BREEDING OF SUITABLE MUNGBEAN GENOTYPES FOR CULTIVATION IN BANGLADESH

BY

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DEDICATED
TO
THE MEMORY
OF
MY PARENTS

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Date :

The Author

Certificate

This is to certify that the research work embodying the results reported in this thesis entitled "Breeding of suitable mungbean genotypes for cultivation in Bangladesh" has been carried out at the experimental field of Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh and at some other locations of the country under our guidance.

It is further certified that the research work presented herein is original and suitable for submission for awarding the degree of Doctor of Philosophy.

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CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDIX TABLES

Chapter- I
INTRODUCTION

INTRODUCTION

Grain legumes comprising pulses and major oilseeds are an important group of crops in South and Southeast Asia because of their high nutritive value, nitrogen fixation capability, wide adaptability and amenability to varying cropping patterns. The pulses include all grain legumes which are harvested for dry grain only, such as dry beans, chickpea, dry peas, pigeon pea, broad beans, cowpea, lentil, etc. The dry beans include mungbean, blackgram, adzuki bean, ricebean, horsegram and grasspea. Among these, mungbean [*Vigna radiata* (L.) Wilczek] is praised for its easy digestibility, high protein content and low production of flatulence.

In 1824 Savi described the genus *Vigna* and dedicated it to Domenico Vigna who was a professor of Botany in Pisa. Initially the genus contained only a few species having a simply bent keel with the style carrying a beard on the inner side below the stigma. The Linnean genus *Phaseolus* was at that time very large and heterogeneous and included the species with their style either coiled or curved, in contrast to *Vigna* with styles from simply bent to more or less at a right angled position. The mungbean was included in the genus *Phaseolus*. In 1954, Wilczek transferred mungbean (*Phaseolus radiatus* L.) to *Vigna*.

The mungbean is an annual, semi-erect to erect or sometimes twining deep-rooted herb, 25 to 100 cm tall (Hooker, 1879; Prain, 1903; Piper and Morse, 1914; Backer and van den Brink, 1963; Purseglove, 1974; Brouk, 1975 and Ahmed *et al.*, 1995). The stems are branching from the base and covered with short fine brownish hairs. The leaves are alternate and trifoliate or sometimes with five leaflets which are medium to dark green, broadly

ovate, sometimes lobed, rounded at the base and pointed at the tip, 5 to 12 cm long and 2 to 10 cm wide. From 10 to 25 flowers are borne in axillary clusters or racemes. The flowers are greenish to bright yellow with a gray tinged keel, 1 to 1.75 cm in diameter. The pods that radiates horizontally in whorls, are cylindrical, straight to strongly curved and pointed at the tip. At maturity, the pods are glabrous or have short hairs, 5 to 14 cm long and 4 to 6 mm wide having 6 to 20 seeds per pod. Seeds are nearly round or oblong. Seed coat colour is green, yellow, brown, black or mottled. Seed luster is either glossy or dull. Dull seeds are coated with a layer of the pod inner membrane, which may be translucid or pigmented (Watt *et al.*, 1977). The testa is reticulated with numerous fine wavy ridges and cross walls (Bose, 1932 and Watt and Marechal, 1977). Each seed weight ranges between 15 to 85 mg. When dried, pods may burst open, shattering the seeds. Seed germination is epigeal. Flowers are self-fertile and highly self-pollinated. Flowering is indeterminate and continues over a period of several weeks. Pods mature about 20 days after flowering. Rapid senescence does not occur.

Major climatic factors affecting adaptation of mungbean are photoperiod, temperature, precipitation and solar radiation. Windstorm and hail may cause severe damage to this crop. High humidity sometimes causes development of foliage diseases. Mungbean strains differ in response to photoperiod. Flowering is delayed as the photoperiod is extended. The amount of delay will be affected by (a) the length of the photoperiod and (b) the genetic response of the mungbean strains. As the photoperiod is lengthened from 12 to 16 hours, flowering in some short-season early strains may be delayed only a few days, but photoperiod sensitive strains may be delayed as much as 30 to 40 days (Bashandi and Poehlman, 1974).

Mungbean is normally grown in the summer season which grows within a mean temperature range of about 20-40^{0}C. In a Phytotron experiment with mungbean, Rawson and Craven (1979) reported that the low photoperiod sensitive strains produced the highest seed yield at 24^{0}C and the photoperiod sensitive strains produced the highest seed yield at 27^{0}C. Seed yield is drastically reduced beyond 30^{0}C mean temperature. Warm temperature is essential for rapid germination of mungbean seeds. Studies at AVRDC indicate that 29 to 31^{0}C are the optimum temperature for good germination. Rate of germination declined slowly below 25^{0}C and virtually ceased below 11.5^{0}C (Simon *et al.*, 1976).

Mungbean does not grow well where the annual precipitation is above 1,000 mm (Jain and Mehra, 1980). Prolonged rains during pod ripening period result in molding of the seeds, or even sprouting of seeds in the pod. Seed quality deteriorates from the cyclic wetting and drying of seeds (Imrie *et al.*, 1987). Mungbean cannot tolerate waterlogged conditions. It has a reputation for drought tolerance. For high seed quality, mungbean should ripen during a bright, rain-free period. The effect of drought stress on net photosynthesis of mungbean was measured at AVRDC (AVRDC, 1978). When leaf water potential was below -2 bars, net photosynthetic rate was reduced, indicating extreme sensitivity to water stress.

Mungbean is suitable for use in multiple cropping systems. It is used in three types of multiple cropping systems, (a) rely cropping, in which mungbean is planted in sequence with other crops, (b) intercropping, in which mungbean and another crop are interplanted in alternate rows and (c) mixed cropping, where crops are planted together in mixtures. Mungbeans are generally grown without using chemical fertilizers. Nitrogen fertilizer reduces the rhizobial activity and nitrogen fixation in legumes. However, with

mungbeans, there are reports that a small amount of nitrogen fertilizer as a starter dose is beneficial (Moolani and Jana, 1965; Tucker and Matlock, 1969; K. K. Singh *et al.*, 1975; T. Singh *et al.*, 1975; Sandhu *et al.*, 1978; C. Singh and Yadav, 1978; PCARR, 1977; Nalampang, 1978 and Park, 1978).

The mungbean is susceptible to many diseases/organisms, such as virus, fungi and nematodes. Several diseases like mungbean yellow mosaic virus (MYMV), *Cercospora* leaf spot (CLS) caused by *C. canescens* or *C. cruenta*; powdery mildew (PM) caused by *Erysiphe polygoni*; root disease complex (*Pythium* spp., *Rhizoctonia solani*, *Fusarium* spp.) and root-knot nematode (*Meloidogyne* spp.) can cause serious loss in yield in mungbean (Morton *et al.*, 1982). Other diseases like leaf blight, rust, scab, anthracnose pod rot, damping-off, stem rot, wilt, witches' broom and root-knot also attack mungbean in varying degrees (Singh, 1988). MYMV, CLS and PM are common diseases of mungbean in Bangladesh. Both summer and winter mungbeans are infected with these diseases but the incidence is more severe in winter (Ahmed *et al.*, 1981). The extent of damage due to major diseases is given in Table 1.1.

A large number of pests also attack mungbean in the field as well as in storage and cause economic losses. The most common pests are beanflies (*Ophiomya phaseoli* Tryon.), bruchids (*Callosobruchus chinensis* L.) and bean aphid (*Aphis craccivora* Koch). Although measures for controlling these pests are known, farmers seldom use plant protection measures in mungbean.

Because mungbean along with other pulses supply a cheaper source of protein than animal products, about 80% of pulses are produced in developing countries. Pulses are known as "poor man's" meat but the current high market price of mungbean is changing the image of mungbean as the "poor man's" meat. Mungbean is a rich source of protein, phosphorus and

vitamin A (Table 1.2). Its protein is rich in amino acids like leucine, arginine and lysine (Table 1.2). Although mungbean protein quality, like other legumes, is limited by the low sulphur containing amino acids like cysteine and methionine, both of these amino acids are comparatively higher in mungbean than other food legumes (Engel, 1978). Mungbean is usually considered as an easily-digestible legume which is relatively free from anti-nutritional factors such as flatulence-inducing substances (Rachie and Roberts, 1974).

Table 1.1. The extent of damage due to major diseases in Bangladesh.

Disease	**Causal organism**	**Infection (%)**
Mungbean yellow mosaic virus	Yellow mosaic virus	40
Cercospora leaf spot	*Cercospora cruenta*	20
Powdery mildew	*Erysiphe polygoni*	30
Foot and root rot	*Fusarium oxysporum*	5
Southern blight	*Sclerotium rolfsii*	5
Anthracnose	*Colletotrichum linde-muthianum*	5
Leaf spot	*Myrothecium* spp.	5
Leaf crinkle virus	Leaf crinkle virus	5
Nematode	*Helicotylenchus* spp.	5
Nematode	*Hoplolaimus* spp.	5

Source : Ahmed *et al.* (1981).

Annual mungbean production around the world is estimated at 1.4 million tons harvested from about 3.4 million ha (Anon., 1984a). India alone produces 70% of the total world production (Shanmugasundaram and Poehlman, 1988). Thailand exports about 40% of its total production and ranks as the second major producer of mungbean (Lawn and Ahn, 1985).

Like other Asian countries pulses constitute an important component in the farming systems of Bangladesh from the points of view of crop ecology as well as human and animal nutrition. Pulses occupy about 0.7 million hectares of the total cropped area and produces 0.6 million tons of pulses (BBS, 1993). Till today, pulses provide the only high protein component in the diet of the majority people of the country. Although the area under pulse cultivation is 0.7 million hectares annually, still at today there is an acute shortage of pulses production in relation to their demand. The present per capita availability of pulses is about 6 g/caput/day against the recommended daily allowance of 112 g/caput/day (BARC, 1986). A number of different pulses are grown in various parts of the country and mung bean ranks 5th in respect of area and production (Table 1.3).

Table 1.2. Nutritive value of mungbean.

Item	**Unit**	**Whole grain**	**Split *dal***	**Essential amino acids**	**Whole grains (g/g nitrogen)**
Moisture	g	10.40	10.10	Total N (%)	3.96
Protein	g	24.00	24.50	Arginine	0.50
Fat	g	1.30	1.20	Histidine	0.35
Minerals	g	3.50	3.50	Lysine	0.43
Fibers	g	4.10	0.80	Tryptophan	0.06
Carbohydrates	g	56.70	59.90	Phenylalanine	0.35
Energy	Kcal	334.00	45.10	Tyrosine	0.10
Calcium	mg	124.00	75.00	Methionine	0.10
Phosphorus	mg	326.00	405.00	Cysteine	0.06
Iron	mg	7.30	8.50	Threonine	0.20
Vitamin A.I.U.	mg	158.00	83.00	Leucine	0.51
Thiamine	mg	0.47	0.72	Isoleucine	0.35
Riboflavin	mg	0.39	0.15	Valine	0.32
Niacin	mg	2.10	2.40		

Source : Singh (1988).

Table 1.3. Area (A) and production (P) of major pulses in Bangladesh ('000 ha and '000 tons, respectively).

Crop	1982-83		1983-84		1992-93		1993-94	
	A	P	A	P	A	P	A	P
Grasspea	93	73	242	170	245	186	245	188
Lentil	73	44	240	161	208	163	208	168
Chickpea	54	40	113	87	68	53	85	62
Blackgram	40	28	84	59	68	51	67	52
Mungbean	15	08	60	34	53	31	54	30
Other pulses	-	-	-	-	49	32	44	30
Total	735	496	738	512	728	523	722	519

Source : BBS (1993).

The above table indicates that there is a big gap in area and production of mungbean as well as other pulses in 1982-83 and 1983-84. The Bangladesh Bureau of Statistics gave one explanation that in 1983-84, there was a house-to-house agricultural census which revealed that earlier estimates on area and production of pulses were not correct, rather the area had increased by more than 300% compared to 1982-83. So, in 1983-84 BBS has revised the estimates of pulses area and production (BBS, 1987). Under this situation till now it is very hard to rely on the correctness of the statistics published by the Bangladesh Bureau of Statistics. However, according to BBS, like other pulses mungbean is also showing a declining trend in area under cultivation and production.

Research on this crop though initiated in Bangladesh during the early 1950s but very little progress has so far been made. Till now farmers cultivate only the local cultivars and they hardly use improved management practices. As a result, its average seed yield is very low (600-700 kg). Using both

conventional and mutation breeding techniques Bangladesh Institute of Nuclear Agriculture (BINA) and Bangladesh Agricultural Research Institute (BARI) have been carrying out research on this crop during the last decade. The concerned scientists of BINA collected exotic and local germplasm and evaluated them in different agro-ecological zones. For this purpose, a large number of mungbean genotypes were collected from AVRDC and other mungbean producing countries.

In Bangladesh, mungbean is mainly grown as a sole crop under rainfed conditions in two seasons (Pattern I ; January to April in the greater districts of Barisal, Patuakhali, Noakhali, Faridpur, Chittagong and Comilla) and (Pattern II, September to December in the districts of Jessore, Dhaka, Rangpur, Dinajpur, Rajshahi, Pabna and Kishoregonj). Data on temperature, annual precipitation for both mungbean growing seasons and sunshine hours of Bangladesh are given in Table 1.4.

About 83% of the total area of mungbean are cultivated during the period, January to March. The remaining 17% area is cultivated during September to December. Crops grown during September to December period can be harvested by single picking as most of the pods mature at the same time due to water stress. The golden-seeded varieties/cultivars are generally grown in this period. In both periods, seeds are sown by the broadcast method under minimum tillage. Almost no other management practices are used for this crop. The area under cultivation and production of mungbean in both the season are given in Table 1.5.

Efforts were made to improve the seed yield of this crop through varietal improvement and by shifting the time of sowing of this crop. It has been found that this crop could be grown during the period from March to June in order to get a higher economic return. At present less than 5% of the

Table 1.4. Weather data for mungbean growing areas where mungbean is grown in the period January to April (Pattern I) and September to December (Pattern II).

Month	Pattern I (January- March)			Pattern II (September- December)			Solar radiation (Sunshine hours)
	Temperature (^{0}C)		Annual precipitation (2615 mm)	Temperature (^{0}C)		Annual precipitation (1700 mm)	
	Max.	Min.	Monthly Average	Max.	Min.	Monthly Average	Monthly Average
January	26	13	20	26	11	5	10.8
February	28	16	30	28	13	10	9.8
March	32	20	60	32	18	140	10.1
April	33	23	120	32	22	240	9.6
May	33	24	225	32	24	300	7.1
June	32	26	500	32	25	310	5.1
July	31	26	550	32	25	340	6.5
August	31	26	500	34	25	200	8.1
September	32	25	340	35	25	100	7.0
October	31	24	200	33	23	30	8.3
November	28	21	50	28	17	15	8.7
December	26	15	20	26	12	10	10.9

Source : Rahman and Miah (1988).

total area is covered under mungbean cultivation during this period. Cultivation of improved mungbean varieties like Mubarik (developed by BARI) and BINAMOOG-2 (developed by BINA) during this period replacing the low-yielding aus rice has already shown some promise. Further breeding of high yielding varieties with seed dormancy, tolerance to rain and/or early maturity will greatly enhance the success of this newly introduced system. Mungbean is the only pulse crop which could be grown in Bangladesh during the entire year in three main seasons (Begum *et al.*, 1980). Being a short-duration crop it fits well into the existing cropping pattern. Replacement of local low yielding cultivars/land races by the high yielding varieties may improve and increase the total mungbean production of the

country. Vast areas in the northern portion of the country including the Barind Tract are left fallow after aus or jute harvest until the planting of winter crop like wheat. Mungbean could be grown in this gap. Development of high yielding varieties and motivation of the farmers to grow this crop will certainly increase the area and production of mungbean in this country.

Table 1.5. Mungbean area under cultivation, production, productivity and cropping pattern in Bangladesh (By greater districts).

Districts	**Area (ha)**	**Production (t)**	**Seed yield (kg/ha)**	**Percent of total area**	**Cropping pattern and type of mungbean grown**
Barisal	16,603	6,275	380	31	Pattern I
Patuakhali	14,498	8,990	620	27	Aman rice (July-Dec.)
Noakhali	7,063	5,005	710	13	Mungbean (Jan.-Mar.)
Faridpur	3,642	2,435	670	7	Aus/ Jute (Apr.-Jul.)
Comilla	1,496	1,025	690	3	
Chittagong	846	805	950	2	Green seeded
Sub-total	**44,148**	**24,535**	-	**83**	
Jessore	2,561	1,870	730	5	Pattern II
Kushtia	1,794	1,460	810	3	Aus rice/Jute (Apr.-Jul.)
Dinajpur	1,761	1,275	720	3	Mungbean (Sept.- Dec.)
Dhaka	909	525	580	2	Fallow/Wheat (Dec.-
Khulna	686	420	610	1	Apr.)
Kishoregonj	310	285	920	1	
					Yellow seeded
Sub-total	**8,021**	**5,835**	-	**15**	
Other 11 districts	1,104	770	697	2	
Total	**53,273**	**31,140**	**585**	**100**	

Source : Monthly Statistical Bulletin of Bangladesh (Dec., 1993).

The yield potential of the existing local mungbean cultivars is low due to various reasons. A survey of published account reveals that the major constraints responsible for low production of mungbean is as follows :

Varietal aspects

a. Lack of resistance to three major diseases, namely, Mungbean Yellow Mosaic Virus (MYMV), *Cercospora* Leaf Spot (CLS) and Powdery Mildew (PM) in case of mungbean grown in the period, September-December and two major diseases, namely MYMV and CLS in case of mungbean grown in late winter (January-March) and summer season (March-May). In addition to these diseases mungbean is susceptible to some other diseases also.

b. Genetic variability is extremely narrow in the local cultivars and land races. Most of the cultivars/varieties grown have no cognizable variation among them in any character (Shaikh and Rahman, 1990).

c. All the mungbean varieties grown in Bangladesh are small seeded type contributing directly to lower seed yield.

d. Varieties/cultivars do not differ in plant types suitable for different agro-climatic regions.

e. Most of the mungbean varieties are photoperiod sensitive. Early or late sowing or changes in photoperiod reduce yield drastically.

f. Asynchronous pod maturity results in decreased seed yield (Ahmed *et al.*, 1978) particularly in case of summer mungbean.

g. Undesirable plant types such as bushy and spreading habits and trailing tendency under abundant moisture regimes (Shaikh *et al.*, 1982).

h. Lack of dormancy in seeds lead to weather damage in the field. Most of the cultivated strains mature in rainy season, seeds rot inside the pod or germinate before harvesting (Imrie *et al.*, 1985; Shaikh *et al.*, 1988 and Ahmed *et al.*, 1988).

Other aspects

a. The production and distribution of the seeds of improved varieties have not been commensurate with the needs of the country. The lack of replacement of local cultivars/land races with improved varieties bred locally has resulted in the stagnation of seed yield (Singh, 1988).

b. Low priority assigned by the farmers in cultivating mungbean because of the risk of crop loss due to natural hazards.

c. Poor management practices due to lack of awareness among farmers about modern production technology.

In the present study the following efforts were made to evolve disease resistant and high yielding mungbean varieties :

a. Evaluation of varietal characters and seed yield of some local and exotic genotypes and mutants and the selected lines were compared with the lines developed through crossing of a local mutant and an AVRDC line.

b. A local mutant line was crossed with two exotic lines superior in one or more desirable characters. The diversity in morphological characters of the varieties used in the crossings was utilized in studying their genetic behavior.

c. Studies on the inheritance of MYMV and seed coat colour.

Chapter- II
REVIEW OF LITERATURE

REVIEW OF LITERATURE

A. Genetic Resources

The International Board for Plant Genetic Resources (IBPGR) has given high priority for genetic conservation of several pulse crops including mungbean. Since 1976 IBPGR has supported several exploration and collection missions for pulse crops. A working group has also been formed to collect and conserve the pulse germplasm. Based upon the information and known existing diversity of mungbean, the following areas have been selected for exploration and collection of this pulse. The areas are Burma, China, Thailand, Afghanistan, Indonesia, Iran, Philippines; Malaysia, Eastern Africa, Madagascar, South Africa and Caribbean Island. The working group has identified Asian Vegetable Research and Development Center (AVRDC), Taiwan for base collection and Institute of Plant Breeding, University of the Philippines at Los Banos (IPB-UPLB), Philippines for storing duplicate samples of mungbean. At present more than 5,000 germplasm is kept in the gene bank of AVRDC, Taiwan. The Institute of Crop Germplasm Resources (ICGR), China also maintains 3,000 germplasm of mungbean. In Bangladesh BINA and BARI are maintaining about 500 mungbean germplasm (Anishetty and Moss, 1988).

B. Evaluation of Germplasm

Various research workers have collected mungbean genotypes and classified them by grouping the strains which are similar in nature (Piper and Morse, 1914; San Miguel, 1916; Bose, 1932; Yohe and Poelhman, 1972; Gill *et al.*, 1975). Bose (1932) based his classification on seed colour, flower colour, pod colour, foliage colour, growth habit and time of maturity. Similar

characteristics were used by Caguicla (1933). Descriptors used by Gill *et al.* (1975) were more complete providing information on maturity, seed weight, seed yield, protein content and disease scores for yellow mosaic virus, bacterial blight and *Cercospora* leaf spot. Based on the above information a descriptors for mungbean has been developed by the International Board for Plant Genetic Resources (IBPGR, 1985). Plant height, days to flower, days to mature, number of branches per plant, number of pods per plant, 100-seed weight, seed yield/plant, seed coat colour and reaction to three major diseases like MYMV, CLS and PM were considered important for mungbean.

C. Qualitative Inheritance in Mungbean :

Genetic studies in mungbean were started in India by Bose in 1939. A total of 45 genes have so far been described for this species (Fery, 1980). A list of mungbean [*Vigna radiata* (L.) Wilczek] genes is presented in Appendix Table 8.2.

It has been mentioned by some researchers that inheritance studies relating to colour of plant structures are often difficult to interpret because they involve shades of colour which were named without reference to standard colour charts and the nomenclature differs with different researchers. Sometimes this led to duplicate names for a particular gene. Inheritance of seed coat texture and colour creates special problem. Dull seed coat colour is reported to be dominant over shiny (Bose, 1939; van Rheenen, 1965; K. B. Singh and J. K. Singh, 1970; and Murty and Patel, 1972, 1973). Watt *et al.* (1977) reported that dull seeds are covered with a texture layer originating from the inner pod membrane. When this layer is removed a shiny seed coat is visible.

Photoperiod insensitivity was reported to be dominant over photoperiod sensitivity (Verma, 1971 and Tiwari and Ramanujam, 1976b). Verma (1971) concluded that photo-insensitiveness is probably governed by a single recessive gene. Swindell and Poehlman (1978) worked in a series of controlled photoperiods, identified a dominant or partially dominant gene for photoperiod sensitivity in a mungbean genotype.

In addition to the above, genes have been reported for resistance to pathogens causing bacterial leaf spot, *Cercospora* leaf spot, mungbean yellow mosaic virus (Thakur *et al.*, 1977b) and cucumber mosaic virus (Sittiyos *et al.*, 1979). Genes have also been identified governing flowering (Tiwari and Ramanujam, 1976b); presence of pubescence (Murty and Patel, 1972, 1973); leaf margin shape (D. Singh and Mehta, 1953; Sen and Ghosh, 1959); plant growth habit (Pathak and Singh, 1963); and pod clusters (T. P. Singh and K. B. Singh, 1970).

D. Quantitative Inheritance in Mungbean

a. Association of plant characters and seed yield

i) Plant height

Positive and significant association between plant height and seed yield was obtained by Giriraj and Vijayakumar (1974), Sandhu *et al.* (1988), Gupta and Singh (1969) and Singh and Malhotra (1970a). On the other hand, negative correlation of plant height with seed yield was found by Ahmed *et al.* (1978).Correlation studies suggest that maximum yield is associated with large plants (Gupta and Singh, 1969; Joshi and Kabaria, 1973; Yohe and Poehlman, 1975). Islam *et al.* (1993) found that plant height was not significantly associated with yield but had significant relationship with seeds per plant and pods per plant. Sandhu *et al.* (1988) found that plant height has

a positive correlation with days to flower, days to maturity, number of branches, cluster per plant, pods per plant, pod length and seeds per pod, thereby indicating that early flowering and early maturing lines were shorter and late flowering, late maturing lines were taller. There are also reports that shorter, more compact plants with high harvest index and more determinate growth habit are suited to short summer season, high plant population and multiple cropping patterns where mungbean is grown for short period between two major crops (L. Singh, 1975).

ii) Days to flower and maturity

Medhi *et al.* (1980) found no variability for days to flowering in mungbean germplasm. Mungbean usually flower for a month or more (Mac Kenzi *et al.*, 1975). Mungbean plants may contain flowers, green or immature pods and ripe pods at the same time which require several pickings. Therefore, one of the major objectives of mungbean breeding is to select shorter length of flowering period so that more or less uniform matured lines could be developed.

iii) Number of branches per plant

Sandhu *et al.* (1988) found positive association of number of branches with pods per plant, plant height, seeds per pod and seed yield. Pokle and Patil (1975), K. K. Singh *et al.* (1976) and Ahmed *et al.* (1978) found a positive relation of branches per plant with seed yield.

iv) Number of pods per plant

Mungbean, in general, flowers abundantly, but a large number of flowers and pods abscise. Pod set in a sparse plant density was reported to be 50% (AVRDC, 1974). Savithri *et al.* (1978) reported that less than 25% of the

flower buds become pods. This is a very important yield contributing character. Highly positive correlation between pods per plant and seed yield has been reported by Gupta and Singh (1969) and Ahmed *et al.* (1978). Similar association in mungbean has also been reported by Singh and Singh (1973), Giriraj and Vijay Kumar (1974), Sandhu *et al.* (1988), Pun and Villareal (1989), Basir *et al.* (1992), Islam *et al.* (1993). It was observed by Malik *et al.* (1988) that an increase in seed yield of the F_1 hybrids was due to an increase in cluster and number of pods. Oseni *et al.* (1992) reported that pods per plant is one of the best indicators of seed yield for almost all other grain legumes.

v) 100-seed weight

Ahmed *et al.* (1978) found a negative correlation between bigger seed size with seed yield per plant. Negative association between seed size and seed yield was also obtained by Malhotra *et al.* (1974). On the other hand, Gupta and Singh (1969), Singh and Malhotra (1970b) obtained positive association between these characters.

vi) Seed yield per plant

The per hectare average seed yield of mungbean is very low in the tropics (only 0.41 t/ha, Anon., 1984b). Many reasons for low yield have been described in the chapter "Introduction" of this thesis. Breeding for improved plant type was emphasized initially to obtain high yield. The new improved plant type refers to more compact plants with high harvest index, more determinate growth habit and reduced photoperiod sensitivity. With the development of improved plant type, the yield potential of AVRDC mungbean cultivars has increased from 0.3 to 1.0 t/ha to 2.75 t/ha under high

population density of 400,000 plants/ha (Anon., 1984b). Seed yield is a complex character. Many workers have shown that a number of yield contributing characters are responsible for increased seed yield in this crop. Ahmed *et al.* (1978) showed number of primary branches, number of pods per plant had significant positive correlation with seed yield per plant while days to first flowering, days to maturity and plant height had a negative correlation in a set of genotypes they studied. Sandhu (1978) evaluated 2,719 genotypes and found that seed yield had a positive correlation with pods per plant, plant height, number of branches, pod length and seeds per pod but found no association with 100-seed weight, days to flowering and days to maturity. They suggested that early maturing types having bolder seeds could be combined with high number of pods per plant in order to attain higher seed yield. Pun and Villareal (1989) obtained a highly significant positive correlation between seed yield and seedling vigour, number of clusters per plant, number of pods per plant, number of seeds per pod, number of branches per plant and 100-seed weight. However, they did not find any correlation between seed yield and plant height. Basir *et al.* (1992) found a high positive correlation between seed yield and number of filled pods per plant and they observed through multiple regression analysis that three cluster, i.e., number of filled pods per plant, number of seeds per pod and 100-seed weight gave significant contribution to seed yield. The path coefficient analysis also revealed that one out of three characters is important to be concerned, i.e., number of filled pods per plant. Islam *et al.* (1993) also found that seed yield per plant had a close association with pods per plant and seeds per plant whereas 100-seed weight had negative significant relationship with seeds per plant and pods per plant.

Other plant characters that have been suggested as possible indirect selection criteria for seed yield include seed size, number of seeds per pod (Chandel *et al.*, 1973; Krishnaswami *et al.*, 1973; Pokle and Patil, 1975; Yohe and Poehlman, 1975; cluster number (Krishnaswami *et al.*, 1973; Malhotra *et al.*, 1974; Singh and Singh, 1973), pod length (Giriraj and Vijayakumar 1974; Gupta and Singh 1969; Tomar *et al.*, 1973), number of pods per peduncle (Chandel *et al.*, 1973); number of seeds per plant (Joshi and Kabaria 1973); weight of seeds per plant (K. K. Singh *et al.*, 1976), days to maturity (Singh *et al.*, 1968); seed weight of 10 pods (Singh *et al.*, 1968). Yadav *et al.* (1979) found that seed yield was positively associated with net assimilation rate at the post-flowering stage and with leaf-area ratio at the pre-flowering stage.

b. Heritability of seed yield and associated characters

Heritability estimates of yield and associated characters in mungbean have been reported by Gupta and Singh (1969); Empig *et al.* (1970), K. B. Singh and Malhotra (1970a), Tomar *et al.* (1972), Joshi and Kabari (1973), Verraswamy *et al.* (1973); Holker and Raut, (1993); and A. Singh and K. P. Singh (1995). Fery (1980) has summarized the broad sense heritability estimates for various characters of mungbean including the seed yield. Published broad sense heritability estimates for plant height and branch number obtained by various workers ranged from 7.9 to 96.9% and 26.05 to 85.2%, respectively (Table 2.1).

Published broad sense heritability estimates of earliness characters (days to flower or days to maturity) ranged from 31.0 to 99.0% (Table 2.1). Bose (1939), Sen and Ghosh (1961) and Tiwari and Ramanujam (1976b) suggested that early maturity is dominant or partially dominant over late maturity while Singh and Singh (1974a) suggested that late maturity is

partially dominant over early maturity. Several authors have analyzed such relationships and concluded that the earliness characters are largely controlled by loci with additive gene action (Chowdhury *et al.*, 1971; Giriraj 1973; Godhani *et al.*, 1978; Singh and Singh 1974a; Swindell and Poehlman 1976; Tiwari and Ramanujam 1974; Yohe and Poehlman, 1975). Murty *et al.* (1976) and Swindell and Poehlman (1978) reported that dominance x dominance gene action is involved in the expression of days to flower. Tiwari and Ramanujam (1976b) noted F_2 segregations of 13 moderately early plants to 3 late plants and they suggested that earliness is under digenic control.

Table 2.1. Broad sense heritability estimates for growth habit characters and earliness parameters in mungbean [*Vigna radiata* (L.) Wilczek].

Reference	h^2 %			
	Plant Height	**Branches/ Plant**	**Days to Flower**	**Days to Mature**
Bhargava *et al.* (1966)	96.8	66.0	-	-
Chowdhury *et al.* (1971)	87.3	34.5	94.9	-
Empig *et al.* (1970)	27.0	-	62.0	71.2
Giriraj (1973)	96.9	-	99.0	-
Gupta and Singh (1969)	-	50.9	39.5	-
Joshi and Kabaria (1973)	7.9	-	-	81.5
Murty *et al.* (1976)	75.0	57.0	88.8	-
Pokle and Numulwar (1975)	96.3	85.2	69.0	-
Swindell and Poehlman (1978)	-	-	59.0	-
Singh and Malhotra (1970b)	-	-	65.1	61.4
Tomar *et al.* (1972)	83.0	31.0	-	-
Veeraswamy *et al.* (1973)	88.5	78.9	90.6	79.0
Tickoo *et al.* (1988)	68.2	26.0	91.2	47.3

Pod length is moderately to highly heritable under most environmental conditions. Published heritability estimates ranged from 6.0 to 95.0% (Table 2.2). There is no general agreement about the nature of gene action for pod length. The association of high heritability and high genetic gain reported by Chowdhury *et al.* (1971) indicates that additive gene action is important. Pokle and Numulwar (1975), however, speculated that non-additive gene action is important because their high heritability estimate was associated with low genetic gain. Singh and Singh (1974a) concluded that both additive and logarithmic or multiplicative gene action are important. Murty *et al.*(1976) showed that pod length is influenced by dominance, dominance x dominance, and additive x additive gene action but Godhani *et al.* (1978) found only additive and additive x additive or dominance gene effects.

Number of seeds per pod is at least moderately heritable under most environmental conditions. Published heritability estimates ranged from 6.0 to 83.0% (Table 2.2). The data of Singh and Singh (1974a), Swindell and Poehlman (1976) and Yohe and Poehlman (1975) indicate that this character is controlled predominantly by loci with additive gene effects. Singh and Jain (1971) and Tiwari and Ramanujam (1974), however, found that both additive and non-additive gene action are important. Singh and Jain (1971) observed partial to over-dominance and speculated that dominance genes govern the inheritance of number of seeds per pod. Murty *et al.* (1976) showed that dominance x dominance gene action was important.

Shattering of pods at maturity is a serious problem in mungbean. Verma and Krishi (1969) showed that the shattering characteristic is completely dominant to the non-shattering characteristics and probably conditioned by a single gene pair. P. Singh *et al.* (1975) found that the matured pods of the blackgram do not shatter and they attempted to transfer

this character into the mungbean. The shattering characteristic was dominant in the F_1 plants of the interspecific cross, but the non-shattering characters could not be recovered in the F_2. P. Singh *et al.* (1975) concluded that resistance to shattering is quantitatively inherited.

Table 2.2. Listing of published broad-sense heritability estimates for pod and seed characters in mungbean [*Vigna radiata* (L.) Wilczek].

Reference	h^2 %			
	Pod length	**Seeds per Pod**	**100-seed weight**	**Protein (%)**
Bhargava *et al.* (1966)	66.0	41.3	85.3	-
Chowdhury *et al.* (1971)	88.6	39.0	98.6	-
Empig *et al.* (1970)	-	10.0[1]	51.2[1]	-
	-	49.0[2]	85.0[2]	-
Giriraj (1973)	89.7	70.2	97.0	-
Gupta and Singh (1969)	89.9	58.7	92.9	-
Joshi and Kabaria (1973)	-	12.3	-	-
Malhotra and Singh (1976)	-	-	-	50.8
Murty *et al.* (1976)	74.0	78.0	-	-
Pokle and Numulwar (1975)	95.0	68.3	95.3	-
Singh and Malhotra (1970b)	33.3	30.5	88.9	-
Singh and Singh (1974b)	-	-	-	73.5[3]
Tomar *et al.* (1972)	31.0	26.0	97.0	-
	6.0	6.0	-	-
	79.0	83.0	-	-
Veeraswamy *et al.* (1973)	53.4	60.1	-	-
Tickoo *et al.* (1988)		56.16	71.99	

[1] Average of 5 F_2 populations.
[2] F_3 populations.
[3] Narrow sense heritability estimate.

Seed size is highly heritable under most environmental conditions. Published heritability estimates for 100 seed weight, a common index of seed size, ranged from 51.2 to 97.0% (Table 2.2). The association between high heritability estimates and high genetic advance estimates that have been reported by a number of researchers, indicate that additive gene action plays an important role in the inheritance of this character (Bhargava *et al.* 1966; Chowdhury *et al.* 1971; Giriraj, 1973; Pokle and Numulwar, 1975; Singh and Malhotra, 1975). The diallel analysis of Singh and Singh (1972) and Yohe and Poehlman (1975) provided additional evidence that additive gene action is of appreciable magnitude. Singh and Singh (1974a) observed that logarithmic or multiplicative gene action is functioning. Tiwari and Ramanujam (1974) showed that seed size is also conditioned by some loci with non-additive gene effects. Sen and Murty (1960) found that small seed size is dominant over larger seed size and they speculated that large seeded mungbean evolved from small seeded types through the accumulation of recessive genes with additive effects. Their data indicate that it might be possible to further increase seed size by crossing among large seeded cultivars.

It has been found by many researchers that dull, rough seed surface is monogenically dominant over glossy, smooth seed surface (Bose, 1939; Murty and Patel, 1973; Sen and Ghosh, 1959; K. B. Singh and J. K. Singh, 1970; van Rheenen, 1965).

Singh and Singh (1973) and Malhotra and Singh (1976) reported that protein content of mungbean seeds is moderately heritable. Singh and Singh (1973) showed that both additive and non-additive gene action are important in the inheritance of protein content but additive gene action plays the predominant role. Singh (1974) also concluded that both additive and non-

additive gene action are important. He found that high protein content appears to be controlled by dominant genes. Malhotra and Singh (1976) concluded that the simultaneous improvement of yield and protein would be difficult. They showed, for example, that the direct effects of seeds per pod and seed yield per plant on protein content were negatively correlated and the r was relatively high. But Sandhu *et al.* (1994) found that Tryptophan content (r = 0.09) and protein content (r = 0.24) were not associated with seed yield nor with each other (r = 0.16) indicating seed yield and protein content could be improved simultaneously. Tiwari and Ramanujam (1976a) found that protein content is conditioned largely by additive gene action. They showed that both additive and non-additive gene action are equally important for methionine content.

Seed yield is moderately heritable under most environmental conditions. Published heritability estimates for number of pods per plant ranged from 21.7% to 90.4% (Table 2.3). Singh and Jain (1971) and Singh and Singh (1972) reported partial dominance for seed yield and partial to over-dominance for number of pods. Yohe and Poehlman (1975) concluded that these characters are predominantly controlled by loci with additive gene actions but the analysis of Singh and Jain (1971), Singh and Singh (1974 a, b) and Tiwari and Ramanujam (1974) indicated that both additive and non-additive gene action are important. Bhargava *et al.* (1966), Giriraj (1973), Joshi and Kabaria (1973) Pokle and Numulwar (1975) and Veeraswamy *et al.* (1973) reported high expected genetic gains for various yield components that are indicative of strong additive gene effects. Other studies indicate that the role of additive gene action is minimal. Singh and Singh (1972) showed that non-additive gene action is important for both seed yield and number of pods. Godhani *et al.* (1978) concluded that the dominance gene effects are

principally responsible for seed yield whereas non-additive epistatic gene effects are responsible for number of pods. Murty *et al.* (1976) showed that dominance x dominance gene action is involved to a considerable extent in the expression of both seed yield and number of pods.

Seed yield is determined by contributions from several yield components. The direct and indirect contributions to yield of specific yield components have been measured by path coefficient analyses (K. B. Singh and Malhotra, 1970b; T. P. Singh and Singh, 1973; Chandel *et al.*, 1973; Giriraj and Vijayakumar, 1974; Malhotra *et al.*, 1974; Pokle and Patil, 1975; Bhaumik and Jha, 1976 and Ko and Choe, 1976). Pods per plant were shown to contribute indirectly through seeds per pod and seed weight. Plant height and number of branches contributed indirectly to seed yield through pods per plant. Tall plants with many branches were capable of producing many pods. The studies confirmed the importance of a large number of pods per plant to obtain high seed yield, which was established also by correlation analyses.

E. Germplasm Sources and Collection

The initial step in a breeding programme is the collection of germplasm with a wide range of genetic variability. Breeders need to get their working germplasm from :

- improved local cultivar/varieties,
- varieties and breeding lines from existing breeding programmes or germplasm collections and
- closely related wild species.

Local varieties are often low yielding but may possess characteristics that can give stable production in the local environment. Improved varieties, whether developed locally or received from other sources with high yield

potential, generally provide the most valuable material for a breeding programme (Horst, 1961). An extensive breeding programme was developed at AVRDC, with several hundred crosses made annually from genetically diverse parent materials. Seeds from segregating progenies of these crosses were distributed to mungbean breeders (Park and Yang, 1978).

Germplasm of mungbean is collected for future use. The largest collections, which contain more than 5,000 accessions, have been kept at AVRDC. National germplasm collections of mungbean are maintained in Bangladesh (498 accessions), Institute of Crop Germplasm Resources (ICGR), CAAS, Beijing, China (3,000 accessions), Instituto Colombiano Agropecuario, (ICA), Palmira Vally, Colombia (135 accessions), Punjab Agricultural University (PAU), Ludhiana, India (3,000 accessions), NBPGR, New Delhi, India (2,200 accessions), Central Research Institute for Food Crops (CRIFC), Sukamandi, Indonesia (2,172 accessions), Malang Research Institute for Food Crops (MARIF), Malang, Indonesia (867 accessions),National Biological Institute (NBI), Bogor, Indonesia (100 accessions), National Institute of Agricultural Research (NIAR), Tsukuba, Japan (124 accessions), GRL-PARC, Islamabad, Pakistan (627 accessions), Institute of Plant Breeding, University of the Philippines at Los Banos (IPB-UPLB), Philippines (5,736 accessions), Southern Regional Plant Introduction Station (SRPIS-USDA), Experiment, Georgia, USA (3,800 accessions), University of Missouri (UM), Columbia, Missouri, USA (2,100 accessions) (Anishetty and Moss, 1988).

F. Breeding Objectives

Mungbean is generally regarded as a low yielding crop and its yield fluctuates widely under different environmental conditions. So, emphasis is given to improve not only its seed yield but also its yield stability.

a. Seed yield

Breeding for improved seed yield in mungbean involves (1) accumulation of genes for genetic potential for high seed yield (2) incorporation of genes for tolerance to stress conditions into varieties of high yield potential which limits the expression of genetic potential and (3) incorporation of genes into varieties which are responsible for disease and/or insect pests resistance. A few approaches are being made by the breeders to develop mungbean varieties with high yield potential. The first approach is to evaluate a large number of genotypes over a series of environments and select a line or variety with the superior yield. With this approach, sometimes it is not possible to identify characteristics of the variety which contribute to the high yield potential. A second approach ' biometrical methods' is used to evaluate the relationship or contributions of the individual yield components to the total yield. With this method correlation and path coefficient analyses have identified the importance of high pod number for obtaining high yields. A third approach is directed toward evaluation of strains for physiological processes such as source-sink relationships, harvest-index and others. The biometrical and physiological approaches are more precise than the first method and are useful in identifying parent materials for hybridization programmes. A disadvantage of both biometrical and physiological approach is that these are very time consuming and could not be used to large number of varieties and crosses.

b. Plant type

To obtain high yield in mungbean, emphasis has been given to plant type (Jain, 1975). In pulses, ideal plant type refers to shorter, more compact plants with a high harvest index, reduced photoperiod sensitivity, early in maturity and more determinate in growth habit. This type of plants are suitable for short summer seasons, high plant populations and multiple cropping programme where mungbean is grown in between two major crops. This plant type is associated with maximum seed yield per day over a short growing season although not necessarily with maximum seed yield per hectare. In contrast to this plant type, correlation studies suggest that maximum yield per hectare is associated with large plants which have greater height and branching (Prasad, 1959; Gupta and Singh, 1969; Joshi and Kabaria, 1973; Malhotra *et al.*, 1974; Yohe and Poehlman, 1975). Saini and Das (1979) found a late variety to exceed the yield of early varieties in seasons with abundant sunshine but to be lower in yield in a cloudy season.

c. Early and uniform maturity

Early maturity in mungbean is needed to fit the crop in multiple cropping systems. Imrie *et al.* (1987) found that earliness was due to major gene effects with earliness dominant to lateness. Earliness is determined by days from planting to opening of the first flower or days to ripening of first pod. In mungbean, flowering normally continues over a period of several weeks because of its indeterminate growth habit. Reduction in the length of the flowering period to get more uniform maturity is a major objective in mungbean breeding.

d. Diseases and insect resistance

Mungbean is host to many diseases. Disease may affect production of mungbean in various ways. Seedling diseases reduce plant stands in the field. Root diseases and nematodes alter or destroy root tissues and interfere with normal water and mineral uptake and by blocking the vascular system they can cause stunting and wilting of the plants. Leaf diseases destroy leaves or portion of leaves, reduce photosynthetic area and disrupt normal physiological processes. Virus diseases may cause stunting, leaf yellowing, leaf curling, flower deformation and reduction in pod development The major disease control procedures involve (a) cultural practices, (b) use of chemicals and (c) breeding of resistant varieties. Cultural practices like removal and destruction of infected plants and crop rotation can reduce the disease development. Insecticides and fungicides may reduce the incidence of insect attack and foliar diseases. But in mungbean chemicals are rarely used to control diseases by the farmers as mungbean is considered to be a low income crop. Breeding for resistance to diseases is also an important objective for mungbean. Among the diseases MYMV, CLS and PM are considered to be more serious problem of mungbean breeding.

i) Mungbean yellow mosaic virus (MYMV)

The mungbean yellow mosaic disease is transmitted by the whitefly, *Bemisia tabaci* Gen. is the most devastating viral disease of mungbean in the Indian subcontinent and adjacent areas (Nariani, 1960; Nene *et al.*, 1972; Ahmed and Harwood, 1973; Iwaki and Auzay, 1978; Legaspi *et al.*, 1978; Grewal, 1978; Ahmed *et. al.*, 1978; Ahmed *et al.*, 1988). Many isolates of MYMV have been obtained from different hosts and regions in India. All the isolates are transmitted by whitefly (*Bemisia tabaci*), but not by sap

inoculation or through seeds. Isolates from Bangladesh, Pakistan and Sri Lanka have similar transmission characteristics. Typical geminate particles, measuring 15-18 x 30 nm, have been observed in uranyl acetate-stained plant extracts of naturally infected plants of bambara groundnut, french bean, groundnut, horsegram, lima bean, mungbean and soybean (Muniyappa *et al.*, 1987). Like other gemini viruses the genome of MYMV has two circular single-stranded DNA molecules, commonly known as DNA-A and DNA-B. Both molecules are required for infectivities (Honda and Ikegami, 1986). Symptoms of MYMV first appear as a small spot on leaves and sometimes whole leaf becomes yellow due to virus attack. Diseased plants become stunted, maturity is delayed and a few pods or no pods develop. If the plants are infected at an early stage, may be killed before flowering. Young unfolded leaves are better source of the virus than old leaves (Krishnareddy, 1989). Transmission studies have been done by Rathi and Nene (1976) and Murugesan and Chelliah (1977). The whitefly acquires the virus during 15 to 60 minute feeding period. After a 3 to 8 hour incubation period the virus is transmitted during a 10 to 60 minute inoculation period. It was found by their study that a single whitefly is sufficient to inoculate 8 to 32 plants, and 10 flies inoculated all of 20 plants. The virus is classified as a circulative type. It persists in the male adult whitefly for three days and in the female adult for 10 days (Rathi and Nene, 1974). Varieties of mungbean differ in the types of reaction. Susceptible varieties exhibit a yellow mottle reaction and the resistant varieties exhibit a necrotic mottle (Nair *et al.*, 1974). It has been found by the researchers that tolerance to mungbean yellow mosaic virus is controlled by a single recessive gene (Thakur *et al.*, 1977b; Malik *et al.*, 1988). Other researchers found that resistance is governed by two recessive genes (Shukla *et al.*, 1978; Sandhu *et al.*, 1985). However, Reddy and Singh

(1993) concluded that resistance to MYMV is governed by one dominant and one recessive gene. The term 'resistant' has been variably used to refer to lines developing no visible symptoms (Gurha *et al.*, 1982) or necrotic mottle (Nene *et al.*, 1972), having less than 2% (Chaudhary *et al.*, 1981) or less than 10% yellow mosaic incidence (Singh, 1979), or getting infected late. Despite these inconsistencies many resistant mungbean varieties/lines have been identified in the countries where the disease is prevalent. Still durability of resistance to yellow mosaic virus is a problem. A number of mungbean collections were found consistently resistant for 7 years, some other for 6 years and many others for even shorter periods (Singh *et al.*, 1988).

Following points need to be considered for further improvement of MYMV resistance:

- Identification of stable sources of resistance to MYMV in mungbean and related species like *Vigna radiata* var. sublobata, *V. mungo* and *V. umbellata* based on multilocational trials (Verma and Sandhu, 1991).
- Identification of the mechanism of resistance to the virus and the vector.
- Generation of information on the variability of the virus and the vector and on diversity of genes governing resistance/tolerance to the virus and vector and,
- Combining the diverge genes for resistance/tolerance to the vector and the virus with genes for high yield and other biotic and abiotic stresses.

ii) *Cercospora* leaf spot (CLS)

The epidemiology of CLS has been studied and yield loss due to this disease was estimated to be 10% in resistant cultivars (Anon., 1984a). AVRDC has identified several breeding lines that are resistant to CLS.

Cercospora leaf spot causes severe leaf spotting and defoliation of mungbean in humid areas of Southeast Asia (Legaspi *et al.*, 1978; Catedral and Lantican, 1978; Grewal, 1978; Duangploy, 1978; Somaatmadja and Sutarman, 1978). The principal pathogen is *Cercospora canescens* Ell. and G. Martin, although C. *cruenta* has been reported to be a pathogen on mungbean in the Philippines (Ilag *et al.*, 1978). The disease first appears on the leaf as brown leaf spots with grayish white centers and reddish brown margins which causes premature defoliation and loss in yield. As the disease advances, lesions are developed on the stems and pods. The disease spreads by the spores from soil debris. Spores of *C. canescens* are primarily air borne and some may be seed borne. The disease is most prevalent during the rainy season. Disease severity increases during flowering and pod formation. Conidia production on detached leaves was higher in darkness than in normal light and optimum at 27^0c and 96% humidity (Rath and Grewal, 1973). Thakur *et al.* (1977a) found that resistance to CLS is conditioned by the dominant gene.

iii) Powdery mildew (PM)

Powdery mildew is a common foliar disease of mungbean. The disease is prevalent in dry weather with temperatures between 22 to 26^0c and relative humidity of 80 to 88% (Ilag *et al.*, 1978). In Asia, the disease is common in the cool, dry months and rarely a problem in the warm rainy season. The pathogen, *Erysiphe polygoni* D. C., is highly specialized and infects both mungbean and blackgram. The disease first appears as ash gray spots on the upper surface of the leaves and as the fungus spreads, mycelium covers the leaf surface, giving the leaves a powdery white appearance. In advanced stages, stems and pods become infected and older leaves defoliated. If the

infection occurs during flowering, yields are reduced by 21% (Soria and Quebral, 1973). Infection after pod set have only slight effect on seed yield. Besides the above mentioned diseases mungbean is attacked by several other bacterial, fungal and virus diseases.

G. Hybridization

When superior lines of mungbean are identified and characterized, hybridization is used to combine the desirable characteristics of two or more lines into one strain. After hybridization, selection is used to isolate desirable lines from segregating generations and tested for performance in yield trials. Earlier, hybridization did not receive much attention in mungbean breeding. Either local varieties or selections from local varieties were grown. Now hybridization is used extensively and almost all the new varieties are the result of this breeding procedure. The use of hybridization has increased because of the availability of desired new lines from where breeders can choose parent combinations with greater precision and improved crossing procedure so that higher percentage of seed set is obtained. It may be mentioned here that flowering behaviours and crossing techniques have been described by many researchers. Bose (1939) mentioned that flowers of mungbean are borne in clusters of 10 to 20 in axillary or terminal racemes. Pollination occurs at night, beginning around 9 to 10 p.m. and is completed around midnight. Early in the next morning the flowers begin to open, remain in full bloom until shortly before noon and then begin to close and are fully closed by late afternoon. Mungbean is a self pollinated crop and cleistogamy is common (Narasimham, 1929) but outcrossing by small pollen-carrying insects may occur. The outcrossing averages around 2 to 5% (van Rheenen, 1964; AVRDC, 1977) but it varies with the variety and the season. Flower

shedding in mungbean is common. Flower shedding is increased by high temperatures and desiccating winds during the flowering period. The crossing procedure in mungbean is not difficult but seed set is often low due to the high amount of pod shedding after artificial cross pollination. Crossing is usually done using the technique described by Buishand (1956) for beans , as modified by Boling *et al.* (1961). Emasculation is done by pushing one side of the standard and the corresponding wing petal outward with a dissecting needle and removing one-half of the keel petal and anthers with forceps, taking care not to injure the stigma. For the pollen source, mature flowers are selected in which the anthers have dehisced. The pollen covered stigma is brushed on the stigma of the emasculated flower for pollination. After pollination the wing and the standard petal are returned to their original position, covering the pollinated stigma to prevent it from drying out. Highest pod set is obtained by emasculating in the evening with pollination in the following morning (T. P. Singh and Malhotra, 1975). About 20% pod set is normal, although 60% pod set with an average seed set of 6 seeds per pod has been reported from AVRDC (Park and Yang, 1978).

Heterosis or hybrid vigour in mungbean following intervarietal crosses has been reported by Bhatnagar and Singh (1964), Misra *et al.* (1970), K. B. Singh and Jain (1970), Ramanujam *et al.* (1974), Swindell and Poehlman (1976); Ko (1979) and Naidu and Satyanarayana (1993). Experimental results showed that, the increase in seed yield of the hybrids over the midparent ranged from 17% to 208% and the increase of the hybrids over the high parent ranged from 1% to 188%. The hybrid was significantly higher in seed yield than the midparent in only 23 out of 58 crosses and significantly higher than the high parent in only 6 out of 33 crosses. The low proportion of crosses with significant heterosis suggests that a large number of hybrid

combinations need to be made in a mungbean improvement programme in order for superior cross combinations for seed yield to be identified. In addition to seed yield, positive heterosis was reported for characteristics related to plant size, such as height, number of branches, and branch length. Malik *et al.* (1988) observed absence or negative heterosis for seed weight. Generally hybrids were early maturing than the midparent. Heterosis for protein content was observed but the magnitude of the heterosis was small (T. P. Singh and Singh, 1973). Out of 25 crosses, only 3 exhibited significant heterosis for methionine content (Tiwari and Ramanujam, 1976a). With the closed pollination system in mungbean, it is unlikely that heterosis will be exploited commercially in this crop.

The success of cross breeding approach depends on a suitable choice of parents to be combined, on the genetic control of the desired characters and whether selection of the characters is easily possible in the segregating generations. The characters may be qualitative or quantitative. In case of qualitative characters such as disease resistance, plant height, plant structure, fruit number, fruit colour, fruit shape, fruit shattering, the selection of parents is comparatively easy because phenotypic differences reflect genotypic differences for such characters. The environment does affect the expression of these characters but not very strongly. Suitable plants are easily selected and the characters are not genetically complex. Selection for these characters in segregating populations results in rapid genetic advance.

But breeding for quantitative character such as seed yield is much more difficult. Under this situation the breeder must select for qualitative (or visible) characters first, because the selections must confirm to a certain desired agronomic types (e.g., disease resistance, height, earliness, non-shedding of grains, seed size etc.). Normally, these characters are strongly

heritable and therefore, selections for these characters in the early generations (F_2, F_3) of a cross will reduce the large population, retaining only the desired types.

Table 2.3. Published broad sense heritability estimates for seed yield characters in mungbean.

Reference	h^2 %			
	Pods per Plant (no.)	**Pods per Plant (wt.)**	**Seeds per Plant (no.)**	**Seeds per Plant (wt.)**
Bhargava *et al.* (1966)	87.9	-	-	69.9
Chowdhury *et al.* (1971)	53.8	-	-	56.9
	50.9[1]	-	-	-
	50.4[2]	-	-	-
Empig *et al.* (1970)	24.6[3]	-	27.6[3]	8.6[3]
	31.0[4]	-	26.0[4]	47.0[4]
Giriraj (1973)	77.7	-	-	79.1
Gupta and Singh (1969)	47.8	-	-	51.1
Joshi and Kabaria (1973)	90.4	-	87.9	84.2
Murty *et al.* (1976)	78.0	73.0	-	75.0
	-	10.0[5]	-	14.0[5]
Pokle and Numulwar (1975)	21.7	-	-	59.0
Singh and Malhotra (1970b)	30.9	-	-	27.5
Tomar *et al.* (1972)	43.0	-	-	38.0
	48.0	-	-	28.0
	59.0	-	-	79.0
Veeraswamy *et al.* (1973)	61.5	58.2	-	47.2

[1] Number of pods on main shoot, [2]Number of pods on side branches, [3] Average of 5 F_2 populations, [4] F_3 population, [5] Narrow sense heritability.

The pedigree method of selection has been used in the selection of a wide range of qualitative characters and also for seed yield. The method is

useful because single plant and progeny evaluation for qualitative characters is easy to perform. In this case assessment is done visually and a large number of progenies can be handled. After the selection of qualitative characters, a sufficiently large number of segregates (lines) could be retained for evaluation for the quantitative character(s) at F_4, F_5, F_6, or later generations. The pedigree method of breeding is good for crops where plants are grown in open spacing.

Chapter- III
MATERIALS AND METHODS

MATERIALS AND METHODS

A. Materials

For evaluation and selection of suitable genotypes 25 local and 6 mutant lines and 193 exotic lines along with one control were used. The country of origin and accession numbers of these lines are described in Table 3.1. The following varieties/lines of mungbean were used for hybridization :

1. MB-55-4 : This is a small seeded mutant line which was developed through gamma irradiation by the Bangladesh Institute of Nuclear Agriculture (BINA). The plants are dwarf and photo-sensitive, i.e., grow in short day photoperiod. The line is resistant to Mungbean Yellow Mosaic Virus (MYMV), but susceptible to both *Cercospora* Leaf Spot (CLS) and Powdery Mildew (PM). Due to its tolerance to MYMV and yellow seed coat colour, this line was selected to use in hybridization programme.

2. VC-1560D : The line was developed at the Asian Vegetable Research and Development Center (AVRDC), Taiwan through hybridization. This bold seeded line has been released as a variety in the Philippines, Australia and Vietnam (Fernandez and Shanmugasundaram, 1988). This variety was reported to be resistant to CLS. When grown in Bangladesh it showed resistance to CLS in both summer and winter, but was susceptible to MYMV and PM in both the seasons. The line was chosen for its bold seeded

character, resistance to CLS and erect plant habit.

3. ML-37 : The line was developed in India and reported to be resistant to Mungbean Yellow Mosaic Virus (MYMV) and *Cercospora* Leaf Spot (CLS) in a few countries.

Table 3.1. Country of collection, accession numbers and total number of genotypes studied

Country	**BINA accession numbers (MB)**	**Total no. of genotypes**
Australia	142, 161, 201-222	24
Bangladesh	Winter type : 6, 7, 54-56, 63-68 = 11 Mutants : 57-62 = 6 Summer : 76-87 + 3 local = 15	32
China	69-75	7
India	1-5, 8-11, 23-27, 44-45, 94-95,132-141, 143-147, 152-160, 162-165	46
Indonesia	15-18	4
Iran	12-14	3
South Korea	91, 97, 109	3
Pakistan	102	1
Philippines	20-22, 28-37, 89, 93, 101, 150, 151, 166-172	25
Sri Lanka	19, 38-43,46-53	15
Taiwan	88, 92, 96, 98, 103-108, 110-131, 173-200	60
Thailand	100	1
USA	90, 99, 148-149	4
Total		**225**

Table 3.2. Morphological characteristics of the varieties/lines used in this study.

- **During winter**

Characters	**MB-55-4**	**VC-1560D**	**ML-37**
Days to flower	34.0	35.0	34.0
Days to mature	76.0	80.0	75.0
Plant height (cm)	32.0	40.0	39.0
Number of branches/plant	2.0	2.0	1.6
Number of pods/plant	17.0	5.0	8.0
Pod length (cm)	6.0	9.0	6.0
Number of seeds/pod	9.0	12.0	11.0
100-seed weight (g)	2.8	6.5	3.7
Seed yield/plant (g)	4.2	3.5	3.0
Stem hairiness	Hairy	Glabrous	Hairy
Pod hairiness	Dense	Nil	Scanty
Seed shape	Globular	Oblong	Oblong
Seed coat colour & luster	Yellow dull	Green shiny	Green shiny
Cotyledon colour	Yellow	Yellowish white	Yellowish white
Disease reactions			
MYMV	Resistant	Susceptible	Susceptible
CLS	Tolerant	Tolerant	Tolerant
PM	Susceptible	Susceptible	Susceptible

- **During Summer**

Characters	MB-55-4	VC-1560D	ML-37
Days to flower	Did not flower	33.0	32.0
Days to mature	-	85.0	76.0
Plant height (cm)	-	51.0	39.0
Number of branches/plant	-	2.0	2.0
Number of pods/plant	-	12.0	32.0
Pod length (cm)	-	9.5	6.5
Number of seeds/pod	-	13.0	10.0
100-seed weight (g)	-	6.6	4.0
Seed yield/plant (g)	-	7.5	7.6
Stem hairiness	-	Glabrous	Hairy
Pod hairiness	-	Nil	Scanty
Seed shape	-	Oblong	Oblong
Seed coat colour & luster	-	Green shiny	Green shiny
Cotyledon colour	-	Yellowish white	Yellowish white
Disease reactions			
MYMV	-	Tolerant	Tolerant
CLS	-	Resistant	Tolerant
PM	-	Resistant	Susceptible

B. Methods

All the experiments were conducted under the Plant Breeding and Genetics Division of the Bangladesh Institute of Nuclear Agriculture (BINA), Mymensingh. The different experimental procedures followed during evaluation of germplasm, hybridization, inheritance of tolerance to MYMV, inheritance of seed size and seed coat colour, evaluation of selected

segregants at different locations and selection procedures in the subsequent generations are described below:

a. Evaluation of germplasm

Seeds of all the germplasm were sown in March, 1986 at the experimental farm of Bangladesh Agricultural Research Institute (BARI), Ishurdi. The soil of that farm was sandy loam with pH 6.5-7.0. Fertilizer was applied @ 20 kg Urea, 40 kg TSP and 20 kg MP/ha. The experiment was conducted in 15 x 15 Lattice design with two replications. Seeds were sown in hills of one m^2 grid, each hill having 20-30 plants.

Data on number of days to first flowering, pod maturity and disease reaction in respect of MYMV, CLS and PM in field conditions were recorded. Plants were grown without applying any fungicide in order to assess the reaction of the above diseases. Reactions to MYMV, CLS and PM were scored using the scale described in Table 2.3.

Before harvesting the number of plants/hill was counted. Data on plant height, number of branches/plant and number of pods/plants were collected on five randomly picked plants from each plot. The pods were sun-dried, threshed, cleaned and weight of 100-seeds were taken. The seven highest yielding genotypes were selected and the means and ranges of their varietal characters computed as a separate group. A local cultivar (MB-87) was also included in this group as a check.

b. Observation trial of the selected genotypes with F_4 lines

A few hybrid lines (MC-41, MC-84, MC-103, MC-219 and MC-246) which were selected earlier from a cross between a mutant (MB-55-4) and AVRDC line (V-2773) were evaluated with the selected genotypes (MB-1,

MB-8, MB-45, MB-94, MB-95, MB-183 and MB-197) at BINA farm, Mymensingh during summer, 1987 along with the control (MB-87) and one parent (V-2773). The other parent (MB-55-4) does not flower in summer and was excluded from the trial. The experiment was conducted following randomized complete block design with three replications having unit plot size of 2.5 x 2.0 m. Data on varietal characters such as days to flower, days to maturity, plant height, number of pods per plant, number of seeds per plant, 100-seed weight, seed yield per plant, seed colour and luster and reactions to MYMV, CLS and PM was recorded.

c. Preliminary yield trial

Based on the result of observation trial, five promising lines (hybrid line, MC-246 and four exotic summer lines, MB-1, MB-8, MB-94 and MB-197) with two controls (MB-87 and Mubarik), and a parent (V-2773) were subjected to preliminary yield trial in the year 1988 at two locations, viz., Bangladesh Jute Research Institute (BJRI) farm, Kishoreganj and RARS farm, Ishurdi. The experiment was conducted following randomized complete block design with three replications. The unit plot size was 4.0m x 2.5m. Data on days to flower, days to maturity, plant height, number of pods per plant, 100-seed weight, seed yield kg/ha and disease reactions was recorded.

d. Advanced yield trial

During 1989, three promising summer mungbean lines along with two controls were put into an advanced yield trial at four locations, viz., Ishurdi, Kishoreganj, Faridpur and Barisal. The experiment was laid out in randomized complete block design with three replications having unit plot size of 4.0m x 5.0m. Only seed yield kg/ha was recorded to evaluate the lines.

e. Zonal yield trial

In the year 1990 , the high yielding line MC-246 along with two controls were put into zonal yield trials at five locations. The locations were Barisal, Rangpur, Faridpur, Mymensingh and Ishurdi. The experiments of Barisal, Faridpur and Mymensingh were partially damaged by rain and storm and yield performances of the strains were not satisfactory hence the experiments were repeated in the year 1991 at all the locations as in the previous year. The newly released variety Kanti was included as one of the controls in 1990 and 1991 experiments instead of Mubarik. In both the years the experiments were laid out in randomized complete block design with four replications. Unit plot size was 4.0m x 5.0m. Data on seed yield kg/ha was recorded.

f. On-farm and on-station trial

On farm trials of MC-246 along with the released variety Kanti of BARI were conducted through the Department of Agricultural Extension (DAE) at seven locations, namely, Barisal, Faridpur, Ishurdi, Satkhira, Rangpur, Trisal and Mymensingh. On-Station trials were conducted at three locations. The locations were Mymensingh, Trisal and Ishurdi. Data on seed yield and disease reactions were recorded.

g. Variation in *dal*, seed coat and protein %

Seeds of MC-246 and few other elite lines and 2 controls were decorticated. The cotyledons were separated from the seed coat and the weight was taken separately. Protein % of the strains were estimated by using the Kjeldahl's method.

h. Hybridization

Reciprocal crosses between MB-55-4 and ML-37, MB-55-4 and VC-1560(D), and ML-37 and VC-1560(D) were done in the glass house of BINA in winter, 1985 following the hybridization procedure described by Boling (1961). Emasculation was done by pushing one side of the standard and the corresponding wing petal outward with a dissecting needle and removing one half of the keel petal and the anthers with forceps by taking care not to injure the stigma. For the pollen source, mature flowers were selected in which the anthers have dehisced. The pollens were brushed lightly across the stigma of the emasculated flower to complete the pollination. After pollination, the wing and the standard petal were returned to their original position covering the pollinating stigma to prevent it from drying out. Emasculation were done in the evening with pollination in the following morning. Details of the cross combinations and selections made in following generations are described Table 3.3 and 3.4.

For hybridization, data were collected on the number of flowers pollinated, the number of pods set and the number of mature pods harvested. Pod setting was recorded four days after pollination. Pods abscising 14 days after pollination were considered to be late aborted pod.

i) Growing of F_1 population

The F_1 hybrids, together with parents, MB-55-4 and VC-1560D were grown in winter (September, 1985) in the farm of BINA, Mymensingh in a randomized complete block design with three replications. Each unit plot had eight plants spaced 10 cm apart. The spacing between rows was 30 cm. Data were recorded from four sample plants of the F_1 generation and parents from

each replication for the characters namely days to flowering and maturity, plant height, number of branches/plant, number of pods/plant, pod length, seeds/pod, 100-seed weight and seed yield/plant.

Table 3.3. Number of plants and families selected in F_2, F_3 and F_4 generations (winter).

Cross number and combination	Number of selections made		
	F_2 plants	F_3 plants	F_4 lines
1. MB-55-4 x ML-37	20	1	1
2. ML-37 x MB-55-4	7	2	0
3. MB-55-4 x VC-1560D	134	41	11
4. VC-1560D x MB- 55-4	45	16	2
5. ML-37 x VC-1560D	0	0	0
6. VC-1560D x ML-37	0	0	0
Total	206	60	14

ii) Growing of F_2 generation in winter

Half of the seeds of the three crosses were sown separately to raise F_2 populations along with F_1s and parents in September, 1986 at BINA farm, Mymensingh. Sowing was done in 3m long rows. Row to row and plant to plant spacings were 30 and 10 cm, respectively. A local MYMV and CLS susceptible line (MB-63) was replicated after every 5 rows as a spreader to identify virus and CLS infection from natural sources. No insecticide was applied in order to maintain high population of the MYMV vector, the whitefly (*Bemisia* sp.). The F_2 progeny was screened carefully and selection of individual plants were made on the basis of disease resistance and seed yield. Data on the following characters, such as days to flowering and maturity, plant height (cm), number of branches/plant, number of pods/plant,

pod length (cm), seeds/pod, seeds/plant, 100 seed weight (g), seed colour and luster, disease reactions (MYMV, CLS and PM) and seed yield/plant (g) were recorded from the plants selected in the field. Plants with lower seed yield than the parents were discarded. Finally seeds of 206 individual F_2 plants were selected for further studies in F_3. Accession numbers were given to all the selected F_2 plants.

Table 3.4. Number of plants and families selected in F_2, F_3 and F_4 generations (summer)

Cross number and combination	Number of selections made		
	F_2 plants	F_3 plants	F_4 lines
1. MB-55-4 x ML-37	0	0	0
2. ML-37 x MB-55-4	4	0	0
3. MB-55-4 x VC-1560D	0	0	0
4. VC-1560D x MB- 55-4	106	21	11
5. ML-37 x VC-1560D	15	2	0
6. VC-1560D x ML-37	11	1	1
Total	136	24	12

iii) Growing of F_3 generation in winter

Seeds of all the 60 selected plants were sown to raise F_3 populations in winter, 1987. The seeds of individual plants were sown in two lines of 2.5m long with three replications along with parents. Each line having at least 25 seeds. Row to row and plant to plant distances were 30 and 10 cm, respectively. Recommended cultural practices were used throughout the growing period of the crop. True breeding lines were selected from F_3 populations. Selections were made on the basis of resistance to MYMV, CLS and PM, higher number of pods, bold seed size, yellow seed coat colour and

higher seed yield than the parents. With regard to days to flower and maturity, number of branches/plant lower means than control were the basis of selection which are desired for this crop. Five plants were picked up at random from each line for recording data as described earlier.

The mean values of each character except seed colour and disease reaction were analyzed statistically. The mean values of the characters were plotted against seed yield/plant.

iv) Growing of F_4 generation in winter

Fourteen F_4 promising lines (selected in F_3) were grown along with parents in winter, 1988 at BINA farm, Mymensingh. The experiment was conducted following randomized complete block design with three replications. Unit plot size was 2.5m x 4.0m. Row to row and plant to plant distances were 30 and 10 cm, respectively. Fertilizer was applied @ 20 kg Urea, 40 kg TSP and 20 kg MP /ha. In the field, data on days to flowering and maturity, disease reactions were taken and after harvest, data on different varietal characters were taken from five randomly picked plants from each replication. Seeds of each plot were threshed, cleaned and dried separately before taking the weight of seeds of each plot and then plot seed yield was converted to kg/ha. The lines which produced higher seed yield than the parents were selected.

v) Growing of F_2 generation in summer

The remaining half of the seeds obtained from F_1 generation of the three cross combinations were sown in summer (March, 1987) at RARS farm, Ishurdi. The experiment was laid out in 3m long rows. The row to row and plant to plant distances were 40 and 10 cm, respectively. A local MYMV and

CLS susceptible line (MB-87) was replicated after every 5 rows as a spreader. No insecticide was applied during the growing period of the population. Data on days to flowering and maturity, plant height (cm), number of branches/plant, number of pods/plant, pod length (cm), seeds/pod, seeds/plant, number of weathered seeds/plant, 100-seed weight (g), seed colour and luster, disease reactions, seed yield/plant (g) were recorded from the plants selected in the field. Plants which was susceptible to diseases and producing lower seed yield than the parents were discarded. Finally seeds of 136 individual F_2 plants were kept separately for growing as F_3 plant progeny. Accession numbers were given to all the selected F_2 plants.

vi) Growing of F_3 generation in summer

As in winter seeds of selected plants from F_2 generation were sown in summer at RARS, Ishurdi. There were three replications for each selected line and seeds were grown in two lines of 2.5m long in each replication. Plant to plant and line to line to distances were 10 and 40 cm, respectively.

Data on 5 randomly chosen plants from each replication was taken as was taken in F_3 of winter. The mean values of the characters were plotted against seed yield/plant. Based on the data superior lines were selected to grow F_4 population for further study.

vii) Growing of F_4 generation in summer

Only 12 promising F_3 lines were selected to grow F_4 in summer. The experiment was conducted at two locations, viz., Ishurdi and Barisal in summer, 1989 with these 12 lines. These locations were chosen because these areas are considered the best summer mungbean areas and Barisal produces highest mungbean among the greater districts. The experiments

were conducted in randomized complete block design with three replications. Unit plot size was 2.5m x 4.0m. Spacings between rows and plants were 40 and 10 cm, respectively. Data on disease reactions, days to flower and maturity were taken in the field. For other necessary data five plants were selected randomly from each plot. Seed yield/plot was converted to kg/ha. Only a few lines were selected to assess their yield potential in the next generation.

viii) Inheritance of tolerance to MYMV

Seeds of the cross number 3 (MB-55-4 x VC-1560D) were grown to raise F_2 population along with F_1's and parents in September, 1986 at BINA farm, Mymensingh. The sowings were made in 3m long rows. The row to row and plant to plant spacings were 30 and 10 cm, respectively. A local MYMV and CLS susceptible line was replicated after every 5 rows as a spreader to identify virus and CLS infection from natural sources. No insecticide was applied in order to maintain high population of the vector, the whitefly (*Bemisia* spp.). Data on MYMV infection were taken at the time of pod formation when about 90% of the plants in the spreader line were infected with MYMV. The rating scale which is presented in Table 3.5 was used during the study. Observations were recorded on the incidence of MYMV in the parents, F_1, F_2 and F_3 generations (including reciprocals). The parent line, MB-55-4 was resistant to MYMV under field conditions while the other one (VC-1560D) was susceptible to this disease. Goodness of fit was determined by χ^2 test for segregation ratio.

ix) Inheritance of seed coat colour

The experimental material consisted of the parents, F_1, F_2 and backcross generations of two mungbean strains, VC-1560D and MB-55-4 having green

and yellow seed coat colour, respectively. The seed coat colour of the dry seeds of individual plants were visually recorded. Variation in the intensity of colour within a group was not taken into consideration. The F_1, F_2 and backcross generations along with their parents were studied.

Intermediate scales were used in scoring all the diseases for intermediate severity levels. The mean disease severity score for each line/strain was calculated by averaging the scores obtained from each line/strain.

Table 3.5. Rating scale for MYMV, CLS and PM used in the present study (Source: Singh *et al.*, 1988).

MYMV :

Rating	Plants/ foliage affected	Reaction
1	Completely free	Resistant
3	Traces of necrotic mottle	Moderately resistant
5	Moderate necrotic mottle	Tolerant
7	Restricted yellow mottle	Moderately susceptible
9	Completely yellow mottle	Susceptible

CLS :

Rating	Percentage affected	Reaction
1	Completely free	Resistant
3	Brown spots covering up to 10% leaf area	Moderately resistant
5	Bigger spots covering up to 20% leaf area	Tolerant
7	Lesions covering up to 40% leaf area	Moderately susceptible
9	Lesions covering more than 60% leaf area	Susceptible

PM :

Rating	Percentage of leaf area affected	Reaction
1	No symptoms	Resistant
3	10-25% leaf area mildewed	Moderately resistant
5	40-50% leaf area mildewed	Tolerant
7	60-75% leaf area mildewed	Moderately susceptible
9	>75% leaf area mildewed	Susceptible

C. Statistical Methods

The data collected on different quantitative characters in F_1, F_2, F_3 and F_4 generations were statistically analyzed using the procedures of the PC packages, the MSTAT-C (Freed, 1992).

a. Analysis of variance

In most of the experiments, the breeder is interested in estimating the component of variances. One can achieve it through Analysis of Variance (ANOVA). It helps in sorting out variance due to different sources, e.g., variation observed can be partitioned into two parts, one representing the variation between the genotypes and the other within the families of genotypes. The second objective of analysis of variance is to provide basis for test of significance. The analysis of variance was done on the pattern shown in Table 3.6.

Table 3.6. Pattern of analysis of variance

Source	D.F.	S.S.	M.S.	F value
Replications	(r-1)			
Families	(f-1)	M1		
Error	(r-1)(f-1)	M2		
Total	(rf-1)			

b. Analysis of coefficients of variability

Range, means with their standard deviations and standard errors were calculated on family and population basis in each cross along with their parents. The parameters of variability such as variance and coefficients of variation were calculated on the basis of family and population using the

above packages and the standard statistical procedures (Snedecor and Cochran, 1967). The induced variability was analyzed by estimating the following components of the mean and variance :

Family mean : The mean of a character based on the data collected from five plants in a family.

Population mean : It was the variance for a character between different families within a cross.

Interfamily mean : It was the variance for a character between different families within a cross.

Intrafamily variance : This was the variance of a character among the randomly selected plants within a family.

Population variance : This was the interplant variance of a character which was averaged over all the families in a cross.

Intrafamily coefficient of variability: The intrafamily coefficient of variability of a particular character was estimated using the following method :

$$\text{Intrafamily CV} = \frac{\sqrt{\text{Intrafamily variance}}}{\text{Family mean}} \quad X\ 100$$

Population coefficient of variability : It was calculated using the population variance and population mean for a character of a particular cross.

$$\text{Population CV} = \frac{\sqrt{\text{Population variance}}}{\text{Population mean}} \quad X\ 100$$

c. Estimation of components of variation and genetic parameters :

According to Burton (1952) the phenotypic variance (Vp) and genotypic variance (Vg) are used to compute the components of variation and genetic parameters as described below :

i). **Components of variation**

Phenotypic coefficient of variation (PCV)

$$= \frac{\sqrt{Vp}}{\text{Mean}} \times 100$$

Genotypic coefficient of variation (GCV)

$$= \frac{\sqrt{Vg}}{\text{Mean}} \times 100$$

ii). **Genetic parameters**

Heritability (broad sense) : Heritability (h^2) in broad sense was estimated as the ratio obtained by dividing the genotypic variance to the phenotypic variance as shown below :

$$h^2 = \frac{Vg}{Vp} \times 100$$

Genetic advance : The expected gain in selection (GA) was calculated as percentage of mean which is given below :

$$GA = \frac{Vg \times K}{\sqrt{Vp} \times \text{Mean}} \times 100$$

Where, K = 2.06 (Selection intensity at 5% level)

d. Analysis of variability in F_2, F_3 and F_4 generations

The analysis of variability was done by estimating the components of mean and variance as in the previous generation.

e. Analysis of performance of genotypes in F_3 and F_4 generations

In order to compare the mean performance of the selected mutants and control, the breeders often calculate the Critical Difference (C.D.) by using the following formula :

CD = S.E. X t

Where, S.E. = Standard Error of the difference of genotypes mean to be compared and is equal to :

S.E. + (2.EMS/r)½

Where, EMS = Error Mean Sum of Square

r = Number of replication

t = Tabulated value at 5% or 1% level of significance for Degree of Freedom of Error Mean Square.

If the mean difference between any two genotypes is greater than the calculated the value of C.D. then the difference is taken to be significant.

f. Selection of promising families

During the present investigation the characters which were studied are briefly described below :

Days to first flower : The total number of days taken by the plants from the date of sowing to the opening of first flower. Strains not flowering in summer within

60 days after sowing was considered as photoinsensitive.

Days to pod maturity : Total number of days taken for pod maturity from its sowing date to about 90% of its pods turning black.

Plant height : Length of a plant in centimeter from soil surface to the tip of the main stem.

Branches/plant : Total number of branches with pods on the main stem.

Pods/plant : Total number of mature pods (Weathered or unweathered) produced by a plant counted at harvest.

Seeds/plant : Mean number of seeds of five plants.

Seeds/plant : Mean number of seeds of five plants.

100-seed weight : Weight in gram of sun dried 100 seeds taken at random immediately after harvest of a particular strain.

Seed colour : Two types of seed colour : yellow (Y) and green (G) were recorded after harvest.

Seed luster : It was classified into shiny (S) and dull (D).

Seed yield : Single plant seed yield in case of individual plant selection and plot yield in case of different

trials were recorded. Seeds were cleaned and sun-dried before weighing.

Reactions to MYMV, CLS and PM : Plants in each plot were scored at the maximum pod-filling stage when the susceptible strains were severely affected. The severity of the diseases was scored by observing the percentage of affected leaves and the remaining plant parts and assigning 1-9 rating scale as described in Table 2.6. Reactions to MYMV appeared as bright yellow patches to complete yellowing of the leaves and other parts of plant. The reactions to CLS appeared as brown to black spots of varying size on the leaves and other parts of a plant and reactions to PM appeared as white patches of fungal mycelium to complete whitening of the leaves and other parts of a plant.

Chapter-IV
EXPERIMENTAL RESULTS

EXPERIMENTAL RESULTS

A. Evaluation of Germplasm

Among the 225 genotypes studied, 11 local winter lines (MB-5, MB-6, MB-54 to MB-56 and MB-63 to MB-68) and 6 mutant lines (MB-57 to MB-62) showing delayed flowering up to 60 days from sowing were considered to be photosensitive types. These lines/mutants were excluded from the experiment and data from the remaining 208 genotypes were recorded (Appendix Table 8.1). The varietal characters that were studied and analyzed during the evaluation of germplasm are described below:

Plant height

The plant height of 208 genotypes varied from 29 to 80 cm with a mean of 50 cm (Table 4.1). Among these, plant height of 3 genotypes were within 29-30 cm, 33 within 31-40 cm, 84 within 41-50, 52 within 51-60 cm, 21 within 61-70 and 15 within 71-80 cm (Fig. 4.1). The plant height of selected eight genotypes ranged from 32 to 65 cm with a mean of 41.9 cm (Table 4.2). The genotypes MB-183 and MB-197 were the tallest (65 cm) among the selected lines while MB-94 was the shortest (32 cm) (Table 4.2).

Days to flower

The mean time of first flowering from the date of seeding was 33 days with a range from 28 to 39 days (Table 4.1). Among these genotypes, 6 flowered within 28-29 days, 32 within 30-31 days, 55 within 32-33 days, 88 within 34-35 days, 25 within 36-37 days and only 2 within 38-39 days (Fig. 4.2). On the other hand, the mean time of flowering for the selected genotypes was 30 days with a narrow range from 28 to 30 days (Table 4.2). Among the selected lines the Accession No. 197 flowered first in 28 days and all other lines flowered in 30 days (Table 4.2).

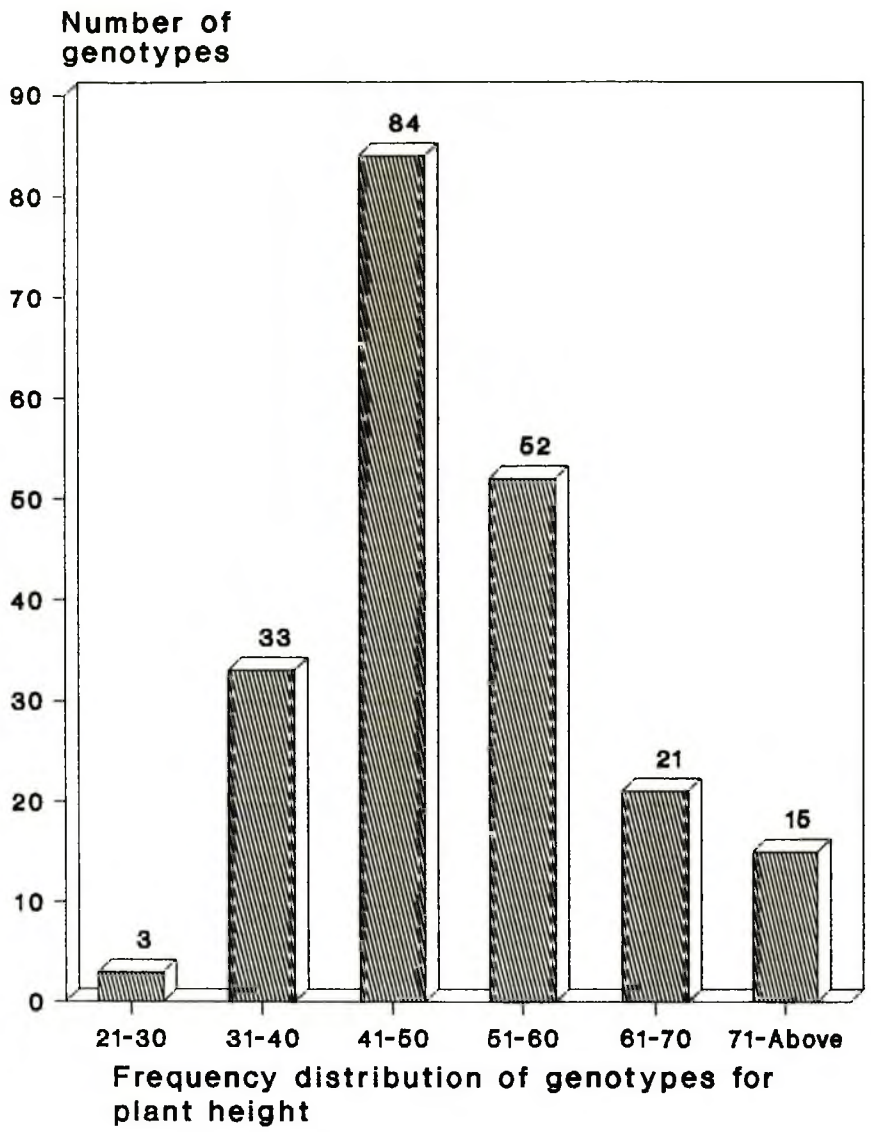

Fig. 4.1. Distribution of 208 genotypes for plant height.

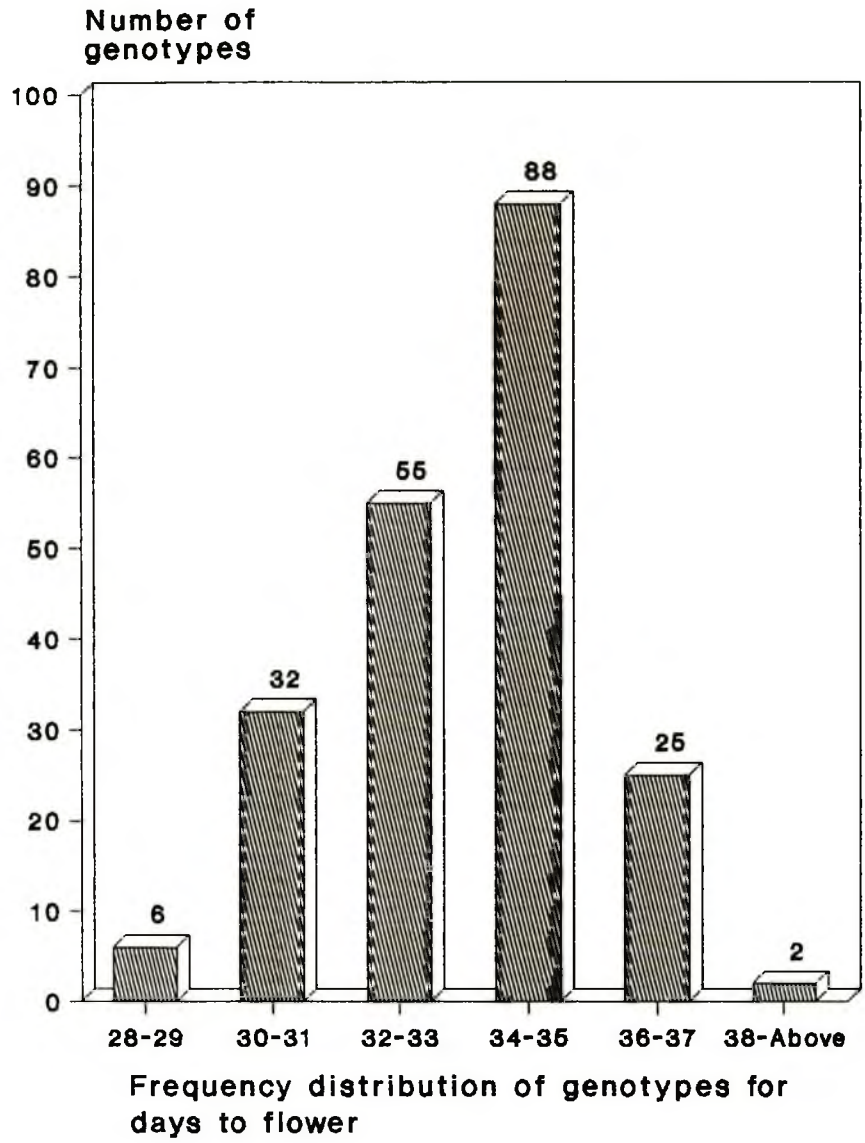

Fig. 4.2. Distribution of 208 genotypes for days to flower.

Days to mature

The mean days to pod maturity of all the genotypes were 80 days with a range from 65 to 94 days (Table 4.1). Among these, only one genotype matured very early, i.e., within 65 days from the date of sowing, 15 matured within 66-70 days, 26 within 71-75 days, 105 within 76-80 days, 38 within 81-85 days, 21 within 86-90 days period and the very late maturing genotypes among these batches were only 2 which took 91-95 days to mature (Fig. 4.3). On the other hand, eight selected genotypes matured within a shorter period (65-80 days) having a mean of 74 days (Table 4.2).

Table 4.1. Variation among the 208 mungbean genotypes for varietal characters and seed yield/plant.

Characters	Unit	Range	Mean	S.D.	CV (%)
Plant height	cm	29.0-80.0	50.0	11.2	22.4
Days to flower	Day	28.0-39.0	33.2	2.1	6.3
Days to mature	Day	65.0-94.0	79.6	5.0	6.8
Branches/plant	No.	0.0-3.0	1.7	0.7	41.2
Pods/plant	No.	3.0-22.0	10.2	3.8	37.2
100-seed weight	g	2.5-7.0	4.0	0.9	22.5
Seed yield/plant	g	0.6-8.2	2.4	1.2	50.0

Number of branches/plant

The number of branches/plant varied from 0 to 3 among the genotypes. The mean number of branches/plant was 1.7 (Table 4.1). Among these, 5 genotypes produced no branch at all, 72 had only one branch, 112 had two branches and 19 produced three branches/plant (Fig. 4.4). The selected genotypes produced 2-3 branches/plant with a mean of 2.5. Among these four

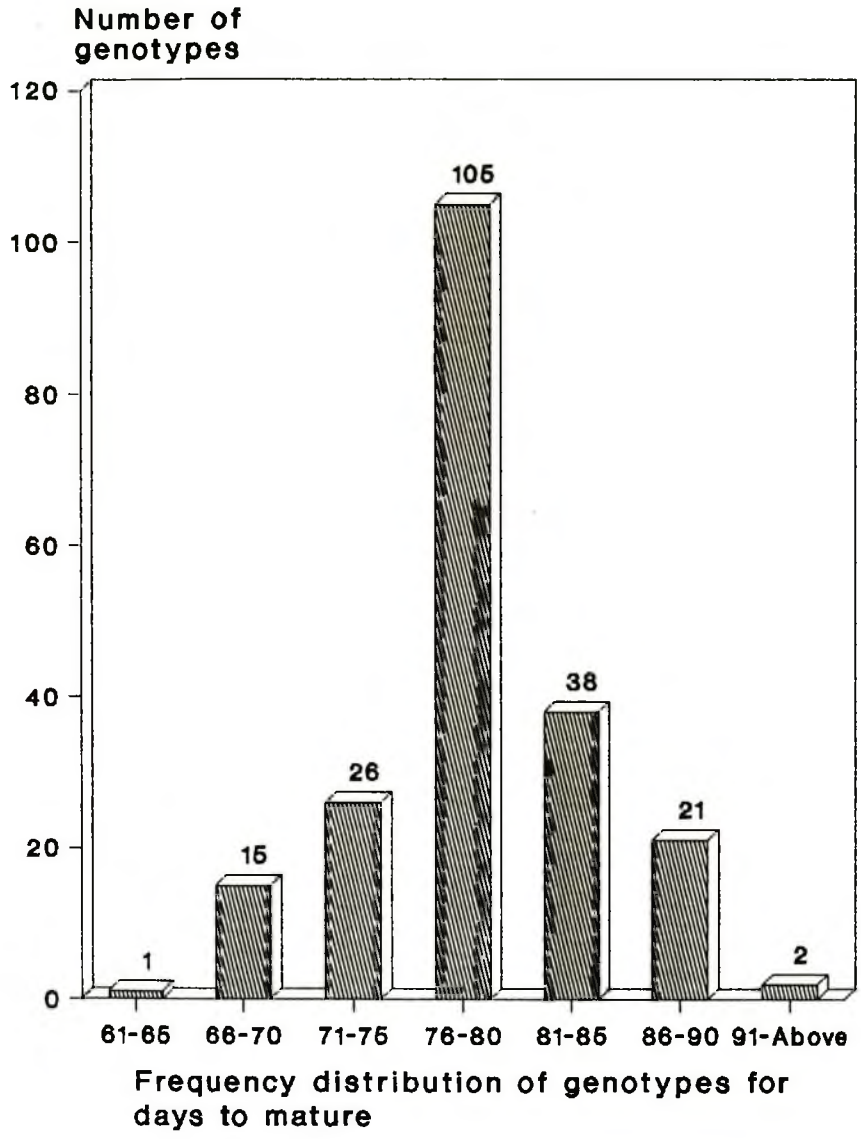

Fig. 4.3. Distribution of 208 genotypes for days to mature.

genotypes produced two branches/plant and other four produced three branches/plant (Table 4.2).

Number of pods/plant

The important yield component, number of pods/plant varied from 3 to 22 pods with an average of 10 pods (Table 4.1). Among the 208 genotypes, 23 produced 1-5 pods, 91 produced 6-10, 79 produced 11-15, 12 produced 16-20 and only 3 produced 21-25 pods/plant (Fig. 4.5). Higher number of pods/plant was observed among the selected eight genotypes with a mean of 20 pods/plant. Among the genotypes, three viz., MB-8, MB-45 and MB-95 yielded the highest number of pods (22 pods/plant) while MB-87 produced the lowest number of pods (17 pods/plant) (Table 4.2).

100-seed weight

The mean seed size (100-seed weight) was 4.03 (g) with a wide range from 2.5 to 7.0 (g) (Table 4.1). Among these 100-seed weight of 41 genotypes were between 2.1-3.0, 99 genotypes between 3.1-4.0, 47 genotypes between 4.1-5.0, 16 genotypes between 5.1-6.0 and 5 genotypes between 6.1-7.0 (Fig. 4.6). On the other hand, 100-seed weights of the selected genotypes were higher in average (4.2 g) with a range of 3.0-6.0 (g). Among the selected genotypes 100-seed weight of MB-183 was the highest (6.0 g) while it was the lowest in the local genotype MB-87 (3.0 g) (Table 4.2).

Seed yield/plant

For seed yield/plant the genotypes showed a wide range of variability (0.6-8.2g) with a mean of 2.4 (g) (Table 4.1). Among these, seed yield of 86 genotypes were between 0.1-2.0 (g), 111 between 2.1-4.0, 5 between 4.1-6.0, 4 genotypes between 6.1-8.0 and 2 genotypes above 8.0 (g) (Fig. 4.7). Only those genotypes, which had produced at least 6.0 (g) of seeds/plant, were

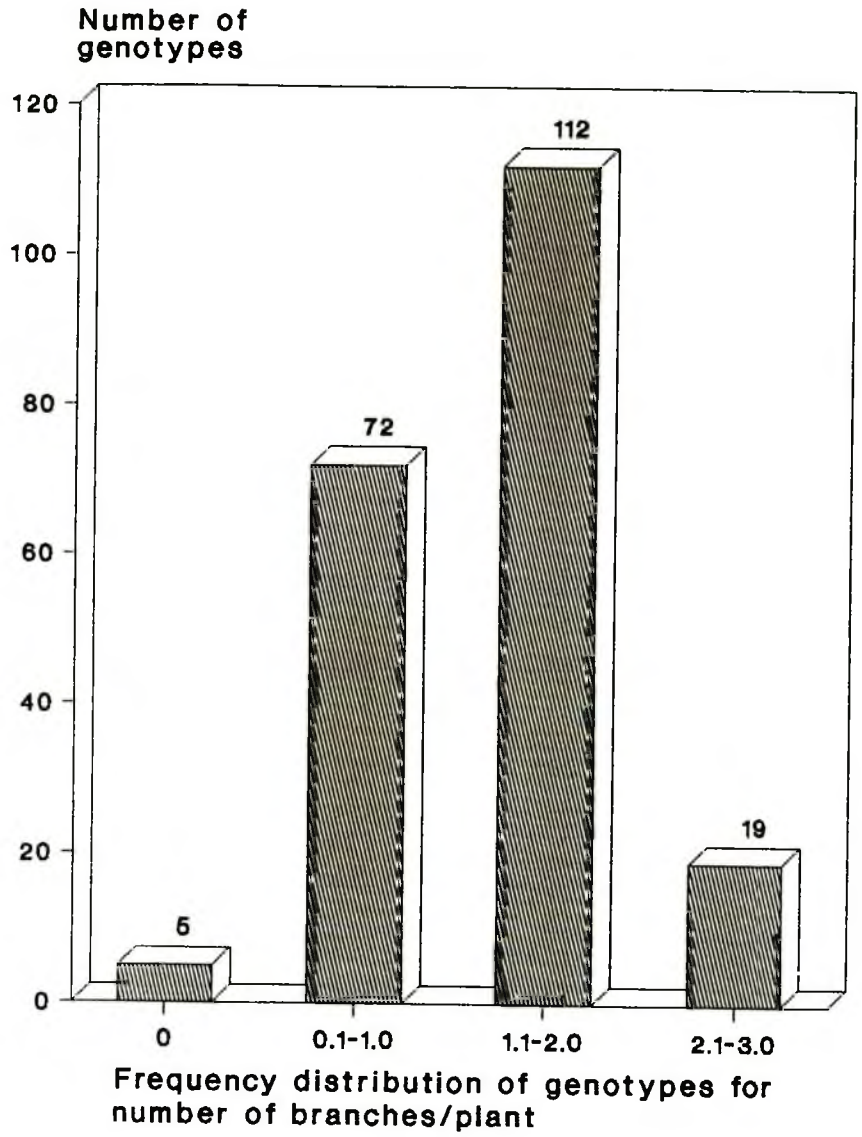

Fig. 4.4. Distribution of 208 genotypes for branches/plant.

selected. A local line (MB-87) which produced 4.5 (g) seeds/plant was kept as a check for further comparative trials (Table 4.2).

Table 4.2. Data on varietal characters of 8 selected genotypes.

Characters	Mungbean accession numbers*								Mean	Range
	1	8	45	87	94	95	183	197		
Days to flower	30	30	30	30	30	30	30	28	30	28-30
Days to mature	68	65	72	78	73	75	80	80	74	65-80
Plant height (cm)	44.5	32.0	37.0	40.5	30.5	35.0	65.0	65.0	41.9	32-65
Branches/plant	2	2	2	2	3	3	3	3	2.5	2-3
Pods/plant	20	22	22	17	18	22	18	18	20	17-22
100-seed weight (g)	3.5	3.5	4.0	3.0	3.5	3.8	6.0	6.0	4.2	3.0-6.0
Seed yield/plant (g)	6.1	6.2	6.9	4.5	6.0	6.8	8.2	8.2	6.5	4.5-8.2
Seed colour**	GS	GS	GS	GD	GS	GS	GS	GS	-	-
Reactions to diseases* **										
MYMV	T	T	T	S	T	T	S	T	-	-
CLS	T	T	T	S	S	T	R	T	-	-
PM	T	T	R	T	T	R	R	T	-	-

* Origin of the accessions is presented in Appendix Table 8.1

** GS= Green Shiny, GD= Green Dull

*** R= Resistant, T= Tolerant and S= Susceptible

Seed coat colour

Seed colour and luster was studied before sowing of these genotypes. Among these 111 genotypes had green shiny seed coat colour, 93 had green dull seed coat colour, 2 had black mosaic seed coat colour, 1 had brown seed coat colour and another yellow dull seed coat colour.

Among the selected genotypes seven had green shiny seed coat and only one (local MB-87) had green dull seed coat colour (Table 4.2).

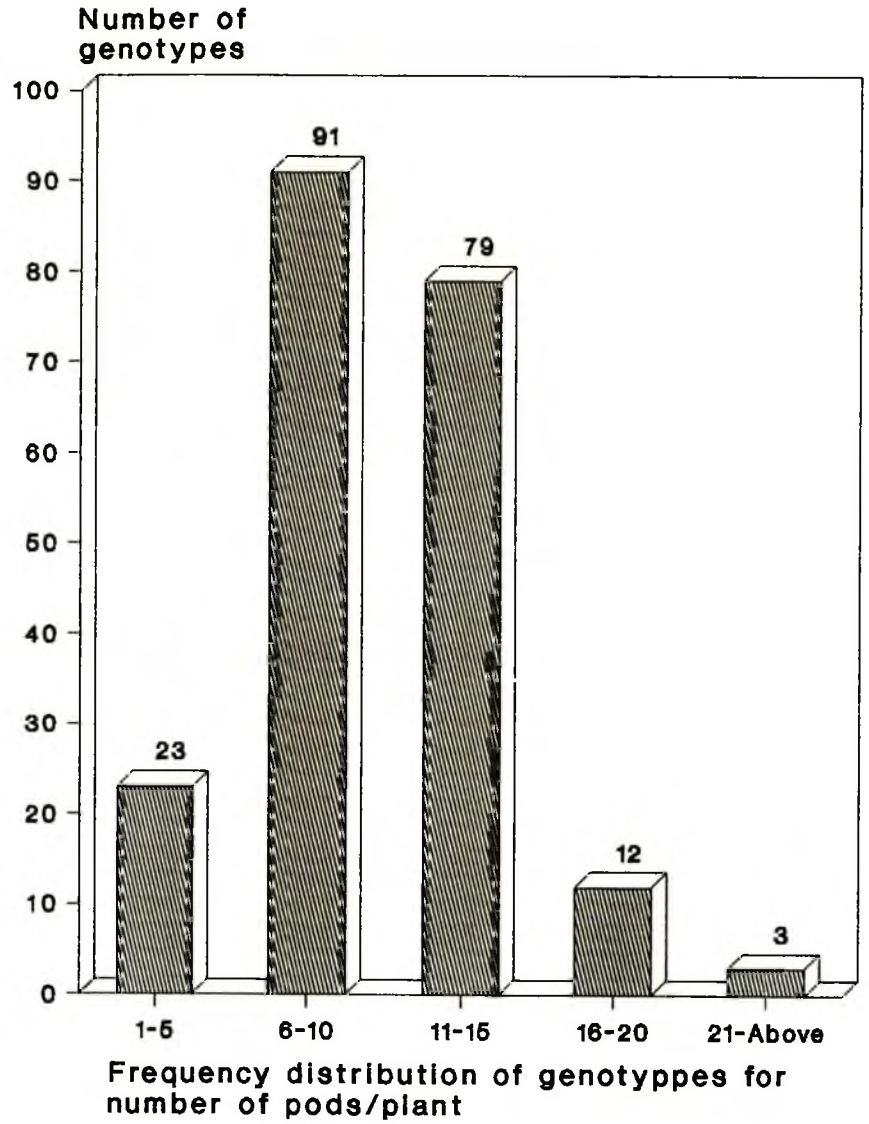

Fig. 4.5. Distribution of 208 genotypes for number of pods/ plant.

Reaction to three major diseases

MYMV: Among the genotypes studied none was found to be resistant to this virus. The genotypes were classified into two groups for this disease, i.e., tolerant and susceptible. Among the 208 genotypes, 25 were tolerant to this disease (12%) and 183 were susceptible (88%) whereas among the selected genotypes six were tolerant (75%) and only two were susceptible (25%) (Table 4.3).

CLS : Only one (0.5%) of 208 genotypes showed resistance to this disease whereas 94 (45%) and 114 (55%) genotypes showed tolerance and susceptibility, respectively to this disease. Among the selected genotypes, one was resistant (13%), five (63%) were tolerant and only two (25%) were susceptible to this disease (Table 4.3).

PM : PM caused less damage to these genotypes and among the 208 genotypes, 49 (24%) showed resistance and 159 (76%) showed tolerance to this disease. Among the selected genotypes, three (37.5%) were resistant and five (62.5%) were tolerant to this disease (Table 4.3).

Although the main basis for selection in this study was seed yield (minimum 6.0 g/plant), all the selected genotypes showed resistance/tolerance to one or more diseases under study, e.g., MB-1 and MB-197 showed tolerance to all the three diseases, MB-45 and MB-95 showed tolerance to both MYMV and CLS and resistance to PM (Table 4.2).

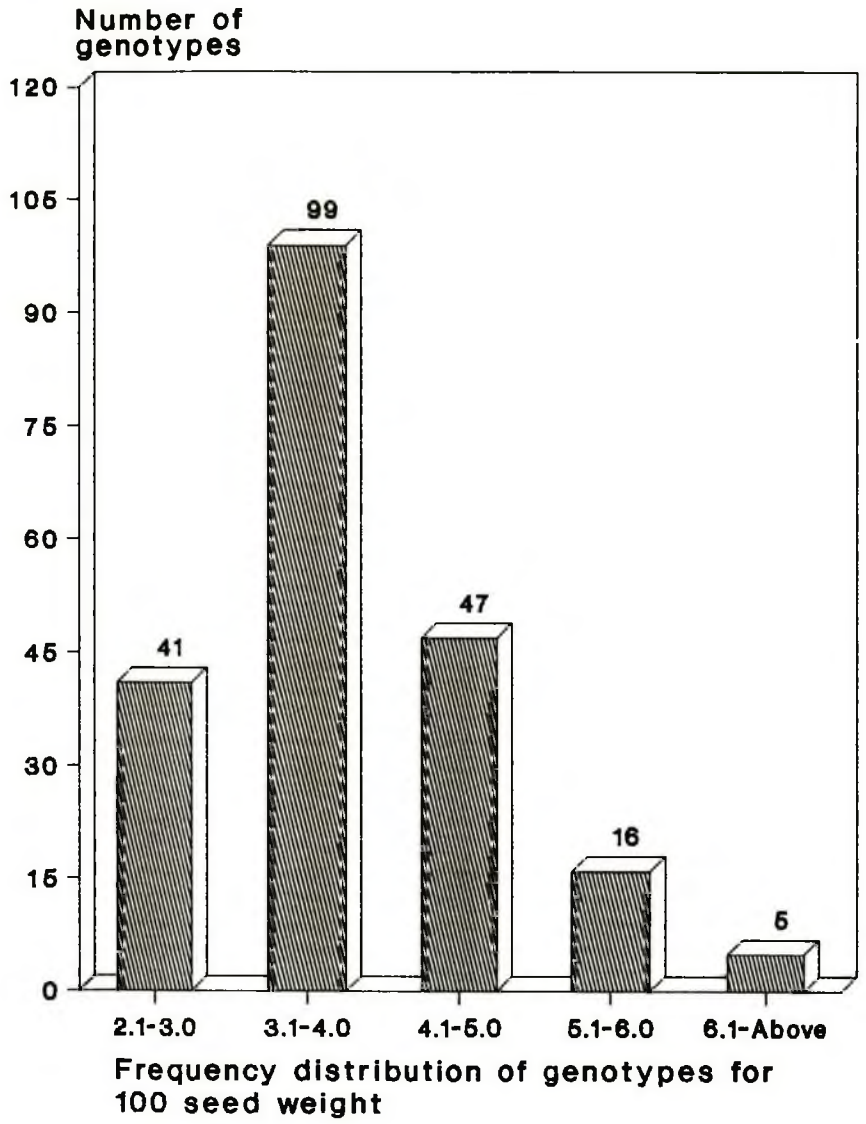

Fig. 4.6. Distribution of 208 genotypes for 100-seed weight.

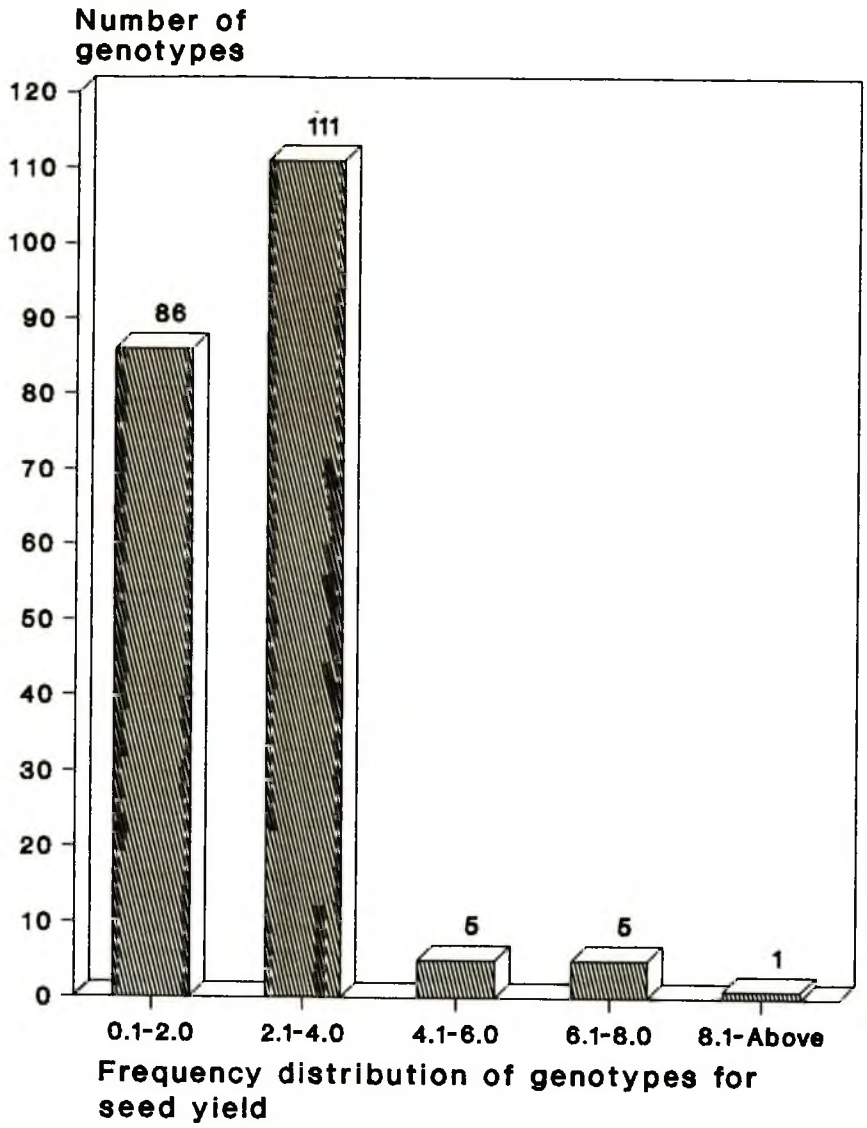

Fig. 4.7. Distribution of 208 genotypes for seed yield/ plant.

Table 4.3. Reaction of mungbean genotypes to three major diseases.

Diseases	Among 208 genotypes						Among selected 8 genotypes					
	Resistant		Tolerant		Susceptible		Resistant		Tolerant		Susceptible	
	No.	%	No.	%	No.	%	No.	%	No.	%	No.	%
MYMV	-	-	25	12	183	88	-	-	6	75	2	25
CLS	1	0.5	94	45	114	55	1	13	5	63	2	25
PM	49	24	159	76	-	-	3	37.5	5	62.5	-	-

B. Observation Trial

Performance of twelve selected lines with their parents as control were put under observation trial during summer of 1987 is presented in Table 4.4. Reactions of these lines to three major diseases are also included in this table.

All the strains flowered within a short range of period, i.e., from 28 to 33 days (Table 4.4). The maturity period ranged from 65 to 80 days. MB-8 was found to be early maturing while MB-197 was late maturing. Plant height varied from 60 to 80 cm. The strain MB-41 was the shortest and the strain MB-45 was the tallest of all the strains studied. Wide range of variations were observed in number of pods/plant, seeds/plant, 100-seed weight and seed yield/plant. Variations ranged from 10 to 28 in pods/plant, 83 to 250 in seeds/ plant, 2.5 to 6.0 (g) in 100-seed weight and 3.5 to 10.0 (g) in seed yield/plant. MC-246 produced the highest number of pods/plant (28), seeds/plant (250) and seed yield/plant (10.0 g). On the other hand, MB-183 gave the lowest number of pods/plant (10), seeds/plant (83) but its seed size was the highest (6.0 g/100 seeds) of all the genotypes which resulted in moderate seed yield/plant (5.0 g). The highest seed yield per plant was produced by the strain MC-246 (10.0 g) and the lowest by the strain MC-219 (3.5 g). Seed coat colour and lustre of the strain were similar to that found in the previous study.

Reaction of the strains to the three diseases varied. Two strains (MC-246 and MB-1) were found to be resistant, seven showed tolerance and the remaining strains along with the parent were susceptible to this MYMV. Further, none of the strains showed resistance to CLS, seven strains and the parent were tolerant and the remaining strains were susceptible to this disease. All the strains were, however, scored to be tolerant to PM.

Table 4.4. Seed yield, varietal characters and disease reactions of the selected summer mungbean strains in the observation trial.

Cross/ Acc. No.	Days to flower	Days to mature	Plant ht. (cm)	Pods/ plant (No.)	Seeds /plant (No.)	100-seed wt (g)	seed yield/ pl. (g)	Seed coat colour	Disease reactions*		
									MYMV	CLS	PM
MC-41	33	69	60	12	123	3.4	4.2	GD**	S	T	T
MC-84	32	72	74	15	128	3.5	4.5	GD	T	S	T
MC-103	30	70	68	14	105	3.8	4.0	GS	T	S	T
MC-219	32	70	78	10	92	3.8	3.5	GD	S	S	T
MC-246	32	70	76	28	250	4.0	10.0	GD	R	T	T
MB-1	31	70	78	24	225	3.2	7.2	GS	R	T	T
MB-8	28	65	68	23	210	3.0	6.3	GS	T	T	T
MB-45	31	72	80	12	111	4.5	5.0	GS	T	S	T
MB-94	32	70	75	22	203	3.2	6.5	GS	T	T	T
MB-95	30	70	65	15	145	4.0	5.8	GS	T	T	T
MB-183	32	78	69	10	83	6.0	5.0	GS	S	T	T
MB-197	33	80	74	15	134	5.8	7.8	GS	T	S	T
MB-87 (Local)	33	78	75	16	148	2.5	3.7	GD	S	S	T
V-2773 (Parent)	33	78	73	20	136	4.4	6.0	GS	S	T	T

* R = Resistant, T = Tolerant, S = Susceptible.
** GD = Green Dull, GS = Green Shiny.

C. Preliminary Yield Trial

Performance of five selected lines and the local MB-87 under preliminary yield trial during the summer, 1988 at two locations is summarized in Table 4.5.

Table 4.5 shows that all the strains flowered within a very short range of period at both Ishurdi and Kishoregonj. The maturity periods of the strains were also narrow. At Ishurdi, the range of maturity was from 65 to 75 days while at Kishoregonj from 66 to 83 days. At both the places MB-8 matured earlier than all other strains/variety. The strain took 65 and 66 days to mature at Ishurdi and Kishoregonj, respectively. The strain V-2273 was late maturing at both the locations. It matured in 85 days at Ishurdi and 83 days at Kishoregonj. A narrow range of variability was observed in case of plant height. Plant height of the strains varied from 68 to 80 cm and 67 to 85 cm at Ishurdi and Kishoregonj, respectively. The strain MB-197 was the tallest (80 cm) at Ishurdi and MB-94 was found to be tallest at Kishoregonj. The local cultivar MB-87 was found to be the shortest strain at both the locations. Number of pods per plant varied widely at both the locations. The range of pods per plant was from 12 to 26 at Ishurdi and 8 to 16 at Kishoregonj. The strain MC-246 produced the highest number of pods per plant at both the locations. On the other hand MB-94 and MB-87 produced the lowest number of pods per plant at Ishurdi and V-2773 and MB-87 produced the lowest number of pods per plant at Kishoregonj. The seed size also varied widely at both the places. Seed size of MB-197 was the largest (5.4 g/100 seeds and 5.2 g/100 seeds at Ishurdi and Kishoregonj, respectively). Wide range of variation was also observed among the strains in respect of seed yield at both the locations. Performances of the strains regarding seed yield were better at

Ishurdi than Kishoregonj. Significantly higher seed yield was obtained by the strain MC-246 both at Ishurdi (1655 kg/ha) and Kishoregonj (600 kg/ha).

Variation was observed among the strains in respect of three major diseases in both the locations. The line MC-246 showed resistant and tolerant reaction to MYMV at Ishurdi and Kishoregonj, respectively. The line was tolerant to CLS and PM at both the locations.

Table 4.5. Varietal characters and seed yield data of selected summer mungbean strains in the preliminary yield trial at two locations during 1988.

Strain/ Variety	Days to flower	Days to matu-rity	Plant height (cm)	Number of pods / plant	100-seed wt. (g)	Seed yield (kg/ha)	Disease reaction		
							MY MV	CLS	PM
Location : Ishurdi									
MC-246	32	70	74	26	4.0	1655a	R	T	T
MB-1	32	68	78	14	3.0	729c	T	T	T
MB-8	30	65	76	20	2.8	1232b	T	T	T
MB-94	30	72	77	19	2.8	1136b	T	T	T
MB-197	32	78	80	12	5.4	868bc	T	S	T
V-2773 (Parent)	32	85	72	14	4.2	870bc	S	S	T
MB-87 (Local)	30	70	68	12	2.2	611c	S	S	T
Mubarik (Control)	32	75	79	20	3.3	1253ab	S	S	T
Location : Kishoregonj									
MC-246	33	72	79	16	3.7	606a	T	T	T
MB-1	32	67	75	11	3.0	372bc	S	T	T
MB-8	30	66	76	11	2.5	379bc	S	T	T
MB-94	30	72	85	14	2.7	509ab	T	T	T
MB-197	32	77	80	8	5.2	322c	S	T	T
V-2773 (Parent)	32	83	83	10	4.0	310c	T	S	T
MB-87 (Local)	32	72	67	10	2.1	279b	S	S	T
Mubarik (Control)	32	73	69	14	3.3	541ab	S	S	T

* Figures with same letters in the column (under each location) did not differ significantly at 5% level.

D. Advanced Yield Trial

Seed yield performance of five selected lines and controls and checks calculated from the advanced yield trials at four locations during summer, 1989 are summarized in Table 4.7 and the combined analysis of variance is presented in Table 4.6.

Combined analysis of variance for seed yield showed that all the items viz., Genotype (G), Locations (L) and their interaction (G x L) were highly significant. This suggested that (a) the genotypes differed significantly in their yield performances, (b) locations have significant effect on the genotypes and (c) the genotypes have different performances under different environments (Table 4.6).

Table 4.6. Combined analysis of variance for seed yields of five promising lines of summer mungbean over 5 locations during 1989.

Source of variation	Degrees of freedom	Mean square values	F values
Genotype (G)	4	827249.67**	6429.53
Location (L)	3	1374503.08**	10682.88
G x L	12	72829.83**	566.05
Error	38	128.66	

** Significant at 1% level.

Table 4.7 shows that the line MC-246 produced the highest seed yield at all the four locations and gave an average yield of 1355 kg/ha. Among the 4 locations, the highest seed yield was obtained at Barisal (1823.3 kg/ha) followed by Ishurdi (1616.7 kg/ha). It was also observed that the strain MB-87, a local cultivar that was collected from *Bhola* Island also performed well at Barisal. On the other hand, the lines MB-94, MB-8 and *Mubarik* performed well at Ishurdi. Overall performances of the strains were poor at Kishoregonj.

Table 4.7. Mean seed yield (kg/ha) of five summer mungbean strains in yield trials at 4 locations during 1989.

Strains / Varieties	Locations				Average
	Ishurdi	Kishoregonj	Faridpur	Barisal	
MC-246	1616.7a	740.0a	1240.0a	1823.3a	1355a
MB-94 (V-2272)	1400.0a	693.2a	1191.7a	1180.0b	1116ab
MB-8	983.4bc	463.4b	963.7ab	773.3c	796bc
Mubarik (Control)	958.4bc	341.7b	841.7b	790.0c	733bc
MB-87 (Control)	906.7c	372.5b	872.5b	1160.0b	828b
Mean of locations	1173.0	522.1	1021.9	1145.3	-

Means followed by same letters in columns are not significantly different at 1% level according to DNMRT.

E. Zonal Yield Trial

Seed yield performance of two selected lines compared to a check variety obtained from the zonal yield trials at 5 locations during summer, 1990 are presented in Table 4.9 and combined analysis of variance calculated from these data are given in Table 4.8.

The combined analysis of variance showed that the variances due to Genotypes (G), Locations (L) and Genotype x Location (G x L) interaction for the seed yield were highly significant, which indicated that the genotypes had significant differences between them and the locations had significant effects on the performances of different genotypes (Table 4.8).

The result (Table 4.9) revealed that overall performances of the strains were very poor at Barisal, Faridpur and Mymensingh. This was due to heavy rain and storm at these locations at different stages of crop growth. However, MC-246 produced significantly higher seed yield (1483 kg/ha) than both the controls at Ishurdi. The strain also produced higher seed yield at Mymensingh

(393.0 kg/ha) and Rangpur (850.0 kg/ha) but the seed yield was not significantly different from *Kanti* at both the locations.

Table 4.8. Combined analysis of variance for seed yield of one promising line of summer mungbean along with 2 controls at 5 locations during 1990.

Source of variation	Degrees of freedom	Mean square values	F values
Genotypes (G)	2	200635.467**	
Location (L)	4	1279154.733**	
G x L	8	93282.133**	
Error	42	4255.216**	

** Significant at 1% level.

Table 4.9. Mean seed yield (kg/ha) of MC-246 compared to 2 controls in zonal yield trial at five locations during 1990.

Strains/ Varieties	Locations					Average
	Barisal	Faridpur	Ishurdi	Mymensingh	Rangpur	
MC-246	625.0a	583.5b	1483.0a	393.0a	850.0a	786.9a
MB-87 (Control)	655.0a	562.0b	1081.0b	266.5b	383.0b	589.5c
Kanti (Control)	408.0b	601.5a	1093.0b	374.0a	817.0a	658.7b
Mean of locations	562.7	582.3	1219.0	344.5	683.3	-

Means followed by same letters in columns are not significantly different at 1% level according to DNMRT.

Seed yield performance of two selected lines and a control obtained from zonal yield trial involving 5 locations in 1991 and the analysis of variance calculated from these data are summarized and presented in Table 4.10 and 4.11, respectively.

Table 4.10. Combined analysis of variance for seed yield of one promising line of summer mungbean along with 2 controls at 5 locations during 1991.

Source of variation	Degrees of freedom	Mean square values	F values
Genotype (G)	2	714157.267**	
Location (L)	4	3606047.600**	
G x L	8	230430.350**	
Error	42	4999.397**	

** Significant at 1% level.

Combined analysis of variance for seed yield showed that the genotypes (G) differed significantly and similar result was also found in case of locations (L). Significant mean square value of the item (G x L) revealed that the performances of different genotypes in different locations varied significantly i.e. genotype and location interaction is highly significant (Table 4.10).

Table 4.11. Mean seed yield (Kg/ha) of improved summer mungbean strain MC-246 compared to 2 controls in zonal yield trials at 5 locations during 1991.

Strains/varieties	Locations					Average
	Barisal	Faridpur	Ishurdi	Mymensingh	Rangpur	
MC-246	2001.0a	1019.0a	1993.0a	496.0a	816.0a	1265.0a
MB-87 (Control)	1587.5b	875.0b	1578.0b	441.0b	517.0b	999.7b
Kanti (Control)	1617.5b	655.0c	1063.0c	560.0a	850.5a	949.1b
Mean of locations	1735.3	849.7	1544.7	499.0	727.8	-

Means followed by same letters in columns are not significantly different at 1% level according to DNMRT.

The line MC-246 produced significantly higher seed yield (2001.0 Kg/ha) than both the controls at Barisal. The line also produced higher seed

yield at Ishurdi and Faridpur. While at Mymensingh and Rangpur the variety *Kanti* (Control) produced the highest seed yield, although the seed yield of *Kanti* was not significantly different than that of MC-246 at both the locations. It was also observed that overall performance of the strains was at their best at Barisal (1735.3 Kg/ha) followed by Ishurdi (1544.7 Kg/ha). The lowest seed yield was obtained at the Mymensingh location (499.0 Kg/ha). In both the years (1990 and 1991) performances of the strains at Rangpur were almost similar. In the year 1990 mean seed yield at Rangpur was 683.3 Kg/ha and in 1991 it was 727.8 Kg/ha. In both the years MC-246 produced the highest average seed yield when 5 locations were considered. In 1990, the strain produced seed yield of 786.9 Kg/ha followed by *Kanti* (658.7 Kg/ha) and in the year 1991 this strain produced seed yield of 1265.0 Kg/ha followed by MB-87 (999.5 Kg/ha).

F. On-Farm and On-Station Trial

Seed yield performance of the finally selected line MC-246 compared to a control variety *Kanti* under on-farm and on-station trials are presented in Table 4.12.

In both on-farm and on-station trials the MC-246 produced higher seed yield compared to the control *Kanti* at all the locations (Table 4.12). The strain produced the highest seed yield (1440.0 kg/ha) at the farmers' fields of Ishurdi followed by Faridpur (1225.0 kg/ha). The percentage of seed yield over *Kanti* varied widely among the locations. At Ishurdi the increase was 28% and at Faridpur 19%. In the on-station trials also, the strain MC-246 produced higher seed yield compared to *Kanti* at all the three locations. The highest seed yield was obtained at Ishurdi (1460.0 Kg/a) followed by Faridpur (1015.0 Kg/ha) which was 16% and 8% higher than *Kanti*, respectively. It

was also observed that on an average MC-246 produced 1015 Kg seeds/ha and *Kanti* produced 866.0 Kg seed/ha. The mean percentage of seed yield of MC-246 over *Kanti* was 16%.

Table 4.12. Yield performance of MC-246 and *Kanti* at farmers' field and on-station in different locations during 1992.

Locations	**Variety/ Strain**		**% increased over *Kanti***	**Disease reactions**
	MC-246	***Kanti***		
ON-FARM				
Barisal	1189	1041	14	In all the places MC-246 was tolerant to CLS and MYMV.On the other hand *Kanti* was susceptible to both the diseases.
Faridpur	1225	1030	19	
Ishurdi	1440	1124	28	
Satkhira	1084	933	16	
Rangpur	579	481	20	
Trisal	810	715	13	
Mymensingh	870	705	23	
ON-STATION				
Mymensingh	480	450	6	
Faridpur	1015	944	8	
Ishurdi	1460	1255	16	
Mean	1015	868	16	

The Field Evaluation Team of the National Seed Board visited most of the experiments and they recommended that the strain MC-246 might be released as a national variety for growing in the summer mungbean growing regions. Accordingly, application was submitted to the National Seed Board (NSB). After thorough evaluation, the strain was released by the NSB under the name, BINAMOOG - 2 (Plate - 1).

G. Variation in *Dal*, Seed Coat and Protein (%)

Variation in percentages of *dal*, seed coat and protein of some selected lines were determined in 1990-91 and are summarized in Table 4.13 which shows that *dal* % of MC-246 was 88.90 which was a little lower than the AVRDC line VC-1000 (89.2 %) but slightly higher than MB-87 and *Kanti*. Not much variation was also found in case of protein %. Protein percentage of MC-246 was 24.95.

Table 4.13. Variation of *dal* (%), seed coat (%) and protein content (%) of some mungbean strains/varieties studied during 1990-91.

Strains/ Varieties	*Dal*	Seed coat	Protein
MC-246	88.9	12.10	24.95
MB-1	88.5	11.51	25.47
MB-8	88.9	10.99	24.75
VC-1000	89.2	11.76	22.97
V-2272	88.8	11.22	24.30
VC-1560D	87.9	12.15	23.75
ML-37	87.7	12.35	25.00
MB-87	87.7	12.35	25.20
Kanti	88.0	12.00	24.14
MB-55-4	87.0	13.00	25.78

Plate 1. Field view of BINAMOOG-2

H. Hybridization

Six different crosses were made in reciprocal ways using three mungbean lines namely, MB-55-4, ML-37 and VC-1560D during the winter of 1985. The results of crossings are summarized in the Table 4.14.

Table 4.14 shows that pod set was the highest (57%) in Cross-3 (MB-55-4 x VC- 1560D) when MB-55-4 was used as the female parent and the pod set was the lowest (39%) in Cross-2 (ML-37 x MB-55-4) when ML-37 was used as the female parent. The highest number of seeds/pod (4 seeds) was obtained in Cross-4 (VC-1560D x MB-55-4) when the strain VC-1560D was used as the female parent and the lowest in Cross-5 (ML-37 x VC-1560D) when ML-37 was used as the female parent.

Table 4.14. Number of flowers pollinated, number of pods set, % of success in crossing, number of mature pods harvested, total seeds obtained and average seeds/pod.

Cross combinations	Number of flowers pollinated	Number of pods set	Percent of success in crossing	Number of mature pods harvested	Total seeds obtained	Average seeds/ pod
1. MB-55-4 x ML-37	175	75	43	70	208	3
2. ML-37 x MB-55-4	166	65	39	58	165	3
3. MB-55-4 x VC-1560D	200	114	57	103	318	3
4. VC-1560D x MB-55-4	195	84	43	72	288	4
5. ML-37 x VC-1560D	172	70	40	69	140	2
6. VC-1560D x ML-37	137	56	41	50	141	3

a. Study of F_1 population

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability

and genetic advance (%) for days to flowering in the F_1 generation of 6 crosses are presented in Table 4.15.

Table 4.15. Mean, range, components of variation, heritability and genetic advance (%) for days to flowering in the F_1 generation of six crosses compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	34.0	32-36	0.91	2.10	1.49	50.9	2.20
ML-37	34.6	34-36	0.66	1.66	1.11	45.0	1.53
VC-1560D	35.2	32-36	0.63	2.14	1.09	26.1	1.15
Cross-1	34.1	31-36	1.30	3.06	2.77	82.0	5.17
Cross-2	33.4	30-37	1.70	6.24	5.03	64.9	6.96
Cross-3	35.2	32-38	1.88	2.80	2.57	83.8	4.84
Cross-4	35.6	31-38	1.54	3.16	2.48	61.7	4.02
Cross-5	35.2	32-37	1.44	2.51	2.07	68.2	3.53
Cross-6	35.0	31-37	1.63	3.10	2.63	72.0	4.60

The result showed that the mean values of all the crosses, except Cross-2 (ML-37 x MB-55-4) with a slight lower mean and Cross-4 (VC-1560D x MB-55-4) with higher mean than the parents, were more or less similar to those of the parents. Greater ranges were observed in days to flowering for all the six crosses than their parental lines. It ranged from 32.0 in MB-55-4 to 36.9 in VC-1560D, and 30.2 in Cross-2 to 38.1 in Cross-3. Coefficient of variation (%) was also greater in the crosses than in the parental lines. It ranged from 1.30 in Cross-1 to 1.89 in Cross-3 and 0.63 in the parent VC-1560D to 0.91 in the parent MB-55-4.

As regards phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), these calculated values were also found to be

higher in the crosses than the parental lines. Similarly, heritability estimates and genetic advances were higher in the crosses than the parental lines.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for days to maturity are presented in Table 4.16.

Table 4.16. Mean, range, components of variation, heritability and genetic advance (%) for days to maturity in the F_1 generation of six crosses compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	73.3	72-76	1.35	1.01	0.58	32.7	0.70
ML-37	75.3	72-77	1.42	1.02	0.61	35.6	0.75
VC-1560D	80.4	79-88	1.03	1.19	0.63	28.0	0.69
Cross-1	73.4	69-78	2.07	1.50	1.24	69.2	2.12
Cross-2	75.4	70-79	2.56	2.17	1.82	70.5	4.15
Cross-3	78.1	71-81	2.33	1.95	1.77	82.1	3.30
Cross-4	79.5	72-80	2.74	1.33	1.86	78.2	2.14
Cross-5	80.7	79-83	2.76	1.42	1.24	76.2	2.23
Cross-6	80.0	77-81	2.21	1.13	0.97	73.5	1.72

The result showed variation in the means of all the parents and crosses. Higher mean value was found in Cross-5 followed by VC-1560D and Cross-6. Moreover, wider ranges of means in days to maturity were observed in almost all crosses than the parental lines. It ranged from 72.0 in MB-55-4 to 88.1 in VC-1560D, on the other hand, 69.0 in Cross-1 to 83.1 in Cross-5. Coefficient of variability (%) was also found to be greater in these crosses

than the parental lines. It ranged from 2.03 in Cross-6 to 2.83 in Cross-2 while the parental values ranged from 1.03 in VC-1560D to 1.70 in MB-55-4.

Phenotypic- (PCV) and genotypic coefficient of variation (GCV) were higher in the crosses than the parental lines. Similarly, heritability estimates and genetic advances were also higher in these crosses than the parental lines.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for plant height are presented in Table 4.17.

Table 4.17. Mean, range, components of variation, heritability and genetic advance (%) for plant height in the F_1 generation of six crosses compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	31.7	30.0-34.2	1.26	3.07	1.82	34.9	2.21
ML-37	38.6	36.2-41.3	1.24	3.11	1.92	38.2	2.44
VC-1560D	41.3	39.8-41.7	0.95	1.93	1.18	37.7	1.49
Cross-1	33.2	30.1-36.3	2.18	4.75	3.52	55.1	5.39
Cross-2	35.1	30.5-38.8	2.50	3.48	2.37	46.3	3.33
Cross-3	36.1	35.3-39.4	2.73	1.99	1.72	75.0	3.08
Cross-4	38.5	35.2-41.0	1.98	2.28	2.01	77.8	3.65
Cross-5	40.7	34.9-42.2	1.76	1.83	1.68	83.6	3.16
Cross-6	40.9	33.2-42.6	1.71	1.90	1.67	76.8	3.02

Mean plant height of the parents, MB-55-4, ML-37 and VC-1560D were 31.7, 38.6 and 41.3 cm, respectively. The plant height in the crosses ranged from 33.2 cm in Cross-1 to 40.9 cm in Cross-6; and the mean heights of F_1 families were found to be greater in the crosses than their parents. Coefficient of variability was found to be comparatively high in the F_1s of all

the crosses. All the crosses also showed high estimates of PCV, GCV, heritability and genetic advance.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for number of pods/plant in F_1 generation of six crosses are summarized in Table 4.18.

Table 4.18. Mean, range, components of variation, heritability and genetic advance (%) for number of pods/plant in the F_1 generation of six crosses compared to the parental lines .

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	17.4	16-19	3.78	5.30	3.72	49.2	5.37
ML-37	12.1	11-13	4.15	4.47	3.09	48.1	4.42
VC-1560D	5.2	4-7	3.42	7.19	4.30	35.7	5.29
Cross-1	19.2	12-24	6.77	12.41	10.42	70.5	18.02
Cross-2	14.5	9-18	8.14	15.8	13.48	72.8	23.69
Cross-3	18.0	10-22	9.23	13.03	11.38	76.4	20.50
Cross-4	9.7	6-13	6.70	17.20	14.40	70.3	24.88
Cross-5	9.1	7-18	6.59	12.88	11.04	73.5	19.51
Cross-6	5.9	3-14	7.12	22.80	18.94	69.0	32.41

The result showed that the mean number of pods/plant were 17.4 and 12.1 in MB-55-4 and ML-37, respectively while VC-1560D had only 5.2 pods/plant. Cross-1 and Cross-3, involving MB-55-4 as mother, and Cross-2, involving ML-37 as mother, gave higher number of pods/plant (14.5 - 19.2 pods) than the parents. Cross-4, Cross-5 and Cross-6, involving ML-37 and VC-1560D as mother, gave lower number of pods/plant (5.9 - 9.7). The ranges of mean varied greatly in the crosses compared to those of the parents.

Coefficient of variability ranged from 6.59 in Cross-5 to 9.23 in Cross-3 while in the parents it ranged from 3.42 in VC-1560D to 4.15 in ML-37. PCV and GCV were also higher in the crosses than the parents. Heritability and genetic advance (%), in turn, also exhibited higher values over the parents.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for number of seeds/plant in the F_1s of six crosses are presented in Table 4.19.

Table 4.19. Mean, range, components of variation, heritability and genetic advance (%) for number of seeds/plant in the F_1 generation of six crosses compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	154.1	150-160	2.49	2.05	1.36	44.3	1.87
ML-37	93.5	86-97	2.87	3.23	2.25	48.7	3.23
VC-1560D	54.5	46-68	2.23	3.57	1.79	25.3	1.85
Cross-1	164.1	125-195	4.42	5.25	4.55	74.9	8.12
Cross-2	122.0	99-165	4.72	6.27	5.32	72.1	9.32
Cross-3	175.7	140-209	5.29	5.81	4.85	69.5	8.33
Cross-4	95.3	61-126	5.12	7.29	5.89	65.2	9.82
Cross-5	96.8	78-83	3.61	6.57	5.39	67.2	9.10
Cross-6	69.8	67-98	4.02	6.15	4.86	62.4	7.92

The result showed that the parents, MB-55-4, ML-37 and VC-1560D had 154.1, 93.5 and 54.5 seeds/plant, respectively. Cross-3 produced the highest number of seeds/plant (175.7). Cross-1 and Cross-2 gave 164.1 and 122.0 seeds/plant, respectively. Whereas Cross-4, Cross-5 and Cross-6 produced 95.3, 96.8 and 69.8 seeds/plant, respectively. The ranges of

population means varied greatly in the crosses compared to their parents. Variations were greater in Cross-1 and Cross-3 than the remaining four crosses. Coefficient of variability (%) was observed to be higher (almost double) in the F_1 populations than the parents. Similarly, higher estimates of PCV, GCV, heritability and genetic advance were also found in these crosses than the parents.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for 100-seed weight in F_1s of six crosses are presented in Table 4.20.

The weight of 100-seed in VC-1560D (parent) was found to be the highest, i.e., 6.49 (g) while that in MB-55-4 and ML-37 was 2.74 and 4.09 (g), respectively. Only Cross-4 and Cross-6 showed considerably higher 100-seed weight, i.e., 5.94 and 6.05 (g), respectively than that found in the remaining crosses. The population mean was greater in Cross-3, Cross-4 and Cross-6 than that recorded in other crosses and parents. Coefficient of variability was higher in the crosses than that observed in their parents. High PCV and GCV estimates were recorded in the crosses, which resulted in appreciably high heritability estimates and genetic advances over the parents.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for seed yield/plant in F_1s of six crosses are presented in Table 4.21.

Table 4.20. Mean, range, components of variation, heritability and genetic advance (%) for 100-seed weight in the F_1 generation of 6 crosses compared to the parental lines.

Parent/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	2.74	2.50-2.90	1.09	4.16	1.99	23.1	1.98
ML-37	3.95	3.81-4.32	1.22	4.77	2.44	26.3	2.58
VC-1560D	6.40	6.20-6.55	0.92	1.54	0.69	20.0	0.63
Cross-1	2.97	2.70-3.51	3.70	7.18	5.93	68.0	10.24
Cross-2	4.03	3.51-4.50	3.97	5.02	5.02	70.7	8.71
Cross-3	3.12	2.48-6.29	3.85	6.95	6.12	78.7	11.27
Cross-4	5.94	3.70-6.05	3.36	4.08	3.40	69.5	5.84
Cross-5	4.06	3.73-4.38	3.69	3.56	2.80	61.9	4.55
Cross-6	6.05	3.78-6.25	2.80	1.95	1.65	71.4	2.87

While all the progeny of crosses gave higher seed yield, their parents MB-55-4, ML-37 and VC-1560D produced lower seed yield of 3.54, 3.41 and 3.32 g/plant, respectively. Cross-3 and Cross-4 produced 5.24g and 5.43 g/plant, respectively. Other crosses except Cross-5 produced more than 4.0 g/plant. Coefficient of variability (%) in the crosses was considerably higher than parents. Genotypic coefficient of variation in the crosses ranged from 11.41 in Cross-6 to 16.60 in Cross-4 while in the parents, MB-55-4, ML-37 and VC-1560D the estimates were 2.68, 2.81 and 11.23, respectively. Heritability estimates and genetic advances were also found to be higher in the crosses than their parents.

Table 4.21. Mean, range, components of variation, heritability and genetic advance (%) for seed yield/plant in the F_1 generation of 6 crosses compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	3.54	3.20-3.83	1.41	4.25	2.68	40.9	3.53
ML-37	3.41	3.22-3.71	1.76	3.93	2.81	51.1	4.13
VC-1560D	3.32	2.68-4.32	1.55	21.06	11.23	28.5	12.35
Cross-1	4.21	3.01-5.62	5.98	16.16	14.05	75.6	25.17
Cross-2	4.44	3.22-5.81	5.17	14.64	13.26	82.2	24.78
Cross-3	5.24	2.74-6.58	7.47	14.77	13.13	79.1	24.08
Cross-4	5.43	3.20-7.18	4.22	19.29	16.60	74.1	29.43
Cross-5	3.72	2.71-4.69	4.61	16.51	13.53	67.1	22.83
Cross-6	4.07	2.66-6.21	3.68	12.18	11.41	87.8	22.03

b. Study of F_2 generation in winter

Among the six crosses, 20 plants were selected from Cross 1 (MB-55-4 x ML-37), 7 from Cross 2 (ML-37 x MB-55-4) 134 from Cross 3 (MB-55-4 x VC-1560D) and 5 from Cross 4 (VC-1560D x MB-55-4). F_2 plants of Cross-5 (ML-37 x VC-1560D) and Cross-6 (VC-1560D x ML-37) were susceptible to diseases and no plant was selected from the progeny of the above two crosses (Table 3.3).

The mean, range, coefficient of variability (CV%), components of variation i.e. phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for the seven characters and seed yield in the F_2 generation are summarized in Tables 4.22 to 4.28 and the results are discussed below.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for days to flowering in F_2 are presented in Table 4.22.

Mean days to flowering were 34.2 for MB-55-4, 36.3 for ML-37 and 35.2 for VC-1560D. Variation was smaller among the four crosses compared to the F_1 generation, which ranged from 34.1 in Cross-1 to 36.2 in Cross-3. Population means were found to be smaller in the parents than the crosses. Coefficients of variation were higher in the crosses (1.19 - 1.67) than in the parents (0.53-0.77) in this generation. Phenotypic and genotypic coefficients of variation were also higher in the crosses than in their parents. Similar results were also found in respect of heritability and genetic advance.

Table 4.22. Mean, range, components of variation, heritability and genetic advance (%) for days to flowering in the F_2 generation of four crosses compared to the parental lines .

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	34.2	33.8-35.5	0.53	3.04	2.17	51.1	3.20
ML-37	36.3	35.0-36.8	0.77	2.40	1.76	53.8	2.66
VC-1560D	35.2	34.4-36.0	0.65	2.30	1.71	55.1	2.61
Cross-1	34.1	32.2-37.0	1.67	3.09	2.72	78.0	4.96
Cross-2	34.5	32.7-36.4	1.45	3.43	4.14	83.7	5.92
Cross-3	36.2	31.8-37.4	1.19	3.32	3.06	85.4	5.83
Cross-4	35.3	34.2-37.1	1.27	3.54	3.21	82.3	6.00

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability

and genetic advance (%) for days to maturity in F_2 are presented in Table 4.23.

Mean of parents, MB-55-4, ML-37 and VC-1560D were 75.1, 78.5 and 80.6, respectively for days to maturity. While those in the crosses were 78.9 (Cross-1), 84.5 (Cross-2), 81.2 (Cross-3) and 83.5 (Cross-4). Range of variation in population means was greater in the crosses than in the parents. Coefficients of variability were very high in the crosses compared to the parents. Components of variation (PCV and GCV) were comparatively high in the crosses, which showed high heritability and genetic advance.

Table 4.23. Mean, range, components of variation, heritability and genetic advance (%) for days to maturity in the F_2 generation of four crosses compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	75.1	73.0-77.0	1.06	1.37	0.97	53.9	1.47
ML-37	78.5	78.2-79.1	0.89	1.32	0.95	52.0	1.42
VC-1560D	80.6	80.2-80.9	0.94	1.14	0.80	49.1	1.16
Cross-1	78.9	75.3-81.2	2.45	2.00	1.86	86.5	3.56
Cross-2	84.5	76.3-87.1	2.44	1.81	1.67	84.3	4.15
Cross-3	81.2	79.7-83.0	2.60	2.10	1.79	83.26	3.61
Cross-4	83.5	78.6-85.2	2.57	1.96	1.80	84.3	3.40

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for plant height in F_2 are presented in Table 4.24.

The result showed that plant height of MB-55-4, ML-37 and VC-1560D was 28.0, 39.8 and 41.6 cm, respectively. In the crosses, the highest plant height was recorded in Cross-2 (41.1 cm) and the lowest in Cross-1

(30.5 cm). Plant height in Cross-3 and Cross-4 was 32.7 and 33.9 cm, respectively. Ranges of plant height means were almost similar in the parents and the crosses. However, CV (%) was higher in the crosses than the parents. GCV in the crosses was found to be nearer to PCV which resulted in high heritability and genetic advance. GCV ranged from 1.14 to 2.18 in parents and 4.14 to 4.49 in the crosses. All the crosses had high heritability values (78.5 - 82.4) while the parents had comparatively lower values (36.3 - 44.2). Genetic advance ranged from 5.74 to 8.20 in the crosses while the values ranged from 2.35 to 2.77 in the parents.

Table 4.24. Mean, range, components of variation, heritability and genetic advance (%) for plant height of four crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	28.0	27.0-28.8	0.71	3.61	2.18	36.3	2.77
ML-37	39.8	36.8-41.2	0.63	2.66	1.14	42.9	2.35
VC-1560D	41.6	40.0-43.8	0.75	2.92	1.94	44.2	2.66
Cross-1	30.5	28.4-32.4	3.44	5.07	4.49	78.5	8.20
Cross-2	41.1	37.7-42.8	1.97	3.53	4.14	79.0	5.74
Cross-3	32.7	29.6-35.1	2.91	4.30	3.90	82.4	7.30
Cross-4	33.9	28.8-36.7	2.92	4.88	4.38	80.7	8.11

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for number of pods/plant in F_2 are presented in Table 4.25.

Table 4.25. Mean, range, components of variation, heritability and genetic advance (%) for number of pods/plant of four crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	14.9	11.6-18.0	3.29	6.58	4.20	40.7	5.53
ML-37	11.4	7.3-14.4	3.95	8.83	5.79	42.9	7.81
VC-1560D	6.0	4.2-8.0	3.67	5.84	5.78	58.8	6.11
Cross-1	20.8	14.0-24.3	5.29	10.56	10.29	95.0	20.65
Cross-2	34.5	20.7-39.0	5.50	13.31	10.20	88.1	16.10
Cross-3	12.9	8.2-17.3	6.32	12.97	11.66	80.8	21.60
Cross-4	13.6	8.9-19.4	5.87	13.09	11.97	83.6	22.54

Mean number of pods/plant of three parents, MB-55-4, ML-37 and VC-1560D were 14.9, 11.4 and 4.0, respectively. Cross-1 and Cross-2 produced 20.8 and 34.5 pods/plant, respectively while Cross-3 produced 12.9 pods/plant and Cross-4 gave 13.6 pods/plant. Ranges of mean were wider in all the crosses than the parents. Higher coefficient of variability (5.29 - 6.32) was observed in the crosses while in the parents it ranged from 3.29 to 3.95. Components of variation (PCV and GCV) and genetic parameters (heritability and genetic advance) were also higher in the crosses than the parents. Genotypic coefficient of variation in the crosses ranged from 11.97 in Cross-4 to 10.20 in Cross-2 while the parental values ranged from 4.20 in MB-55-4 to 5.79 in ML-37. The highest heritability was found in Cross-1 (95%) followed by Cross-2 (88.1%) while the parents showed 40.7% in MB-55-4, 42.9% in ML-37 and 58.8% in VC-1560D. Cross-4 had the highest genetic advance (22.54) followed by Cross-3 (21.60) and Cross-1 (20.65) while the values in parents were 5.53 in MB-55-4, 7.81 in ML-37 and 6.11 in VC-1560D.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for number of seeds/plant in F_2 generation are presented in Table 4.26.

Table 4.26. Mean, range, components of variation, heritability and genetic advance (%) for number of seeds/plant of four crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	144.8	126.0-180.0	5.39	1.13	0.77	46.20	1.07
ML-37	110.4	95.0-116.4	5.86	1.54	1.05	46.40	1.47
VC-1560D	57.3	38.5-62.1	5.99	1.90	1.25	43.97	1.72
Cross-1	188.1	151.5-210.3	13.41	2.15	2.03	81.70	3.92
Cross-2	347.5	324.6-361.4	11.59	2.09	2.97	81.22	3.82
Cross-3	138.8	116.7-152.3	14.72	2.90	2.72	81.91	5.21
Cross-4	158.7	133.4-171.8	13.33	2.21	2.15	90.40	4.25

All the crosses produced appreciably greater number of seeds/plant. Cross-2 produced the highest number of seeds/plant (347.5) followed by Cross-1 (188.1 seeds). Cross-3 and cross-4 gave 138.8 and 158.7 seeds/plant, respectively. The parents, MB-55-4, ML-37 and VC-1560D produced 144.8, 110.4 and 57.3 seeds/plant, respectively. Ranges of mean values were also wider in the crosses than the parents. Coefficient of variation(%) was also greater in the crosses, ranging from 11.59 to 14.72. The coefficients of variation and the genetic parameters (heritability and genetic advance) were also higher in the crosses compared to the parents.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability

and genetic advance (%) for 100-seed weight in F_2 are presented in Table 4.27.

Table 4.27. Mean, range, components of variation, heritability and genetic advance (%) for 100-seed weight (g) of four crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	2.81	2.60-2.90	0.71	3.56	1.59	20.0	1.47
ML-37	3.91	3.70-4.23	0.77	2.43	1.81	55.6	2.78
VC-1560D	6.73	6.62-6.94	0.45	2.05	1.24	36.8	1.55
Cross-1	2.73	2.44-3.00	2.93	9.62	8.59	79.7	15.80
Cross-2	2.60	2.31-2.85	2.31	6.08	5.30	76.0	9.52
Cross-3	4.14	3.80-4.28	1.45	4.39	3.82	75.8	6.85
Cross-4	4.49	3.93-5.75	1.56	5.50	4.56	68.9	7.80

Mean 100-seed weight in Cross-1 and Cross-2 was lower, 2.73g and 2.60g, respectively than the parents. In MB-55-4 and ML-37 100-seed weight was 2.81g and 3.91g, respectively. Cross-3 and Cross-4 gave moderate seed weight of 4.14g and 4.49g. Mean 100-seed weight of VC-1560D was 6.73g, which was recorded to be the highest of all. Variation in ranges of means was more or less similar in parents and crosses. However, CV (%) values in crosses were higher (1.45 - 2.93) than the parents (0.45 - 0.77). Genotypic coefficient of variations ranged from 3.82 (Cross-3) to 8.59 (Cross-1) while in the parents it ranged from 1.24 (VC-1560D) to 1.81 (ML-37). Heritability estimates were also higher in the crosses (68.9 - 79.7%) than the parents (20.0 - 36.8%). The highest genetic advance was found in Cross-1 (15.80) followed by Cross-2 (9.52) while all the parents produced lower genetic advance (1.47 - 2.72).

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for seed yield/plant in F_2 are presented in Table 4.28.

The result showed that cross-2 produced the highest mean seed yield/plant (8.75g) followed by cross-4 (6.53g). The other two crosses, cross-1 and cross-3, produced 4.95 and 5.45g seed yield/plant, respectively.

Table 4.28. Mean, range, components of variation, heritability and genetic advance (%) for seed yield/plant (g) of four crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
MB-55-4	3.93	2.91-5.03	6.62	18.54	13.77	55.2	21.08
ML-37	4.08	3.87-4.20	4.41	17.14	12.43	52.6	18.56
VC-1560D	3.55	3.41-3.69	5.07	16.95	11.72	47.8	16.69
Cross-1	4.95	4.50-9.22	16.16	19.60	17.35	78.4	31.66
Cross-2	8.75	6.80-10.30	10.85	13.73	12.88	88.0	24.89
Cross-3	5.45	4.35-6.15	7.52	22.52	21.01	87.0	40.37
Cross-4	6.53	4.78-8.07	15.77	19.74	18.18	84.8	34.49

c. Study of F_3 generation in winter

The analysis of variance (mean squares) and the mean performances of the selected F_3 families and parents for seed yield and six other characters are presented in Tables 4.29 and 4.30. Mean, range, coefficient of variability of the traits over F_3 families and parents separately are also summarized and presented in Table 4.31. The result (Table 4.29) showed significant differences among the entries (families and parents) for all the characters. Coefficients of variation (%) were found to be lower in parents compared to the crosses for all the characters (Table 4.31).

Tables 4.30 and 4.31 show that the mean time of first flowering from the date of seeding was 33 days with a range from 31 to 36 days. Among these, 9 families flowered in 31 days, 12 in 32 days, 19 in 33 days, 7 in 34 days, 9 in 35 days and 4 in 36 days (Fig. 4.8). On the other hand, the mean time of flowering for the parents was 32 days with a narrow range from 31 to 33 days (Table 4.30). The data on days to flower and seed yield/plant was plotted on a graph. The characters showed a normal distribution (Fig. 4.8). A truncation point for days to flower was drawn on 34 days and for seed yield it was drawn on 9.0 (g). Eight families (MC-14, MC-37, MC-38, MC-58, MC-65, MC-98, MC-107 and MC-149) were selected on the basis of these two characters.

The mean days to pod maturity for all the families were 80 days with a range from 70 to 96 days (Table 4.30 and 4.31). Among these, only one family (MC-180) matured early, i.e., in 70 days from sowing, 26 matured within 71-75 days, 22 within 76-85 days, 10 within 86-95 days and only one in 96 days (Fig. 4.9). The parents, on the other hand, matured within a shorter range of period (75-81 days) with a mean of 77 days. The data on days to mature and seed yield was plotted on a graph. Truncation point for days to mature was set on 85 days keeping the seed yield/plant at 9.0 (g) (Fig. 4.9). On the basis of these two characters 9 families (MC-14, MC-37, MC-38, MC-65, MC-95, MC-98, MC-99, MC-107 and MC-149) were selected.

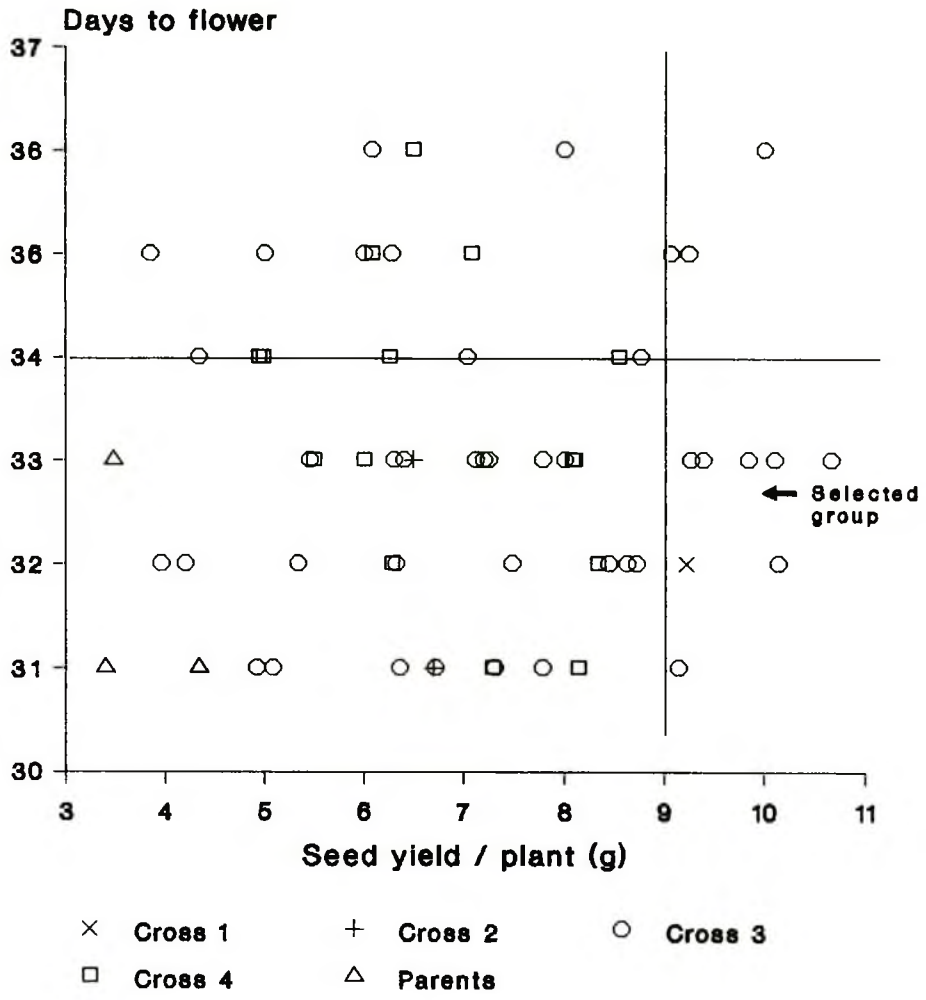

Fig. 4.8 Distribution of parents and F_3 families (winter) of the progeny of four cross combinations for days to flower and seed yield.

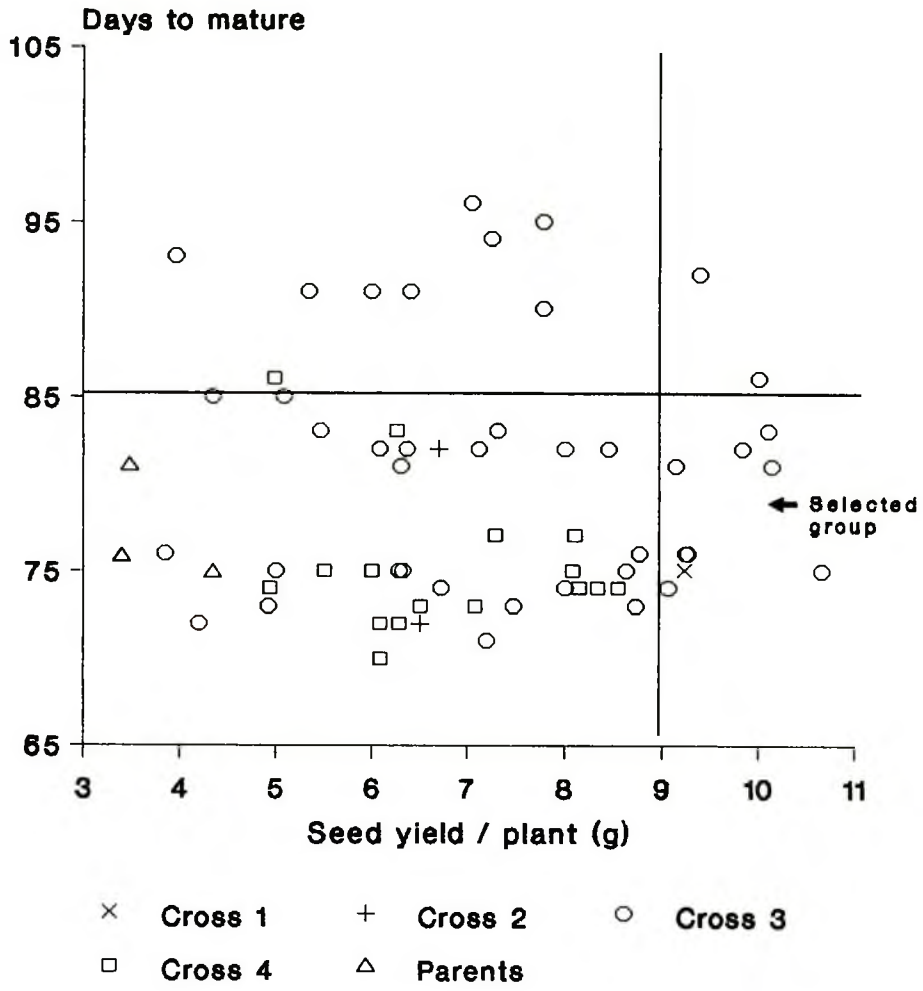

Fig. 4.9 Distribution of parents and F_3 families (winter) of the progeny of four cross combinations for days to mature and seed yield.

Table 4.29. Analysis of variance (mean square values) of the selected families along with their parents for different varietal characters.

Source of variation	DF	Days to flowering	Days to maturity	Plant height (cm)	Pods/ plant (No.)	Seeds/ plant (No.)	100-seed weight (g)	Seed yield/ plant(g)
Genotypes	62	7.01**	141.63**	238.64**	130.49**	11959.80**	3.90*	19.15*
Error	124	0.47	0.57	2.11	2.63	152.35	0.01	0.63

*, **Significant at 5 and 1% level of probability.

The plant height of 60 families varied from 20.1 to 55.1 cm with a mean of 36.8 cm (Tables 4.30 and 4.31). Among these, the plant height of 10 families was within 20.1-30 cm, 31 within 31.1-40 cm, 18 within 40.1-50 and 1 was 55.1 cm. The plant height of parents ranged from 30 to 41 cm with a mean of 36 cm (Table 4.30). The family MC-163 was the tallest (55.1 cm) among the selected families while the family MC-180 was the shortest (20.1 cm) (Table 4.30). The data on plant height and seed yield were plotted on a graph to select families for further trial. The truncation point for plant height was drawn on 40 cm keeping the seed yield /plant at 9.0 (g) (Fig. 4.10). Nine families were selected on the basis of these two characters. The families were MC-14, MC-37, MC-38, MC-58, MC-60, MC-65, MC-99, MC-107 and MC-149.

The number of pods/plant of 60 families varied from 10 to 25 pods with an average of 17 pods (Table 4.30, 4.31 and Fig. 4.11). Among the 60 families, 25 produced 10-15 pods, 25 produced 16-20, and 10 produced 21-25. Lower number of pods/plant was observed among the parents with a mean of 10 pods/plant. Among the families the highest number of pods was produced by the family MC-94 (25 pods/plant) while the lowest number of

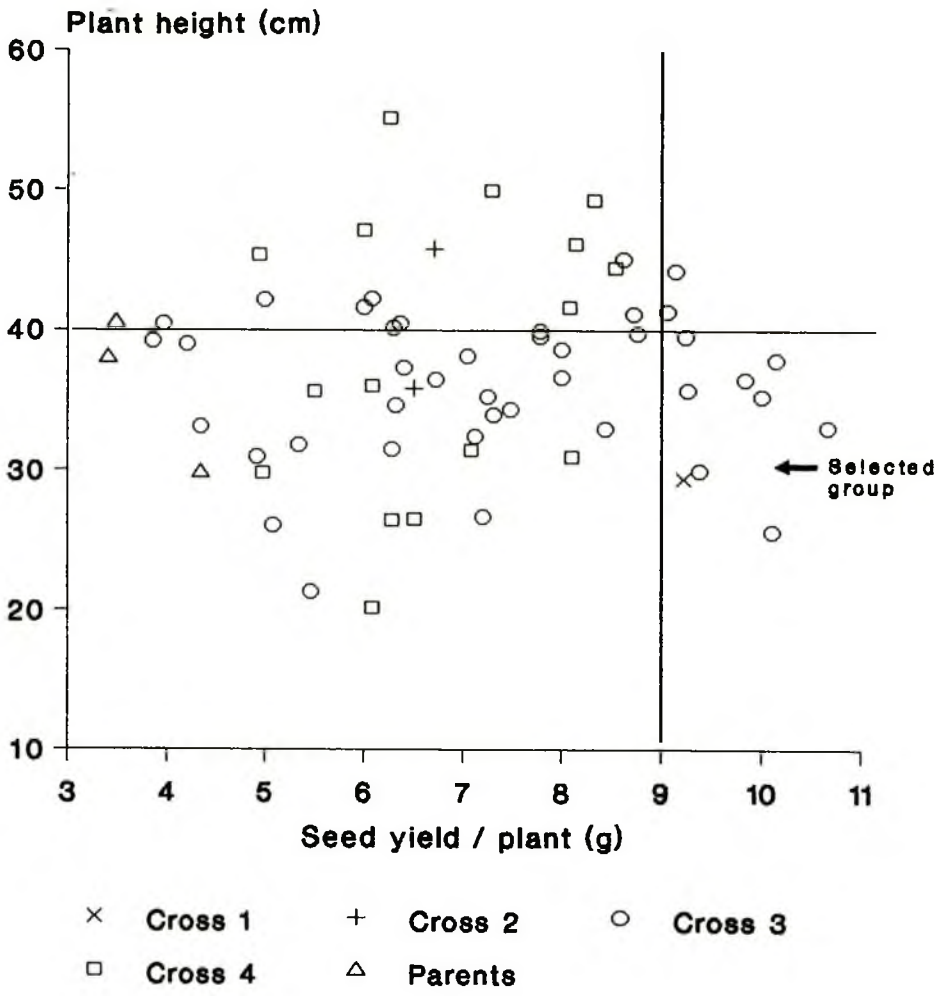

Fig. 4.10. Distribution of parents and F_3 families (winter) of the progeny of four cross combinations for plant height and seed yield.

pods (10 pods/plant) was produced by the family MC-140. When the data on pods/plant was plotted along with seed yield/plant on a graph it showed a normal distribution (Fig. 4.11). Truncation point for pods/plant was drawn on 20 pods and for seed yield/plant on 9.0 (g). On the basis of these two characters 10 families were selected. The families were MC-14, MC-37, MC-38, MC-60, MC-65, MC-95, MC-98, MC-99, MC-107 and MC-149.

Among the 60 families, number of seeds/plant ranged from 110 to 265 with a mean of 167. Among these, 23 produced 100-150 seeds, 17 produced 151-200 seeds, 19 produced 201-250 seeds and only one family produced more than 251 (265) seeds/plant (Tables 4.30, 4.31 and Fig. 4.12). On the other hand, the parents produced the lowest number of seeds/plant (55-150) with a mean of 100 seeds/plant. Among the families, the highest seeds/plant was produced by the family MC-14 (265 seed/plant) and the lowest by the family MC-180 (110 seeds/plant). The data on seeds/plant and seed yield/plant were plotted on graph and for selection of families truncation point for seeds/plant was drawn on 200 seeds/plant and seed yield/plant on 9.0 (g) (Fig. 4.12). Ten families were selected on the basis of these two characters. The families were MC-14, MC-30, MC-37, MC-38, MC-60, MC-95, MC-98, MC-99, MC-107 and MC-149.

The seed size (100-seed weight) varied widely in selected families. The seed weight ranged from 3.0 to 6.0 (g) with a mean of 4.44 (g) (Tables 4.30, 4.31 and Fig. 4.13). Among these 100-seed weight of 14 families were between 3.0-4.0 (g), 25 between 4.1-5.0 (g) and 20 families between 5.1-6.0 (g). Among the selected families, 100-seed weight of the family MC-201 was the highest (6.0 g) while it was the lowest in family MC-41 (3.00 g). The parent VC-1560D had the highest seed weight (6.38 g) and none of the families was found to exceed this seed weight (Table 4.30). Data on 100-seed

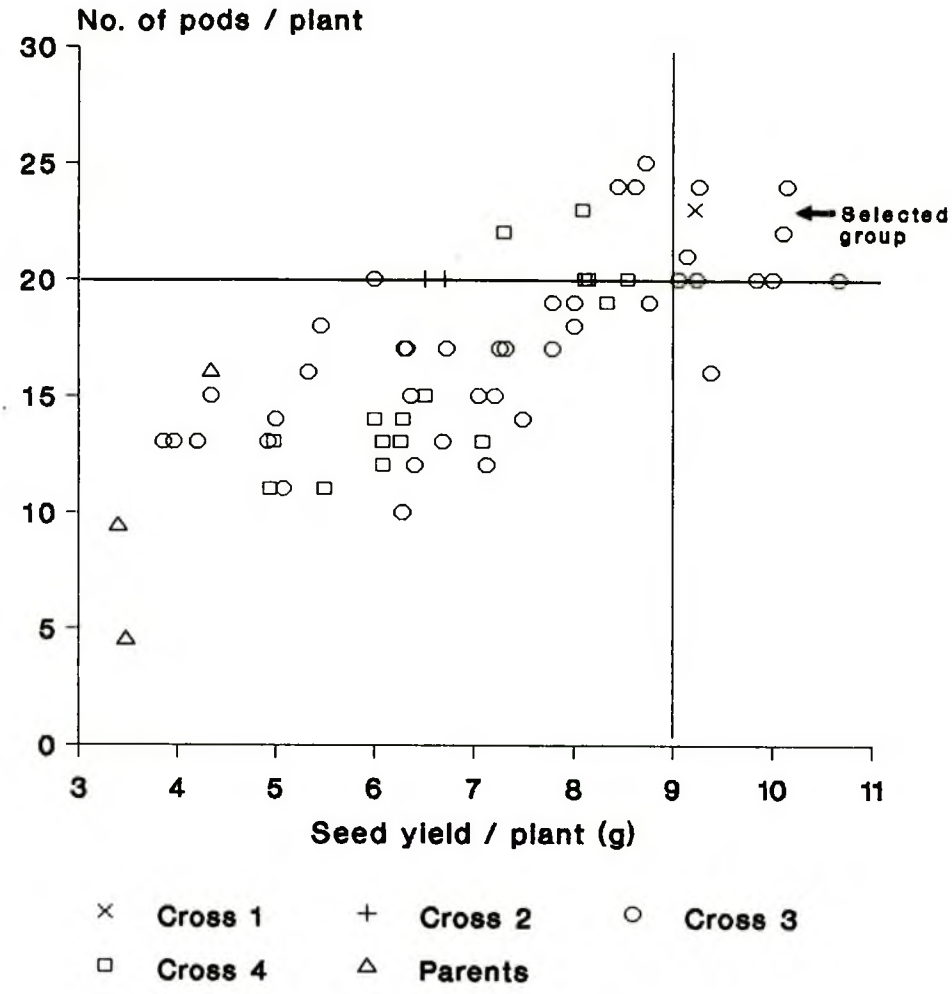

Fig. 4.11. Distribution of parents and F_3 families (winter) of the progeny of four cross combinations for number of pods/plant and seed yield.

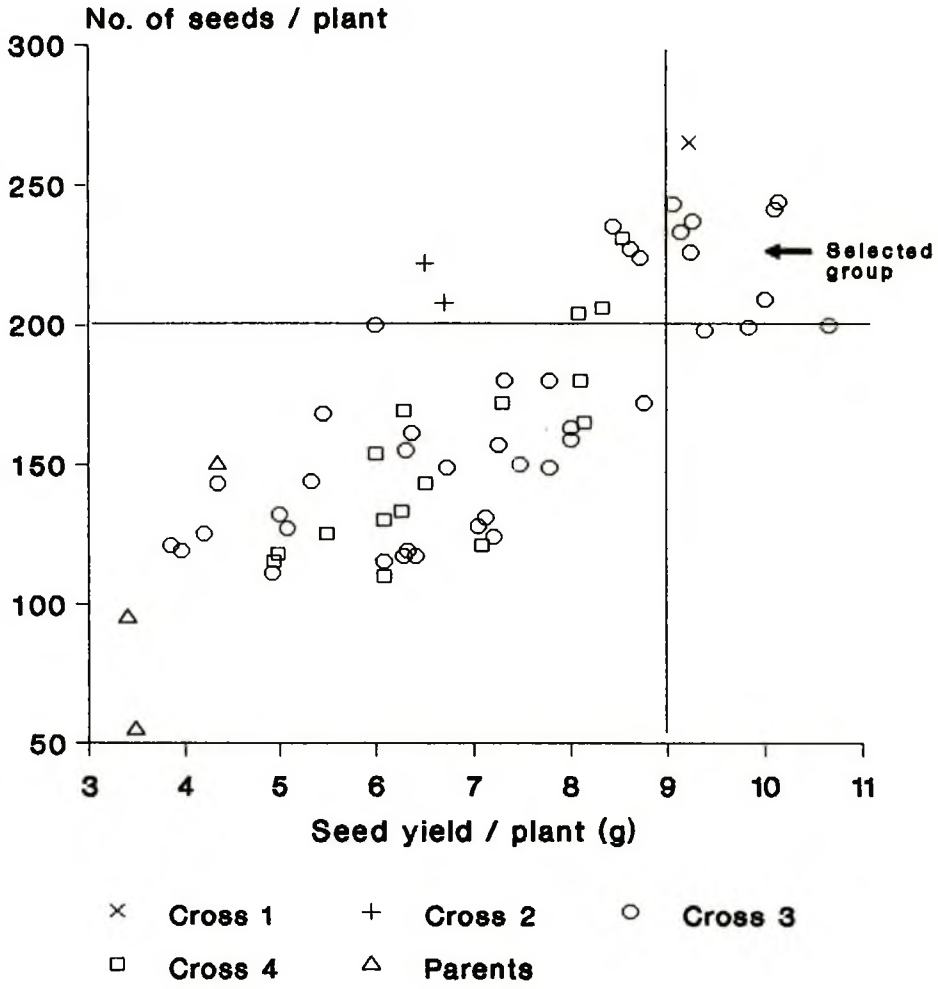

Fig. 4.12. Distribution of parents and F_3 families (winter) of the progeny of four cross combinations for number of seeds/plant and seed yield.

weight and seed yield/plant were plotted on a graph and a truncation point for 100-seed weight was set on 4.0 (g). Truncation point for seed yield was 9.0 (g) (Fig. 4.13). Ten families were selected on the basis of these two characters. The families were MC-37, MC-38, MC-58, MC-60, MC-65, MC-95, MC-98, MC-99, MC-107 and MC-149.

For seed yield/plant the genotypes showed a wide range of variability. It ranged from 3.85 to 10.66 (g) with a mean of 7.16 (Table 4.30). Among these, 5 families were between 3.1-5.0 (g), 22 between 5.1-7.0 (g), 22 between 7.1-9.0 (g) and 11 between 9.1-11.0 (g). Seed yield of the parents was very low. The range was from 3.40 to 4.34 (g) with a mean of 3.74.

For scoring three diseases namely, MYMV, CLS and PM the families were classified into three groups : resistant, tolerant and susceptible. Among the 60 families, 19 were resistant, 25 tolerant and 16 susceptible to MYMV (Table 4.30). Among the 3 parents, only one (MB-55-4) was resistant and other two were susceptible to MYMV. Results of CLS showed that out of 60 families, 11 were resistant, 27 were tolerant and 22 were susceptible to this disease (Table 4.30). On the other hand, all the three parents were tolerant to CLS. Reactions to PM indicate that 34 families were resistant and 26 were tolerant to this disease (Table 4.30). None of the families were found to be susceptible to PM. All the parents were tolerant to PM. On the basis of resistance to these three diseases, three families were selected although seed yield of these lines was below 9.0 g/plant. The families were MC-30, MC-184 and MC-196. Thus, a total of 14 families were selected for growing in the F_4 generation on the basis of different characters studied in F_3 (Appendix Table 8.3).

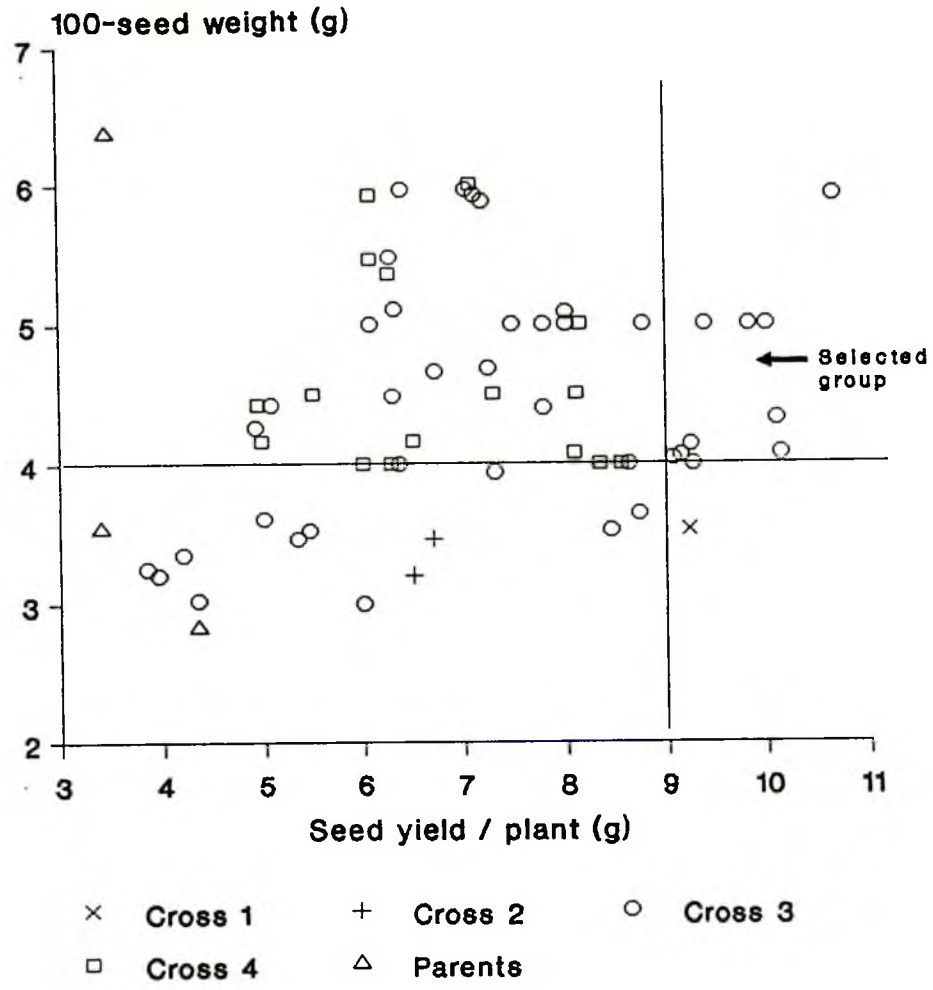

Fig. 4.13. Distribution of parents and F_3 families (winter) of the progeny of four cross combinations for 100-seed weight and seed yield.

Table 4.30. Mean performance of 60 selected families along with their parents for different varietal characters.

Parents/ selected families	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (no.)	Seeds/ plant (no.)	100-seed wt.(g)	Seed yield/ plant (g)	Disease reactions		
								MY MV	CLS	PM
Parents										
MB-55-4	31	75	29.8	16	150	2.83	4.34	R	T	T
ML-37	31	76	38.0	9	95	3.53	3.40	S	T	T
VC-1560D	33	81	40.5	4	55	6.38	3.48	S	T	T
Cross 1										
MC-14	32	75	29.3	23	265	3.52	9.22	R	T	T
Cross 2										
MC-21	31	82	45.8	20	208	3.46	6.70	T	S	T
MC-22	33	72	35.8	20	222	3.20	6.50	T	S	T
Cross 3										
MC-23	31	74	36.4	17	149	4.66	6.72	R	S	T
MC-25	33	94	35.2	17	157	4.68	7.25	T	T	T
MC-26	32	93	40.4	13	119	3.20	3.96	S	T	R
MC-28	31	95	39.9	19	180	4.40	7.78	T	T	R
MC-29	34	85	33.1	15	143	3.02	4.34	S	S	R
MC-30*	32	82	32.9	24	235	3.52	8.44	R	R	R
MC-31	35	76	39.2	13	121	3.24	3.85	S	R	T
MC-32	33	82	40.4	15	161	4.00	6.36	T	R	R
MC-34	35	75	42.1	14	132	3.60	5.00	T	S	T
MC-35	32	72	39.0	13	125	3.34	4.20	S	T	R
MC-36	33	81	40.1	17	155	4.48	6.30	T	S	R
MC-37	33	76	35.7	24	237	4.00	9.26	T	T	R
MC-38	32	81	37.8	24	244	4.08	10.14	R	T	R
MC-39	31	83	33.9	17	180	3.94	7.31	R	S	T
MC-40•	32	75	45.0	24	227	4.00	8.62	T	T	T
MC-41	35	91	41.6	20	200	3.00	6.00	T	S	R
MC-52	32	91	31.8	16	144	3.46	5.34	S	R	R

Parents/ selected families	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (no.)	Seeds/ plant (no.)	100-seed wt.(g)	Seed yield/ plant (g)	Disease reactions		
								MY MV	CLS	PM
MC-58	33	95	29.9	16	198	5.00	9.38	R	T	T
MC-60	36	86	35.2	20	209	5.00	10.00	R	T	R
MC-65	33	82	36.4	20	199	5.00	9.83	R	T	T
MC-74	33	71	26.6	15	124	5.88	7.20	T	T	R
MC-82	33	82	38.6	19	159	5.08	8.00	T	T	T
MC-83	32	75	34.6	17	119	5.10	6.32	T	S	R
MC-89	31	73	30.9	13	111	4.26	4.92	S	R	R
MC-90	33	82	32.4	12	131	5.92	7.12	T	S	R
MC-92	33	83	21.3	18	168	3.52	5.46	S	S	R
MC-94	32	73	41.1	25	224	3.64	8.72	T	T	R
MC-95	35	74	41.3	20	243	4.04	9.06	R	R	T
MC-98	31	81	44.2	21	233	4.06	9.14	R	T	T
MC-99	35	76	39.5	20	226	4.14	9.24	R	T	R
MC-107	33	83	25.6	22	241	4.32	10.10	R	T	R
MC-116	31	85	26.0	11	127	4.42	5.08	S	S	T
MC-127	34	96	38.1	15	128	5.96	7.04	T	T	T
MC-131	33	91	37.3	12	117	5.96	6.40	R	S	T
MC-138	33	90	39.5	17	149	5.00	7.78	R	S	R
MC-140	35	75	31.5	10	117	5.48	6.28	S	T	R
MC-142	36	74	36.6	18	163	5.00	8.00	T	T	R
MC-148	36	82	42.2	13	115	5.00	6.08	S	T	T
MC-149•	33	75	33.0	20	200	5.92	10.66	T	T	R
MC-152	34	76	39.7	19	172	5.00	8.76	T	S	T
MC-155	32	73	34.3	14	150	5.00	7.48	S	R	R
Cross 4										
MC-159	31	77	49.9	22	172	4.50	7.29	T	S	R
MC-161	32	74	49.2	19	206	4.00	8.33	T	S	T
MC-163	34	83	55.1	13	133	5.36	6.26	T	S	R

Parents/ selected families	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (no.)	Seeds/ plant (no.)	100-seed wt.(g)	Seed yield/ plant (g)	Disease reactions		
								MY MV	CLS	PM
MC-171	31	74	46.1	20	165	5.00	8.14	T	T	T
MC-174	33	75	41.6	23	204	4.08	8.08	R	S	R
MC-180	35	70	20.1	13	110	5.92	6.08	R	T	T
MC-181	34	86	29.8	13	118	4.16	4.98	S	S	R
MC-184*	36	73	26.5	15	143	4.16	6.50	R	R	R
MC-186	34	74	45.3	11	115	4.42	4.94	S	R	T
MC-187	33	75	35.6	11	125	4.50	5.50	T	S	R
MC-190	34	74	44.4	20	231	4.00	8.54	T	T	R
MC-195	33	77	30.9	20	180	4.50	8.10	R	S	R
MC-196*	32	72	26.4	14	169	4.00	6.28	R	R	R
MC-197	35	72	36.0	12	130	5.46	6.08	S	T	T
MC-200	33	75	47.1	14	154	4.00	6.00	S	R	T
MC-201	35	73	31.4	13	121	6.00	7.08	S	T	T

• Yellow seeded families.
* Selected on the basis of multiple disease resistance .
MYMV = Mungbean Yellow Mosaic Virus, CLS = Cercospora Leaf Spot and PM = Powdery Mildew.
R = Resistant, T = Tolerant and S = Susceptible.

Table 4.31. Variation among 60 selected families along with their parents for different varietal characters.

Characters	Among the F_3 families				Among the parents			
	Range	Mean	S. D.	CV(%)	Range	Mean	S. D.	CV(%)
Days to flower	31-36	33	1.46	4.41	31-33	32	1.15	0.47
Days to mature	70-96	80	7.07	8.88	75-81	77	3.21	0.27
Plant height (cm)	20.1-55.1	36.8	7.00	19.03	29.8-40.5	36.1	5.60	15.51
Pods/plant	10-25	17	4.01	23.48	4-16	10	6.03	16.36
Seeds/plant	110-265	167	43.39	26.03	55-150	100	47.7	14.70
100-seed wt. (g)	3.0-6.0	4.44	0.83	18.69	2.83-6.38	3.18	0.49	15.40
Seed yield/plant (g)	3.85-10.66	7.16	1.70	23.74	3.40-4.34	3.74	0.52	13.90

d. Study of F_4 generation in winter

Analysis of variance (mean squares) of the selected 14 F_4 families and 3 parents for different characters is presented in Table 4.32. The result showed that the entries (14 F_4 families and 3 parents) differed significantly among themselves. Coefficients of variation (%) were higher in F_4 lines than the parents in the present study also (Table 4.34).

Table 4.32. Analysis of variance (mean square values) of the selected 14 families along with their parents for different varietal characters.

Source of variation	DF	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (No.)	Seeds/ plant (No.)	100-seed weight (g)	Seed yield kg/ha
Genotypes	16	10.74**	175.58**	54.79**	64.65**	7972.06**	2.18**	99121.46**
Error	32	2.13	1.03	2.63	5.40	31.25	0.03	4004.96

**Significant at 1% level of probability.

The mean time of first flowering from the date of seeding was 33 days with a range from 30 to 36 days (Table 4.33 and 4.34) . Among these, 3 families flowered in 30 days, 4 in 32 days, 1 in 33 days, 2 in 34 days, 3 in 35 days and 1 in 36 days (Fig. 4.14). Mean time of flowering for the parents was 32 days with a narrow range from 31 to 34 days (Tables 4.33 and 4.34). Among the selected families, MC-30, MC-99 and MC-184 were early and produced 1st flower in 30 days and family MC-65 was late which flowered in 36 days time (Table 4.33 and Fig. 4.14). The data on days to flower and seed yield were plotted on a graph. The characters showed a normal distribution (Fig. 4.14). A truncation point for days to flower was drawn on 34 days and for seed yield the truncation point was drawn on 1100 kg seed yield/ha. Only

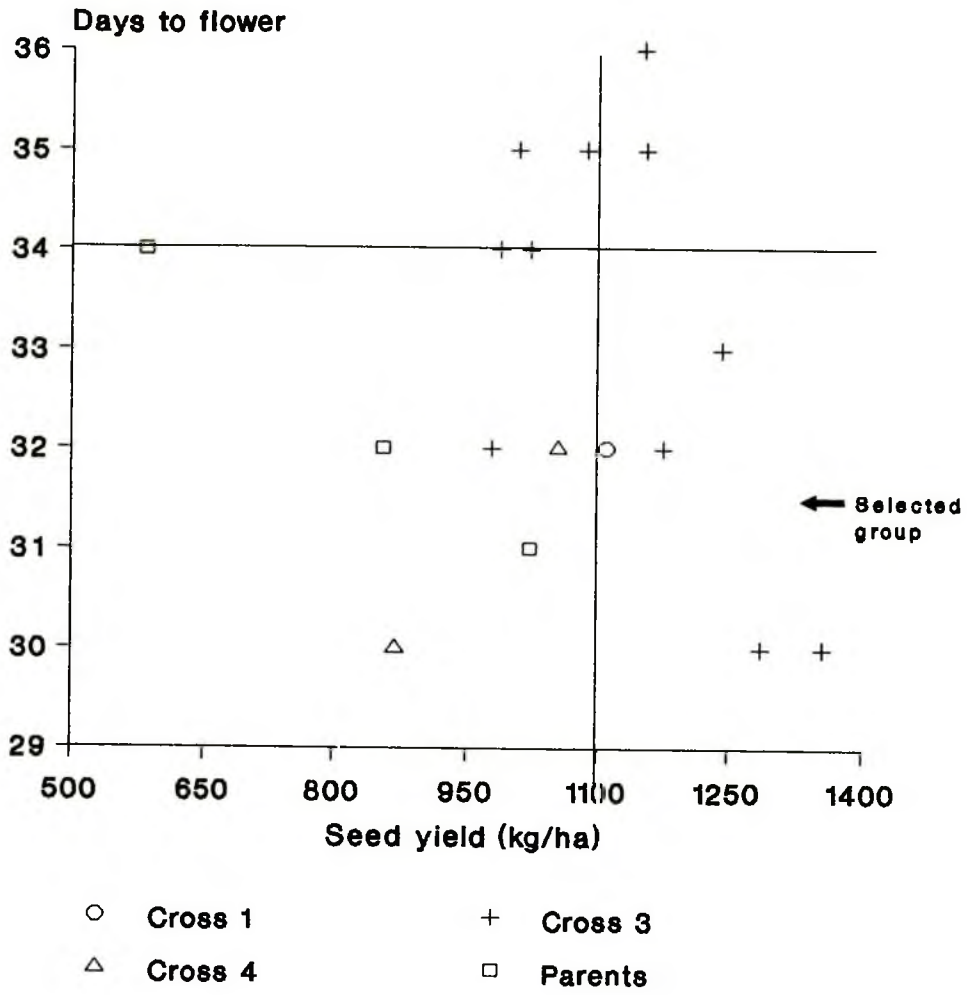

Fig. 4.14. Distribution of parents and F_4 families (winter) of the progeny of three cross combinations for days to flower and seed yield.

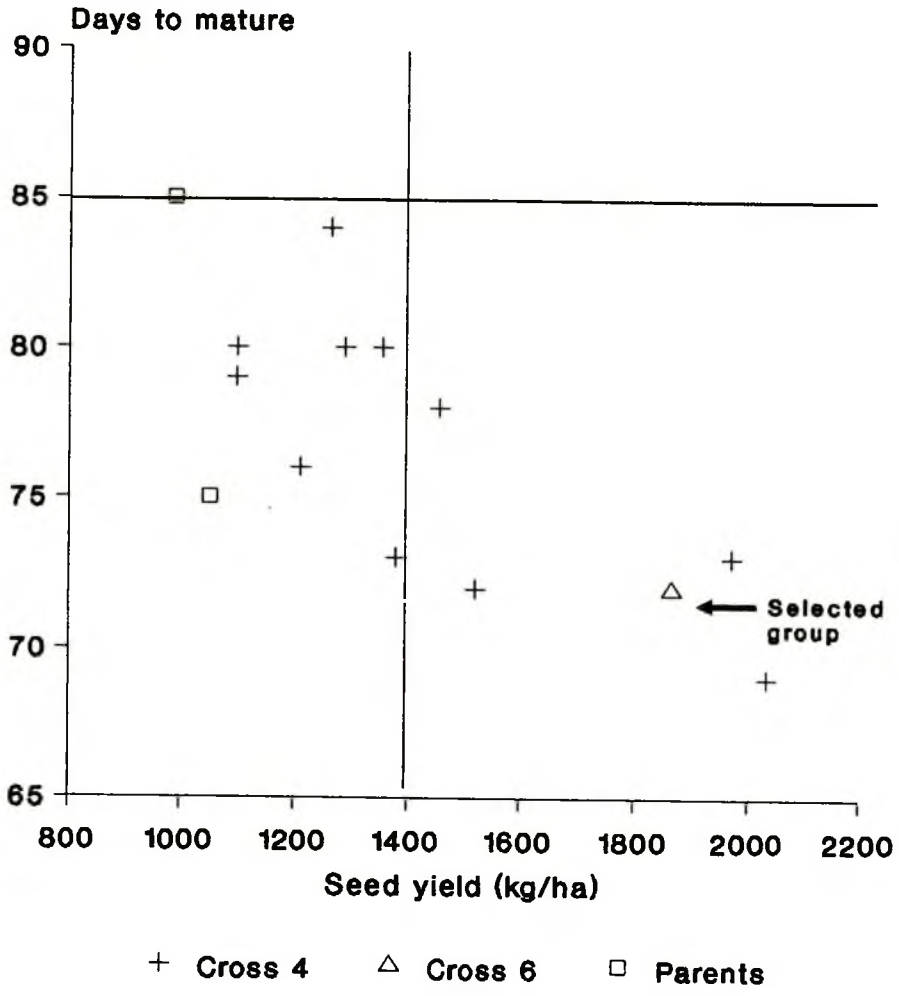

Fig. 4.15. Distribution of parents and F_4 families (winter) of the progeny of three cross combinations for days to mature and seed yield.

5 families were selected on the basis of these two characters. The families were MC-14, MC-30, MC-38, MC-99 and MC-107.

The mean for days to pod maturity for all the 14 families was 81 days with a range from 70 to 95 days (Tables 4.33 and 4.34). Among these, 2 families matured in 70 days, 4 in 75 days, 3 in 80 days, 2 within 81-85 days, one in 90 days and two in 95 days (Fig. 4.15). The parents matured within a shorter range of period from 75 to 81 days with a mean of 77 days. The data on days to mature and seed yield were plotted on a graph. Truncation point for days to mature was set on 85 days keeping the seed yield kg/ha at 1100 (Fig. 4.15). On the basis of these two characters 5 families (MC-14, MC-30, MC-38, MC-99 and MC-107) were selected.

The plant height of all the families varied from 27.3 to 42.6 cm with a mean of 34.7 cm (Tables 4.33 and 4.34). Among these, the family MC-107 was dwarf (27.3 cm tall). Among the other families, 5 were 30-35 cm tall, the height of 7 families fell within 36-40 cm and that of one was 42.6 cm. The plant height of parents ranged from 29.5 to 41.4 cm with a mean of 36.2 cm (Tables 4.33 and 4.34). The data on plant height and seed yield were plotted on a graph to select families on the basis of the above two characters. The truncation point for plant height was taken on 40 cm keeping the seed yield kg/ha at 1100 (Fig. 4.16). Six families were selected on the basis of these two characters. The families were MC-14, MC-30, MC-38, MC-58, MC-99 and MC-107.

The number of pods/plant varied from 14 to 24 pods with an average of 20 pods (Tables 4.33 and 4.34). Among the families, one family produced 14 pods, 5 produced 15-18 pods, 4 produced 19-21 pods and 4 produced 22-24 pods/plant. On the other hand, the parents produced lower number of pods than most of the families. Among the families, the highest number of pods

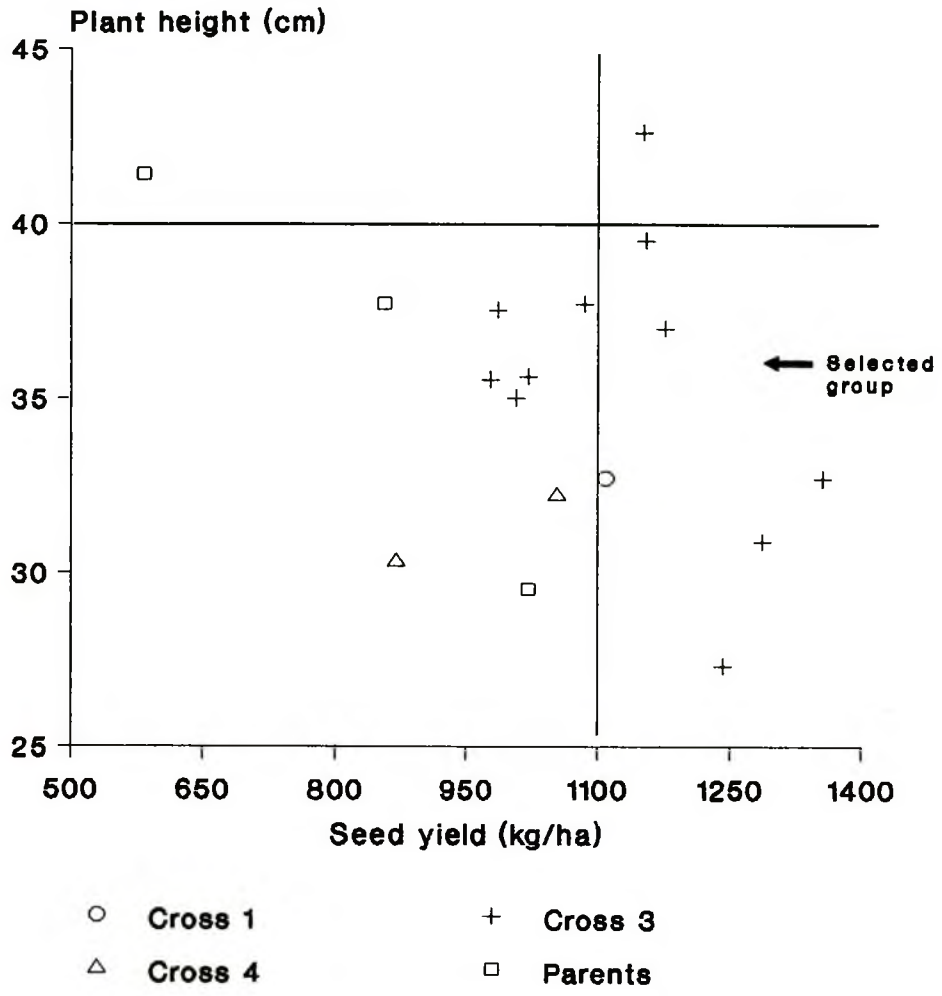

Fig. 4.16. Distribution of parents and F_4 families (winter) of the progeny of three cross combinations for plant height and seed yield.

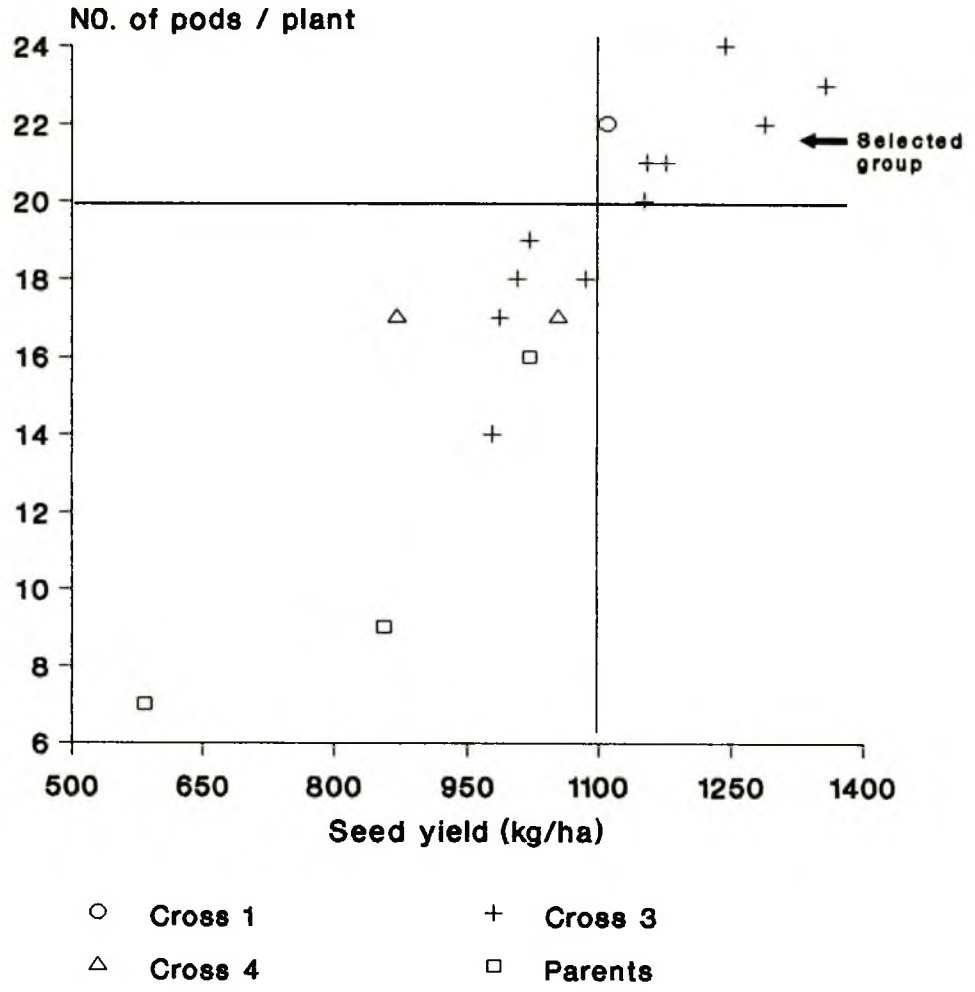

Fig. 4.17. Distribution of parents and F_4 families (winter) of the progeny of three cross combinations for number of pods/plant and seed yield.

was produced by the Family MC-107 (24 pods/plant). The data on pods/plant were plotted along with seed yield/ plant on a graph (Fig. 4.17). Truncation point for pods/plant was drawn on 20 pods and for seed yield on 1100 (kg/ha). On the basis of these two characters 7 families were selected. The families were MC-14, MC-30, MC-38, MC-58, MC-65, MC-99 and MC-107.

Number of seeds/plant among the 14 families ranged from 150 to 256 with a mean of 207. Among these, 7 families produced 150-200 seeds/plant, 6 produced 201-250 seeds and one produced 256 seeds. The data on seeds/plant and seed yield/plant were plotted on graph and for selection of families truncation point for seeds/plant was drawn on 200 and for seed yield on 1100 (kg/ha) (Fig. 4.18). Seven families were selected on the basis of these two characters. The families were MC-14, MC-30, MC-38, MC-58, MC-65, MC-99 and MC-107.

The range of seed weight was from 3.4 to 5.9 (g) with a mean of 4.2 (g) (Tables 4.33 and 4.34). Among these, the 100-seed weight of 8 families were between 3.1-4.0 (g), 5 families between 4.1-5.0 (g) and one family over 5.0 (g). In general, the seed size of the selected families was found to increase in the F_4 over F_3 families. This increase may be due to selection pressure on larger seed size. The parent VC-1560D is characterized by the highest seed weight (6.0 g) and none of the families was found to exceed this parameter (seed weight) (Table 4.33). Data on 100-seed weight and seed yield/plant were plotted on a graph with truncation points for 100-seed weight at 4.0 (g) and for seed yield on 1100 (kg/ha) (Fig. 4.19). Five families were selected on the basis of these two characters. The families were MC-38, MC-58, MC-65, MC-99 and MC-107.

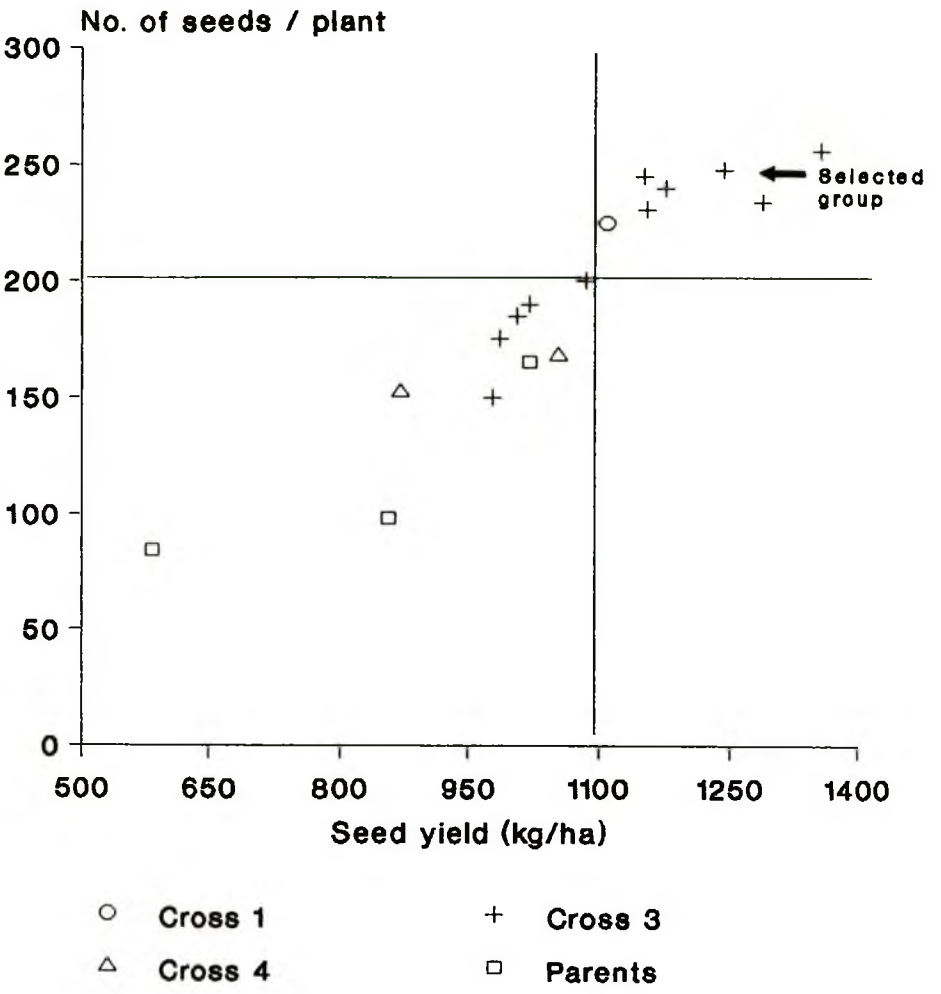

Fig. 4.18. Distribution of parents and F_4 families (winter) of the progeny of three cross combinations for number of seeds/plant and seed yield.

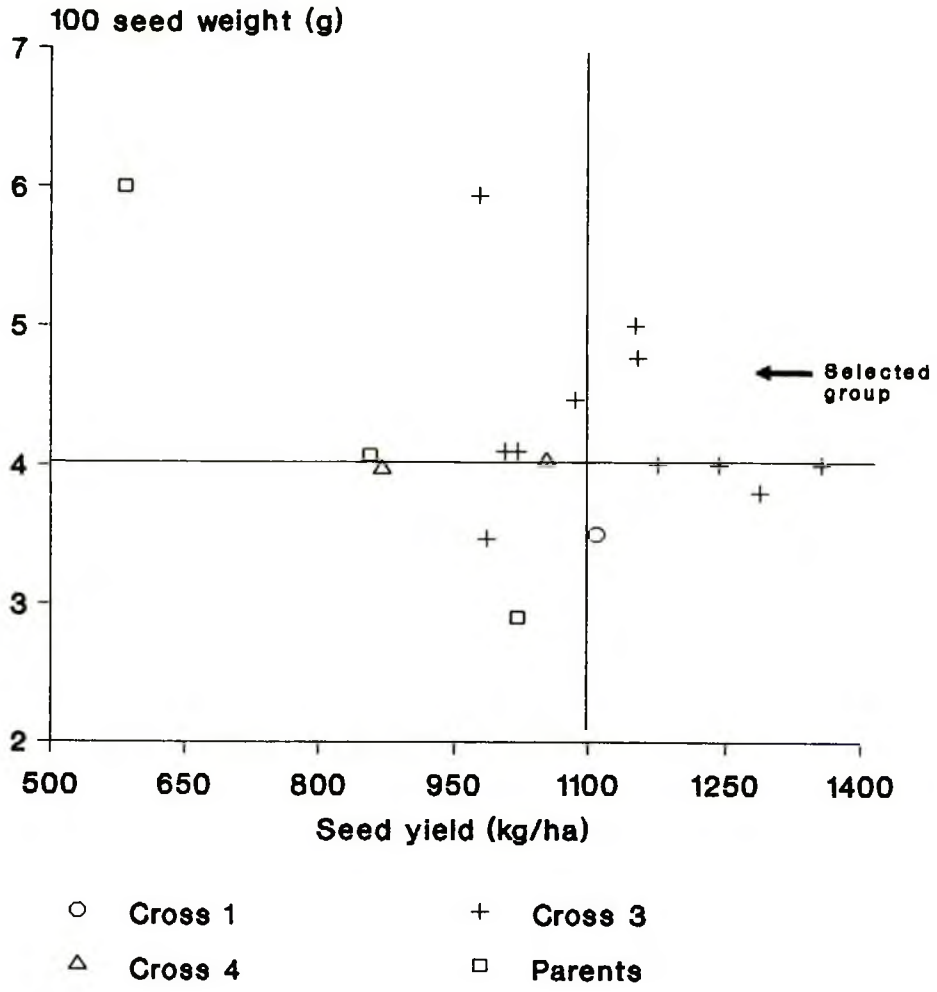

Fig. 4.19. Distribution of parents and F_4 families (winter) of the progeny of three cross combinations for 100-seed weight and seed yield.

Table 4.33. Mean performance of 14 selected families along with their parents for different varietal characters.

Parents / selected families	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (no.)	Seeds/ plant (no.)	100-seed wt. (g)	Seed yield/ kg/ha	Disease reaction		
								MY MV	CLS	PM
Parents										
MB-55-4	31de	75e	29.5gh	16ef	165h	2.9g	1021fg	R	T	T
ML-37	32cde	76e	37.7cd	9g	98j	4.1d	856h	S	T	T
VC-1560D	34abc	81d	41.4ab	7g	84k	6.0a	583i	S	R	T
Cross 1										
MC-14	32cde	75e	32.7ef	22abc	225d	3.5f	1109def	R	S	T
Cross 3										
MC-30	30e	70f	35.0de	22abc	234cd	3.8de	1287ab	R	T	S
MC-37	35ab	84c	30.9fg	18c-f	185f	4.1d	1007fg	T	S	T
MC-38	32cde	75e	37.0d	21a-d	240bc	4.0d	1176cd	T	T	S
MC-58	35abc	95a	39.5bc	21a-d	231cd	4.7c	1154cde	T	S	T
MC-60	35ab	90b	37.7cd	18c-f	200e	4.5c	1085d-g	S	T	T
MC-65	36a	95a	42.6a	20a-e	245b	5.0b	1151cde	R	S	T
MC-95	34abc	85c	35.6de	19b-e	190f	4.1d	1021fg	S	T	T
MC-98	34abc	80d	37.5cd	17def	175g	3.4ef	987g	S	S	T
MC-99	30e	70f	32.7ef	23ab	256a	4.0d	1356a	R	R	T
MC-107	33bcd	80d	27.3h	24a	248ab	4.0d	1242bc	R	T	S
MC-149	32cde	75e	35.5de	14f	150i	5.9a	978g	S	T	T
Cross 4										
MC-184	30e	75e	30fgh	17def	152i	3.9d	870h	S	S	T
MC-196	32cde	80d	32fg	17def	168gh	4.0d	1054efg	T	S	T

Means with same letter(s) in a column do not differ significantly at 1% level of probability, according to DNMRT.

Seed yield ranged from 870 to 1356 (kg/ha) among the families with a mean of 1106 (Tables 4.33 and 4.34). Among these, seed yield of one family was 870 kg/ha, that of 6 between 950-1100 kg/ha, 5 between 1101-1250 kg/ha and 2 between 1250-1400 kg/ha. Seed yield of the parents was low (583-1021 kg/ha) with a mean of 820 kg/ha.

Table 4.34. Variation among 14 selected families along with their parents for different varietal characters.

Characters	Among the F_3 families				Among the parents			
	Range	Mean	S. D.	CV(%)	Range	Mean	S. D.	CV(%)
Days to flower	30-36	33	2.03	6.78	31-34	32	1.53	4.73
Days to mature	70-95	81	8.25	10.23	75-81	77	3.21	4.15
Plant height (cm)	27.3-42.6	34.71	4.07	11.73	29.5-41.4	36.2	6.09	6.82
Pods/plant (no.)	14-24	20	2.82	14.46	7-16	11	4.73	4.33
Seeds/plant (no.)	150-256	207	37.09	17.92	84-165	116	43.29	7.43
100-seed wt. (g)	3.4-5.9	4.2	0.65	15.40	2.9-6.0	4.3	1.56	6.03
Seed yield (kg/ha)	870-1356	1106	132.84	12.02	583-1021	820	221.21	6.98

The families were classified into three groups for scoring disease resistance against MYMV, CLS and PM. Among the families, 5 were resistant, 4 tolerant and the remaining 5 were susceptible to MYMV (Table 4.33). Among the 3 parents, MB-55-4 was resistant and the other two were susceptible to MYMV. Out of 14 families, one was resistant, 6 tolerant and 7 susceptible to CLS (Table 4.33). As against this, one parent (VC-1560D) was resistant and the other two (MB-55-4 and ML-37) were tolerant to CLS. None of the families was found resistant to PM. Out of the 14 families, 11 were tolerant and 3 susceptible to this disease. All the parents were tolerant to PM.

A total of 7 families were selected for growing the F_5 generation on the basis of different characters (Appendix Table 8.4). Out of these, two families, MC-30 and MC-99 were released in 1997 under the name 'BINAMOOG-3' and 'BINAMOOG-4', respectively (Plate - 2 and Plate - 3).

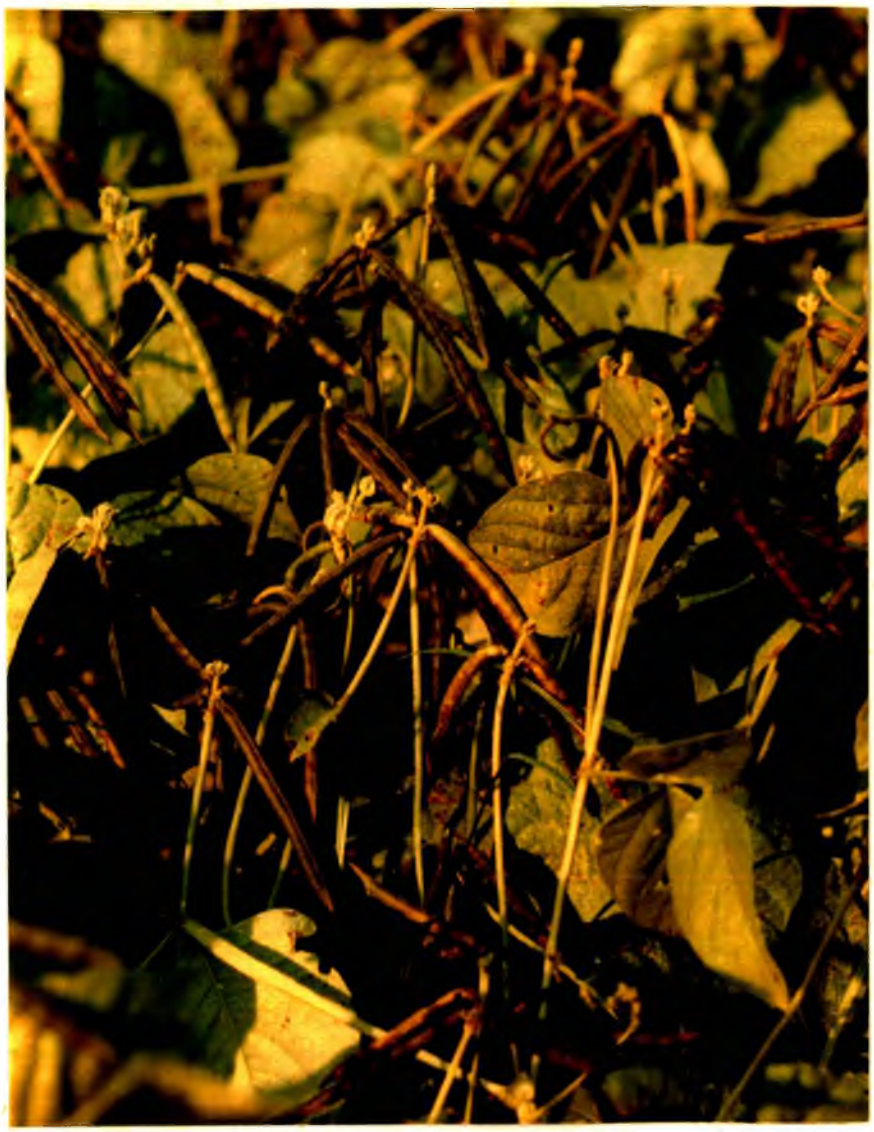

Plate 2. Field view of BINAMOOG-3

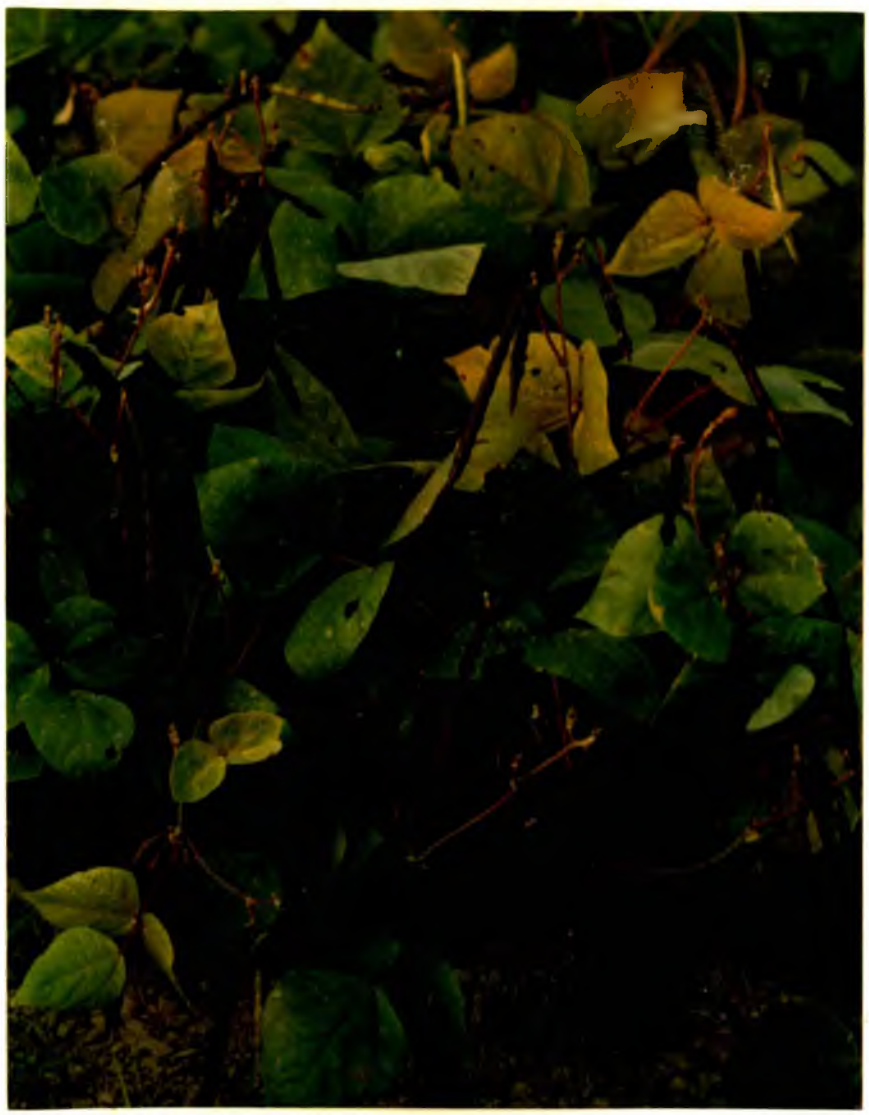

Plate 3. Field view of BINAMOOG-4

e. Study of F_2 generation in summer

The mean, range, coefficients of variability (CV%), components of variation i.e. phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for seven characters in the F_2 generation are summarized in Tables 4.35 through 4.41 and the results are discussed in the following paragraphs.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for days to flower in the F_2 are presented in Table 4.35.

Table 4.35. Mean, range, components of variation, heritability and genetic advance (%) for days to flower of six crosses in the F_2 generation compared to their parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
ML-37	32.1	31-34	0.59	3.57	2.51	49.2	3.63
VC-1560D	33.2	31-35	0.81	2.53	1.88	54.9	2.87
Cross-1	31.7	29-35	1.70	4.04	3.63	80.6	6.72
Cross-2	32.2	28-36	1.93	3.83	3.48	82.2	6.49
Cross-3	31.4	28-34	1.82	3.56	3.12	76.8	5.63
Cross-4	32.6	29-36	1.50	3.65	3.26	79.6	5.99
Cross-5	31.8	27-34	1.60	2.63	2.30	74.3	4.18
Cross-6	31.2	28-35	1.47	3.27	2.78	72.1	4.86

Mean days to flower were 32.1 in ML-37 and 33.2 in VC-1560D. The other parent did not flower in summer, so it was not included in the study. All the crosses showed considerable variation in this character. However, the range of mean was found to be wider in the crosses than the parents (Table

4.35). The CV (%) was also higher in the crosses ranging from 1.47 in Cross-6 to 1.93 in Cross-2 than the parents (0.59-0.81). The phenotypic components of variation ranged from 2.63 in Cross-5 to 4.04 in Cross-1 while ML-37 and VC-1560D had 3.57 and 2.53, respectively. Heritability estimates were substantially higher in the crosses (72.1-82.2%) than the parents (49.2-54.9%). The highest genetic advance (6.72%) was shown by the Cross-1 followed by Cross-2 (6.49) while the lowest by VC-1560D (2.87) and ML-37 (3.63).

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for days to maturity in the F_2 are presented in Table 4.36.

Table 4.36. Mean, range, components of variation, heritability and genetic advance (%) for days to maturity of six crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
ML-37	73.4	71-75	1.09	1.40	1.00	50.5	2.71
VC-1560D	82.8	80-85	1.23	1.13	0.78	52.9	1.23
Cross-1	75.6	69-78	2.45	2.14	1.98	85.1	3.75
Cross-2	78.6	69-85	2.86	2.22	2.07	87.2	3.98
Cross-3	78.8	71-80	2.22	2.39	2.13	79.4	3.91
Cross-4	81.1	72-84	2.61	2.28	2.12	86.3	4.05
Cross-5	77.6	70-85	2.55	1.96	1.80	84.0	3.40
Cross-6	78.9	70-84	2.05	2.18	1.93	78.6	3.53

Mean values of all the crosses ranged from 75.6 to 81.1 which were higher than the parents ML-37 (73.4) and lower than VC-1560D (82.8) (Table

4.36). Ranges of means were higher in the crosses than in the parents. The Cross-2 had the highest coefficient of variation (2.86 %) followed by the Cross-1 (2.45 %) while the variation was 1.09 % in ML-37 and 1.13 % in VC-1560D. Both the components of variation were higher in the crosses than in the parents. Heritability was greater in the crosses (79.4-87.2 %) than the parents (50.5-52.9 %). Genetic advance was the highest in Cross-4 (4.05) followed by Cross-2 (3.98) and lowest in VC-1560D (1.23).

The mean, range, coefficients of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for plant height in the F_2 are presented in Table 4.37.

Table 4.37. Mean, range, components of variation, heritability and genetic advance (%) for plant height of six crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
ML-37	38.9	36-40	0.90	3.11	1.93	38.6	2.47
VC-1560D	49.2	45-52	0.79	3.10	1.96	40.0	2.56
Cross-1	49.7	43-57	2.94	4.00	3.74	87.6	7.21
Cross-2	48.1	41-56	2.87	4.43	4.04	83.1	7.59
Cross-3	46.7	39-55	1.88	3.86	3.47	80.6	6.41
Cross-4	49.5	42-59	2.50	3.91	3.46	78.5	6.33
Cross-5	48.3	40-54	1.98	3.73	3.31	78.7	6.04
Cross-6	47.4	41-53	2.15	3.84	3.29	73.2	5.80

Means of all the crosses were close to the parent VC-1560D (49.2) but while much higher than the parents ML-37 (38.9) regarding plant height (Table 4.37). Ranges of means were wider in the crosses than the parents and

the lowest values in the range of all crosses were higher than that of ML-37. The CV (%) ranged from 1.88 in Cross-3 to 2.94 in Cross-1 while ML-37 and VC-1560D showed 0.90 and 0.79, respectively. The highest PCV and GCV (4.43 and 4.04, respectively) were found in Cross-2 which was closely followed by Cross-1 while lowest in the parents. Heritability and genetic advance had higher values as in the characters described above (Table 4.37).

The mean, range, coefficients of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for pods/plant in the F_2 are presented in Table 4.38.

Table 4.38. Mean, range, components of variation, heritability and genetic advance (%) for pods/plant of six crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
ML-37	16.7	13-18	3.23	7.03	4.31	37.5	5.44
VC-1560D	10.4	9-13	3.55	9.41	5.99	40.5	7.86
Cross-1	16.5	8-22	5.57	12.32	11.60	88.6	22.49
Cross-2	17.8	9-23	5.90	11.28	10.36	84.4	19.62
Cross-3	17.2	14-21	4.65	12.18	10.44	73.5	18.45
Cross-4	22.5	14-31	8.22	11.10	10.65	92.2	21.10
Cross-5	15.8	10-22	5.19	11.20	9.51	72.1	16.64
Cross-6	18.0	11-28	6.66	9.05	7.80	74.4	13.87

The highest number of pods/plant was found in Cross-4 (22.5) followed by Cross-6 (18.0) and Cross-2 (17.8) while the parents VC-1560D produced the lowest number of pods/plant (10.5) and ML-37 produced 16.7 pods/plant (Table 4.38). Other crosses, i.e., Cross-1, Cross-3 and Cross-5 produced 16.5,

17.2 and 15.8 pods/plant, respectively. Range of mean was observed to be narrow in parents while it was much wider in the crosses. The highest CV (%) was estimated in Cross-4 (8.22) followed by Cross-6 (6.66) while the lowest in the parents (3.23 and 3.55). Components of variation (PCV and GCV), heritability and genetic advance were substantially higher in the crosses than the parents. Cross-4 showed the highest heritability (92.2 % followed by the Cross-1 (88.6 %). Appreciably higher genetic advance was found in Cross-1 (22.49) and Cross-4 (21.10).

The mean, range, coefficients of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficient of variation, heritability and genetic advance (%) for seeds/plant in the F_2 are presented in Table 4.39.

Table 4.39. Mean, range, components of variation, heritability and genetic advance (%) for seeds/plant of six crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
ML-37	99.9	91-110	1.32	1.69	1.11	43.4	1.51
VC-1560D	120.1	115-125	1.04	1.96	1.25	41.0	1.66
Cross-1	129.6	116-145	2.64	2.24	2.00	79.5	3.67
Cross-2	107.7	96-131	2.83	3.69	3.24	77.5	5.88
Cross-3	111.2	85-141	2.21	2.89	2.60	80.4	4.79
Cross-4	189.2	126-290	3.24	3.01	2.76	84.1	5.22
Cross-5	144.9	94-201	2.52	2.22	1.97	78.7	3.60
Cross-6	118.8	81-190	1.78	2.59	2.27	76.5	4.08

Number of seeds/plant was 99.9 and 120.1 in ML-37 and VC-1560D, respectively. Plants of Cross-4 produced 189.2 seeds/plant followed by Cross-

5 (144.9) (Table 4.39). Other crosses produced more number of seeds/plant than ML-37. One plant produced the highest number of seeds/plant (290) in Cross-4. Heritability in Cross-4 was also higher (84.1 %). Genetic advance was 5.88 and 5.22 in Cross-2 and Cross-4, respectively.

The mean, range, coefficient of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for 100-seed weight in F_2 are presented in Table 4.40.

Table 4.40. Mean, range, components of variation, heritability and genetic advance (%) for 100-seed weight of six crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
ML-37	3.97	3.80-4.10	1.26	3.37	2.10	38.9	2.70
VC-1560D	6.03	5.90-6.20	1.33	2.29	1.48	42.1	1.98
Cross-1	4.09	3.50-5.10	3.18	4.30	3.87	80.6	7.15
Cross-2	4.34	3.40-5.80	2.76	3.79	3.34	77.8	6.07
Cross-3	4.45	3.30-5.20	3.37	3.41	3.10	82.6	5.80
Cross-4	5.51	4.10-6.50	3.63	4.14	3.85	86.5	7.38
Cross-5	4.64	3.80-6.10	2.59	4.26	3.73	76.9	6.74
Cross-6	4.50	3.30-5.60	2.22	3.65	3.06	70.4	5.29

One hundred seed weight of ML-37 and VC-1560D was 3.97 and 6.03g, respectively. All the crosses had higher 100-seed weight (4.09-5.51) than the parent ML-37 but lower than the VC-1560D (Table 4.40). Range of mean was found to be wider in all the crosses than the parents. Coefficients of variability (%), components of variation and genetic parameters were observed to be higher in the crosses than the parents. The highest heritability

was found in Cross-4 (86.5 %) followed by Cross-3 (82.6 %) and Cross-1 (80.6 %). Cross-4 also showed highest genetic advance (7.38) followed by Cross-1 (7.15) and Cross-5 (6.74).

The mean, range, coefficients of variability (CV%), components of variation, i.e., phenotypic- and genotypic coefficients of variation, heritability and genetic advance (%) for seed yield/plant in the F_2 are presented in Table 4.41.

Table 4.41. Mean, range, components of variation, heritability and genetic advance (%) for seed yield / plant of six crosses in the F_2 generation compared to the parental lines.

Parents/ Crosses	Mean	Range	CV (%)	PCV	GCV	h^2	GA (%)
ML-37	3.85	3.30-4.80	5.19	19.21	12.01	39.90	15.77
VC-1560D	5.35	3.90-6.20	4.67	23.08	14.98	42.10	20.00
Cross-1	3.66	2.80-5.20	15.57	22.94	20.48	79.70	37.67
Cross-2	3.82	2.60-4.30	10.21	22.85	20.70	82.00	38.60
Cross-3	4.35	2.70-5.70	9.20	18.40	16.18	77.30	29.30
Cross-4	7.86	4.60-12.50	17.0	21.39	20.10	89.00	39.21
Cross-5	5.24	2.80-10.50	12.40	17.20	15.09	77.00	27.27
Cross-6	5.00	3.10-7.20	10.40	19.08	16.67	76.40	30.02

The highest number of pods and seeds/plant resulted in maximum seed yield/plant (7.86 g) in Cross-4 (Table 4.41). The parents ML-37 and VC-1560D produced 3.85 and 5.35 (g) seed yield/plant, respectively. Cross-1 and Cross-2 gave lower seed yield/plant (3.66 and 3.82 g, respectively). On the other hand, Cross-3, Cross-5 and Cross-6 gave 4.35, 5.24 and 5.0 (g) seed yield/plant, respectively which were lower than VC-1560D. Wider range of

mean was observed in the crosses than the parents. Cross-4 showed the highest CV of 17.0 % followed by Cross-1 (15.57 %). Coefficients of variability were lower in the parents. Similarly all other estimates in the crosses were substantially higher than parents. Both heritability and genetic advance were greater in Cross-4 followed by Cross-2.

f. Study of F_3 generation in summer

Analysis of variance (mean squares) for different characters of the selected 24 families and the parental lines is presented in Table 4.42. The result showed that these families and the parents differed significantly in all the characters studied. One of the parents namely, MB-55-4 did not flower in summer due to its photosensitive character (Table 4.43). As expected, coefficients of variation (%) were higher in the F_3 families compared to their parents (Table 4.44).

Tables 4.43 and 4.44 show that the mean time of first flowering was 32 days with a range from 30 to 35 days. Among these, 9 families flowered in 30 days, one in 31 days, 5 in 32 days, another 5 in 34 days and the remaining 4 in 35 days (Fig. 4.20). The time of flowering for both the parents was 33 days (Table 4.44). The data on days to flower and seed yield/plant were plotted on a graph. The characters showed a normal distribution (Fig. 4.20). A truncation point for days to flower was drawn on 34 days and for seed yield/plant was drawn on 9.0 g/plant. Nine families were selected on the basis of these two characters. The families were MC-14, MC-18, MC-21, MC-26, MC-36, MC-46, MC-66, MC-80 and MC-106.

The mean days to pod maturity for all the families was 77 days with a range from 70 to 85 days (Tables 4.43 and 4.44). Among these one family (MC-18) matured very early, i.e., within 67 days from sowing, 9 matured

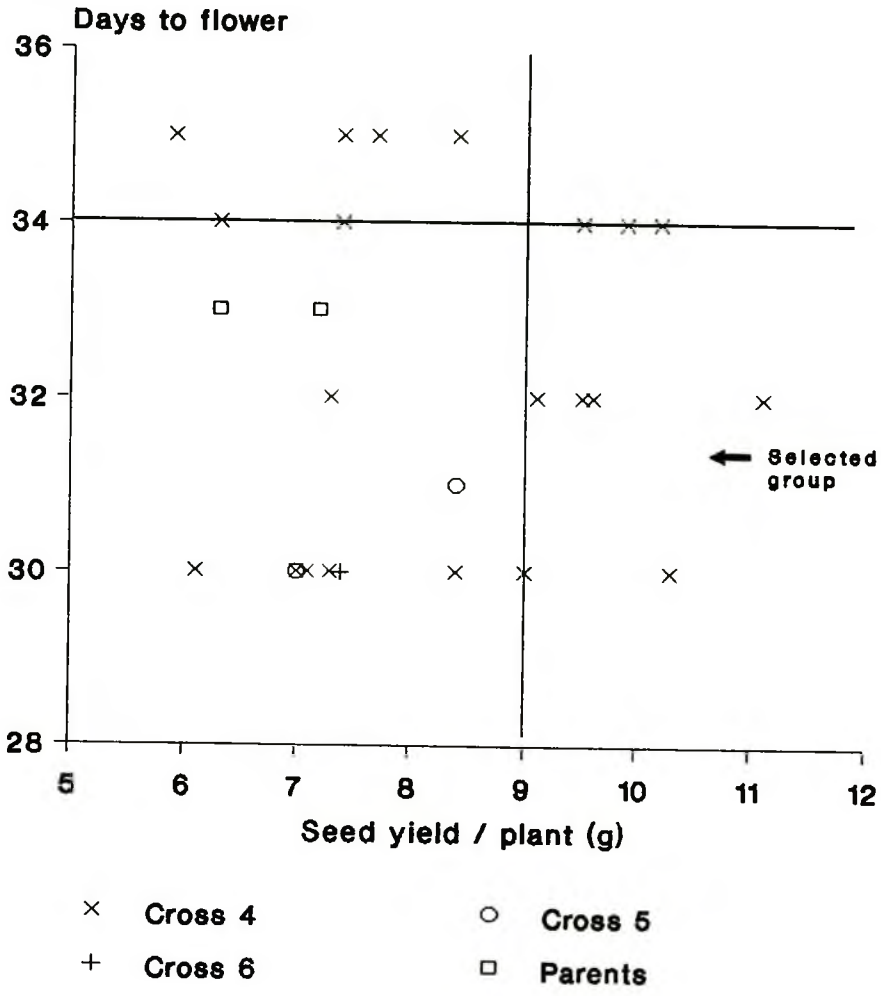

Fig. 4.20. Distribution of parents and F_3 families (summer) of the progeny of three cross combinations for days to flower and seed yield.

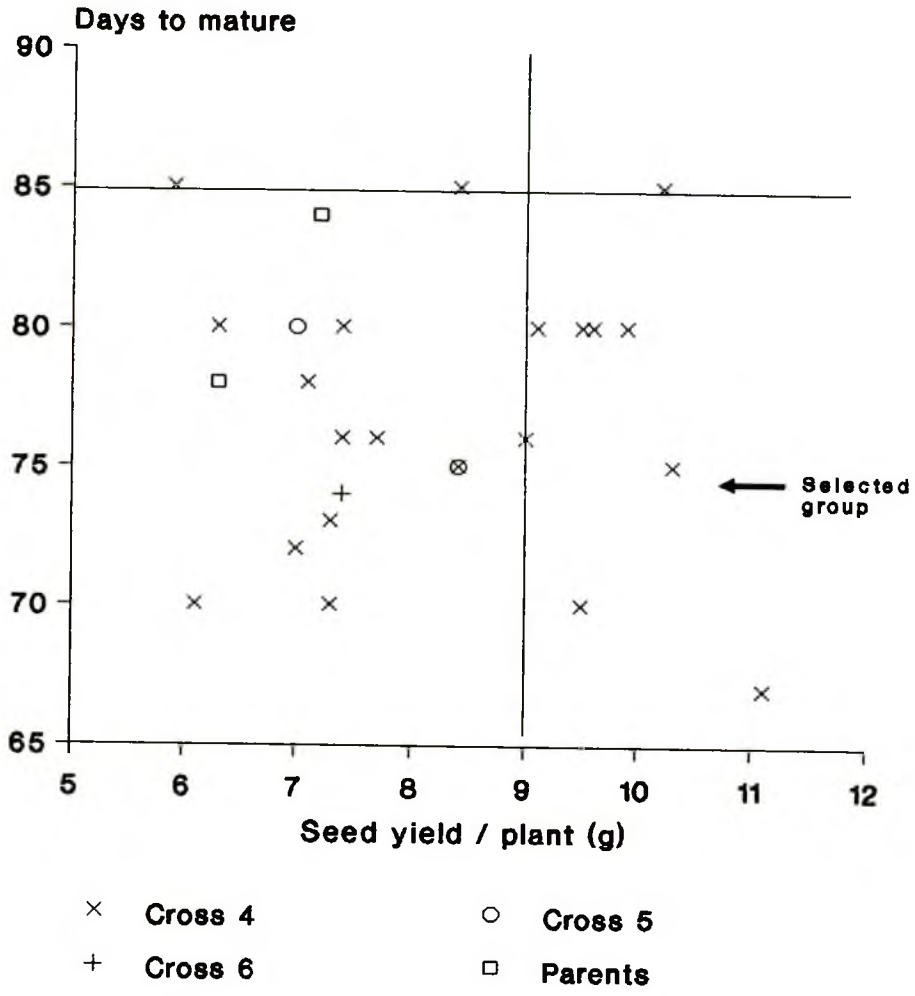

Fig. 4.21. Distribution of parents and F_3 families (summer) of the progeny of three cross combinations for days to mature and seed yield.

within 70-75 days, 11 matured within 76-80 days and 3 matured in 85 days (Fig. 4.21). The parents matured within a shorter range of period (78-84 days) with a mean of 81 days. The data on days to mature and seed yield /plant were plotted on a graph. Truncation point for days to mature was set on 85 days keeping the seed yield/plant at 9.0 (g) (Fig. 4.21). On the basis of these two characters 9 families (MC-14, MC-18, MC-21, MC-26, MC-36, MC-46, MC-66, MC-80 and MC-106) were selected.

The plant height of 24 families varied from 32.0 to 55.0 cm with a mean of 45.6 cm (Table 4.43 and 4.44). Among these, plant height of 3 families were within 30.1-35.0 cm, 5 within 35.1-40.0 cm, 6 within 40.1-50.0 and 10 were above 50.0 cm. The plant height of parents ranged from 38.0 to 50.0 cm with a mean of 44.0 cm (Table 4.44). The family MC-8 was the tallest (56.0) among the selected families while the family MC-47 was the shortest (31.2 cm) (Table 4.43). The data on plant height and seed yield/plant were plotted on the graph paper to select families for further trial. The truncation point for plant height was drawn on 40 cm keeping the seed yield /plant at 9.0 (g) (Fig. 4.22). Four families were selected on the basis of these two characters. The families were MC-18, MC-46, MC-66, and MC-106.

The number of pods/plant varied from 15 to 30 pods with an average of 23 pods (Tables 4.43 and 4.44 and Fig. 4.23). Among the 24 families, 6 produced 15.1-20.0 pods, 9 produced 20.1-25.0 and the remaining 9 produced above 25 pods. The lower number of pods/plant was observed among the parents with a mean of 13.5 pods/plant. Among the families, the highest number of pods was produced by the family MC-106 (30 pods/plant) while the lowest number of pods (15 pods/plant) was produced by the family MC-113. When the data on pods/plant was plotted along with seed yield/plant on a graph it showed a normal distribution (Fig. 4.23). Truncation point for

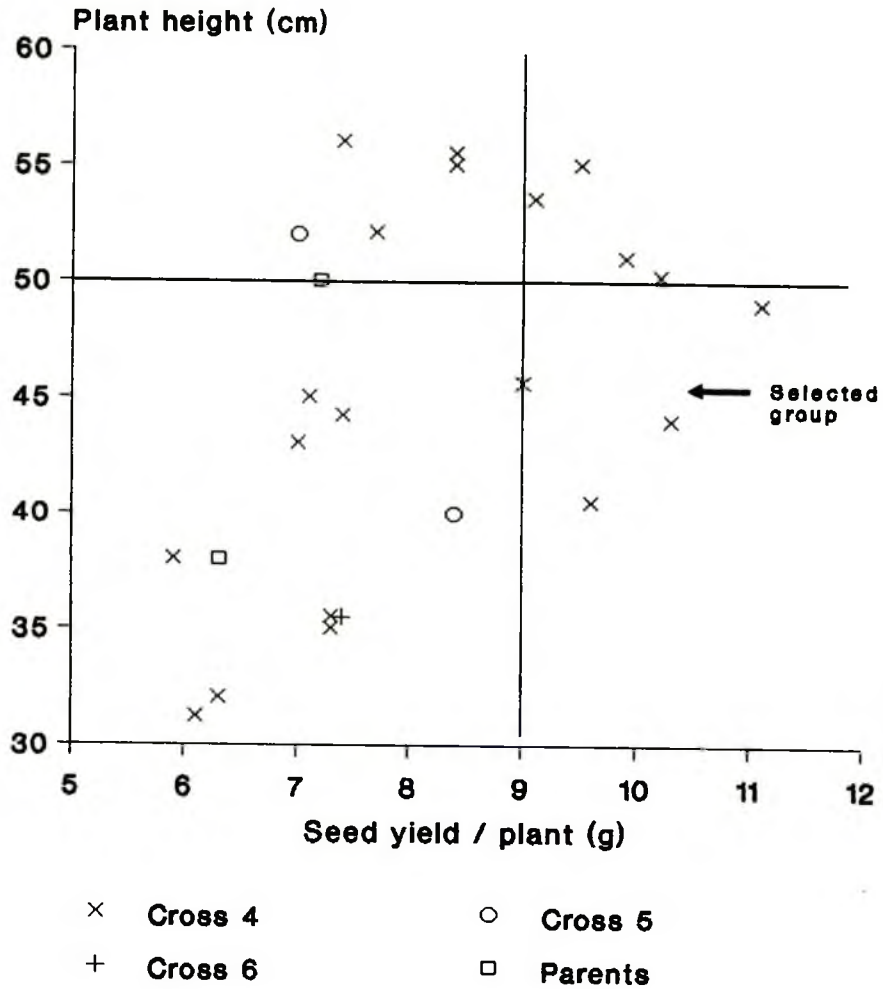

Fig. 4.22. Distribution of parents and F_3 families (summer) of the progeny of three cross combinations for plant height and seed yield.

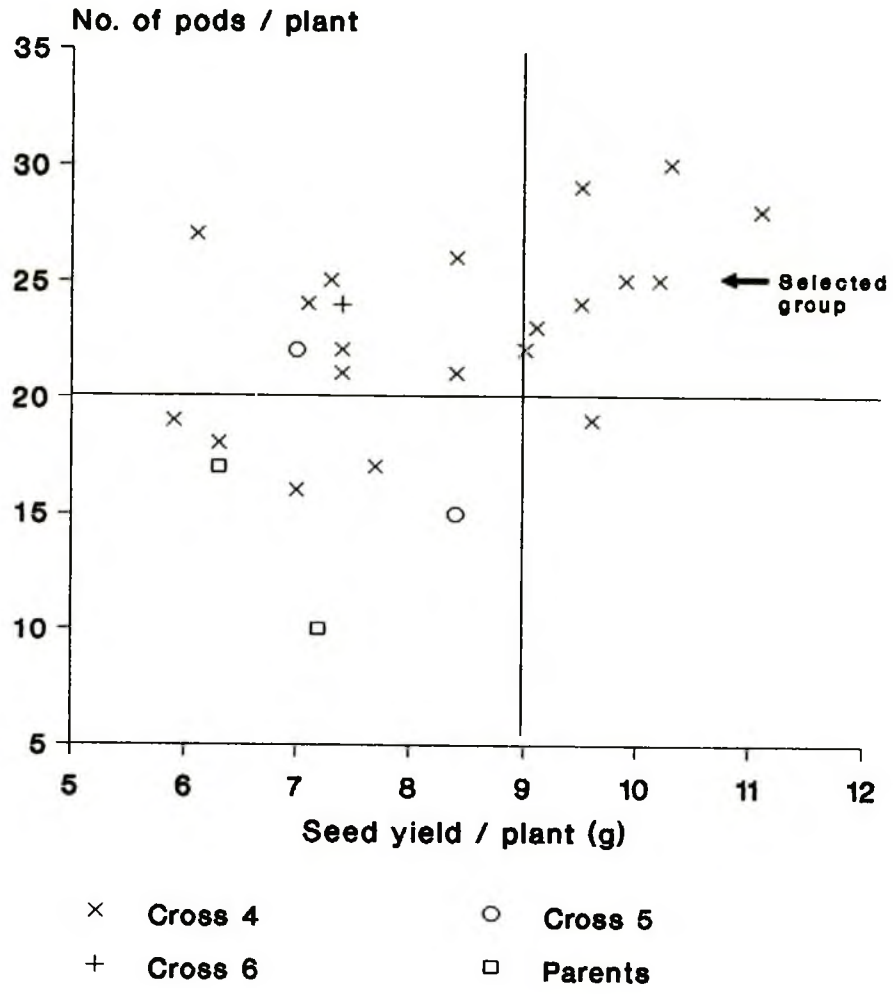

Fig. 4.23. Distribution of parents and F_3 families (summer) of the progeny of three cross combinations for number of pods/plant and seed yield.

pods/plant was drawn on 20 pods/plant and for seed yield/plant on 9.0 (g). On the basis of these two characters 8 families were selected. The families were MC-14, MC-18, MC-21, MC-26, MC-36, MC-46, MC-80 and MC-106.

Number of seeds/plant among the families ranged from 140 to 288 with a mean of 214. Among these, one produced 101-150 seeds, 5 produced 151-200 seeds, 15 produced 201-250 seeds and 3 produced more than 250 seeds/plant (Table 4.43 and Fig. 4.24). On the other hand, the parents produced the lowest number of seeds/plant (122-165) with a mean of 143.5 seeds/plant. Among the families, the highest seeds/plant was produced by the family MC-36 (288 seed/plant) and the lowest by family MC-113 (140 seeds/plant). The data on seeds/plant and seed yield/plant were plotted on a graph and for selection of families truncation point for seeds/plant was drawn on 200 seeds/plant and seed yield/plant on 9.0 (g) (Fig. 4.24). Eight families were selected on the basis of these two characters. The families were MC-14, MC-18, MC-21, MC-26, MC-36, MC-46, MC-80 and MC-106.

The seed size (100-seed weight) varied widely in the selected families. The range of seed weight was 3.0-6.0 (g) with a mean of 4.01 (g) (Table 4.43 and 4.44). Among these, 100-seed weight of 11 families were between 3.1-4.0 (g), 9 between 4.1-5.0 (g) and 3 betweene 5.1-6.0 (g). Among the selected families, 100-seed weight of the Families MC-66 and MC-113 was the highest (6.0 g) while it was the lowest in families MC-46 and MC-47 (3.0 g). The parent VC-1560D had the highest seed weight (6.01 g) and none of the families was found to exceed this seed weight (Table 4.43). Data on 100-seed weight and seed yield/plant were plotted on the graph and a truncation point for 100-seed weight was set on 4 (g). Truncation point for seed yield was 9.0 (g) (Fig. 4.25). Seven families were selected on the basis of these two

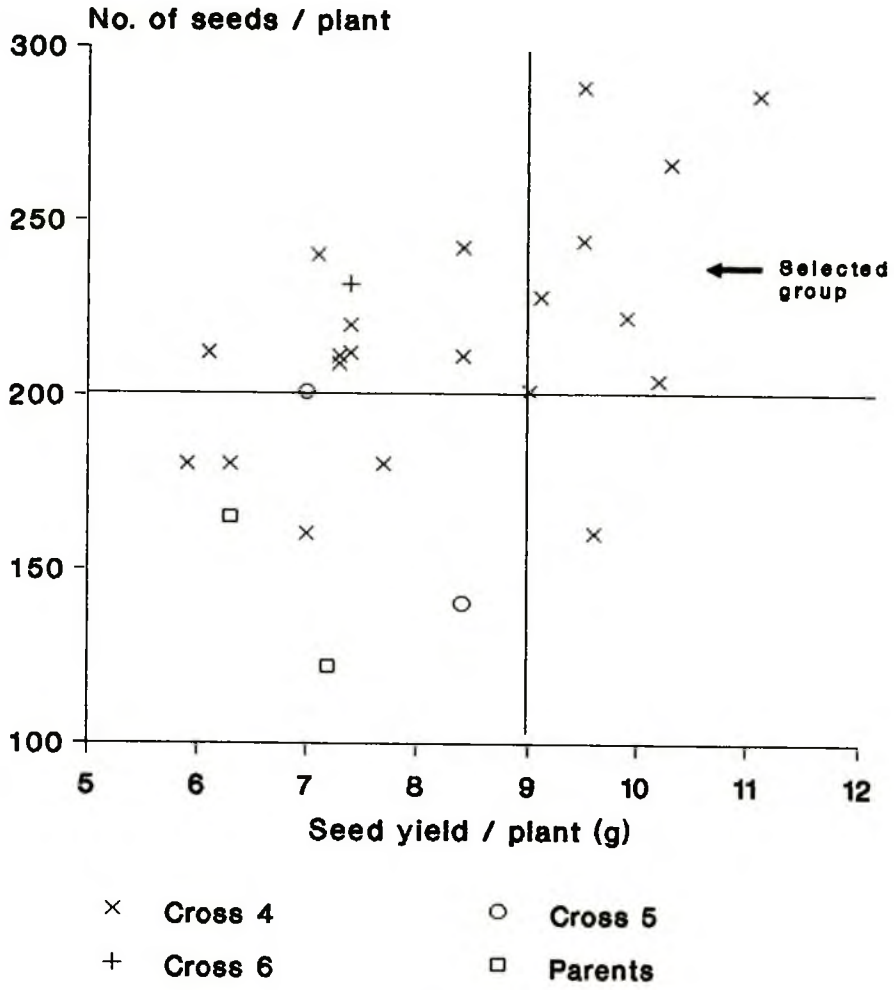

Fig. 4.24. Distribution of parents and F_3 families (summer) of the progeny of three cross combinations for number of seeds/plant and seed yield.

characters. The families were MC-14, MC-18, MC-21, MC-26, MC-46, MC-66 and MC-80.

Seed yield/plant of the families ranged from 5.9 to 11.1 (g) with a mean of 8.18 (g) (Table 4.44). Among these, seed yield of one family was below 6 (g), 4 between 6.1-7.0 (g), 7 between 7.1-8.0 (g), 4 between 8.1-9.0 (g), 5 between 9.1-10.0 (g), 2 between 10.1-11.0 (g) and one family was above 11.0 (g). Seed yield of the parents were very low. The range was from 6.3 to 7.2 (g) with a mean of 6.75 (g) (Table 4.44).

The families were classified into three groups (Resistant, Tolerant and Susceptible) through scoring of infection by three diseases namely MYMV, CLS and PM. Among the 24 families, 10 were resistant, 9 tolerant and 5 susceptible to MYMV (Table 4.43). Among the 2 parents, none was resistant to MYMV. Scoring against CLS showed that out of 24 families, 6 were resistant, 11 tolerant and 7 susceptible to this disease (Table 4.43). On the other hand, one of the parents was found to be resistant and the other was susceptible to CLS. Scores for PM indicated that out of 24 families, 21 resistant and 3 tolerant to this disease (Table 4.43). None of the families was found to be susceptible. Both the parents were tolerant to PM. On the basis of resistance to these three diseases three families, MC-48, MC-69 and MC-130, were selected for further trial in the next generation although their seed yield/plant was below 9.0 (g).

A total of 9 families were selected on the basis of association of different varietal characters and seed yield and three (MC-48, MC-69 and MC-130) were selected on the basis of multiple disease resistance. A total of 12 families (MC-14, MC-18, MC-21, MC-26, MC-36, MC-46, MC-48, MC-66, MC-69, MC-80, MC-106 and MC-130) were selected for growing in F_4 generation (Appendix Table 8.5). Among the selected families, 11 were from

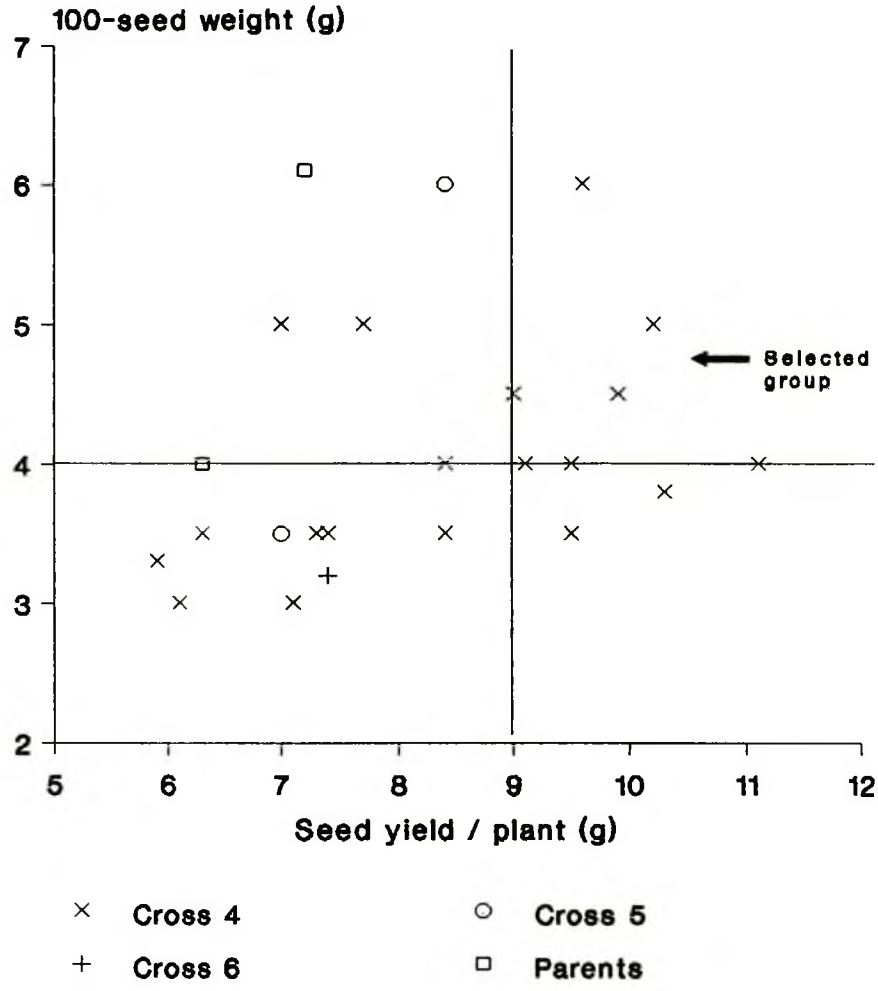

Fig. 4.25. Distribution of parents and F_3 families (summer) of the progeny of three cross combinations for 100-seed weight and seed yield.

Cross-4 (VC-1560D x MB-55-4) and only one was from Cross-6 (VC-1560D x ML-37).

Table 4.42. Analysis of variance (mean square values) of the selected 24 families along with two parents for different varietal characters.

Source of variation	DF	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (No.)	Seeds/ plant (No.)	100-seed weight (g)	Seed yield/ plant (g)
Genotypes	25	10.09**	74.91**	190.51**	72.17**	5015.03	2.54**	6.31**
Error	50	0.40	1.15	1.20	3.90	3.74	0.01	0.02

**Significant at 1% level of probability.

Table 4.43. Mean performance of 24 selected families along with their parents for different varietal characters.

Parents/ selected families	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (No.)	Seeds/ plant (No)	100-seed wt. (g)	Seed yield/ plant(g)	Disease reaction		
								MYMV	CLS	PM
Parents										
MB-55-4	Did not flower			-	-	-	-	-	-	-
ML-37	33	78	38.0	17	165	4.0	6.3	T	S	T
VC-1560D	33	84	50.0	10	122	6.1	7.2	T	R	T
Cross 4										
MC-5	35	76	52.1	17	180	5.0	7.7	T	S	R
MC-8	34	76	56.0	22	220	3.5	7.4	S	T	R
MC- 14	32	70	55.0	24	244	4.0	9.5	T	T	R
MC-18	32	67	49.0	28	286	4.0	11.1	R	R	R
MC-21	34	80	51.0	25	222	4.5	9.9	T	T	T
MC-26	34	85	50.2	25	204	5.0	10.2	T	T	R
MC-30	35	80	44.2	21	212	3.5	7.4	S	T	R
MC-34*	34	80	32.0	18	180	3.5	6.3	S	S	R
MC-35*	35	85	38.0	19	180	3.3	5.9	T	S	R
MC-36	34	80	55.0	29	288	3.5	9.5	R	T	R

Parents/ selected families	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (No.)	Seeds/ plant (No)	100-seed wt. (g)	Seed yield/ plant(g)	Disease reaction		
								MY MV	CLS	PM
MC-42	30	76	45.6	22	201	4.5	7.1	S	T	R
MC-43	35	85	55.0	26	242	3.5	8.4	T	S	R
MC-46*	30	78	45.0	24	240	3.0	9.0	R	T	R
MC-47*	30	70	31.2	27	212	3.0	6.1	S	T	R
MC-48•	30	70	35.0	25	209	3.5	7.3	R	R	R
MC-53	32	73	35.5	25	211	3.5	7.3	R	S	R
MC-66	32	80	40.5	19	160	6.0	9.6	T	R	R
MC-69•	30	75	55.5	21	211	4.0	8.4	R	R	R
MC-79	30	72	43.0	16	160	5.0	7.0	T	S	R
MC-80	32	80	53.5	23	228	4.0	9.1	R	T	R
MC-106	30	75	44.0	30	266	3.8	10.3	R	R	R
Cross 5										
MC-113	31	75	40.0	15	140	6.0	8.4	T	R	T
MC-118	30	80	52.0	22	201	3.5	7.0	R	S	R
Cross 6										
MC-130•	30	74	35.5	24	232	3.2	7.4	R	T	T

* Yellow seeded families

• Selected on the basis of multiple disease resistance.

MYMV = Mungbean Yellow Mosaic Virus, CLS = Cercospora Leaf Spot and PM = Powdery Mildew.

R = Resistant, T = Tolerant and S = Susceptible.

Table 4.44. Variation among 24 selected families along with their parents for different varietal characters.

Characters	Among the F 3 families				Among the parents			
	Range	Mean	S. D.	CV(%)	Range	Mean	S. D.	CV(%)
Days to flower	30-35	32	2.01	6.26	33-33	33	0	0
Days to mature	70-85	77	4.96	6.46	78-84	81	4.24	5.23
Plant height (cm)	32.0-55.0	45.60	8.11	17.79	38.0-50.0	44	8.49	9.30
Pods/plant	15-30	23	4.01	17.60	10-17	13.5	4.95	6.67
Seeds/plant	140-288	214	37.07	17.35	122-165	143.5	30.40	11.18
100-seed wt. (g)	3.0-6.0	4.01	0.85	21.20	4.0-6.1	5.05	1.48	9.31
Seed yield/plant (g)	5.9-11.1	8.18	1.39	9.48	6.3-7.2	6.75	0.64	4.77

g. Study of F_4 generation in summer

The analysis of variance (Mean squares) of the 12 F_4 selected families and parents for different characters is presented in Table 4.45. The result showed significant differences among the F_4 families and parents for all the characters studied. Coefficient of variation (%) was higher in F_4 hybrid lines compared to the parents (Table 4.47).

Table 4.45. Analysis of variance (mean square values) of the selected 12 families along with their parents for different varietal characters.

Source of variation	DF	Days to flowering	Days to maturity	Plant height (cm)	Pods/ plant (No.)	Seeds/ plant (No.)	100-seed weight (g)	Seed yield kg/ha
Genotypes	13	3.51**	68.24**	99.12**	61.68**	5797.02**	2.47**	347847.43**
Error	26	1.29	0.99	6.77	1.02	18.50	0.01	8797.65

**Significant at 1% level of probability.

It was observed in the Tables 4.46 and 4.47 that the mean time of first flowering from the date of seeding of 12 selected families was 32 days with a range from 30 to 34 days. Among these, 2 families flowered in 30 days, 4 in 31 days, 4 in 32 days, one in 33 days and the remaining one in 34 days (Fig. 4.26). On the other hand, both the parents flowered in 32 days. The data on days to flower and seed yield were plotted on a graph. The characters showed a normal distribution (Fig. 4.26). A truncation point for days to flower was drawn on 34 days and for seed yield was drawn on 1400 kg/ha. Five families were selected on the basis of these two characters for growing in the next generation. The families were MC-14, MC-18, MC-66, MC-106 and MC-130.

The mean days to pod maturity for all the families was 76 days with a range from 69 to 84 days (Tables 4.46 and 4.47). Among these, only one family MC-18 matured early, i.e., in 69 days from sowing, 4 within 70-75

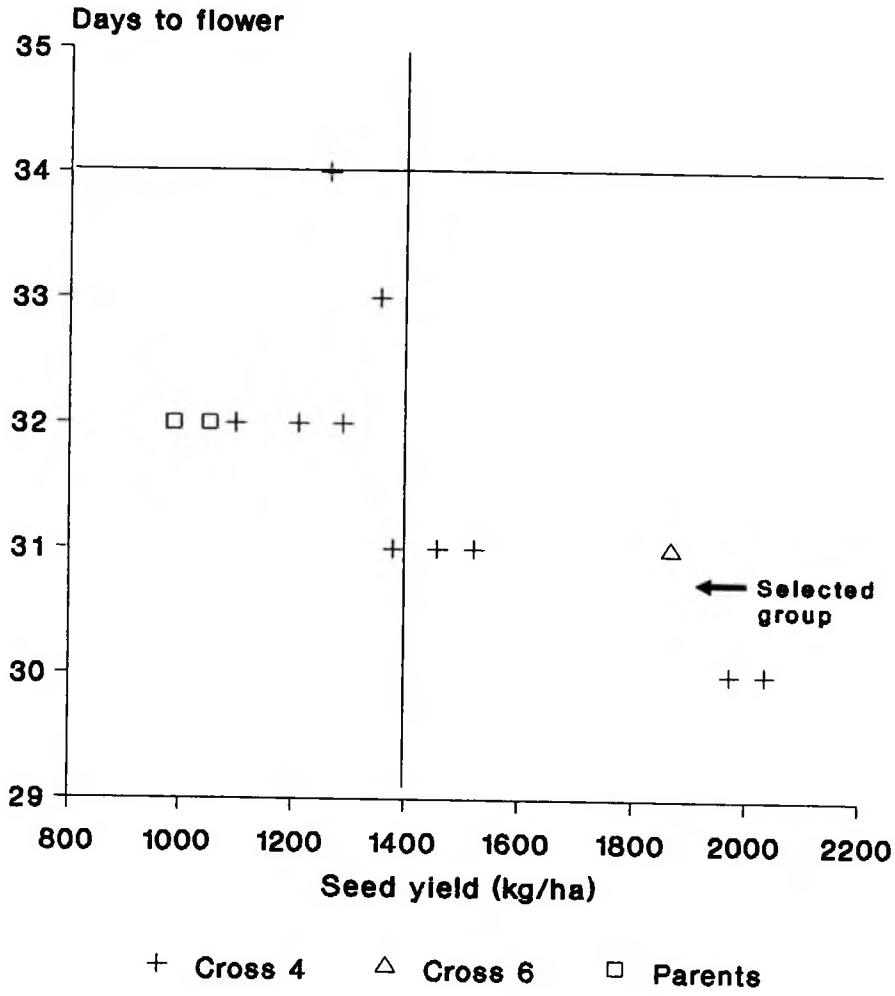

Fig. 4.26. Distribution of parents and F_4 families (summer) of the progeny of two cross combinations for days to flower and seed yield.

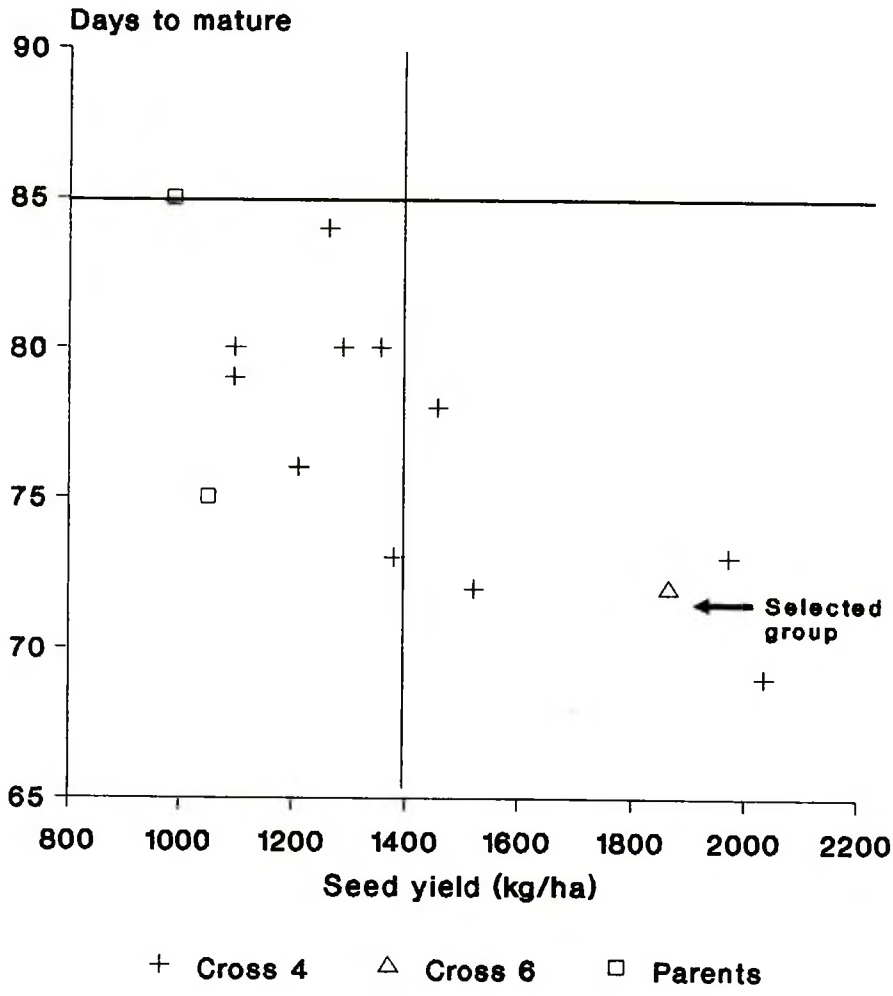

Fig. 4.27. Distribution of parents and F_4 families (summer) of the progeny of two cross combinations for days to mature and seed yield.

days and 7 within 76-85 days (Fig. 4.27). The parents, on the other hand, matured within a shorter range of period (75-85 days) with a mean of 80 days. The data on days to mature and seed yield were plotted on a graph. Truncation point for days to mature was set on 85 days keeping the seed yield at 1400 kg/ha (Fig. 4.27). On the basis of these two characters 5 families (MC- 14, MC-18, MC-66, MC-106 and MC-130) were selected.

The plant height of 12 selected families varied from 33.6 to 50.7 cm with a mean of 45.2 cm (Tables 4.46 and 4.47). Among these, plant height of one family was 33.6 cm, 2 within 35.1-40 cm, 2 within 40.1-45 cm, 5 within 45.1-50 cm and 2 above 50 cm (Fig. 4.28). The plant height of parents ranged from 40.2 to 50.5 cm with a mean of 45.4 cm (Table 4.47). The data on plant height and seed yield were plotted on the graph paper. The truncation point for plant height was drawn on 50 cm keeping the seed yield at 1400 kg/ha (Fig. 4.28). Five families were selected on the basis of these two characters. The families were MC-14, MC-18, MC-66, MC-106 and MC-130.

The number of pods/plant varied from 20 to 29 pods with an average of 24 pods (Tables 4.46 and 4.47). Among the families, 10 produced 20-25 pods and 2 produced more than 25 pods. Lower number of pods/plant was observed among the parents (Fig. 4.29) with a mean of 15 pods/plant. When the data on pods/plant was plotted along with seed yield on a graph it showed a normal distribution (Fig. 4.29). Truncation point for pods/plant was drawn on 20 and for seed yield at 1400 kg/ha. On the basis of these two characters 5 families were selected. The families were MC-14, MC-18, MC-66, MC-106 and MC-130.

Among the 12 families, number of seeds/plant ranged from 178 to 300 with a mean of 235. Among these, one family produced 178 seeds, 9 produced 200-250 seeds and the remaining two 2 produced above 250 seeds

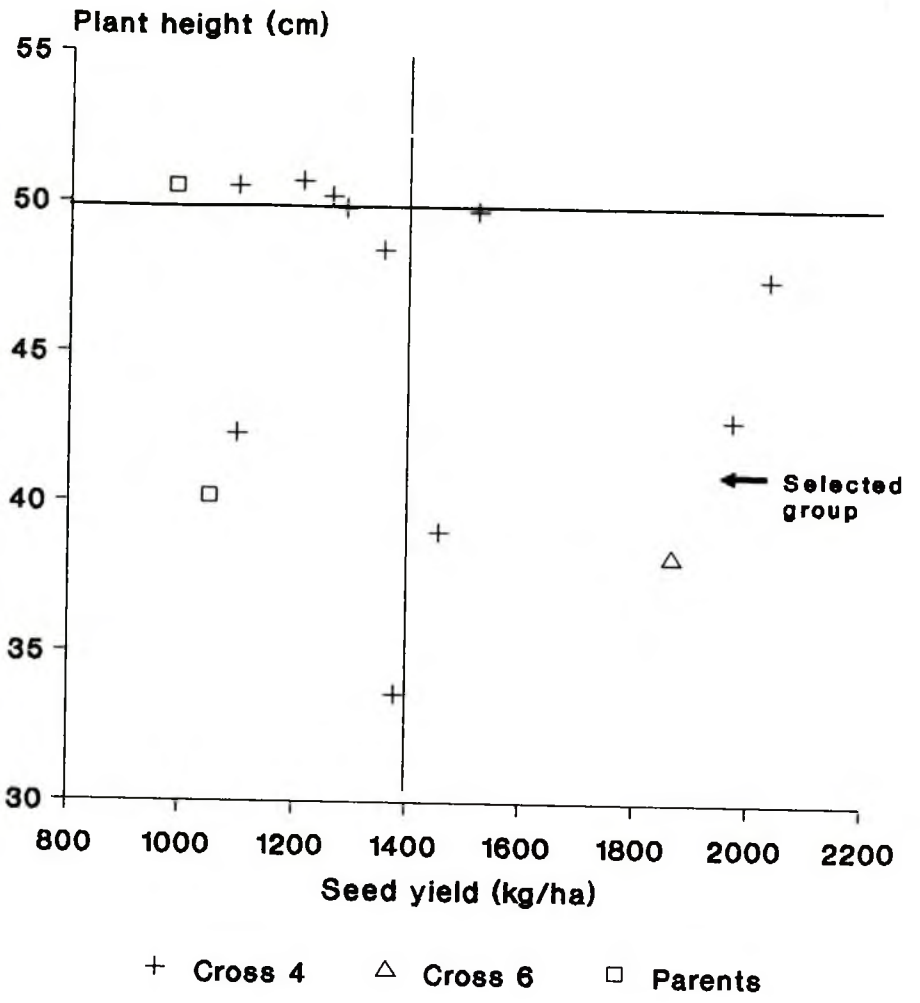

Fig. 4.28. Distribution of parents and F_4 families (summer) of the progeny of two cross combinations for plant height and seed yield.

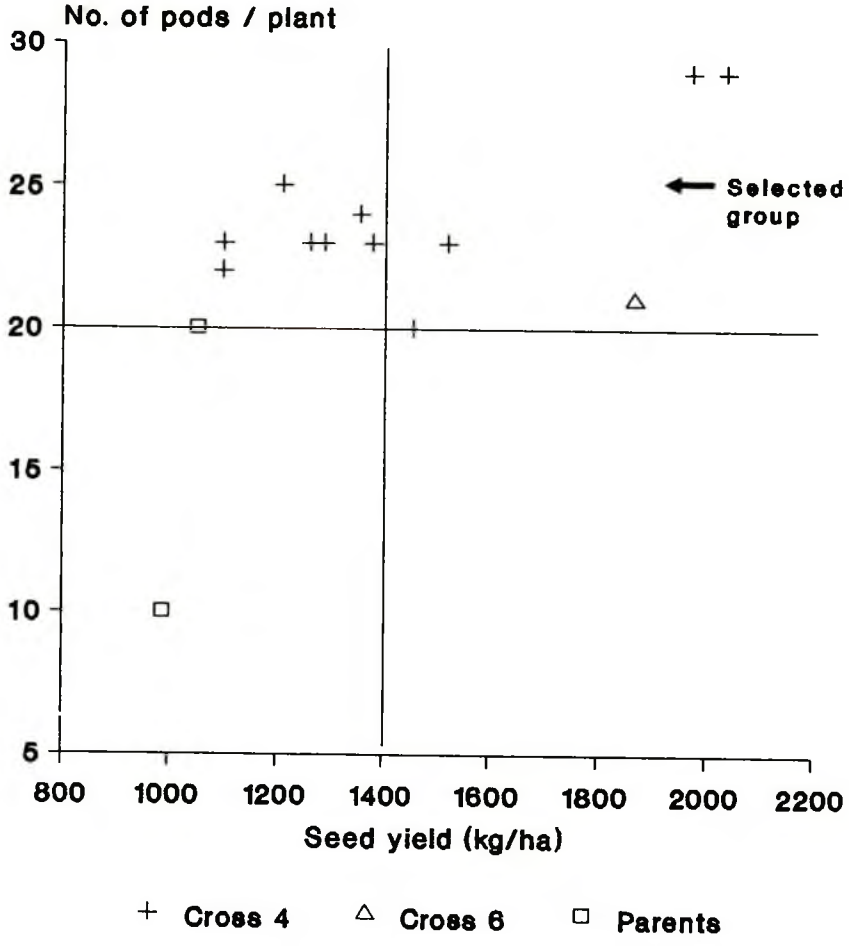

Fig. 4.29. Distribution of parents and F_4 families (summer) of the progeny of two cross combinations for number of pods/plant and seed yield.

(Table 4.46 and Fig. 4.30). On the other hand, the parents produced the lowest number of seeds/plant (124-187) with a mean of 156 seeds/plant. Among the families, the highest seeds/plant was produced by the family MC-18 (300 seed/plant) and the lowest by the family MC-69 (178 seeds/plant). The data on seeds/plant and seed yield were plotted on graph and for selection of families. Truncation point for seeds/plant was drawn on 200 and seed yield at 1400 kg/ha (Fig. 4.30). Five families were selected the basis of these two characters. The families were MC-14, MC-18, MC-66, MC-106 and MC-130.

The seed weight of the selected families ranged from 3.0 to 6.0 (g) with a mean of 4.1 (g) (Tables 4.46 and 4.47). Among these, 100-seed weight of 9 families were between 3.0-4.0 (g) , 2 between 4.1-5.0 (g) and one was 6.0 (g). Data on 100-seed weight and seed yield/plant were plotted on a graph and a truncation point for 100-seed weight was set on 4.0 (g). Truncation point for seed yield was at 1400 kg/ha (Fig. 4.31). Three families were selected on the basis of these two characters. The families were MC-14, MC-18 and MC-66. The range of seed yield of the selected families was from 1097 to 2034 kg with a mean of 1460.8 kg/ha (Tables 4.46 and 4.47).

Among these, seed yield of 2 families were between 1001-1200 kg, 5 between 1201-1400 kg, 2 between 1401-1600 kg and 3 between 1801-2100 kg/ha. Seed yield of the parents was low. The range was from 987 to 1051 kg with a mean of 1019 kg/ha.

The families were classified into three groups (Resistant, Tolerant and Susceptible) for scoring three diseases such as MYMV, CLS and PM. Among the 12 families, 4 were resistant, 6 tolerant and 2 susceptible to MYMV (Table 4.46). Among the 2 parents, one (ML-37) was tolerant and the other one (VC-1560D) was susceptible to MYMV. Out of 12 families, 2 were resistant, 8 tolerant and 2 susceptible to CLS disease (Table 4.46). On the

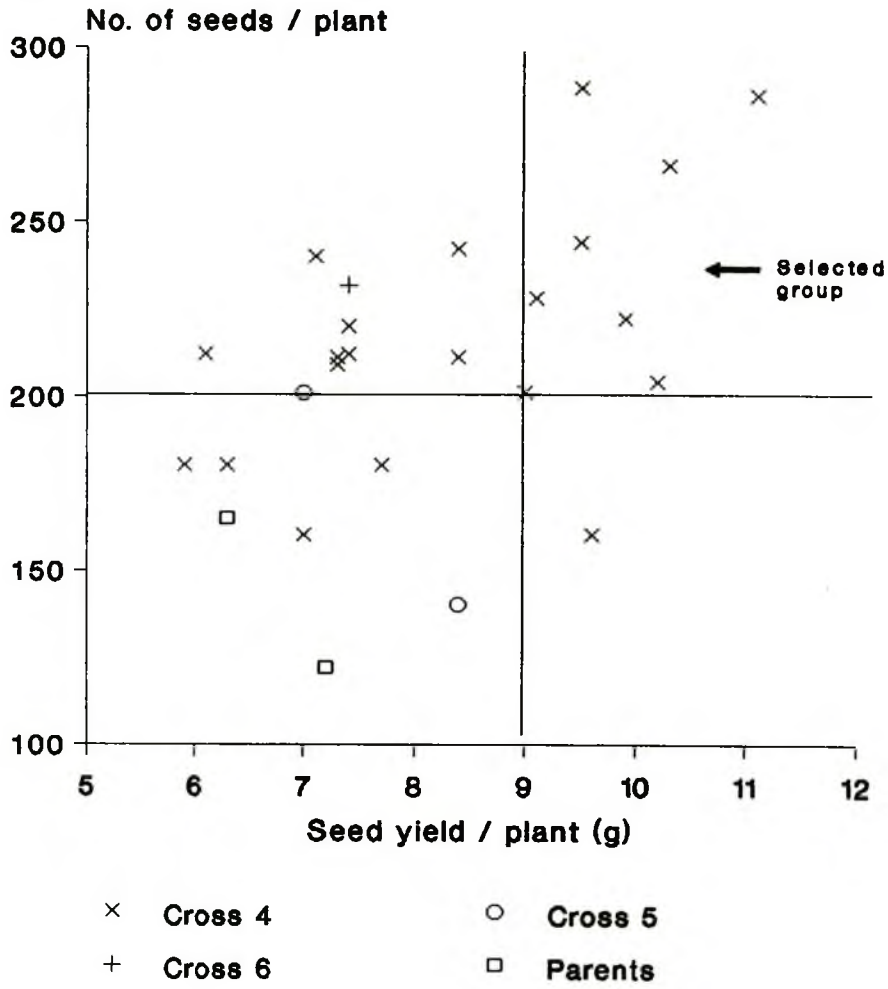

Fig. 4.30. Distribution of parents and F_4 families (summer) of the progeny of two cross combinations for number of seeds/plant and seed yield.

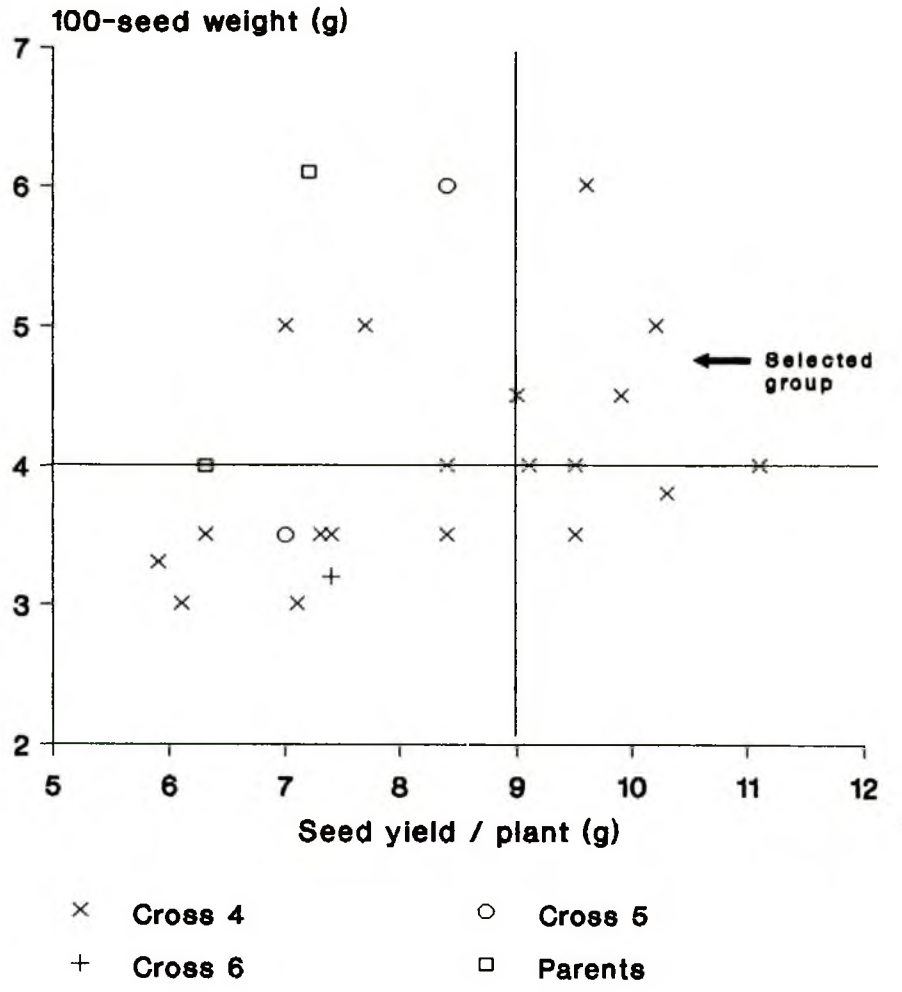

Fig. 4.31. Distribution of parents and F_4 families (summer) of the progeny of two cross combinations for 100-seed weight and seed yield.

other hand, one parent was resistant and the other was susceptible to this disease. Scores for PM indicated that 8 families were resistant, 2 tolerant and 2 susceptible (Table 4.46).

Table 4.46 . Mean performance of 12 selected families along with their parents for different varietal characters.

Parents / Selected families	Days to flower	Days to mature	Plant height (cm)	Pods/ plant (No.)	Seeds/ plant (No.)	100-seed wt. (g)	Seed yield/ kg/ha	Disease reaction		
								MYMV	CLS	PM
Parents										
MB-55-4	Did not flower			-		-	-	-	-	-
ML-37	32abc	75d	40.2b	20f	187h	3.8c	1051gh	T	S	S
VC-1560D	32abc	85a	50.5a	10g	124j	6.0a	987h	S	R	T
Cross 4										
MC-14	31bc	72e	49.7a	23cd	231e	4.0d	1521c	T	T	R
MC-18	30c	69f	47.5a	29a	300a	4.0d	2034a	R	R	R
MC-21	33ab	80b	48.4a	24bc	234de	4.5c	1354cde	T	T	S
MC-26	34a	84a	50.2a	23cd	213f	5.0b	1261ef	R	S	R
MC-36	32abc	76d	50.7a	25b	250c	3.5f	1209efg	T	T	S
MC-46	32abc	80b	42.3b	23cd	240d	3.0g	1098fgh	T	S	R
MC-48	31bc	73e	33.6c	23cd	254c	3.5f	1378cde	R	T	T
MC-66	31bc	78c	39.0b	20f	201g	6.0a	1456cd	T	T	R
MC-69	32abc	79bc	50.5a	22de	178i	4.0d	1097fgh	S	T	T
MC-80	32abc	80b	49.8a	23cd	209f	4.0d	1287de	S	T	R
MC-106	30c	73e	42.8b	29.0a	279b	3.8e	1970ab	R	R	R
Cross 6										
MC-130	31bc	72e	38.2b	21.0ef	234de	3.5f	1865b	T	T	R

Means with same letter(s) in a column do not differ significantly at 1% level of probability, according to DNMRT.

A total of 5 families were selected on the basis of different characters studied in F_4 for further evaluation (Appendix Table 8.6). After few years of evaluation, application was made to the National Seed Board (NSB) for releasing one family, MC-18 under the name 'BINAMOOG-5' for cultivation in summer season (Plate - 4).

Plate 4. Field view of MC-18

Table 4.47. Variation among 12 selected families along with their parents for different varietal characters.

Characters	Among the F_4 families				Among the parents			
	Range	Mean	S. D.	CV(%)	Range	Mean	S. D.	CV(%)
Days to flower	30-34	32	1.16	3.67	32-32	32	0	0
Days to mature	69-84	76	4.50	5.91	75-85	80	7.07	4.83
Plant height (cm)	33.6-50.7	45.2	5.80	12.83	40.2-50.5	45.4	7.28	6.03
Pods/plant	20-29	24	2.77	11.54	10-20	15	7.07	7.13
Seeds/plant	178-300	235	33.50	14.25	124-187	156	45.55	9.20
100-seed wt. (g)	3.0-6.0	4.1	0.79	19.27	3.8-6.0	4.9	1.55	0.69
Seed yield kg/ha	1097-2034	1460.8	326.20	22.33	987-1051	1019	45.25	4.44

I. Inheritance Study of MYMV

Like previous study the mutant line MB-55-4 was found to be resistant to MYMV and VC-1560D susceptible to this disease. The F_1 plants of the cross (MB-55-4 x VC-1560D) and the reciprocal were all susceptible to MYMV suggesting that MYMV resistance is a recessive character controlled by nuclear gene(s). The F_2 segregation in the cross MB-55-4 x VC-1560D and VC-1560D x MB-55-4 showed a close fit to the 15 highly susceptible/ susceptible : 1 resistant ratio. The F_3 progenies were in the ratio of 7 (highly susceptible/ susceptible) : 8 (segregating) : 1 (resistant). Thus it can be concluded that MYMV resistance is governed by two recessive genes (Table 4.48).

Table 4.48. Segregation for resistance to MYMV in F_2 and F_3 generations in mungbean.

Cross combination	Generation	Observed segregation			Expected ratio	χ^2	P
		Suscep -tible	Segre- gating	Resis- tant			
MB-55-4 x VC-1560D	F_2	52	0	4	15 : 1	0.097	0.70-0.80
MB-55-4 x VC-1560D	F_3	44	47	5	7 : 8 : 1	0.105	0.90-0.95
VC-1560Dx MB-55-4	F_2	155	0	10	15 : 1	0.077	0.70-0.80
VC-1560D x MB-55-4	F_3	76	80	9	7 : 8 : 1	0.436	0.80-0.90

J. Inheritance Study of Seed Coat Colour

The F_1 plants of the cross and its reciprocal had green seed coat colour. The result indicate that there were no cytoplasmic factors involved in the inheritance of this trait. The F_2 and backcross data of this cross is summarized in Table 4.49. It is revealed from the data that F_2 population gave a ratio of 3 green : 1 yellow seed coat. The backcross generation with the dominant parent, VC-1560D, had all 21 plants with green seed coat colour, while the backcross generation involving the recessive parent MB-55-4 gave a ratio of 1 green : 1 yellow seed coat colour. The chi-square list gave a good fit of monogenic inheritance with complete dominance of green seed coat over yellow.

Table 4.49. Breeding behaviour of F_2 and backcross populations of the cross VC-1560D x MB-55-4.

Cross combination	Generation	Expected ratio	Number seed coat colour			P
			Green	Yellow	Total	
VC-1560D x MB-55-4	F_2	3 : 1	239	78	317	0.75-0.90
BC1(VC-1560d x F_1)	-	-	21	-	21	-
BC2 (MB-55-4 x F_1)	-	1 : 1	8	12	20	0.25-0.50
	F_3	3 : 1	214	70	284	0.75-0.90

F_3 population comprising 31 families (22 with green seed coat and 9 with yellow) was studied. Among the 22 families with green seed coat colour, eight breed true and 14 segregated into 3 green x 1 yellow. All the 9 families with yellow seeds bred true.

DISCUSSION

A. Evaluation of Germplasm

Germplasm is the basic source for crop improvement. Improved crop varieties are being developed through the evaluation and selection of germplasm around the world. In mungbean, a large number of improved varieties have been developed through selection from the germplasm (Shanmugasundaram, 1988 and 1998). In the present study, the main aim was to select high yielding and/or disease resistant lines from 225 germplasm for future use in the breeding programme.

Among the 225 germplasm studied, 11 local lines (winter type) and 6 mutants which were developed at BINA through γ-irradiation did not flower when these were grown in summer season because of their sensitivity to photoperiod. From the remaining 208 germplasm, seven exotic and one local genotypes were selected mainly on the basis of seed yield and disease resistance. The genotypes that produced 6.0 (g) or more seed yield/plant and were resistant to at least two major diseases out of three such as mungbean yellow mosaic virus (MYMV), *Cercospora* leaf spot (CLS) and powdery mildew (PM) were selected. The only exception was made in selecting the local line (MB-87) which was the highest yielding among the local genotypes.

The main basis for selecting the highest yielding genotypes was seed yield/plant and resistance to diseases like MYMV, CLS and PM; but their mean days to flower, days to mature and plant height were less than for the 208 germplasm (Tables 4.1 and 4.2). This indicates that in this group of mungbeans, having characters like late flowering, late maturity and tallness were not associated with higher seed yield. On the other hand, mean number of pods/plant, number of branches/plant and 100-seed weight of the selected

genotypes was higher than the mean value of 208 genotypes indicating positive relationship of the above characters with higher seed yield.

The varietal characters of the 208 genotypes studied and findings of the other researchers in respect of these characters are described below.

a. Plant height

Many researchers found wide range of variability in plant height of mungbean genotypes. Paroda and Thomas (1988) evaluated 2,200 mungbean accessions and reported that maximum number of accessions fell in the frequency class of 41-51 cm for plant height. This range has similarity with the present study. Among the 208 genotypes studied, plant height of 84 genotypes ranged from 41 to 50 cm. Sandhu *et al.* (1988) found significant positive association between plant height and seed yield in one experiment and at the same time, they did not find any association between these two characters in another experiment. It indicated that the taller plants might not be always higher yielding types. Ahmed *et al.* (1978) also found negative correlation of plant height with seed yield. On the other hand, Gupta and Singh (1969), Singh and Malhotra (1970b) obtained positive correlation with seed yield. Correlation studies suggested that higher seed yield is associated with large plant (Gupta and Singh, 1969; Joshi and Kabaria, 1973; Yohe and Poehlman, 1975). Islam *et al.* (1993) found that plant height had no significant relationship with seed yield but had significant relationship with seeds per plant and pods per plant. Sandhu *et al.* (1988) found that plant height had a positive correlation with days to flower, days to maturity, number of branches, cluster per plant, pods per plant, pod length and seeds per pod, thereby indicating that early flowering and early maturing lines were shorter while late flowering and late maturing lines were taller. In the present

study, similar relationships were also found among the selected lines (Table 4.2). There are reports that shorter, more compact plants with high harvest index and more determinate growth habit are suited to short summer season, high plant population and multiple cropping patterns where mungbean is grown for the short period between two major crops (L. Singh, 1975).

b. Days to flower and maturity

Mungbean usually flowers for a month or more (Mac Kenzi *et al.*, 1975) and plants may contain flowers, green or immature pods and ripe pods at the same time, which require several pickings. Therefore, one of the major objectives of mungbean breeding is to select plants with shorter length of flowering period so that more or less uniform matured lines could be developed. Genotypes with low photoperiod sensitivity are generally early maturing. In the present study, a narrow range of variability was found in case of days to flowering. Medhi *et al.* (1980) also found no variability for days to flowering. It was observed in case of selected lines of this study that range of variability regarding days to flowering and maturity was narrower than to all the 208 genotypes indicating that the selected lines were more uniform in flowering and maturity.

c. Number of branches per plant

It was found in the present study that plants without any branch or with only one branch was low yielding. The selected high yielding lines had 2-3 branches per plant. Sandhu *et al.* (1988) found positive association of number of branches with pods per plant, plant height, seeds per pod and seed yield. Ahmed *et al.* (1978) also found a positive relation of branches per plant with seed yield.

d. Number of pods per plant

Number of pods per plant is one of the best indicators of seed yield for almost all grain legumes (Oseni *et al.*, 1992). Mungbean, in general, flowers abundantly, but a large number of flowers and pods abscise. Pod set in a sparse plant density was reported to be 50% (AVRDC, 1974). Savithri *et al.* (1978) reported that less than 25% of the flower buds become pods which is the most important yield contributing character. It was found in the present study that all the selected lines had more number of pods/plant, which indicated the positive relationship of this character with higher seed yield. In fact, pods/plant was the best yield contributing character of all the characters studied in 208 germplasm. Highly positive correlation between pods per plant and seed yield was reported by Gupta and Singh (1969). Singh and Singh (1973), Giriraj and Vijayakumar (1974), Sandhu *et al.* (1988), Pun and Villareal (1989), Basir *et al.* (1992) and Islam *et al.* (1993) also reported similar association in mungbean. It was observed by Malik *et al.* (1988) that an increase in seed yield of the F_1 hybrids was due to an increase in cluster and number of pods. They reported that the negative heterosis for seed size and pod length and positive heterosis for other yield contributing characters, viz. number of pods, seeds per pod and number of branches. This finding was similar to the previous reports of Singh and Jain (1970) and Malhotra (1983). Sandhu *et al.* (1988) also found that pods per plant had a positive correlation with plant height, number of branches, cluster per plant, pod length, seeds per pod and seed yield, but no association with 100-seed weight, days to flowering and days to maturity. This suggests that early maturing types having bolder seeds could be combined with types having higher number of pods per plant in order to obtain higher seed yield.

e. 100-seed weight

Generally two types of mungbean is grown in Bangladesh. These are i) golden yellow or yellow seeded cultivars grown in winter which are low yielding, photosensitive and have tendency to shatter but has a consumer preference for its colour and good flavour; ii) another type is comparatively high yielding, photo-insensitive, has less tendency to shatter but their seed coat colour is green. Both the types are small seeded (100-seed weight 2.5-3.0g). Since mungbean is mostly splitted and used as *dal* in Bangladesh, large seed size is not a factor for the consumer. Preference is only for well filled mature seeds. Bigger seeded varieties are mainly grown in Taiwan, the Philippines, Thailand and Australia where a substantial quantity of mungbean is used for sprouting. It was found in the present study that mean seed size (100-seed weight) of the selected lines was bigger than the mean seed size of all the 208 germplasm. This indicates that bigger seed size had positive effect on seed yield in this group of mungbeans. Gupta and Singh (1969), Singh and Malhotra (1970a) obtained positive association between these characters. On the other hand, Malhotra *et al.* (1974) and Ahmed *et al.* (1978) obtained negative association between seed size and seed yield.

f. Seed yield per plant

The per hectare average seed yield of mungbean is low in the tropics, only 0.41 t/ha (Anon., 1984b). Many reasons for low yield have been described in the chapter "Introduction" of this treatise. Breeding for improved plant type was initially emphasized to obtain high yield. The improved plant type in mungbean refers to more compact plants with high harvest index, more determinate growth habit and reduced photoperiod sensitivity. With the development of improved plant type, yield potential of

the AVRDC mungbean cultivars has increased from 1.0 t/ha to 2.75 t/ha under high population density of 400,000 plants/ha (Anon., 1984b). In the present study, some of the improved lines obtained through AVRDC performed better in respect of seed yield.

Seed yield is a complex character. Many workers have reported that a number of yield contributing characters were responsible for increased seed yield in this crop. Ahmed *et al.* (1978) showed that number of primary branches and number of pods per plant had significant positive correlation with seed yield per plant while days to first flowering, days to maturity and plant height had a negative correlation in a set of genotypes they studied. Sandhu (1978) evaluated 2,719 genotypes and found that seed yield had a positive correlation with pods per plant, plant height, number of branches, pod length and seeds per pod but found no association with 100-seed weight, days to flowering and days to maturity. He suggested that early maturing types having bolder seeds could be combined with high number of pods per plant in order to attain higher seed yield.

Basir *et al.* (1992) found a highly positive correlation between seed yield and number of filled pods per plant. Islam *et al.* (1993) also found that seed yield per plant had a close association with pods per plant and seeds per plant whereas 100-seed weight had negative significant relationship with seeds per plant and pods per plant.

Tikko *et. al.* (1996) proposed a plant type with thick stem, 2-3 erect branches, shorter internodes, clusters of pods in the top 60-75% of the nodes, small and thick leaves, long and thick pods, 12-18 seeds/pod as ideal to obtain high yield. He also mentioned that physiologically, the yield increase has to come from large seed size and more number of pods since seed number/pod is fixed.

g. Seed coat colour

In Bangladesh, there is a preference for yellow seeded mungbean. But among the 208 germplasm there was only one genotype (MB-24)with yellow seed coat colour. This genotype was found low yielding and susceptible to diseases. Seed coat colour was studied mainly to see the purity of the genotypes.

h. Reaction to three major diseases

i) Mungbean yellow mosaic virus (MYMV)

Mungbean Yellow Mosaic Virus is the most devastating viral disease of mungbean (Nariani, 1960; Nene *et al.*, 1972; Ahmed and Harwoord, 1973; Benigo and Dolores, 1977; Varma *et al.*, 1991 and Verma and Sandhu, 1991).This is a serious disease of mungbean in Bangladesh also. Both summer and winter mungbean cultivars are infected with this disease and the incidence is more severe in winter season (Ahmed *et al.*, 1981). There are claims that MYMV causes damage to mungbean crop up to 40% (Ahmed *et al.*, 1981). But in India some researchers found that this disease could cause up to 100% damage to this crop (Nene *et al.*, 1972). Ahmed *et al.* (1978) also found in their studies that in the severe cases specially in case of exotic strains there was complete yellowing of leaves and infected plants were stunted. Some of these lines bore a few flowers and almost no pods were formed. The yield losses in naturally infected susceptible cultivars vary with the time of infection. Early infected plants had more severe symptoms than late infected ones. Chlorosis, stunting and reduced branching contributed to yield losses.

In the present study, MYMV infection was a very important factor for determining seed yield of a particular genotype. Among 208 genotypes studied, none was found to be resistant to this disease. Although three lines of

India, such as Acc. No. 41 (ML-1), Acc. No. 94 (ML-5) and Acc. No. 95 (ML-3) were reported to be resistant to this disease by many researchers (Fernandez and Shanmugasundaram, 1988; Gill *et al.*, 1975; Chhabra and Kooner, 1980), but in the present investigation, only two lines ML-3 and ML-5 were found to be tolerant to this disease and ML-1 was found to be susceptible. This might be due to different races of virus and for favourable environmental conditions. Another line, Acc. No. 45 (ML-37) which was reported to be resistant to MYMV (Sandhu, 1978) was found tolerant in this study. It may be mentioned here that out of eight selected lines six were tolerant to this disease (Table 4.2). This finding indicates that high yielding lines are associated with MYMV resistance/tolerance.

ii) *Cercospora* leaf spot (CLS)

Cercospora leaf spot is a serious pathogen of mungbean. The disease occurs both in summer and winter seasons in Bangladesh. The epidemiology of CLS was studied and yield loss due to CLS was estimated to be 10% in resistant cultivars (Anon., 1984a). AVRDC has identified several breeding lines, which are resistant to CLS. Three such lines such as Acc. No. 95, Acc. No. 140 and Acc. No. 183 were evaluated in the present study. Among these three, only one (Acc. No. 183) showed resistance to this disease. It may be mentioned here that this accession is the only resistant line found in the present study. Among other two lines Acc. No. 95 showed tolerance and Acc. No. 140 showed susceptibility to this disease.

iii) Powdery mildew (PM)

Occurrence of the powdery mildew disease was not serious during the present investigation. It was observed that the disease appeared after the

formation of pods, for this reason the effect was little. Among the selected lines, three were resistant and all other was tolerant to this disease. Among 208 genotypes, none was found to be susceptible. It means that incidence of this disease during summer is not prevalent.

B. Yield Trials

Yield trials were conducted with the eight selected genotypes from 208 germplasm and five selected F_4 lines for further screening. Yield trials are the prerequisite of National Seed Board for registering new varieties. Trials conducted under the present study are described below:

a. Observation trial

The selected 8 genotypes were put under observation trial along with 5 true breeding F_4 lines (MC-41, MC-84, MC-103, MC-219 and MC-246) in summer, 1987. The F_4 lines were developed earlier through a cross between a mutant line MB-55-4 of BINA and the AVRDC line V-2773 (MB-95). The line V-2773 originated in India (Fernandez and Shanmugasundaram, 1988) was reported to have high level of resistance to CLS and PM and was also reported to be the source of resistance to MYMV. The line was officially released in Indonesia in 1983 under the local name 'Nuri'.

It was observed from the result (Table 4.4) that the F_4 line MC-246 out yielded all the genotypes/lines studied in the observation trial. This might be due to its high number of pods and resistance to MYMV and tolerance to two other major diseases. It was also observed from the result that the lines with resistance/tolerance to three major diseases performed better than the genotypes/lines susceptible to the diseases. Although the line V-2773 was reported to be resistant to MYMV in some countries, it showed susceptibility

to this disease in this observation trial indicating that true resistance to this disease is absent in this line.

Five lines including the local cultivar (MB-87) were selected on the basis of higher seed yield and resistance to the diseases for growing them in preliminary yield trial.

b. Preliminary yield trial

Preliminary yield trial was conducted at two locations, e.g., at Ishurdi and Kishoregonj in summer, 1988. The result showed that seed yield potential of these lines, in general, was much higher at Ishurdi compared to Kishoregonj. The reason for low yield at Kishoregonj in summer may be due to excessive rainfall during the growing and ripening period, which caused damage to this crop. This indicates that summer mungbean cultivation in this area is not profitable. In fact, farmers of this area do not cultivate summer mungbean and even they are not aware that mungbean could be cultivated in summer season. However, MC-246 produced the highest seed yield both at Ishurdi and Kishoregonj. Arwooth *et al.* (1988) also observed variation of seed yield in mungbean in different sowing season and in different locations. Only three lines, MB-8, MB-94 and MC-246 were selected on the basis of higher seed yield performance and resistance to diseases for further evaluation in the following year.

c. Advanced yield trial

Three lines selected from the preliminary yield trial were grown in the advanced yield trial at 4 locations of the country in summer, 1989. 'Mubarik' a released variety of BARI and the local line MB-87 were included in this trial as check. The locations were Ishurdi, Kishoregonj, Faridpur and Barisal.

It was observed that location had significant effect on seed yield of the lines studied. Yield performances of the lines was better in summer mungbean growing areas like Ishurdi, Faridpur and Barisal compared to Kishoregonj. MC-246 was selected for zonal yield trials due to its superior performance in all the 4 locations.

d. Zonal yield trial

Zonal yield trials with MC-246 were conducted in 1990 and 1991 at 5 locations, Barisal, Faridpur, Ishurdi, Mymensingh and Rangpur. New high yielding variety 'Kanti' of BARI was included in this trial instead of 'Mubarik'. The experiment of 1990 at Barisal, Ishurdi and Mymensingh were partially damaged by rain and performance of the lines at Rangpur was not satisfactory. However, the experiment was repeated in 1991 at all the 5 locations. In this year MC-246 produced significantly higher seed yield at three locations, i. e., at Barisal, Ishurdi and Faridpur while Kanti produced the highest seed yield at two other locations, i. e., at Mymensingh and Rangpur. Summer mungbean is mainly grown in the southern part of Bangladesh and it was found in these experiments that the newly developed strain MC-246 was very suitable for that area.

e. On-farm and on-station trial

On-farm trial was conducted in the farmers' field at Barisal, Faridpur, Ishurdi, Satkhira, Rangpur, Trisal and Mymensingh and on-station trials were conducted at BINA farm, Mymensingh; BJRI farm, Faridpur and BINA sub-station farm, Ishurdi in summer, 1992. The line MC-246 was found superior to 'Kanti' in respect of seed yield and disease incidence (Table 4.12).

After thorough field evaluation by the Field Evaluation Team of the National Seed Board the line MC-246 was released under the name, BINAMOOG-2 for cultivation all over Bangladesh particularly in the southern districts.

C. Hybridization

Reciprocal crosses between MB-55-4 and ML-37, MB-55-4 and VC-1560D, and ML-37 and VC-1560D were made to combine the desirable characters. The main characteristics of these three genotypes have been described in the preceding chapter 'Materials and Methods'.

It was observed in the study that in the reciprocal crosses between MB-55-4 and VC-1560D (Cross-3 and Cross-4), the percentage of success in crossing was the highest (57%) when MB-55-4 was used as a female parent (Table 4.14). Maximum number of desirable single plants was also selected in winter from this cross combination in the F_2 (Table 3.3). This might be due to the adaptiveness of the local mutant line MB-55-4 under our climatic conditions. Again in this cross combination when VC-1560D was used as the female parent, maximum number of desirable single plants were found to be suitable for selection in F_2 summer. The possible reason might be the photo insensitive character of the exotic line VC-1560D that was better suited in warm season. The mutant MB-55-4 is a photosensitive genotype and does not flower in long day photoperiod. For this reason, in summer a smaller number of desirable plants were likely to be found suitable for selection. It may be mentioned that the photoinsensitive character is dominant over photosensitive and this character is controlled by a single gene pair (Verma, 1971). However, Swindell and Poehlman (1978) identified a dominant or partially dominant gene (Ps), for sensitive to photoperiod in a mungbean genotype. They found

that the gene was expressed when the genotype was grown in 14-16 hour photoperiod regime, but not expressed in a 12- hour photoperiod.

In the cross combination MB-55-4 and ML-37 (Cross-1 and Cross-2), almost similar results were found as in Cross-3 and Cross-4 in selecting F_2 single plants. From the cross combination, ML-37 and VC-1560D, it was not possible to select suitable single plants from F_2 winter. This might be due to the exotic origin of both the lines, which were also susceptible to MYMV. However, a few F_2 single plants were found suitable for selection in this cross combination in F_2 summer.

The selected lines in both the seasons in F_2 were carefully screened and 60 and 24 individual plants were selected from winter and summer, respectively. After evaluation of F_3 generation 14 and 12 true breeding lines were selected for winter and summer, respectively.

a. Genetic study of F_1 and F_2 population

Genetic study on seed yield and six yields related characters were made in the non-segregating (F_1) and segregating (F_2) generations separately. For this study, F_1s of six crosses including parents were raised. Harvested F_2 seeds were divided in two halves for raising F_2 winter and summer separately. Data of seven characters including seed yield of both the generations, F_1 and F_2, were subjected separately to analyze phenotypic- and genotypic coefficients of variation, heritability and genetic advance following Burton (1952), Burton and De Vane (1953), Johnson *et al.* (1955) and Hanson *et al.* (1956). Results on genetic analysis revealed the following features as discussed below.

Results of analyses on phenotypic coefficients of variation (PCV) involving crosses and parents revealed that the values of each analysis varied greatly showing wide range within themselves for each character in a

generation irrespective of seasons. For example, PCV values for days to flowering in F_1 showed wide range and varied greatly within themselves and similarly PCV values of this trait in F_2 in each season showed wide range varying greatly within them. Similar trend was also observed in the results of genotypic coefficients of variation (GCV). These values of different crosses and parents in each generation irrespective of seasons varied greatly and showed wide ranges for a character.

It was observed from the results that the PCV and GCV values of the crosses i.e., the hybrid population in all cases irrespective of generations and seasons, except in few cases, were greater as it was expected than those of the parental values in all the characters. Moreover, PCV values were found larger than their corresponding GCV values but the differences between these two coefficients were low in all the characters and generations. This suggested that major part of the phenotypic variations of all the characters was of genetic in nature and the environmental effects were lower on the studied characters

Heritability estimates also showed wide range of variation in each generation for each character. The estimates of the parents were comparatively lower than those of all the crosses irrespective of F_1 and F_2 generations. All the heritability estimates of the crosses were high, except the case F_1 of Cross 2 in case of plant height where the value was moderate. High heritability estimates for different characters in mungbean have been detected earlier by many investigators as summarized in Table 2.1 and Table 2.2. High heritability value does not necessarily mean an increase in genetic advance (Johnson *et al.*, 1955). Thus, in this study, the hybrid population, both F_1s and F_2s did not exhibit high genetic advance in all the characters. In comparison to different characters, it was observed that the estimates of genetic advance

were high in all the crosses of hybrid population in case of number of pods/plant and seed yield/plant. High genetic advance accompanied by high heritability in these two traits indicated that the additive gene effects control these characters as has been reported earlier by Panse (1957) and Morton *et al.* (1982). Johnson *et al.* (1955) suggested that heritability estimate in combination with genetic advance was more reliable than heritability alone for predicting selection effect. Thus, in the present study high GCV and heritability values coupled with high genetic advance in all the crosses and generations, selection for number of pods/plant and seed yield /plant in all the crosses would be effective and satisfactory for practical breeding purposes. Tickoo *et al.* (1988) in 1000-seed weight, plant height and nodes/plant in mungbean and Hamid *et al.* (1994) in plant height and seed size of mungbean found high estimates of heritability accompanied by high genetic advance values. They indicated the additive nature of these characters for which the breeders for effective selection in mungbean could give attention. Earlier to these works, many investigators, such as Bhargava *et al.* (1966) for plant height and pods/plant, Paramasivan and Rajasekaran (1980) for pod length, 100-seed weight and seed yield and Shamsuzzaman *et al.* (1983) for number of branches/plant and number of pods/plant in mungbean also found high estimates for these two parameters and identified these characters where selection can be applied. With the help of these two parameters having high estimates, effective selection could be made in other pulses, which have been reported earlier by Srivastava *et al.* (1972) for pod length and number of seeds/pod in pea, by Singh *et al.* (1981) for number of pods/plant in pigeonpea and Apte *et al.* (1987) for 100-seed weight and seeds/pod in cowpea. In the present study, in case of 100-seed weight F_1s of Cross 1, Cross 2 and Cross 3 and F_2s of Cross 1 and Cross 2 of winter exhibited moderately

high genetic advance values accompanied by high values of heritability. This also suggested the additive nature of 100-seed weight of the first two crosses, but the character was more influenced by the environment. Thus, with moderate high genetic advance accompanied by high heritability selection for this character would also be effective only in case of Cross 1 and Cross 2. Similar results have been found by Tickoo *et al.* (1988) for seeds/pod and days to flowering in mungbean. They also found moderate high values of heritability and genetic advance for grain yield/plant. Moderate values of these two parameters were also observed by Hamid *et al.* (1994) for pods/plant in mungbean. According to the above investigators, these four characters would be reliable for effective selection in mungbean.

b. Selection in F_3 and F_4 generations

i) F_3 (winter)

Seeds of all the 206 selected plants were grown in 1987 for further screening. From this population a total of 60 individual plants were selected on the basis of different desirable characters and disease resistance. The mean values of each character were plotted against seed yield/plant separately. The characters showed normal distribution as it was expected. A truncation point for seed yield/plant was set on 9.0 (g). Nine grams seed yield/plant was set on an assumption that if a population of 200,000 were maintained/hectare then approximately 1,800 kg seeds/ha would be obtained. For other characters truncation points were different from each other depending on the nature of character and their relationship with seed yield, e. g., for days to flower truncation point was set at 34 days. Since a short duration mungbean crop is desirable to grow between two major crops, any family, which flowered

beyond 34 days, was discarded. For days to maturity the truncation point was set at 85 days and any family maturing beyond 85 days was discarded. In case of plant height, truncation point was 40cm since there are reports that compact plants with determinate growth habit and reduced photoperiod sensitivity are ideal for higher seed yield (Tickoo *et al.*, 1996). For number of pods/plant and seeds/plant the truncation points were 20 and 200, respectively. Any family that did not produce 20 pods and 200 seeds/plant was rejected. For 100-seed weight since seed size is not considered to be a consumer's preference a compromise was made, i. e., medium seed size was taken into consideration and a truncation point was set at 4.0 g/100 seeds.

It was found that out of 60 families, four (MC-37, MC-38, MC-107 and MC-149) fell in the selected group for all the characters studied. Four families (MC-14, MC-65, MC-98 and MC-99) fell in the selected group for 5 characters except 100-seed weight. It has been mentioned earlier that bigger seed size of mungbean is not important for Bangladesh as most of the people eat mungbean as *dal*. The families MC-60 and MC-95 fell in the selected group for 4 characters; the family MC-58 fell in the selected group for 3 characters (Appendix Table 8.3). In addition to the above-mentioned families, three (MC-30, MC-184 and MC-196) were selected on the basis of multiple disease resistance inspite of their slightly lower seed yield than 9.0 g/plant.

ii) F_4 (winter)

Fourteen promising families were evaluated in F_4. For further selection from these families, mean values of the 6 characters were plotted against seed yield. In case of F_4 all the truncation points for the characters were similar with F_3 except for seed yield. In F_4, seed yield/plot instead of seed yield/plant were recorded and converted into seed yield/ha. Truncation point for seed

yield/ha was set at 1,100 kg. Although a population of 20-25 plants/m^2 was kept during the study in F_4, the expected yield was not obtained from any of the families.

It was observed from the study that the families MC-38, MC-99 and MC-107 fell in the selected group for all the 6 characters. Families MC-14 and MC-30 were in the selected group for 5 characters and families MC-58 and MC-65 were for 4 and 3 characters, respectively (Appendix Table 8.4). In total, seven families were selected in F_4 generation. After evaluation for 7 years (1990-1996), two families, MC-30 and MC-99 were released as 'BINAMOOG-3' and 'BINAMOOG-4', respectively, in 1997 for cultivation in Bangladesh in winter season. Both these varieties are photosensitive in nature.

iii) F_3 (summer)

Seeds of all the 136 selected plants were grown in 3 replications. From this population a total of 24 individual plants were selected on the basis of different desirable characters including disease resistance. Truncation points for all the characters and seed yield/plant were similar as fixed in F_3 (winter).

It was found that out of 24 families, two (MC-18 and MC-46) fell in the selected group for all the characters studied. Families MC-14, MC-21, MC-26, MC-66, MC-80 and MC-106 fell in the selected group for 5 characters and the family MC-36 fell in the selected group for 4 characters (Appendix Table 8.5). Families MC-48, MC-69 and MC-130 were selected on the basis of multiple disease resistance inspite of their seed yield was less than 9.0 g/plant.

iv) F_4 (summer)

Twelve promising families were evaluated in F_4 generation. For further selection from these families mean values of all the 6 characters studied were plotted against seed yield. The truncation points for all the characters were similar to F_3 (summer) except for seed yield. In F_4, seed yield/plot instead of seed yield/plant were recorded and converted into seed yield/ha. Truncation point for seed yield/ha was set at 1,400 kg. Although a population of 20-25 plants/m^2 was kept during the study of F_4, the expected yield was not produced by any of the families. It has been mentioned earlier that if a plant produces 9.0 (g) seeds/plant and if a population of 200,000 is kept, expected seed yield would be 1,800 kg/ha. However, seed yield of the families of F_4 summer was higher compared to the families of F_4 winter. Mungbean is a warm season crop. This may be one of the reasons for increased yield in summer.

It was observed from the study that the families MC-14, MC-18 and MC-66 fell in the selected group for all the 6 characters. Families MC-106 and MC-130 were in the selected group for 5 characters (Appendix Table 8.6). In total, five families were selected from F_4 on the basis of the above mentioned criteria of which MC-18 is likely to be released as a variety (BINAMOOG-5) because of its superior performance.

D. Inheritance Study of MYMV

There are conflicting reports about the genetics of resistance to yellow mosaic viruses in different species of *Vigna*, claiming both susceptibility and resistance to be dominant. However, in most of the cases resistance was shown to be recessive and governed by two genes (Varma *et al.*, 1991). Two

mungbean hybrids obtained through crosses between a resistant and susceptible mungbean, remained free from yellow mosaic in a 2-year trial, whereas the susceptible variety used in the cross had high incidence of yellow mosaic (Misra *et al.*, 1978). Similarly, crosses between a resistant and susceptible variety were all resistant in F_1 and gave a 3 : 1 ratio in F_2 and 1 : 2 : 1 in F_3 indicating that resistance is dominant. Furthermore, crosses between two resistant blackgram varieties produced all resistant in F_1, a 15 : 1 ratio in F_2 and a 7 : 8 : 1 ratio in F_3 indicating that the genes in the two varieties were at different loci (Kaushal and Singh, 1988). The dominant nature of resistance was also supported by crossing between susceptible varieties of mungbean and *Vigna radiata* var. *sublobata* — a wild progenitor of mungbean, which was resistant to MYMV (Ahuja and Singh, 1977). Other researchers suggested that one recessive gene for resistance was involved (Thakur *et al.*, 1977b; Singh and Patel, 1977; Malik *et al.*, 1988).

In contrast to the above findings, like the present study, genetic studies involving many crosses of resistant and susceptible mungbean genotypes showed that resistance to yellow mosaic was governed by two recessive genes and that susceptibility was dominant over resistance (Shukla *et al.*, 1978; Shukla and Pandya, 1985; Sandhu *et al.*, 1985; Reddy and Varma, 1986). In all crosses including the reciprocals, all plants of the F_1 generation were susceptible, plants of F_2 segregated at a ratio of 15 : 1 and F_3 families segregated 7 susceptible : 8 segregating : 1 resistant. Shukla and Pandya (1985) labeled the genes as S_1 and S_2 for susceptibility and identified another gene I in mungbean as an inhibitor, so that the genetic combination of a resistant variety would be $s_1s_2s_2s_2ii$. The inhibitor I function against either gene S_1 or S_2 at a time, and was believed to be cytoplasmic. Further studies on the genetics of resistance to the virus, its vector and both might resolve the

conflicting results on the dominant or recessive nature of resistance to yellow mosaic.

No information is available on the pathogenic variability of the virus and the whitefly. Information on the diversity of genes conferring resistance in different germplasm lines/breeding lines is not available. Similarly, no information is available on the inheritance of tolerance to the whitefly. Such information needs to be generated to diversify the sources of resistance in the recommended varieties and to combine more diverse genes for resistance in the same genotype. However, available information suggests that incorporation of virus resistance can effectively be done by the pedigree or backcross methods (Verma and Sandhu, 1991).

E. Inheritance Study of Seed Coat Colour

Mungbean is used mainly as *dal* in Bangladesh. In the preparation of *dal* the mungbean is splitted and cooked. But in the market when the whole pulse is sold, consumers have preference for bright yellow coloured mungbean commonly known as '*Sonamoog*' means golden mung. It has been found that the local mungbean cultivars that are grown in winter have yellow seed coat colour. These local cultivars are normally low yielding type. To increase the yield of this crop the breeders are now using exotic high yielding genotypes. The exotic genotypes are mostly green seeded. The present study was undertaken to see the inheritance pattern of seed coat colour, so that the yellow seed coat colour could be transferred to the high yielding exotic genotypes. It was observed that a single recessive gene governed the yellow seed coat colour. The monogenic inheritance of the character indicates that the desired colour could be transferred easily through hybridization. Bose (1939) was the first worker to study the genetics of this character and he

postulated that two genes were responsible for seed coat colour. Murty and Patel (1972) found that green seed coat colour was dominant over yellow. van Rheenen (1965) assigned the symbols *G* and *S* to the dominant genes conditioning green and spotted seed coat colours, respectively. Singh and Patel (1977) studied the green and spotted seed colour characters and concluded that a single dominant gene conditioned each.

The works done under the present investigation have resulted in the generation of a) new information on the various parameters studied, b) three new high yielding varieties and c) some highly improved breeding lines which are in the advanced stages of development.

Chapter- VI
SUMMARY

SUMMARY

The research work of the present investigation is summarized below:

A. Evaluation of Germplasm

The main aim of evaluating 225 germplasm was to select high yielding and/or disease resistant lines. Eleven local lines and six mutants did not flower when these were grown in summer season because of their sensitivity to photoperiod. From the remaining 208 germplasm, seven exotic lines and one local line were selected.

The main basis for selecting high yielding genotypes was seed yield/plant with resistance/tolerance to diseases such as mungbean yellow mosaic virus (MYMV), *Cercospora* leaf spot (CLS) and powdery mildew (PM). During selection, it was noted that the mean of days to flower, days to mature and plant height of the selected genotypes were less than the mean of the remaining 208 genotypes. This demonstrated clearly that in this group of mungbeans, characters like late flowering, late maturity and tallness were not associated with higher seed yield. On the other hand, mean number of pods/plant, number of branches/plant and 100-seed weight of the selected genotypes were higher than the mean of the remaining 208 genotypes indicating positive relationship of these characters with higher seed yield.

In regard to diseases, no genotype was found to be resistant to MYMV disease. Of the eight selected lines, six were tolerant to this disease. This finding indicated that high yielding lines were associated with MYMV tolerance. In respect of CLS, only one line (Accession No. 183) showed resistance to this disease. Furthermore, the occurrence of PM was not serious.

The disease appeared after the formation of pods having produced only minor effect on seed yield.

An observation trial in summer, 1987 was conducted with 12 selected lines (seven from the germplasm, five selected F_4 and MB-87). The F_4 line MC-246 outyielded all the genotypes/lines. Ultimately, five lines were selected on the basis of higher seed yield and resistance/tolerance to the above diseases.

The result of the preliminary yield trial conducted in summer, 1988 showed that seed yield potential of the above five lines, in general, was significantly higher at Ishurdi compared to that at the Kishoregonj location. However, only three lines, MB-8, MB-94 and MC-246 were selected. Of these three lines, MC-246 produced the highest seed yield in both locations.

Advanced yield trial with the three selected lines was carried out in 1989 at 4 locations. The locations were found to have significant effect on seed yield. MC-246 was selected for the zonal yield trial due to its superior performance in all the 4 locations.

In the zonal yield trial, the selected line MC-246 produced highest seed yield at three locations, i.e., at Barisal, Ishurdi and Faridpur in the summer of 1991. During the same period the check variety Kanti produced the highest seed yield at two other locations, i.e., at Mymensingh and Rangpur. However, in on-farm trial in 1992 MC-246 was superior to 'Kanti' in respect of seed yield and disease incidence. Summer mungbean is mainly grown in the southern part of Bangladesh and that MC-246 was found suitable for that area.

After a thorough field evaluation by the Field Evaluation Team of the National Seed Board, the line MC-246 was released in 1994 as a variety under the name, BINAMOOG-2 for cultivation all over Bangladesh,

particularly in the southern districts. Till now this has proved to be the highest yielding mungbean variety of summer mungbean in the country.

B. Hybridization

In the reciprocal crosses between MB-55-4 and VC-1560D (Cross-3 and Cross-4), the percentage of success in crossing were highest (57%) when MB-55-4 was used as the female parent. From this cross combination, maximum number of desirable single plants was also selected in F_2 population grown in winter. This might be due to the adaptiveness of the local winter mutant line, MB-55-4 under the climatic conditions of Bangladesh. Again, when the exotic line, VC-1560D was used as the female parent, maximum number of selected single plants were found to be suitable for growing in summer. The possible reason might be the photo-insensitiveness character of the line; VC-1560D that was better suited in warm season. MB-55-4 is a photosensitive genotype that does not flower in long day photoperiod. In cross combination, MB-55-4 X ML-37 (Cross-1 and Cross-2), almost similar results i.e.; suitable F_2 single plants could be selected as in the progeny of Cross-3 and Cross-4.

From the cross combination, ML-37 X VC-1560D, it was not possible to select suitable single plants for winter from among the F_2 population; that might be due to the exotic origin of the two MYMV susceptible lines. However, for summer a few F_2 single plants could be selected.

The phenotypic coefficients of variation (PCV) of crosses and parents revealed that the values varied greatly showing wide range within themselves for each character in a generation irrespective of the season. Similar trend was also observed in the genotypic coefficients of variation (GCV). Except in a few cases, PCV and GCV values of the crosses were greater as expected than

those of the parental values, irrespective of the generation and the season in question were. Moreover, PCV values were found slightly larger than their corresponding GCV values. This suggested that major part of the phenotypic variations was of genetic in nature with low environmental effects.

Heritability estimates in both F_1 and F_2 also showed a wide range of variation than in the parents. Almost all heritability estimates of the crosses were high. In both F_1 and F_2 genetic advance values varied from character to character; these values in respect of all the characters were not the same. Furthermore, these two populations did not exhibit high genetic advance for all the characters. The estimates of genetic advance were high in case of number of pods/plant and seed yield/plant. High genetic advance accompanied by high heritability in these two characters indicated that additive gene effects controlled these characters. High GCV and heritability values coupled with high genetic advance in all the crosses and generations for number of pods/plant and seed yield /plant indicated selection would be effective for practical breeding purposes in all the crosses. In case of 100-seed weight F_1s of Cross 1, Cross 2 and Cross 3 and F_2s of Cross 1 and Cross 2 of winter exhibited moderately high genetic advance values accompanied by high values of heritability. This also suggested the additive nature of 100-seed weight of the first two crosses, but the character was more influenced by the environment. Thus, with moderately high genetic advance accompanied by high heritability, selection for this character would be effective only in case of Cross 1 and Cross 2.

a. Selection in F_3 and F_4 generations (winter)

A total of 60 individual plant progenies were evaluated in F_3. For further selection in this generation, the mean values of each character were

plotted against seed yield/plant separately. A common truncation point for seed yield/plant was set on 9.0 (g). For other characters, truncation points were different from each other depending on the nature of the character and their relationship with seed yield, e.g., truncation point was set at 34 days for days to flower, 85 days for days to maturity, 40 cm for plant height, 20 and 200 for number of pods/plant and seeds/plant, respectively. For 100-seed weight a compromise was made, i.e., medium seed size was taken into consideration and a truncation point was set at 4.0 g/100 seeds.

Out of 60 families 11 (MC-14, MC-37, MC-38, MC-58, MC-60, MC-65, MC-95, MC-98, MC-99, MC-107 and MC-149) were selected on the basis of the above mentioned characters associated with yield. In addition, three (MC-30, MC-184 and MC-196) were selected on the basis of multiple disease-resistance although they produced slightly less than 9.0 (g) of seeds/plant. A total of 14 true breeding families were selected from this generation.

Fourteen promising families were evaluated in F_4. For further selection from these families, the mean values of each character were plotted against seed yield separately. Except seed yield truncated at 1,100 kg/ha truncation points for all other characters were similar to the F_3 winter population. Seven families were selected from this generation. Of them two families, MC-30 and MC-99 were released as varieties as 'BINAMOOG-3' and 'BINAMOOG-4', respectively, in 1997 as winter varieties. These two varieties are photosensitive in nature.

b. Selection in F_3 and F_4 generations (summer)

A total of 24 individual plant progenies were evaluated in F_3. For further selection the truncation point for all the characters was kept similar to

the F_3 winter population. Nine families MC-14, MC-18, MC-21, MC-26, MC-36, MC-46, MC-66, MC-80 and MC-106 were selected. In addition, MC-48, MC-69 and MC-130 were selected on the basis of their disease resistance trait in spite of their slightly lower seed yield less than 9.0 g/plant.

Twelve promising families derived from F_3 were evaluated in the F_4 generation. The truncation points for all the characters were similar to the F_3 (winter) except for seed yield that was truncated at 1400 kg/ha. None of the families produced the expected yield. None the less, seed yield of the families of F_4 summer was higher compared to those of F_4 winter.

Five families (MC-14, MC-18, MC-66, MC-106 and MC-130) were selected from this generation of which MC-18 is likely to be released as 'BINAMOOG-5' because of its superior performance.

C. Inheritance Study of MYMV and Seed Coat Colour

a. MYMV

The reciprocal crosses, MB-55-4 x VC-1560D, yielded only susceptible F_1 individuals and segregated in the ratio of 15 susceptible : 1 resistant in F_2 generation. F_3 families segregated in the ratio of 7 susceptible : 8 segregating : 1 resistant suggesting that resistance for MYMV is governed by two recessive genes and that susceptibility is dominant over resistance.

b. Seed coat colour

The F_2 population of the cross, MB-55-4 x VC-1560D segregated in the ratio of 3 green : 1 yellow suggesting that a single recessive gene is governing the yellow seed coat colour. Because of the monogenic inheritance of the character the desired yellow colour could be easily transferred through hybridization.

Chapter- VII
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Chapter- VIII
APPENDIX TABLES

Appendix Tables

Appendix Table 8.1. Some varietal characters of 208 genotypes studied.

BINA Acc. No. (MB)	Original name/ Accession number of the line/variety	Source of collection (Country)	Days to flower	Days to mat-urity	Plant ht. (cm)	Br../ plant (No.)	Pods/ plant (No.)	100-seed wt. (g)	Seed yield / plant (g)	Seed colo-ur and luster	Disease reactions		
											MY MV	C L S	PM
1	S-8	India	30	68	44.5	2	20	3.5	6.1	GS	T	T	T
2	Pusa Baishakhi	India	30	70	40.5	2	11	3.5	2.5	GS	S	T	T
3	PS-7	India	30	68	40.0	1	12	3.0	2.8	GS	S	T	T
4	PS-10	India	29	68	38.3	2	10	3.0	3.0	GS	S	T	T
5	PS-16	India	30	68	38.0	1	11	3.2	2.7	GS	S	S	T
8	PS-16A	India	30	65	32.0	2	22	3.5	6.2	GS	T	T	T
9	PS-7 A	India	30	68	44.0	2	10	3.2	3.0	GD	S	T	T
10	K-851	India	34	70	44.5	2	9	3.5	2.5	GD	S	T	T
11	H-70-16	India	32	70	46.0	2	14	5.0	4.0	GS	S	S	T
12	Parto	Iran	34	74	48.0	3	4	5.0	1.8	GD	S	S	T
13	Mehre	Iran	35	78	50.0	3	6	5.0	1.1	GS	S	S	T
14	Gohar	Iran	34	79	46.0	3	5	5.5	1.7	GD	S	S	T
15	Kachanj Ijo	Indonesia	34	80	56.0	2	8	6.8	2.5	GS	S	S	T
16	Si Walek	Indonesia	32	72	42.0	2	7	5.5	3.1	GS	S	S	T
17	Arta Ijo	Indonesia	30	73	40.0	2	8	5.0	2.3	GS	S	S	T
18	Maos Karsi	Indonesia	32	72	38.0	2	10	5.5	1.6	GS	S	S	T
19	Bhakti	Srilanka	32	75	38.8	1	6	5.0	2.2	GS	S	S	R
20	BPI mungo	Philippines	35	78	46.8	2	5	5.5	2.3	GS	S	S	R
21	CES-114	Philippines	38	80	48.2	1	4	6.0	1.6	GS	S	S	R
22	CES-115	Philippines	36	80	60.0	2	5	6.5	1.8	GS	S	S	R
23	CES- 55	India	32	72	65.2	1	10	2.5	0.9	BM	S	T	R
24	Yellow mung	India	34	72	51.0	1	12	3.8	2.0	YD	S	S	T
25	LM-6	India	33	73	40.0	0	11	3.5	1.5	GS	S	S	T
26	LM-2016	India	32	70	65.0	2	11	3.5	2.3	GS	S	S	T
27	L-1694	India	34	74	45.0	1	7	3.0	1.8	GD	S	S	T
28	CES-IV-5	Philippines	30	70	60.0	2	7	3.0	1.2	GD	S	S	R
29	CES-5	Philippines	29	70	60.0	2	5	5.5	0.9	GD	S	T	R
30	CES-87	Philippines	34	75	46.8	1	12	4.0	3.0	GD	S	T	R
31	CES-14	Philippines	35	85	58.2	2	10	3.0	1.5	GS	S	S	T
32	CES-4-1	Philippines	36	86	70.0	3	11	3.0	2.1	GD	S	S	T
33	CES-Q-1	Philippines	32	80	63.0	1	8	4.0	2.3	GS	S	S	T
34	CES-10-21	Philippines	30	75	55.0	2	3	4.7	0.6	GS	S	S	T
35	CES-55c	Philippines	31	72	50.0	1	5	5.5	0.6	GS	S	T	R
36	CES-10	Philippines	32	72	65.0	1	12	5.0	3.8	GS	S	S	T
37	MG-50-10A	Philippines	32	70	62.0	2	8	5.0	2.6	GD	S	S	T
38	G-Glabrus	Srilanka	34	72	80.0	2	10	4.8	3.1	GD	S	S	T
39	Type-51-14	Srilanka	37	82	68.0	2	12	3.0	2.3	GD	S.	S	R

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											MY MV	C L S	PM
40	ML-2	Srilanka	35	72	57.0	2	12	3.5	2.5	GS	T	S	T
41	ML-4	Srilanka	35	82	65.0	2	14	3.5	3.6	GS	T	T	T
42	MG-50-G	Srilanka	35	74	48.0	2	10	5.0	4.1	GD	S	T	R
43	Type-51-69	Srilanka	35	70	47.0	1	8	4.0	1.3	GD	S	S	T
44	ML-1	India	35	72.	40.0	0	7	2.5	2.1	GS	S	T	T
45	ML-37	India	30	72	37.0	2	22	4.0	6.9	GS	T	T	R
46	Type-51	Srilanka	34	70	44.0	1	14	4.5	3.6	GD	S	S	R
47	Type-51 Sel 40	Srilanka	32	75	48.0	1	12	4.0	3.2	GD	S	S	R
48	CES-55A	Srilanka	36	75	62.0	2	8	6.0	3.0	GS	S	S	T
49	CES-87	Srilanka	36	87	58.0	2	6	5.0	2.4	GD	S	S	T
50	Type-51 Sel 41	Srilanka	36	87	60.0	2	9	4.5	3.3	GS	S.	S	T
51	M-350	Srilanka	32	70	38.0	1	10	4.6	3.4	GS	S	S	T
52	Type-51 Sel 43	Srilanka	37	80	42.0	1	11	4.0	2.3	GS	S	T	T
53	Vigna sp.	Srilanka	37	82	58.0	2	14	40	2.5	GS	T	T	R
69	Sl-1	China	34	78	78.0	2	12	3.5	2.1	GD	S	S	R
70	Sl-2	China	36	80	62.0	2	10	3.0	1.3	GD	S	T	R
71	Sl-3	China	32	80	58.0	2	11	4.0	2.2	GD	S	S	R
72	Sl-4	China	36	80	60.0	2	10	3.8	1.2	GD	S	S	R
73	Sl-5	China	36	89	55.5	2	10	4.0	2.2	DS	S	S	T
74	Sl-6	China	34	80	47.5	1	5	3.5	1.5	GD	S	T	T
75	Sl-7	China	34	83	36.5	1	8	4.0	1.7	GD	S	T	T
76	Goradaha	Bangladesh	34	83	30.5	1	12	4.0	2.5	GS	T	S	T
77	Takerhat	Bangladesh	34	83	65.0	2	11	3.5	2.6	GD	T	S	T
78	Madhabpasa	Bangladesh	32	79	46.0	2	12	4.0	2.3	DS	T	S	T
79	Chandpasa	Bangladesh	36	84	58.0	2	14	3.2	2.5	GD	T	S	T
80	Sikarpur	Bangladesh	35	84	52.0	2	15	3.5	2.8	GD	S	S	T
81	Gotia	Bangladesh	33	79	50.0	2	12	3.3	3.0	GD	S	S	T
82	Banaripara	Bangladesh	36	87	48.5	2	12	3.0	2.6	GD	S	S	T
83	Hoglakandi	Bangladesh	32	79	48.0	2	11	3.2	3.0	GD	T	S	T
84	Madaripur	Bangladesh	33	78	45.0	2	14	2.8	2.8	GS	T	S	T
85	Babugonj	Bangladesh	34	78	42.0	2	16	3.0	2.1	GD	S	S	T
86	Vjaypur	Bangladesh	33	83	43.5	2	12	3.0	2.8	GD	S	T	T
87	Bhola	Bangladesh	30	78	40.5	2	17	3.0	4.5	GD	S	S	T
88	MG-50-10A	Taiwan	34	80	71.0	2	4	5.0	1.8	GS	S	S	T
89	MG-50-10A(S)	Philippines	34	80	62.0	1	3	5.0	0.6	GS	S	S	T
90	Oklahoma	USA	34	82	58.0	1	5	5.0	1.1	GS	S	S	T
91	MG-30-4	S. Korea	33	80	47.7	2	12	4.0	1.1	GD	S	S	T
92	M-317	Taiwan	34	84	51.4	2	9	2.5	0.8	GD	S	S	T
93	Phlv-18	Philippines	34	80	56.1	2	8	6.0	1.6	GS	S	S	T

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											MY MV	C L S	PM
94	ML-5 (V-2272)	India	30	73	30.5	3	18	3.5	6.0	GS	T	S	T
95	ML-3 (V-2773)	India	30	75	35.0	3	22	3.8	6.8	GS	T	T	R
96	Locl CV-1	Taiwan	34	84	41.5	2	6	3.0	1.2	GD	T	S	T
97	V-2984	S. Korea	35	85	31.8	1	12	3.0	1.3	GS	S	S	T
98	V-3092	Taiwan	30	78	26.5	2	6	4.0	2.0	GD	S	S	T
99	V-3388	USA	34	80	44.5	1	15	4.5	3.2	GD	S	S	T
100	Uthong-1	Thailand	30	75	43.5	2	9	4.0	3.0	GD	S	S	T
101	V-3476	Philippines	32	77	50.0	3	16	2.5	1.0	GS	S	S	T
102	L-6604	Pakistan	36	86	60.0	2	14	2.5	2.8	GS	T	S	T
103	VC-1089-B	Taiwan	34	80	44.0	1	16	2.5	0.6	GD	S	S	T
104	VC-1163-2-2	Taiwan	32	79	52.5	2	13	5.0	2.6	GS	S	S	T
105	VC-1168-2B	Taiwan	34	80	44.0	2	9	4.0	1.5	GS	S	T	T
106	VC-1177-9	Taiwan	24	80	41.2	2	13	4.0	3.0	GS	S	S	T
107	VC-1209-3	Taiwan	32	78	37.5	2	14	3.5	2.6	GD	S	S	T
108	V-2013	Taiwan	35	87	51.0	2	15	4.5	2.4	GS	S	S	T
109	KJ-5	S. Korea	34	80	51.0	2	6	6.0	2.0	GS	S	S	T
110	VC-1089-B-29	Taiwan	38	80	49.0	2	9	7.0	1.8	GS	S	S	T
111	VC-1163-2-2B	Taiwan	36	80	30.4	1	5	6.0	2.1	GS	S	S	T
112	VC-1163-2-2-6	Taiwan	34	80	35.0	1	8	7.0	3.0	GS	S	S	T
113	VC-1177-9-5	Taiwan	34	80	47.0	1	12	5.0	3.2	GD	S	S	T
114	VC-1177-9-6	Taiwan	34	82	45.5	2	8	4.0	2.6	GD	S	S	T
115	1209-3-B	Taiwan	35	84	55.4	1	15	3.5	1.8	GD	S	S	T
116	1209-36-B	Taiwan	30	78	32.0	2	12	2.8	1.2	GS	T	S	T
117	1007-14-1	Taiwan	32	79	43.4	1	15	3.8	3.8	GS	S	S	T
118	1131-B-4	Taiwan	30	79	42.0	2	14	3.6	3.5	GD	S	S	T
119	1392-B-18	Taiwan	32	80	44.8	2	13	4.0	1.8	GS	S	T	R
120	VC-990-2B	Taiwan	34	84	44.0	2	10	4.0	1.9	GD	S	T	T
121	VC-1000-2B	Taiwan	35	84	50.6	1	8	3.0	0.9	GS	S	T	T
122	VC-1053-2B	Taiwan	35	86	41.5	2	7	3.0	2.3	GD	S	S	T
123	VC-1089-2B	Taiwan	34	82	42.2	2	8	5.0	2.4	GS	S	S	T
124	VC-1109-2B	Taiwan	33	80	48.0	1	9	3.0	2.1	GS	S	T	T
125	VC-1137-2B	Taiwan	34	82	43.6	2	10	4.0	2.7	GD	S	T	T
126	VC-1160-2B	Taiwan	34	82	47.0	2	12	3.0	2.5	GS	S	T	T
127	VC-1163-2B	Taiwan	32	80	73.0	3	13	5.0	3.4	GS	S	T	T
128	VC-1168-2B	Taiwan	32	80	54.5	2	4	5.0	1.9	GD	S	T	T
129	VC-1209-2B	Taiwan	30	78	37.5	3	8	3.0	3.2	GS	S	T	T
130	VC-1277-2B	Taiwan	30	78	60.0	1	10	4.0	3.2	GD	S	S	T
131	VC-1392-2B	Taiwan	34	89	80.0	3	3	4.0	1.6	GS	S	T	T
132	LM-612	India	36	94	52.0	2	15	5.5	2.8	GD	S	T	T

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											MY MV	C L S	PM
133	ML-4	India	34	80	55.4	2	5	3.0	3.6	GS	T	S	R
134	ML-28	India	34	80	51.4	2	5	3.0	3.0	GS	S	S	T
135	PLM-689	India	34	80	62.5	3	9	5.0	3.2	GD	S	S	T
136	PLM-888	India	34	80	40.0	1	12	2.5	2.0	GS	S	S	T
137	PLM-926	India	30	78	47.0	2	8	4.5	2.1	GD	S	S	T
138	PLM-932	India	34	87	48.0	2	13	3.6	3.1	GS	S	T	T
139	PLM-944	India	32	80	67.0	3	8	3.0	2.5	GD	S	T	T
140	PLM-945	India	32	80	80.0	1	8	4.0	1.8	GS	S	S	T
141	MO-163	India	32	80	63.5	1	10	4.0	1.4	GS	S	S	T
142	MI-936	Australia	32	80	40.5	1	12	4.5	2.3	GS	S	S	T
143	LM-410	India	34	88	47.0	1	15	4.0	1.5	GD	S	S	T
144	LM-413	India	32	80	46.0	1	13	3.5	1.8	GS	S	S	T
145	MO-194	India	32	80	52.0	2	11	3.4	3.1	GS	S	T	T
146	MO-214	India	32	80	53.0	2	8	3.4	2.6	GS	S	T	T
147	LM-29	India	32	80	57.5	3	12	3.5	3.2	GD	S	T	T
148	MO-701	USA	32	80	56.8	2	13	5.5	1.6	GD	S	T	T
149	MO-773	USA	34	80	49.5	1	10	5.0	1.7	GD	S	T	T
150	M-1746	Philippines	34	80	53.0	2	8	4.5	1.9	GD	S	T	T
151	M-1712	Philippines	34	80	56.0	2	10	4.0	2.3	GD	S	T	T
152	MO-160	India	30	78	51.5	3	12	3.5	3.0	GD	S	T	T
153	MO-162	India	34	80	51.0	1	13	3.5	3.8	GS	S	T	T
154	LM-278	India	34	80	37.0	3	15	3.0	3.6	GS	S	T	T
155	Jalgoan	India	32	80	45.0	1	10	4.0	0.8	GS	S	S	T
156	P-476	India	30	78	47.0	2	11	4.0	2.8	GD	S	T	T
157	LM-094	India	30	78	32.0	1	12	3.5	3.0	GD	S	T	T
158	LM-170	India	32	80	31.8	1	14	4.0	3.2	GS	S	T	T
169	ML-6	India	29	78	44.5	2	16	3.5	3.5	GS	T	S	T
160	LM-168	India	30	80	43.5	2	14	3.0	3.2	BS	T	S	T
161	LM-356	Australia	34	85	50.0	3	8	5.0	2.1	GS	S	S	T
162	LM-404	India	30	77	60.0	2	7	4.0	2.5	GS	S	T	T
163	MO-236	India	34	80	44.7	2	14	3.5	2.8	GS	T	S	T
164	LM-210	India	34	89	52.0	2	10	3.0	1.7	GS	T	T	T
165	LM-171	India	32	78	48.5	2	12	2.5	1.2	GD	S	S	T
166	EG-MG-G-12	Philippines	34	80	33.8	1	11	3.2	2.6	GD	S	S	T
167	MG-50	Philippines	30	75	48.5	1	3	4.0	1.0	GS	S	T	T
168	BPI-91	Philippines	29	75	36.5	0	6	3.5	0.9	GS	S	T	T
169	CES-44	Philippines	36	89	40.0	1	8	3.5	1.7	GD	S	T	T
170	PAEC-1	Philippines	33	80	35.0	1	4	3.0	1.2	GS	S	T	T

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											MY MV	C L S	PM
171	PAEC-2	Philippines	36	87	48.6	2	6	3.0	1.6	GS	S	T	T
172	PAEC-3	Philippines	34	80	52.5	1	8	3.5	1.8	GS	S	T	T
173	VC-2399	Taiwan	30	78	57.6	2	4	4.0	0.6	GD	S	T	T
174	VC-2401	Taiwan	34	80	44.2	2	4	4.5	0.8	GS	S	T	T
175	VC-2402	Taiwan	33	80	42.6	1	6	4.0	0.9	GS	S	T	T
176	VC-2407	Taiwan	30	78	30.8	1	8	4.0	1.2	GS	S	T	T
177	VC-2409	Taiwan	36	89	29.0	1	9	4.5	1.3	GD	S	T	T
178	VC-2414	Taiwan	34	84	31.5	0	7	4.0	1.8	GD	S	T	T
179	VC-2427	Taiwan	34	80	63.0	2	11	4.0	2.0	GD	S	T	T
180	VC-2447	Taiwan	34	80	31.0	1	5	4.0	1.3	GD	S	T	T
181	VC-2468	Taiwan	32	80	55.3	2	8	5.0	3.5	GD	S	T	R
182	VC-2470	Taiwan	36	89	34.7	0	7	4.5	2.2	GS	S	T	R
183	VC-1560D	Taiwan	30	80	65.0	3	18	6.0	8.2	GS	S	R	R
184	VC-1089	Taiwan	34	80	40.5	3	16	3.8	6.0	GD	S	T	T
185	VC-1163	Taiwan	30	75	42.0	1	13	4.0	3.4	GD	S	T	T
186	VC-1482D	Taiwan	35	87	39.0	1	12	4.0	1.8	GD	S	T	R
187	VC-1628A	Taiwan	34	80	47.0	1	10	3.5	1.5	GS	S	T	R
188	VC-2523A	Taiwan	29	78	48.0	1	14	3.5	3.3	GS	S	T	R
189	VC-2527A	Taiwan	32	80	60.5	2	12	5.0	3.1	GD	S	S	R
190	VC-2909A	Taiwan	32	80	53.3	2	10	5.2	2.8	GS	S	S	R
191	VC-2923A	Taiwan	33	80	48.4	2	9	4.3	3.0	GD	S	S	R
192	VC-2919	Taiwan	30	79	58.0	2	8	4.0	1.8	GD	S	S	R
193	VC-2964	Taiwan	32	82	68.6	2	10	4.2	3.5	GS	S	S	R
194	VC-2998A	Taiwan	34	85	40.5	1	12	4.5	2.3	GS	S	S	R
195	VC-3492	Taiwan	34	84	46.0	1	8	4.0	1.4	GD	S	S	R
196	VC-3418	Taiwan	34	84	70.5	2	7	4.0	1.3	GD	S	T	R
197	VC-1000	Taiwan	28	80	65.0	3	18	6.0	8.2	GS	S	T	R
198	Q-10593	Taiwan	35	87	78.0	1	8	3.5	1.8	GD	S	S	T
199	Q-23680	Taiwan	35	85	56.0	2	10	3.5	2.1	GS	S	T	R
200	Q-23681	Taiwan	34	80	42.0	1	8	3.5	1.5	GS	S	S	T
201	CPI-29224	Australia	37	86	43.0	1	12	5.0	3.5	GD	S	T	R
202	CPI-29823	Australia	36	93	78.0	2	14	4.5	3.6	GS	S	T	R
203	CPI-29955	Australia	36	90	76.0	2	7	4.3	1.6	GS	S	T	T
204	CPI-29971	Australia	34	85	70.0	2	6	4.0	1.7	GD	S	T	T
205	CPI-29972	Australia	34	80	49.0	1	10	4.0	3.1	GS	S	T	T
206	CPI-29973	Australia	34	82	47.5	1	5	3.5	1.0	GS	S	T	T
207	CPI-29974	Australia	34	83	45.6	1	8	3.5	1.2	GD	S	S	T
208	CPI-29975	Australia	36	84	52.1	2	11	4.5	3.3	GD	S	T	R

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											MY MV	C L S	PM
209	CPI-29976	Australia	32	80	52.3	2	7	3.0	1.3	GD	S	S	T
210	CPI-31116	Australia	32	80	54.4	2	8	4.2	2.0	GD	S	S	T
211	CPI-42964	Australia	32	80	54.3	2	12	4.0	3.0	GD	S	T	R
212	CPI-42965	Australia	33	82	54.0	2	12	4.0	3.2	GD	S	T	R
213	CPI-56226	Australia	34	80	42.0	1	11	4.0	3.0	GD	S	T	T
214	CPI-60799	Australia	36	84	43.0	1	8	3.8	1.9	GD	S	T	T
215	CPI-60800	Australia	34	82	48.5	1	7	4.5	2.1	GS	S	T	T
216	CPI-60801	Australia	32	80	45.0	1	6	4.0	1.6	GS	S	T	T
217	CPI-60806	Australia	33	82	51.2	2	8	4.5	2.6	GS	S	T	R
218	CPI-60807	Australia	34	84	66.5	2	12	5.0	4.2	GD	S	T	R
219	CPI-60815	Australia	35	86	52.3	2	8	5.5	2.8	GD	S	T	R
220	CPI-60816	Australia	35	85	47.8	2	9	4.0	1.6	GS	S	T	R
221	CPI-60822	Australia	34	80	75.0	2	7	4.2	1.9	GS	S	T	R
222	CPI-60824	Australia	32	80	62.0	2	10	4.0	2.1	GD	S	T	R
L-1	Local-1	Bangladesh	30	78	42.0	2	12	3.0	3.0	GS	T	S	T
L-2	Local-2	Bagladesh	30	78	44.0	1	13	3.0	3.2	GS	T	S	T
	Mubarik	Bangladesh	34	80	78.5	2	18	3.5	4.9	GS	T	S	T

*R = Resistant, T = Tolerant, S = Susceptible and HS=Highly susceptible

** GD = Green Dull, GS = Green Shiny, BM=Black Mosaic

Appendix Table 8.2. List of mungbean [*Vigna radiata* (L). Wilczek] genes.

Preferred Symbol	Synonym	Character	Reference
A	(G)	Green seed coat colour	Bose 1939; van Rheenen 1965
*ab	(a)	Almond biscuit pod colour	Sen and Ghosh 1959
al		Albino seedling	Sen and Ghosh 1960b
B		Dark green seed coat colour	Bose 1939
bf		Buff seed coat colour	Sen and Ghosh 1959
* Bl	(B)	Blue seed coat colour	Sen and Ghosh 1959
*Bla	(B)	Black seed coat colour	Murty and Patel 1972
*Bls	(B)	Bacterial leaf spot resistance	Thakur et al 1977c
Br		Colourless plant pubescence (N must be present)	Sen and Ghosh 1959
*Brn	(Br)	Brown seed coat colour	Murty and Patel 1972
Bsp		Black spot on seed coat	K. B. Singh and J. K. Singh 1970
C	(S.D. Ns)	Dull, rough seed surface. Dominant to glossy, smooth seed surface	Sen and Ghosh 1959
*C-2	(S2)	Dull, rough seed surface-2, Dominant to glossy, smooth seed surface	Bose 1939; Sen and Ghosh 1959; van Rheenen 1965; K. B. Singh and J. K. Singh 1970
*Cl	(C)	Single cluster per node. Dominant over 3 clusters per node	T. P. Singh and K. B. Singh 1970
Cmm		Cucumber mosaic virus, mungbean strain resistance	Sittiyos et al. 1979
*Dp		Dense plant pubescence. Dominant to medium intensity pubescence	Murty and Patel 1973
E	(L)	Lobed leaf margin. Dominant over entire leaf margin. Heterozygote is intermediate	Singh and Mehta 1953; Sen and Ghosh 1959
F		Cercospora leaf resistance	Thakur et al. 1977c
G		Green seed coat colour. Dominant to greenish-yellow	Sen and Ghosh 1959
*Gn	(G)	Green seed coat colour	Murty and Patel 1972
*Grn	(G)	Bottle green seed coat colour	Singh 1973
I-1		Simple inflorescence-1 (I-2 must be present)	Sen and Ghosh 1959
I-2		Simple inflorescence-2 (I-1 must be present)	Sen and Ghosh 1959
Ic		Incised leaflets. Dominant over ovate shape leaflets	Pokle 1972
*in-al	(i)	Inhibitor of albino seedling, al.	Sen and Ghosh 1960b
La	(N)	Lanceolate leaf. Semidominant and lethal when homozygous	Singh and Saxena 1959
lp		Light popcorn pod colour	Sen and Ghosh 1959

Preferred Symbol	Synonym	Character	Reference
M		Mosaic seed coat pattern	Murty and Patel 1972
N		Colourless plant pubescence (Br must be present)	Sen and Ghosh 1959
O		Light-yellowish olive flower colour and deep red veins on pod sutures. Partially dominant to olive yellow flowers and green pod sutures	Bose 1939
P		Purple hypocotyl. Dominant to purple spotted hypocotyl	Sen and Ghosh 1959
*Pe	*(C)	Purple epicotyl. Dominant to purple spotted and green epicotyl	Sen and Ghosh 1959
*Pe^{s}	(c^{b})	Purple spotted epicotyl. Dominant to green epicotyl	Sen and Ghosh 1959
Pg		Pale green flower colour. Dominant to pg^{b} and pg^{n}.	Murty and Patel 1973
* pg^{b}	(Pb)	Bryta yellow flower colour. Dominant to pg^{n}	Murty and Patel 1973
*pg^{n}	(Pn)	Naphthalene yellow flower colour	Murty and Patel 1973
*Pg	(A)	Purple hypocotyl	Swindell and Poehlman 1973
Ps		Photoperiod sensitive	Swindell and Poehlman 1973
R		Red colour of cotyledons, hypocotyl and top of leaflet stalk	van Rheenen 1965
*Sp	(S)	Spotted seed coat	van Rheenen 1965
T		Twining habit	Sen and Ghosh 1959
Tp		Swollen pod tip. Dominant to tapering pod tip	Sen and Ghosh 1959
v		Mungbean yellow mosaic virus resistance	Thakur et al. 1977c
Y		Yellowish green seed coat colour. Gene Yg must be present	Singh 1973
*Yg	(P)	Yellowish green seed coat colour. Gene Y must be present	Singh 1973

Source : Fery 1980.

* Proposed new symbol (Fery 1980).

Appendix Table 8.3. Selection of families in F_3 (winter) on the basis of six characters.

Selected families*	Characters on which the families were selected					
	Days to flower	Days to maturity	Plant height	Pods/ plant	Seeds/ plant	100-seed weight
MC- 14	√	√	√	√	√	-
MC- 37	√	√	√	√	√	√
MC- 38	√	√	√	√	√	√
MC- 58	√	-	√	-	-	√
MC-60	-	-	√	√	√	√
MC-65	√	√	√	√	-	√
MC-95	-	√	-	√	√	√
MC-98	√	√	-	√	√	√
MC-99	-	√	√	√	√	√
MC-107	√	√	√	√	√	√
MC-149	√	√	√	√	√	√
Total	8	9	9	10	9	10

* Families MC-30, MC-184 and MC-196 were selected on the basis of multiple disease resistance

Appendix Table 8.4. Selection of families in F_4 (winter) on the basis of six characters.

Selected families	Characters on which the families were selected					
	Days to flower	Days to maturity	Plant height	Pods/ plant	Seeds/ plant	100-seed weight
MC-14	√	√	√	√	√	-
MC-30	√	√	√	√	√	-
MC-38	√	√	√	√	√	√
MC-58	-	-	√	√	√	√
MC-65	-	-	-	√	√	√
MC-99	√	√	√	√	√	√
MC-107	√	√	√	√	√	√
Total	5	5	6	7	7	5

Appendix Table 8.5. Selection of families in F_3 (summer) on the basis of six characters.

Selected families*	Characters on which the families were selected					
	Days to flower	Days to maturity	Plant height	Pods/ plant	Seeds/ plant	100-seed weight
MC-14	√	√	-	√	√	√
MC-18	√	√	√	√	√	√
MC-21	√	√	-	√	√	√
MC-26	√	√	-	√	√	√
MC-36	√	√	-	√	√	-
MC-46	√	√	√	√	√	√
MC-66	√	√	√	-	-	√
MC-80	√	√	-	√	√	√
MC-106	√	√	√	√	√	-
Total	9	9	4	8	8	7

* Families MC-48, MC-69 and MC-130 were selected on the basis of multiple disease resistance

Appendix Table 8.6. Selection of families in F_4 (summer) on the basis of six characters

Selected families	Characters on which the families were selected					
	Days to flower	Days to maturity	Plant height	Pods/ plant	Seeds/ plant	100-seed weight
MC-14	√	√	√	√	√	√
MC-18	√	√	√	√	√	√
MC-66	√	√	√	√	√	√
MC-106	√	√	√	√	√	-
MC-130	√	√	√	√	√	-
Total	5	5	5	5	5	3