other crops. Traditional breeding efforts need to be continued and augmented to further improve yield potential and yield stability. Tolerance to heat and drought and resistance to Cercospora, powdery mildew, and virus diseases still pose a challenge to breeders and pathologists. While MYMV constitutes a serious hazard in the Indian subcontinent, good progress has been made in India on breeding for MYMV resistance combined with resistance to Cercospora leaf spot and various pests. Other viruses attack mungbean ad reduce yields in local areas. In addition to traditional breeding methods, innovative new approaches such as genotype stability analysis (Dahiya and Singh, 1985; Verma et al., 1978), would help to identify superior parent materials.

Future strategies should be directed toward sustaining high yields in farmer's fields. Utilization of the mungbean's short maturity as an intercrop, or as a short season crop in a multiple cropping system, would increase profitability of growing mungbean. Varietal research needs to be directed toward cultivars with this special utility and resistance to the disease and insect hazards associated with specific cropping patterns. Quality of seeds would be improved by enhancing the sulfur containing aminoacids. Mungbean breeding and evaluation of cultivars must be integrated into the total production system which involves fertility maintenance; disease, insect, and weed control; and efficient labor management.

Mungbean is used to be planted in the marginal land. Recently, however, the newly developed cultivars with high yield, early and uniform maturity, and disease and insect resistance have been planted in extensive areas with appropriate inputs and management to increase the sustainability and farmer's income with the cereal-cereal rotation in Asia.

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Appendix 1 - Mnngbean Germplasm with resistance to MYMV and/or vectors

Mungbean Germplasm and Breeding lines with reported resistance to MYMV

Resistant/tolerant mungbean line[1]

Bangladesh[2]

AVRDC Accs. V 2272, V 3404, V 3485, V 3486
MB 53, MB 57, MB 58, MB 59, MB 133, MB 246
Mutant NOB-10 (25)
Sita Kundu (MB 55)
YH 25

India[2]

A 11/99, 11/395, 12/333, 16-303-20-3-8, 16-303-20-3-8-g (16-303), 20-3-8, 24-2, 57-7, 192-1, 525, 1066, 1122, 2779, 6601, 6602, 10866, 11148, 15044, 15127, 15176, 15225, 15227, 15229
Ac. No. 20, 214, 215, 216, 217, 218, 222, 223, 320
ADT 2
AMRIT (122)
AVRDC Accs. V 1269, V 2181, V 2182, V 2228, V 2294, V 2297, V 2330, V 3119, V 3404, V 3417, V 3466, V 3471, V 3472, V 3485, V 3486, V 3492, V 3493, V 3498, V 3828, V 3962, V 3963, V 3970, V 4075, V 4084, V 4152, V 4232, V 4366, V 4403, V 4409, V 4433, V 4483, V 4542, V 4852
Bulk sample Orrsa
B-2
B R-2
China selection
CO 3,4
EC 2815, 277574, 103127
G 65
Green Mung
H-70-6
Hyb. 4-3, 4-3 A, 12-4
Jawahar 45
Jyoti (Hyb. 4-3)
Kuberi
L 24-2, L 24-2-1
L 23, 45, 52, 53, 61, 65, 66, 80, 87, 115, 127, 129, 143, 213, 271, 304, 323, 349, 404, 294-1
LGG 407, 450
LM 6, 12, 36, 47, 81, 87, 94, 96, 113, 124, 134, 141, 143, 150, 156, 167, 168, 170, 171, 172, 182, 185, 191, 198, 214, 217, 218, 220, 238, 243, 248, 252, 289, 290, 294-1, 298, 310, 316, 354, 355, 356, 364, 383, 392, 404, 438, 459, 492, 496, 508, 509, 520, 529, 531, 542, 625, 626, 630, 662, 671, 686, 687, 692, 695, 696, 711, 744, 755, 775, 784, 873, 1101, 1114
M 13, 21-1, 170
MB 5, 53, 57, 58, 59, 60, 132, 133, 142
Mg-1, Mg 588, Mg 589
MH 83-20, 309
ML 1, 3, 4, 5, 6, 7, 9, 15, 17, 24, 25, 35, 37, 38, 65, 73, 74, 79, 94, 101, 102, 104, 105,

Appendix 1 (cont'cl)

Resistant/tolerant mungbean line

India[2] (cont'd)

ML 109, 113, 116, 124 to 130, 131, 131-1, 132 to 134, 154, 157, 158, 161, 162 to 168, 170, 171, 186, 192, 194, 195, 197, 234, 235, 237, 238, 266, 267, 267-1-84, 268, 269, 272, 274, 278, 282, 284, 285, 286, 288, 289, 290, 296, 298, 302, 304, 306, 307, 313, 314, 315, 322, 326, 336, 337, 338, 353, 359, 360, 368, 369, 370, 371, 372, 375, 376, 382, 388, 390, 393, 394, 395, 405, 408, 409, 418, 421, 422, 423, 427, 428, 435, 436, 437, 438, 459, 466, 475, 484, 489, 506, 520, 536, 537

ML 26-10-3 (Pant Moong 2)
Mohini (S 8)
Moong No. 54
Mu-1

MUG 122, 124, 125, 126, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 144, 145, 169, 170, 173, 175, 176, 242, 262
MUM 1, 2, 3
N 122
No. 525
NDM 88-14
P 1-67, 20, 40, 43-68, 66-68, 68, 82, 84, 86, 91, 94, 131, 156, 179-68, 217, 242, 290, 292, 293, 325, 332, 353-A, 364, 364-68, 366-68, 367, 369, 441-B-2, 453, 473, 614, 617, 670, 679
Pant Moong-1, Pant Moong-2 (ML 26-10-3), Pant Moong-3 (Pant M 3) (UPM 79-4-12)
Ph 419
Plm 1066
PAIYUR-1
PDM 11, 14, 73, 84-139, 84-140, 84-143, 84-146
PIMS 1066
PIMSI
PLN 15
PLS 274
PS 16
PUM 79-4-12
Pusa 101, 105
RATILA
Sabarmati (PIMS 4)
Sona
SML 70
ST 7
SUJATA (Hyb. 12-4)
Tarai Local
Tarai Local 12 m. r.
T44
TPM-1
TV 1132, 1133, 1134, 1135
UI4 80-7
UPM 79-4-12 (Pant Moong 3)
✓ 41 1 6, 4852

Appendix 1 (coned)

Resistant/tolerant **mungbean line**

Pakistan[2]

BRM-114
E-321
M-13-1, M-20-21, M-22-24, M-28
Mut. 19-19, Mut. 20-21, Mut. 121-25, Mut. 131-37, Mut. 94-73, Mut. 131-98. Mut. 13-1
NCM-5, NCM-7, NCM-68, NCM-69, NCM-87
NIAB Mung 121-25, NIAB Mung 19-19, NIAB Mung 20-21, NIAB Mung 13-1
NM 13-1, NM 19-19, NM 20-21, NM 28, NM 51, NM 54, NM 121-25, NM 131-98
NIAB-M 51, NIAB-M 54
Pant Moong No. 1, Pant Mung No. 2, Pant Moong No. 3
Pak 3, Pak 13, Pak 18, Pak 22, Pak 32
Var. RC 71-17, Var. AUM 233
6601, 1429, 3198, 3850, 3854, 3881

Sri Lanka[2]

CES 55 x M13-133F
M-3 0-2
N-4-30-5, N-4-30-11, N-4-30-12, N-4-60-1, N-4-60-3, N-4-60-4, N-4-60-5, N-4-60-6, N-4-60-12, N-4-60-16, N-4-60-21
TV-79-3, 7704, TV-79-6
(CES 55 x M1-3) - 133F

1 The list may contain duplicates, because the same lines may have been assigned a different accession number/name by different institutions.

2 The country refers to that country where the resistance screening has been conducted:

Bangladesh: AVRDC 1979, Chandra et al. 1974, 1980, Jalaluddin & Shaikh 1981, Shaikh et al. 1982, 1983, 1988

India: Ahmad 1975, AVRDC 1981, 1990, Chaudhary et al. 1981, Chhabra et al. 1974, 1979, 1980, 1981, 1988, Chhabra & Kooner 1980, Dahiya et al. 1985, Dey & Singh 1973, Gill et al. 1975, Grewal 1978, Khatri et al. 1971, Kooner et al. 1973, 1977, 1979, Legaspi et al. 1978, Mishra et al. 1978, National Bureau of Plant Genetic Resources 1987, Nene et al. 1972, Nene & Rathi 1976, Pandya et al. 1977, Paroda & Thomas 1988, Ramana 1985, Sandhu 1978, 1980, Sandhu et al. 1985, 1988, Shah et al. 1984, Shukla 1977, Shukla et al. 1978, Shukla & Pandya 1985, Singh 1982, 1986, 1988, Singh et al. 1986, 1977, 1988, 1991, Singh & Patel 1975, 1977, Singh & Sharma 1981, 1983, 1984, Sinta et al. 1988, Sivaprakasam et al. 1974, Thakur et al. 1977, Varma et al. 1973, Verma 1985, Verma et al. 1973, Verma & Sandhu 1992, Verma & Singh 1988, Vidhyasekaran 1976, Virmani 1983, Vinnani et al. 1976.

Pakistan: Bashir et al. 1988, Bashir & Malik 1988, Chandhary et al. 1981, Dey & Singh 1973, Gill et al. 1975, Haq 1980, Malik 1988, 1991, 1992, Malik et al. 1986, Malik & Sarleem 1988, Malik & Sarvar 1988, NIAB 1987, Shakoor et al. 1977

Sri Lanka: Jayasekera & Ariyaratne 1988, Pathirana et al. 1988, Wijetilaka 1989,

Mungbean germplasm with reported vector resistance

Vector resistant/tolerant line	References
India	
G 65 IM 170 LM 47, 141, 170, 364 M 170 ML 1, 3, 5, 6, 7, 15, 24, 186, 192, 194, 195, 197, 235, 337, 423, 428, 711 P 131, 242, 290, 292, 293, 325, 364 T 44 192-1, 10866, 11148, 15127,	Chhabra et al. 1979, 1980, 1981, 1988, Chhabra & Kooner 1980, Kooner et al. 1973, 1977, 1979; Singh 1988

Appendix 2. Pedigree, morphological and agronomic characteristics of mungbean cultivars released in different countries since 1986.

Name of cultivar	Parentage	Year re-leased	Breeder/Institute/ State	Plant type	Seed color	Seed luster	1000-Seed size (g)	Maturity (days)	Yield potential (t/ha)	CLS	PM	BB	MYMV	MMV	Other viruses	Nematode	Root rot	Other diseases
Australia																		
Satin	Tainan #1 x CES 55	1988	CSIRO	erect	green	dull	60	70-90	2.5	MR								
Shantung	EGMY-7 x VC 1560A	1988	CSIRO	erect	green	shiny	70	75-90	2	R	**MR**							
Putland	Berken x Ujjain 16	1991	NTDPIF	branched	green	shiny	45	80-120	2.5			R						
Emerald	VC 3528A Sel.	1994	CSIRO	erect	green	shiny	65	75-90	3	R	R	R						
Black Pearl	Berken mutant	1994	Jamar Farming	erect	black	shiny	60	70-80	2									
Bangladesh																		
BARI Mung 5	NM 92	1997		erect	green								R					
China																		
Zhong Lu #1	VC 1973A	1986	GAAS,. Beijing		green	shiny	60-65	60-75	1.1-4.7									
Xujin #1	VC 1973A	1985	Xuzhou Reg. Agril. Res. Inst.				68.1											
Yue Yin #2	VC 1973A	1986	guangdong AAS															
Elu #2	VC 2778A	1989	Hubei AAS		green	shiny	63.9	87	1.7	R	HR							
V 1381	VC 1381	1989	Hubei AAS		green	shiny			1.6									
Su Lu #1	VC 2768A	1989	Jiangsu AAS						1.5									
Yue Yin #1	VC 2768A		Guangdong AAS															
V 2917	VC 2917A	1989																
India																		
Moti PDM 54/ India	Selection from Bahraich local	1987	IIPR, Kanpur	erect	green	shiny	45	60-65	1.0-1.2	S			R (?)					kharif & summe
Samrat PDM 84-139	ML 20/19 x ML 5	1990	IIPR, Kanpur	erect	green	shiny	45	60-65	1.0-1.5	S			R (?)		M			
Basanti PDM 84/143	ML 20/19 x G 65	1990	IIPR, Kanpur	erect mediumtall	green	shiny	40-43	60-65	1.2-1.5	S			R (?)			MR		

Name of cultivar	Parentage	Year re-leased	Breeder/Institute/ State	Plant type	Seed color	Seed luster	1000-Seed size (g)	Maturity (days)	Yield potential (t/ha)	CLS	PM	BB	MYMV	MIv1V	Other viruses	Nema-lode	Root rot	Other diseases
TARM-1	RUM-5xTPM-1	1996	BARC K.S. Reddy C.R. Bhatia K.B. Wanjari A.J. Patil	spreading	green	shiny	29	79	0.765/ 45% higher than check	S	HR		R	-			MR	Mircophomia S
TARM-2	RUM-5xTPM-1	1992	BARC K.S. Reddy S.E. Pawar C.R. Bhatia D.B. Wanjari E. J. Patil V.N. Nandanwar	spreading	green	shiny	31	82	85% higher over check		HR		MR				MR	S
TARM-18	PDM54xRUM-5	1996	BARC	erect	green	shiny	29	62	0.98	MR	HR		MR		-	-		MR
Korea																		
Nampyeong-nokdu	Kyeonggijarae 5 (V 2984/VC 1089B)	1993	Kyeong Ju Choi/ Jeonnam Prov. RDA/ Korea	erect	green	dull	44		1.3	R	R			MR				
Kuemseong-nokdu	Kyeonggijarae 5/ Bangas all VC 1000C	1995	Ya Seong Lee/ JP RDA/ Korea	erect	green	dull	47		2.06	R	R			R				
Kyeongseon-nokdu	Hongcheonjeokdu / KLA 840102	1997	Hong Sig Kim/ NCES/ Korea	erect	green	dull	49		1.74	R	R			R				
Pakistan																		
NIAB MUNG 51	VC 1973A x 6601 F1 Gamma ray treated	1990	I.A. Malik, M. Salem/ NIAB/ Pakistan	erect	green	shiny	56.0	60-65	1.5-2.5	MS	S		HR	HR				
NIAB MUNG 54	VC 1973A x 6601 Fl Gamma ray treated	1990	Faisalabad/ Pakistan	erect	green	shiny	61.0	60-65	1.5-2.0	T	S		R	R				

Name of cultivar	Parentage	Year re-leased	Breeder/Institute/ State	Plant type	Seed color	Seed luster	1000-Seed size (g)	Maturity (days)	Yield potential (t/ha)	CLS	PM	BB	MYMV	MMV	Other virus	Nema-tode	Root rot	Other diseases
NIAB MUNG 92	VC 2768B x NM 36	1996	Faisalabad/ Pakistan	short	green	shiny	57.0	55-60	2-2.5	R	S		HR	HR				
Philippines																		
PSB-Mg2	VC 3876	1996	AVRDC-POP; BPI-LBNCRDC; R. Matias, F.A. Javilla		dull green	dull	63-65	61-62	1.2-1.3	MR								
PSB-Mg3	VC 2764 (Y)	1996	"		glossy green	shiny	54	60-61	1.0-1.3	MR								
Sri Lanka																		
Marsha	CES-55 x MI-3-133F	1990	H.P. Ariyal Miratne/ FCRDI	semi-erect	yellowish green	shiny	44	55-60	2	S	S	-	R	-	-	-	MR	-
Thailand																		
PSU 1	VC 2768A		Prince of Songkla Univ.	erect	green		72		2.32		R							
Chainat 60	VC 1178 (MG 50-10ACY x ML-6)		AVRDC-TOP		green	white	61		1.37	S	S							
KPS I	VC 1973A (CES1D-21/EG-MG-16)	1986	AVRDC/TOP		green	shiny	66	*65-75*	1.25-3.13	R	R							
KPS II	VC 2778A (BPI glabrus 3// CES 44/ ML 3///CES 1D-21/PHLV 8)	1986	AVRDC/TOP		dark green	white	65	65-75	1.88-3.13									
Vietnam																		
HL 89-E3	IPBM79-9-82	1991	IAS	erect	green	white	50-53	59-62	1.0-1.8	2	-	-	2	-	-	-	-	-
V 87-13	VC 3178A	1991	IAS	erect	green	white	50-54	60-65	1.0-1.8	2	-	-	2	-	-	-	-	

Name of cultivar	Parentage	Year re-leased	Breeder/Institute/ State	Plant type	Seed color	Seed luster	1000-Seed size (g)	Maturity (days)	Yield poten-tial (tlha)	CLS	PM	B13	MYMV	MMV	Other virus	Nenui-tole	Root rot	Other diseases
HL-115	BPI MG7	1994	IAS	erect	green	white	57-60	65-68	1.0-2.1	2			3	-	-	-	-	-
V 91-15	VC 3528A	1995	IAS	erect	green	white	50-60	60-65	1.0-1.8	3		-	1	-	-	-	-	-
V 94-208	VC 4111A	1995	IAS							2	-	-	3	-	-	-	-	-

Remarks:
CLS = Cercospora leaf spot; PM = Powdery mildew; BB = Bacterial blight; MYMV = Mungbean yellow mosaic virus; MMV = Mungbean mottle virus
0 = No symptom, 1-5 increasingly severe disease.
R = Resistant; MR = Moderately resistant; S = Susceptible.

Sources: Dr. Bruce C. Imrie (Australia); Dr. M.L. Chadha (Bangladesh); Dr. R.K. Singh, Dr. S.E. Pawar (India); Dr. Seok-Dong Kim (Korea); Dr. I. Malik (Pakistan); Dr. R. Matias (Philippines); Dr. K.S.D.M. Joseph, Ms. Anula Perera (Sri Lanka); AVRDC-ARC (Thailand); Mr. Bui Viet Nu (Vietnam)