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Mungbean (*Vigna radiata* L. Wilczek): Retrospect and Prospects

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Abstract

Mungbean (*Vigna radiata* L. Wilczek) is economically most important crop of *Vigna* group. It is also known as green gram, golden gram, moong, Chickasaw, Oregon pea, and chop suey bean and this legumes have a strategic position in Southeast Asian countries for nutritional security and sustainable crop production. Being rich in quality protein, minerals and vitamins, they are inseparable ingredients in the diets of a vast majority of Indian population. When supplemented with cereals, they provide a perfect mix of essential amino acids with high biological value. These crops have the ability to fix atmospheric nitrogen (58–109 kg per ha in kg per ha mungbean) in symbiotic association with *Rhizobium* bacteria, which enables them to meet their own nitrogen requirement and also benefit the succeeding crops. This crop has also been reported to smother weed flora appreciably (20–45%) when intercropped with tall cereals or pigeon-pea and consequently, minimize the cost incurred on weed control. On account of short duration and photo-thermo insensitivity, they are considered excellent crops for crop intensification and diversification. A seed of mungbean is highly nutritious containing 24–28% protein, 1.0–1.5% fat, 3.5–4.5% fibre, 4.5–5.5% ash and 59–65% carbohydrates on dry weight basis and provide 334–344 kcal energy. Mungbean protein is considered to be easily digestible. Mungbean are tropical grain legumes widely grown in the sub-tropical countries of South and Southeast Asia. Nevertheless, these crops are cultivated over a wide range of latitudes in the regions where average diurnal temperatures during the growing season are warmer than about 20°C.

Keywords: mungbean, genetics, plant breeding, constrain, biotechnological tools

1. Introduction

Mungbean (*Vigna radiata* L. Wilczek) is cost-effectively most important crops of the pulse group. The mungbean is also known as green gram, golden gram and moong. Mungbean belonging to the subgenus *Ceratotropis* is a diploid species with $2n = 2x = 22$ chromosomes. Worldwide, this crop is of minor importance with restricted geographical distribution, and has cautiously been subjected to detailed

and intensive genetic and cytogenetic investigations. These legumes have a strategic position in Southeast Asian countries for nutritional security and sustainable crop production. Due to rich in quality protein, minerals and vitamins, they are inseparable ingredients in the diets of a vast majority of Indian population. When supplemented with cereals, they provide a perfect mix of essential amino acids with high biological value. Mungbean has the ability to fix atmospheric nitrogen in symbiotic association with *Rhizobium* bacteria, which enables them to meet their own nitrogen requirement and also benefit the succeeding crops [1]. These crops have also been reported to smother weed flora appreciably (20–45%) when intercropped with tall cereals and consequently, reduce the cost incurred on weed control [2]. On account of short duration and photo-thermo insensitivity, they are considered excellent crops for crop intensification and diversification. A seed of mungbean is highly nutritious containing 24–28% protein, 1.0–1.5% fat, 3.5–4.5% fibre, 4.5–5.5% ash and 59–65% carbohydrates on dry weight basis [3] and provide 334–344 kcal energy [4]. Mungbean protein is considered to be easily digestible. The dried grains of mungbean can be split or eaten whole after cooking and made into a soup or dhal. The iron availability in mungbean improves substantially to 7.2–11.3% through cooking practices such as soaking, fermenting and sprouting [5]. Mungbean is also widely relished as sprouts. The germinated grains have higher nutritional value as compared with asparagus or mushroom [6, 7]. Green pods and seeds can be cooked as vegetables. These pulses are frequently fed to children, convalescents and geriatrics or used when “breaking” a long fasting period owing to their ease of digestibility. The haulms are used for fodder and the beans husks and small broken pieces are useful as a feed concentrate. The crops are also grown for hay, green manure and cover crop. Mungbean makes better hay than urad bean as the stems and leaves are less hairy.

2. Origin and domestication

Mungbean is of Indian origin as is evidenced by their occurrence at archeological sites in the continent. *Vigna radiata* is native to north eastern India-Myanmar regions of Asia [8, 9]. *Vigna radiata* var. *sublobata* Verdc. is the closest wild relatives of the cultivated mungbean, respectively, and are regarded as their putative progenitors [10–13]. Based on morphological evidence alone, many researchers have considered var. *sublobata* as progenitor of mungbean [14, 15]. The detailed morpho-chemotaxonomic studies on wide collections of var. *sublobata* [12, 13, 16, 17], cross ability and chromosome pairing evidence [11, 18–20] have led to the conclusion that var. *sublobata* is a polymorphic taxon; two distinct morphological groups of it are the wild progenitors of mungbean and can be designated as *V. radiata* var. *sublobata*. The wild collections have characteristics conducive to domestication like annual growth habit, erect plant type, photoperiod insensitivity, more pods with high number of seeds, and smaller leaves. The present day cultivars of mungbean might have originated from new combinations of the already existing variants, changes in growth habit and seed size have been brought about by possible accumulation of recessive mutant genes [21]. Moreover, during domestication the dehiscent nature of pods and seed hardness of the wild progenitors have been selected out.

3. Ecology

Mungbean is tropical grain legumes widely grown in the sub-tropical countries of South and Southeast Asia [22, 23]. These legumes are grown at low to

intermediate elevations on rainfed ecology. They perform best on good loamy soils with a well distributed rainfall of 750–900 mm per year, but are reasonably resistant to drought and susceptible to water logging. Mungbean is grown in kharif, winter and spring/summer seasons in different agro-ecological regions. Mungbean is grown as sole crops or as intercrops with sugarcane, maize, pearl millet, cotton, groundnut, sorghum and pigeonpea during kharif, as sole relay crop in rice fallows during winter and a sole catch crop during spring/summer seasons.

4. Historical perspective

Pure lines continued even during the early 40s to mid from these landraces were isolated on the basis of colour of stem, foliage, flower, unripe and ripe pods, seed colour and texture and other morphological features. The types selected were best suited in their respective regions mostly under low management. In mungbean, the first promising variety released was Type 1 for cultivation in Uttar Pradesh in 1948. It is a local selection from Muzaffarpur (Bihar). A large number of varieties were developed afterwards through selection from local materials and were released in different states between 1948 and 1970. Some of the important varieties developed through selection are Co 1 and ADT 1 (Tamil Nadu), Jalgaon (Maharashtra), Khargone 1, Krishna (Madhya Pradesh), and G 65 (Punjab). Jawahar 45 (Hybrid 45) released in 1971 in Madhya Pradesh and Type 44 released in Uttar Pradesh in 1972 was perhaps the first varieties developed through hybridization. Afterwards, a number of varieties were developed mainly through selection from the germplasm [24, 25]. Earlier a variety Virat has been released from ICAR—Indian Institute of Pulses Research, Kanpur, Uttar Pradesh; it is mature by 55 days only and fitted to rice wheat cropping system. This has resulted in development of appropriate production technologies and improved varieties besides basic knowledge on these crops.

5. Genetics

Information on the genetics of unusual traits in a crop is crucial for its systematic breeding programmes. Several studies have been conducted to know the genetics of qualitative and quantitative traits in addition resistance to major diseases and insect pests in mungbean, the results of which are presented in **Table 1**.

Qualitative traits	Characteristic	Gene involved	References
Plant type and growth habit	Erect, semi erect, semi-spreading or twining type	Single dominant gene T	[26, 27]
	Twining habit, semi-spreading habit is dominant to erect habit	Single dominant gene	[28]
	Erect, semi erect, semi-spreading or twining type	Dwarf mutant	[29]
	Indeterminate growth habit which inherited independently from leaf shape	Single dominant gene	[30]

Qualitative traits	Characteristic	Gene involved	References
Pigmentation	Purple hypocotyl which is dominant over green hypocotyl	Single gene 'A'	[31]
	'P' gene for the purple hypocotyl and a multiple allelic series 'C', 'C' and 'c' for purple, purple spotted and green epicotyl	Single dominant gene	[32]
	Anthocyanin pigmentation in hypocotyl, epicotyl, stem, petiole and peduncle	Single dominant genes	[28, 33, 34]
	A gene 'R' that conditions red colour of the cotyledons, hypocotyls and top of the leaflet stalk	Single dominant genes	[33]
	Anthocyanin pigmentation in the hypocotyl, epicotyl, stem, petiole, and peduncle	Single recessive gene	[35]
	Anthocyanin in hypocotyl	Two supplementary genes, designated as 'Sh' and 'Ph' with recessive epistatic interaction	[36]
	Purple pigmentation on stem, petiole and veins of leaves	Single dominant gene 'Pppl' with pleiotropic effect	[37]
Stem fasciation	Stem fasciations on the number of floral organs	Single recessive gene 'fsl' with a pleiotropic effect	[38]
Leaf traits	Inheritance of leaf size revealed that large leaflet is dominant over small leaflet	Single dominant gene	[37]
	Pentafoolate leaf	One recessive gene	[39]
	Pentafoolate leaf	Two recessive genes with duplicate gene action	[40]
	Nine foliate leaf mutant	Single recessive gene	[41]
	Induced unifoliata and multifoliata leaf mutants	Single recessive genes	[42]
	Narrow lanceolate leaf	Two recessive genes, 'nil' and 'n12'	[37]
	Lobed trifoliolate leaf is dominant over entire leaf	Single dominant gene	[39, 43]
Chlorophyll mutants	Trilobite leaf	Two dominant genes 'Tib1' and 'T1b2' with duplicate action	[44]
	Chlorophyll mutants have been reported in mungbean with lethal and nonlethal effects. The albino seedling is controlled by monogenic recessive inheritance for the induced xantha, variegata, and greenish yellow chlorina mutants	Single recessive 'al' and 'l' genes	[42]
	Independent monogenic recessive inheritance for albina, chlorina, xantha and virescens types of chlorophyll mutants	Single recessive gene	[45, 46]

Qualitative traits	Characteristic	Gene involved	References
Inflorescence type	Simple inflorescence is governed by two dominant genes ('I1', '12') and double recessive homozygous genotype results in the compound inflorescence	Two dominant genes ('I1', '12')	[32]
	Inheritance of the number of clusters per node shows that a single dominant gene 'C' conditions one cluster per node and its recessive counterpart 'c' determines three clusters per node	Single dominant gene	[47]
	Induced sterility	Single dominant gene	[48, 49]
	A flower mutant with extended stigma and male sterility	Monogenic recessive inheritance	[50]
Flower colour	Four colours of the standard petal namely, red yellow, olive yellow, yellowish olive and light yellowish olive	Single dominant gene	[31]
	Light yellowish olive colour is partially dominant to olive yellow	Single partially dominant gene with gene symbols of 'Pg', 'Pb'	[51]
Pubescence	Dense plant pubescence	Single dominant gene 'Dp'	[51]
	Brown colour of the trait is recessive to colourless and therefore, dominant forms of both the genes are required for colourless pubescence	Two genes 'N' and 'Br'	[26]
	Pod pubescence is dominant over non-pubescence	Single dominant gene	[52]
Pod colour	A gene responsible for flower colour also conditions the colour of unripe pods	Single dominant gene	[31]
	Purple colour on the suture of unripe pod	Single dominant gene	[28]
	Inheritance of dry pod colour for light popcorn and almond biscuit colours	Genes 'lp' and 'lab'	[26]
	Colour of mature pods	Single dominant gene with black dominant over light brown colour	[28]
	Swollen tip is dominant over tapering pod tip	Single dominant gene 'Tp'	[26]
Pod shattering	Pod shattering is dominant to non-shattering	A single gene	[53]
	Resistance to shattering in the interspecific hybrids between mungbean and urd bean was dominant but nonshattering plants could not be recovered in the segregating generations suggesting that the pod shattering is a quantitatively inherited trait	A single gene	[54]

Qualitative traits	Characteristic	Gene involved	References
Seed coat colour	Thickness of the texture layer in seeds is under the quantitative genetic control while inheritance of the brown pigment in the texture layer The presence of brown pigment being dominant to its absence	Two complementary genes	[55]
	Inheritance of mottling in the seed coat is monogenic. The presence of anthocyanin being dominant to its absence. It indicated that the inheritance of black and green seed colours was controlled by a single gene, 'B' with black being dominant over green	A single gene	[56]
	Seed coat colour	A single gene	[57]
	Seed coat colour	Two independent dominant genes	[31]
	Seed coat colour The dominant alleles, 'A' and 'Sp', condition green and spotted seed coat whereas their recessive counterparts confer yellow and non-spotted colours	Two gene pairs	[33]
	Seed colour	Two genes, 'Dgsm1' and 'Dgsm2'	[37]
	Each gene conditioning blue sap colour, buff sap colour and green chloroplast, respectively which together define the seed coat colour	Three gene pairs, 'Br', br and 'G'	[26]
	Seed coat colour	Three-gene model	[58]
	Seed coat colour	Three genes with several modifiers giving mottling patterns on yellow (mmbb ^g g), yellow green (mmBB ^g g), green (mmBBGG) and black (MMBBGG) seed coats	[59]
	Seed coat colour Black, brown, green mosaic, yellow mosaic, amber, green, and yellow seed coat	Four-gene (W, M, 'Br and G)	[60]
Seed coat surface	Inheritance of seed coat colour	Five major genes with non-allelic gene interactions	[39]
	Dull rough seed surface is monogenically dominant over glossy smooth surface and the gene symbols assigned for dull seed coat are 'C'	Single dominant gene	[26, 31, 33, 61]
	Digenic duplicate interaction (D1 and D2) is involved in the inheritance of seed luster, dullness being dominant over shiny	Two dominant gene	[41]

Qualitative traits	Characteristic	Gene involved	References
Cotyledon colour	Green cotyledon is conditioned by which is inherited independently of the red colour present in the hypocotyl and petiole	Single recessive gene 'gc'	[61]
Hard seededness	Hard seededness	Single dominant gene, 'Hdl'	[62]
	Hard seededness	Four QTL	[63]
Photoperiod response	The photoperiod insensitiveness is reportedly dominant over photo-sensitiveness	A single gene	[64]

Table 1.
Genetics of qualitative traits.

6. Production constraints

Traditionally, mungbean has been grown during kharif season. Development of short duration and disease resistant varieties has led their cultivation during spring/summer season in North and central India and during winter (rice fallows) in the coastal peninsula. The major constraints in achieving higher yield are lack of exploitable genetic variability, absence of suitable ideotypes for different cropping systems, poor harvest index, and susceptibility to biotic and abiotic stresses, besides non-availability of quality seeds of improved varieties. The major yield limiting barriers are lack of seedling vigour, excessive flower production, flower drops, poor pod setting, poor harvest index, monocarpic senescence, low response to inputs, narrow adaptation, indeterminate growth habit, staggered maturity and sensitivity to photoperiods and temperature. The phenomenon of compensation among yield components is considered to be main yield limiting factor. Limited variability has been exploited in varietal development programmes of these crops. Pedigree analysis of the released cultivars indicated that a small number of parents with high degree of relatedness were repeatedly used in crossing programmes. Diseases and insect pests cause considerable yield losses to mungbean. Mungbean yellow mosaic virus (MYMV), cercospora leaf spot (*C. canescens*, *C. cruenta*) and powdery mildew (*Erysiphe polygoni* DC) are of considerable economic importance. Mungbean yellow mosaic virus and leaf crinkle during kharif and mungbean yellow mosaic virus during spring in North India and powdery mildew during winter season in coastal peninsula are the major diseases. During the vegetative stage, defoliators like hairy caterpillars, semi-looper and caterpillar are the common pests. Activity of thrips starts at the bud stage and poses serious problems when the crop attains peak flowering, resulting in heavy flower drop. There is no resistant variety against these insect pests. Pre-harvest sprouting especially in mungbean poses a serious threat to timely sown crop during rainy season. Intense heat and hot winds during May-June lead to flower drop and poor pod set in spring/summer crop.

7. Research needs

Varieties developed in the past with resistance to single stress may not be a viable solution as new diseases and insect pests are emerging. Therefore, varieties having resistance to more than one stress provide greater insurance. For mungbean, high yielding cultivars with crop duration of 85–90 days for kharif season and

65–70 days for spring season combining determinate growth habit, high harvest index and reduced photoperiod sensitivity are required. For summer cultivation, extra early varieties of 55–60 days with synchronous maturity are desirable. Vegetative growth should terminate with flowering and assimilates should be transported to developing pods [65, 66]. Recently, large seeded varieties like Pusa Vishal, SML 668, TMV 37, etc., with early and synchronous maturity have been developed which have great market demand. To break the yield plateau in mungbean, there is a need to develop suitable plant type for target environments. In high input cereal-cereal systems, mungbean has to fit in gaps. For this, plant type that is determinate, photo-thermo insensitive, early maturing and high yielding with high harvest index needs to be developed. Good seedling vigour, distinctive vegetative and reproductive phases and high harvest index will be essential components of this plant type. There is good scope to utilize wild and cultivated *Vigna* species to incorporate novel characters and broaden the genetic base.

8. Molecular diversity analysis

Assessment of genetic diversity using RAPD analysis shows close similarity among mungbean cultivars [67]. The study reveals narrow genetic base of Indian cultivars probably due the repeated use of limited ancestors in their pedigrees. This observation has further been confirmed using RAPD [68, 69] and ISSR [70, 71] markers. Amplified fragment length polymorphism (AFLP) markers have also been used in mungbean to test their usefulness in genetic diversity assessment [67]. The long primers yielded significantly higher number of discrete and detectable bands as well as polymorphic bands than 10-base primers. The results show that long primers can be used efficiently for analyzing genetic diversity and the relationships in mungbean germplasm.

9. Mapping of genes/QTLs

Increasing the seed weight has been one of the major objectives to develop high yielding varieties. Molecular markers are now available which are linked to orthologous seed weight loci. RFLP markers to locate major QTLs for orthologous seed weight in mungbean. They found that the genomic regions in cowpea and

Characteristic	Marker	Genes/QTLs/remarks	References
Seed weight	RFLP	Major QTLs	[72]
	RFLP	Suggested a weak association between seed weight and hard seededness in mungbean by analyzing a F ₂ population	[62]
	RFLP	Four loci for hard seededness and 11 loci	[63]
Powdery mildew	RFLP	Genes, ‘13 m’ and ‘Thiz2’ identified in a cross VC3890 × TC1966	[65]
	RFLP	Two QTLs, ‘13MR1’ and ‘PMR2’ have been identified	[73]
	RFLP	A single locus has been identified that explains 86% of variation associated with resistance to powdery mildew in mungbean	[74]

Table 2.
Genes/QTLs/remarks of important traits.

mungbean that have the major effect on seed weight span the same RFLP markers in both the species. These markers are co-linear in arrangement on homologous linkage groups in both the crops. Attempts to breed large and hard seeded varieties of mungbean have not been very successful because of negative genetic correlation between these two traits as a result of pleiotropy or genetic linkage. Studies on the genetic relationship between hard seededness and seed weight, however, are not conclusive. QTL mapping approach using molecular markers have been employed to investigate the linkage relationship between these two traits (**Table 2**).

10. Breeding approach

In order to develop high yielding disease resistant varieties in mungbean, the common breeding methods employed were pure line selection, hybridization followed by pedigree selection, mutation breeding and wide hybridization. While exercising selection, major emphasis has been placed on short duration, photo and thermo-insensitivity, synchronous maturity and resistance to mungbean yellow mosaic virus and powdery mildew. More than 150 varieties have been developed in India employing pure line selection, pedigree method of selection following hybridization, mutation and wide hybridization. The first variety of mungbean was Type 1 developed from local selection of Muzaffarpur (Bihar), which has been extensively been used afterward as one of the parents in hybridization programmes for the development of improved varieties like Type 2, K 851, T 44 and Sunaina. Utilization of T 44 in hybridization has resulted in the development of Pusa Baisakhi which, in turn, has given PIMS 4 and Jyoti. Through mutation breeding, about 14 varieties using gamma rays or occasionally ethyl methane sulphonate as mutagens have been developed. Varieties developed through mutation like CO 4, Pant Moong 2, TAP 7, BM 4, MUM 2 and TARM 1.

10.1 Parental selection

The main reason that the expected yield advances by the conventional component breeding methods have not materialized in mungbean is that the parents used in crossing programmes are not duly evaluated before their use. Seed yield of parents has a positive significant bearing on the yield of the progenies and in the inheritance of this character, additive variance is of paramount importance than the nonadditive variance, although many a times the latter also has significant bearing. The choice of the parents besides on their agronomic attributes like yield and its components must also be based on their genetic diversity, phenotypic stability and combining ability. So logically all the would-be parents must be evaluated by their progeny tests across environments and locations before their use in a crossing programme. A progeny test provides genetic composition of the parental plants and helps in selection of superior ones. In self-pollinated crops like mungbean, many minor genes of additive effect control yield and in any breeding programme, the ultimate goal is to accumulate and harness these genes. High yielding varieties from different genetic backgrounds and carrying different genes for yield when crossed and subjected to replicated progeny tests are expected to generate higher frequency of high yielding plants. Yield stability in mungbean is very important owing to significantly variable response of high yielding varieties across locations and years. Work on stability analysis done in mungbean shows that no high yielding varieties are stable across time and space. All the potential parents in a hybridization programme must be evaluated for their mean yield performance and yield stability, F1 performance, F2 mean yield and the variance generated,

combining ability and their interaction with the important environmental variables. All these variables give a measure of the comparative potential of different F₂ crosses. It is desirable that the progenies of only those parents be advanced beyond F₂ generation that show high grain yield, yield stability, a positive general combining ability for grain yield and that are of distant genetic origin. Progenies of parents with low yield and negative general combining ability for yield must not be advanced beyond F₂ generation. In an intra-species crossing programme, one parent should be a good agronomic base with higher stability and the other parent a good general combiner for yield and its components. Crosses with this strategic selection of parents are expected to give a wide range of genetic variability. To achieve stability and get a true measure of inherent genetic potential, the parental lines must be tested over a number of locations and get their combining ability estimates.

10.2 Component breeding

Fifty years of conventional approach of engineering different yield components in mungbean to build up a new plant type with higher productivity levels has thus far given only modest yield gains over the traditional cultivars. This approach has failed to break the present yield barriers as a whole and bring changes of scale. Based upon correlation analysis of various yield components, selections have been based mainly on number of pods per plant, seeds per pod and 100-seed weight and sometimes also on number of pods per bunch and branches per plant or podding per unit area usually called 'Pod Index'. Pods per plant is by far the most important yield component and almost all the workers have found it having positive correlation with seed yield. It is the best selection index for seed yield and could be increased by increasing number of branches per plant or number of bunches per plant or by increasing the number of pods per bunch. Most of the work has shown that branch number per plant is negatively correlated with seed yield, but bunches per plant has mostly been found to be positively correlated with seed yield. Ramanujam [75] and others have found that pods per bunch and bunches per plant both are positively correlated with yield. Increasing pods per bunch is physiologically constrained in grain legumes owing to fall of flowers and unripe or partially filled pods. It seems the most feasible path to increase seed yield is through increasing number of bunches per plant. This in essence means a plant with more number of nodes with a shorter internode length, with three to four erect branches emerging from the lower to lower-middle nodes at around 20–30° angle with the main stem, and sympodial bearing of pod inflorescences coming from the upper nodes of the main stem, each carrying around 8–10 pods. Number of seeds per pod has been shown mostly positively correlated with seed yield but many workers show it to be negatively correlated with yield. However, an optimal level of 14–16 seeds per pod should be a breeders objective. Seed weight is generally negatively correlated with seed yield but some results have shown it to be positively correlated. The strength of the newly developed second generation varieties like Pusa Vishal and Pusa Ratna lies in the fact that they have more seeds per pod (12–16) with higher 100-seed weight (5.0–5.5 g) without compromising on the pod number per plant. Many researchers advocated cereal mimics with sympodial bearing and suggested increasing pods per plant through the path of increasing the average number of pods per node and building up a soybean like plant type in mungbean [76]. He found the main stem bearing under the control of a single recessive gene and normal conventional bearing to be incompletely dominant. Plant height has been found positively

correlated with seed yield. An optimal upright plant height incorporates more functional nodes and thus more number of pods per plant. After pods per plant, this is the second most important character to be used for selection of seed yield. Owing to their high heritability, 100-seed weight and branch number could be excellent selection criteria but for their unfavorable correlations with yield. Also due to the compensatory mechanisms operating within the plant as a whole, this correlation based selection methodology has not brought the desired productivity levels in mungbean. Alternatively, the best option is direct selection for seed yield on a unit area basis.

10.3 Conventional breeding methods

Most of the high yielding varieties of mungbean bred and released so far have been developed through single cross pedigree method of selection. The single plant selections made in the early generations restrict carrying forward the bulk of created variability, which gets lost quickly giving way to homozygosity with each succeeding generation. This method has served the mungbean improvement programme well in the past, but lately no productivity advances are materializing due to the inherent genetic limitation of the method. The intermitting of selected F_2 plants and selections in the late generations will help to harness most of the desirable genes.

10.4 Early generation testing

The early generation yield trials allow early identification of better performing crosses and F_1 derived lines within the individual crosses. However, selection emphasis is given in later generations only. The F_2 derived family selection is very appropriate in mungbean, which is prone to high GE interactions and low seed increase ratio, which renders pedigree, bulk and single seed decent methods inefficient. The time required is less and emphasis is on grain yield in replicated progeny tests. It was developed in Canada as a modification of bulk method. The F_2 derived family selection takes benefits of early generation yield testing to eliminate efficiently all the undesired materials both between and within the hybrid populations. Replicated yield trials are conducted across locations/environments for early generation selections among and within populations. These selections are further evaluated and final selections for high yield are made in only the best of families or populations. Due emphasis must be given to make site specific selections for different agro-climatic and production systems. Also depending upon the demands of the location and system, input responsiveness of the selections under high management conditions may be tested.

10.5 Mutation breeding

Both physical and chemical mutagens have been employed in improvement of mungbean crop India. The main drawbacks of this method are that the frequencies of desirable mutants are very less, necessitating evaluation of very large population and the difficulty in identification and scoring of micromutations. Tickoo and Chandra [77] using both physical and chemical mutagens could induce significantly higher variability in mungbean for characters like yield per plant, pods per plant, seed number per pod, seed weight, days to flower and harvest index in M_2 generation. Mean values of all the characters had a negative shift in M_2 but after selection changed to positive direction in M_3 but were still associated with significantly

higher interfamily and overall variances than the control populations. Such characters may be incorporated into the cultivated varieties by backcross method. Many a times the selected mutants have been released as new varieties as such for cultivation. Some varieties have been released in India including Pant Mung 2, Co 4, Dhauri, TAP 7, BM 4 and MUM 2 and some in Pakistan including NM 51 and NM 54. The latter two large seeded varieties resistant to MYMV have been developed by hybridization and irradiation of the F_1 seeds.

11. Thrust areas

Resistance to biotic stresses *namely*, mungbean yellow mosaic virus (MYMV), powdery mildew (PM), cercospora leaf spot (CLS), root diseases caused by *Pythium* spp. There is variability in the virulence of MYMV in white fly for incubation of different isolate in mungbean plant for genes governing resistance/tolerance to the virus and tim vector. Gene transfer across species in *Vigna* group has been found difficult. Biotechnological tools are being presently used to overcome these barriers. In the field, spreader row technique has been found to be most effective in screening the materials. However, parental lines to be used in crossing and promising selections before their release for cultivation may she screened under artificial inoculation.

12. Conclusions

Mungbean has the distinct advantage of short crop duration. This fact together with its atmospheric nitrogen fixing ability makes it an indispensable component in various cereal-based cropping systems. Mungbean has tremendous scope for horizontal expansion subject to some committed research inputs to overcome its various productivity bottlenecks. Proper evaluation and utilization of germplasm from secondary and tertiary gene pools by conventional and biotechnological tools immediate priorities. Incorporation of genes from its closely related species for resistance or tolerance to biotic factors like MYMV, bruchids and abiotic factors like sensitivity to photoperiods, high temperatures, drought, waterlogging, pre-harvest sprouting and nutrient use efficiency' and response to irrigation must be accomplished. Breeding for efficient fixing of atmospheric nitrogen has to be priority for higher response to the applied nitrogen in recombination breeding. Mungbean is grown in different seasons and different cropping systems necessitating the development of varieties of different maturity span. The varieties for wheat based cropping systems of Indo-Gangetic-Plains should have crop duration of 60 days with average yield of 1.3–2.0 tonnes per ha.

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Conflict of interest

There is no conflict among the authors.

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