ISSN 1479-2621

Plant Genetic Resources 2(2); 73–80
DOI: 10.1079/PGR200433

The potential of enhanced germplasm for mungbean (*Vigna radiata* (L.) Wilczek) improvement

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Received 15 November 2003; Accepted 19 March 2004

Abstract

Mungbean (*Vigna radiata* (L.) Wilczek), also known as greengram, is the most widely cultivated Asian *Vigna* species. Improved mungbean cultivars have a narrow genetic base that limits yield potential and they are poorly adapted to varying growth conditions in different agro-ecological conditions. The genetic potential of landrace germplasm accessions in genebanks therefore needs to be better exploited. Germplasm core collections are made of a reduced set of representative accessions from the entire diversity maintained by genebanks. This subset of accessions can be used for testing general combining ability with local germplasm in the search for yield enhancement. Core collections also help breeders in selecting parental material that could maximize potential genetic gain from derived hybrid populations. At the National Bureau of Plant Genetic Resources (NBPGR), India, genetic enhancement/prebreeding studies in mungbean have been initiated involving diverse parents mainly from the cultivated gene pool, using the Bureau's core collection as starting material. Germplasm enhancement aims at widening the genetic base of breeding materials by transferring desired genes from unimproved germplasm into enhanced varieties. Mild and decentralized selected material was maintained in target sites across the country. A total of 102 progenies were advanced to F_5 for further selection and use by the breeders in Delhi. The genetic potential of a few selected enhanced progenies with desired plant types and better yield-related traits is presented in this paper. The study clearly demonstrates the potential of germplasm accessions conserved in genebanks for use in large-scale base-broadening efforts in mungbean.

Keywords: core collection; germplasm enhancement; mungbean; *Vigna radiata*

Introduction

Mungbean (*Vigna radiata* (L.) Wilczek), also known as greengram, is one of the most important pulses in Asia. It is the most widely distributed grain legume of the six Asian *Vigna* species and represents an important source of dietary protein in South and South-East Asia, where consumption of animal protein is relatively low. It is used primarily as *dahl* (whole, split or husked beans). Preparations such as weaning foods (porridge, dry mix), snacks (deep fried, crunchies, cookies, breakfast bun), sprouts, noodles, biscuits and textured meat are also made from it. Green pods are cooked as vegetables. The seed coat and broken decorticated cotyledons are fed to livestock and poultry. The dried straw, including the pod shells, is fed to dairy animals. Due to its popularization in non-conventional regions, seasons and crop associations, the area under its cultivation in India has risen considerably in recent years. Unlike cereals and other pulses, the mungbean-growing area has doubled in the last 25 years with an annual rate of 2.5% (Kim, 1994). This growth is very likely to continue because its

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short growth duration makes it suitable for various cropping systems and is much favoured in Asia.

India accounts for about two-thirds of total global mungbean production (Verma and Brar, 1994). Most mungbean cultivars used today in India are largely photosensitive, indeterminate with low harvest index and low grain yield (Tickoo *et al.*, 1988, 1994). The improved varieties developed in earlier phases were invariably pure line selections from local germplasm. The proportion of the improved varieties developed through hybridization or mutation breeding has increased in recent years. These varieties have, however, a narrow genetic base caused by several bottlenecks during domestication, by migration or epistatic and disease effects. Grain legumes have been grown traditionally on marginal lands of low fertility. Thus, even though different species of *Vigna* and other pulses were domesticated several thousand years ago, they are still grown in India in edaphic conditions which are not very different from those in their native habitats. As a result, natural selection has continued to play a major role in the evolution of these crops even after domestication (Jain and Mehra, 1978).

In a recent study (Lakhanpaul *et al.*, 2000), based on randomly amplified polymorphic DNA (RAPD) analysis, the extent of polymorphism in modern Indian mungbean cultivars was found to be moderate to low, and the close similarity between cultivars could be explained by a high degree of commonness in their pedigrees. The narrow genetic base of mungbean cultivars, therefore, emphasizes the need to exploit a larger number of germplasm accessions having diverse morpho-agronomic traits in cultivar improvement programmes. It is widely accepted that any future sustainable increase in crop productivity will require, amongst other things, an increased use of plant genetic resources, through plant breeding. Yet despite the great amount of diversity assembled in collections and available *in situ*, a lack of diversity/variation within the particular pools of genetic resources is encountered. Base-broadening programmes are therefore important in maintaining or increasing current levels of diversity to the benefit of breeders, farmers and other users.

The National Bureau of Plant Genetic Resources (NBPGR), New Delhi, maintains over 2500 accessions of mungbean. Earlier analyses have shown extensive variability for various morphological and yield-related traits (Kawalkar *et al.*, 1996; Bisht *et al.*, 1998a, b). While offering opportunities for base-broadening efforts, the large number of accessions involved is itself a disincentive for exploitation. A core collection strategy offers a more attractive and affordable approach. This paper explores the use of such a strategy for genetic base-broadening of mungbean. We hope that this work will provide the basis for a large-scale genetic base-broadening exercise in mungbean by utilizing the full range of diversity in the existing gene pool.

Materials and methods

To constitute the core collection, 152 mungbean accessions were extracted from 1532 indigenously collected materials, using a Principal Component scoring strategy (Bisht *et al.*, 1998b). Of these, 34 unadapted farmers' landraces were chosen (Table 1) for intercrossing in various combinations. These parental lines represented locally grown genotypes from different agro-ecological regions of the country and lacked wider adaptability primarily due to photoperiod- and thermo-sensitivity, but possessed certain desirable traits such as resistance/tolerance to biotic/abiotic stresses, plant morphology and quality. Only 15–20% of the diversity of the existing mungbean landraces in the genebank were used in the present study.

The selected landraces were used as parents of segregating populations. During the 1998 and 1999 cropping seasons, 132 crosses were made in various combinations between the core collection materials and some well-adapted location-specific improved cultivars (K-841, SML-244, ML-515, Ganga-I, Pusa-9531, TAP-7, PS-16, ML-267, ML-613 and Co-3). A weak and progressively decentralized selection regime was applied in four target environments: the University of Agricultural Sciences, Dharwad, and three NBPGR centres—Cuttack, Amravati and Delhi, in order to exploit genotype × environment interaction and develop location-specific improved germplasm.

At Delhi, the F_2 progenies were grown in replicated trials (two replications) using a randomized block design. Desired types were selected for further advancement in F_3. Further selections were made within replicated F_3 progeny trials. The identity of each of the selected F_2 plant progenies was maintained in the later generations. During the F_3 generation not all the pods were picked from the selected plants for further progeny advancement. The remaining pods of the selected plants were bulk harvested together with the leftover plants. Since mungbean can be successfully grown both in spring/summer (March to June) and the rainy season (July to October), two generations could be advanced in one year at Delhi. Selected progenies were advanced to F_4 and further selections were made in F_4. Selected F_2-derived F_5 progeny lines were grown in a replicated (three replications) randomized block design, adopting recommended agronomic practices both during spring/summer and the rainy cropping season of 2002 at Delhi. The performance of these progenies was compared with

Table 1. Indigenous parental lines used for intercrossing from the core collection

S. No.	Accession	Place of collection/origin	State/source	Days to maturity and other distinct features
1	IC-615-5	Hyderabad	Andhra Pradesh	70–75 days, long pods, high number of seeds per pod, raceme position below canopy, high fruit-setting capacity
2	IC-618-5	Kanpur	Uttar Pradesh	75–80 days, long pods, high fruit-setting capacity
3	IC-2056-2	Kalimpong	West Bengal	70–75 days, synchronous flowering, high fruit-setting capacity, dwarf plant height
4	IC-8917	Jodhpur	Rajasthan	70–75 days, synchronous flowering, high fruit-setting capacity, low susceptibility to bruchid infestation
5	IC-10184-4	Solan	Himachal Pradesh	65–70 days
6	IC-10499	Dhumra	Gujarat	70–75 days, low susceptibility to bruchid infestation
7	IC-12434	Dholi	Bihar	65–70 days
8	IC-24789	Warangal	Andhra Pradesh	70–75 days
9	IC-8592-3	Kotochamba	Himachal Pradesh	65–70 days
10	PLM-21	Arrah	Bihar	75–80 days, synchronous flowering, high fruit-setting capacity
11	PLM-32	Arrah	Bihar	65–70 days, bold seeds
12	PLM-76	Dholi	Bihar	60–65 days
13	PLM-88	Sabour	Bihar	65–70 days, high fruit-setting capacity, bold seeds
14	PLM-125	Arrah	Bihar	60–65 days, bold seeds
15	PLM-184-1	Nagpur	Maharashtra	60–65 days, bold seeds
16	PLM-231	Rewa	Madhya Pradesh	70–80 days, synchronous flowering
17	PLM-334	Jhansi	Uttar Pradesh	55–60 days, bold seeds, synchronous flowering, determinate growth habit, low leafiness
18	PLM-340	Nagon	Himachal Pradesh	75–80 days, synchronous flowering
19	PLM-350	Narela	Himachal Pradesh	65–70 days, high fruit-setting capacity
20	PLM-541	Jabalpur	Madhya Pradesh	60–65 days
21	PLM-562	Giddarbala	Punjab	60–65 days, bold seeds
22	PLM-619	Delhi	Delhi	60–65 days
23	PLM-625	Jaipur	Rajasthan	75–80 days
24	PLM-666	Wankaner	Rajasthan	60–65 days
25	PLM-694	Palanpur	Gujarat	70–75 days
26	PLM-734	Samatra	Gujarat	70–80 days, tall type
27	PLM-748	Jharobi	Gujarat	60–65 days
28	PLM-759	Sendra	Rajasthan	75–80 days
29	PLM-777	Kotputli	Rajasthan	60–65 days
30	PLM-818	Kota-Jhalwa Rd.	Rajasthan	60–65 days
31	PLM-829	Jhirnia	Rajasthan	70–75 days, bold seeds
32	PLM-884	Bhamena	Rajasthan	65–70 days
33	PLM-891	Davod	Rajasthan	70–75 days
34	PLM-1057	Birwa Chik	Karnataka	70–75 days, synchronous flowering

the check varieties particularly for yield and other desired agronomic traits. The range of variation in F_5-selected progeny lines and correlation between various yield-related quantitative traits were also computed using the MSTATC Statistical Package (developed at the Michigan State University, USA). The yield performance of selected F_5 progenies with wider adaptability and desirable plant types was assessed. The F_2-derived F_5 family means were compared with F_2 bulk progeny means and realized genetic gains (Falconer, 1989) were computed for yield-related traits.

Data obtained from the Delhi trials are presented in this paper. At other locations the segregating populations are being advanced for developing location-specific enhanced germplasm, maintaining mild selection, on a longer time-scale of 8–10 years.

Results

From the crossing programme, over 350 individual F_2 plants were selected. Further selections were made in F_3, and 103 F_3 selections were advanced to F_4 and F_5. The range of variation for the yield-related traits of the enhanced F_5 progeny lines grown at Delhi during the 2001 cropping season (both spring/summer and rainy) were assessed. The data presented in Table 2 (for rainy season trials) show good variation for various quantitative yield-related traits for selection by the breeders. The correlation matrix between various pairs of characters is presented in Table 3. The number of clusters per plant is significantly and positively correlated to pod length, number of pods per plant and seed yield. Pod length is significantly and positively correlated to number of seeds per pod, 100-seed weight and seed yield. Days to flower is negatively correlated to seed yield.

At all locations, desirable types have been advanced for developing improved adapted germplasm for use by the breeders. At Delhi, progenies with early maturity and resistance to biotic stresses and reasonably good yield were advanced to F_5. Major emphasis has been given to grain yield which depends on number of pods per plant, number of seeds per pod and 100-seed weight, number of branches, number of functional nodes, capacity to bear flowers and pod-setting rate. A faster vegetative growth during the pre-flowering stage, indicating high dry matter accumulation and higher leaf area index, was monitored by tracking plant height at flowering. Attempts were also made to select progenies/plant types with determinate habit and synchronous maturity. Plants that retained healthy leaves until grain filling was complete were also selected. Suitable plant types were selected for developing ideotypes of different maturity groups ranging from 60 to about 90 days to allow the development of cultivars for different cropping systems/crop combinations. Determinate uniformly maturing plant types were selected to develop ideotypes producing uniform seed quality for all maturity durations.

The performance of 12 superior F_5 lines which performed well with respect to yield and other agronomically desired traits (including low susceptibility to mungbean yellow mosaic virus) under Delhi conditions in both the spring/summer and rainy seasons are presented in Table 4. This shows that most of these selections out-performed the check varieties used in both seasons for seed yield and other related traits. A substantial realized genetic gain was achieved for certain yield-related traits (Table 5). In particular, significant progress was made for the number of clusters per plant (up to 51%), number of pods per plant (up to 98%) and grain yield (up to 73%). Marginal gains for some other traits (number of seeds per pod and 100-seed weight) were also recorded.

Discussion

In the present study, germplasm enhancement activities were undertaken utilizing a selected portion of the existing diversity in the cultivated primary gene pool to illustrate the value of a core collection as an initial starting material for a large-scale base-broadening programme. Such large-scale incorporation programmes represent long-term investments. An understanding of the criteria and indicators of genetic bottlenecks will give useful pointers towards the design of a suitable base-broadening approach. Critical assessments of the state of diversity of the crop, and of the state of use of diversity of the crop, would help to provide a more objective basis for determining future needs and priorities (Cooper *et al.*, 2001; Spillane and Gepts, 2001; Spoor and Simmonds, 2001). Such assessments can include comparative assessments of the total genetic diversity in the crop taxa with that available in the primary gene pool; a comparative assessment of genetic diversity present in the primary gene pool with that present in both *in situ* and *ex situ* genebanks and in breeding pools; an examination of the extent of diversity actually utilized in breeding programmes; and an estimation of the proportion of such genetic diversity used in breeding programmes actually available to farmers in the full range of geographical areas and for the full range of purposes.

Much genetic variation relevant for breeding for higher productivity may have been lost during the development of current populations of mungbean (Jain, 1975). This loss has largely been directed by the force of natural selection, even after crop domestication, which favours alleles responsible for tolerance to biotic/abiotic stresses. However, such useful variation may not have been

Table 2. Diversity in selected core entries of mungbean used as parents and enhanced F_5 progenies

	Core entries				F_5 progenies			
Quantitative characters	Min.	Max.	Mean	CV (%)	Min.	Max.	Mean	CV (%)
Plant height (cm)	29.1	80.0	53.7	21.5	32.5	92.5	60.3	23.7
No. of primary branches	1.0	5.0	2.7	37.6	2.0	6.0	3.2	23.7
Pod length (cm)	5.2	10.1	6.8	14.9	5.5	11.0	6.5	21.5
Days to flowering	40.0	73.0	48.1	14.5	38.0	62.0	44.8	9.15
Days to maturity	65.0	99.0	73.16	8.9	59.0	78.0	62.9	5.9
No. of clusters per plant	2.0	14.0	6.6	47.8	5.0	12.0	8.1	20.9
No. of pods per plant	11.4	52.0	25.3	38.5	15.0	53.0	24.9	23.3
No. of seeds per pod	8.6	12.5	10.9	9.4	9.0	11.0	9.8	5.1
100-seed weight (g)	1.8	5.5	3.5	25.7	2.9	6.2	3.8	23.6
Yield per m^2 (g)	53.0	167.5	117.2	26.8	102.0	201.0	156.7	13.0
Seed protein content (%)	20.5	30.1	24.3	5.7	21.3	28.7	24.8	6.5
Qualitative characters	Frequency distribution (%)				Frequency distribution (%)			
Growth habit	Erect (74), semi-erect (26)				Predominantly erect (91)			
Leafiness	Sparse (15), intermediate (70), abundant (15)				Predominantly intermediate (93)			
Twining tendency	None (74), slight (26)				None (89), slight (11)			
Leaf senescence	No visible senescence (3), slight visible senescence (28), moderate senescence (67), conspicuous concurrent senescence (2)				Predominantly moderate senescence (83)			
Branching pattern	Basal (72), central (25), top (3)				Basal (67), central (33)			
Flowering period	Asynchronous (8), intermediate (78), synchronous (14)				Intermediate (76), synchronous (24)			
Seed colour	Light green (46), dark green (5), green yellow (31), yellow (10), brown (3), brownish green (5)				Light green (42), yellow green (30), yellow (20)			

Min., minimum; Max., maximum; CV, coefficient of variation.

Table 3. Correlation matrix of quantitative yield-related traits for enhanced F_5 progenies

Characters	Days to flowering	Days to maturity	No. of clusters per plant	No. of pods per plant	Pod length	No. of seeds per pod	100-seed weight	Yield per m^2
Days to flowering	1.00							
Days to maturity	0.69**	1.00						
	(0.52**)							
No. of clusters per plant	0.01	0.09	1.00					
	(0.02)	(0.06)						
Pod length (cm)	−0.19	0.01	0.41**	1.00				
	(−0.17)	(0.03)	(0.17)					
No. of pods per plant	−0.03	−0.18	0.26*	0.01	1.00			
	(−0.12)	(−0.14)	(0.18)	(0.03)				
No. of seeds per pod	0.08	0.05	0.19	−0.04	0.36**	1.00		
	(0.06)	(0.01)	(0.12)	(0.07)	(0.23*)			
100-seed weight	−0.23	−0.19	−0.29*	0.02	0.50**	−0.07	1.00	
	(−0.13)	(−0.13)	(−0.13)	(0.04)	(−0.18)	(−0.02)		
Yield per m^2(g)	−0.34**	−0.22	0.36**	0.45**	0.26*	0.07	0.27*	1.00
	(0.21)	(−0.18)	(0.23)	(0.23*)	(0.12)	(0.03)	(0.12)	

*$P < 0.05$; **$P < 0.01$. Correlation coefficients of F_2 base populations are shown in parentheses for comparison.

irretrievably lost, as it is probably still present, perhaps at low frequency, in scattered populations from different agro-ecological conditions. The core collection is a representative set of germplasm accessions from different agro-ecological regions of the country and hence can be expected to contain a reservoir of alleles, which may contribute to higher yield levels under improved levels of agronomic management. But in order to capture these alleles, an extensive hybridization programme, using parental lines that are genetically and geographically diverse, is necessary.

Most of the indigenous landraces in mungbean were collected during the late 1960s and early 1970s. The landrace germplasm has sufficient variability for morphological characters (Bisht *et al.*, 1998b). In the present study, landrace germplasm accessions with local adaptation (but largely unadapted in other environments) have been used. These accessions, however, do not reflect the full range of variability available for most of these traits present in the core collection. There is still plentiful variability available for future use in large-scale base-broadening programmes.

The data derived from trials at Delhi have been presented here in order to demonstrate the potential of genebank-conserved accessions for germplasm enhancement. Selection of F_2-derived superior progenies was made in F_3 for further advancement to F_4 and F_5. The F_3 bulks and selected F_4 progenies are now available for distribution to breeders and other users in the national mungbean improvement programmes. Multi-location testing of the selected F_3 progeny lines and selected F_3 bulks may provide an opportunity to the breeders for selection of suitable plant types for developing location-specific ideotypes by adopting appropriate selection strategies.

The range of variation (Table 3) for various quantitative yield traits shows that there is much variation present in F_5 progenies for further selection by breeders, particularly for number of pod-bearing clusters per plant, pods per plant, pod length and 100-seed weight. Correlation studies (Table 3) of the enhanced F_5 progenies reveal that the number of clusters per plant is positively correlated to pod length, number of pods per plant and seed yield. Pod length is significantly and positively correlated to number of seeds per pod, 100-seed weight and seed yield. These correlations can provide useful criteria for the indirect selection of high-yielding types. Days to flowering was highly correlated to maturity and negatively correlated to seed yield. Flowering time is a direct measure of the length of the vegetative phase. During this phase, the plant establishes the size of the source used during the reproductive phase to determine grain yield. However, too long a vegetative period can have an adverse effect on grain productivity (Bisht *et al.*, 1998a).

A number of F_5 selections show enhanced adaptability as they performed well in both the spring/summer and rainy seasons. Derivatives also performed well in unreplicated trials at other locations, suggesting their inheritance of wide adaptability (materials are available for further selection, on request). These materials achieved a substantial genetic gain over the base population (F_2), particularly with respect to cluster number, pods per plant, 100-seed weight and grain yield. Direct selection for yield *per se* was more efficient than selection on the

Table 4. Performance of a few selected F_5 progenies of some promising crosses for yield-related traits

	Days to flowering		Days to maturity		No. of clusters per plant		No. of pods per plant		Pod length		No. of seeds per pod		100-seed weight		Yield per m^2	
Cross	S	R	S	R	S	R	S	R	S	R	S	R	S	R	S	R
IC-615-5 × PLM-891	41.0	43.0	58.0	60.6	9.0	9.0	47.3	38.6	8.0	8.3	9.5	9.0	4.3	4.7	162.0	171.7
IC-8917 × PLM-891	40.0	45.0	60.5	63.3	8.6	9.0	31.6	34.3	6.0	5.8	10.0	10.0	2.9	3.0	138.0	154.9
IC-8952-3 × PLM-694	42.0	45.0	62.0	64.6	9.6	10.0	30.0	33.6	5.8	5.9	9.5	10.0	3.1	3.4	144.3	165.3
PLM-32 × PLM-891	42.5	45.0	58.5	61.6	8.3	7.6	28.3	30.6	5.5	5.8	9.0	10.0	3.2	3.3	138.5	159.1
PLM-32 × PLM-777	38.5	43.0	60.0	63.0	8.0	8.0	22.6	26.3	5.5	5.7	10.0	10.0	3.0	3.3	142.5	165.0
PLM-562 × IC-10184-4	40.5	43.0	62.0	65.3	7.3	6.6	44.3	27.3	5.7	5.6	10.0	10.0	3.6	3.7	157.3	162.0
PLM-619 × PLM-32	40.0	43.6	62.0	63.3	7.5	7.6	23.3	23.0	5.3	5.7	10.0	10.0	3.5	3.4	139.0	156.0
PLM-666 × PLM-231	38.5	44.6	58.0	62.6	7.3	7.6	22.6	29.3	5.8	5.7	10.0	9.6	3.5	3.6	132.3	149.1
PLM-666 × PLM-734	43.0	44.0	59.5	61.6	7.0	7.3	25.3	24.3	5.8	5.8	9.5	10.0	2.8	2.9	130.3	167.4
PLM-694 × PLM-334	43.0	44.0	60.0	62.3	9.3	11.0	36.5	37.3	5.3	5.8	9.5	9.6	2.9	3.1	158.5	175.7
PLM-759 × PLM-334	38.0	42.6	59.5	63.0	10.0	10.6	37.3	39.0	5.7	5.8	10.5	10.0	3.3	3.2	164.3	188.2
PLM-884 × IC-24789	41.5	45.0	58.5	61.0	7.6	7.3	30.6	25.3	5.7	5.8	9.5	10.0	3.1	3.0	147.3	157.1
K-851 (check)	40.0	40.6	59.5	60.3	6.6	6.0	25.3	25.3	5.5	5.8	10	9.0	3.7	3.8	130.3	141.1
TAP-7 (check)	45.0	60.0	69.0	73.0	6.3	6.0	20.3	21.3	5.6	5.9	9.5	10.0	3.5	3.4	103.4	127.6
Pusa-9531 (check)	43.0	49.0	60.3	62.0	6.3	7.6	21.3	23.3	5.7	5.8	10	10.0	3.5	3.5	105.2	128.0
LSD																
$P < 0.01$	3.67	2.90	6.70	4.50	1.67	1.76	10.70	11.06	0.73	0.61	0.66	0.58	0.61	0.56	23.27	21.57
$P < 0.05$	2.60	2.24	4.30	3.35	1.22	1.32	7.10	8.30	0.51	0.46	0.49	0.43	0.47	0.42	18.13	16.18

S, spring/summer season; R, rainy season.

Table 5. Realized genetic gain[a] (%) in some yield-related traits of selected F_2-derived F_5 progeny means over F_2 bulks for a few promising crosses

S. No.	Selected F_5 progenies from promising crosses	No. of clusters per plant	No. of pods per plant	Pod length	No. of seeds per pod	100-seed weight	Grain yield per m^2
1	IC-615-5 × PLM- 891	29.0	98.0	19.0	11.0	3.0	67.2
2	IC-8917 × PLM-891	29.5	47.7	3.6	11.0	8.1	52.8
3	IC-8952-3 × PLM-694	22.0	29.7	5.9	13.0	8.7	53.2
4	PLM-32 × PLM-891	34.3	26.7	9.4	1.5	9.4	41.5
5	PLM-32 × PLM-777	36.3	75.0	2.5	10.0	9.4	52.3
6	PLM-562 × IC-10184-4	20.2	64.0	2.8	10.0	8.6	48.1
7	PLM-619 × PLM-32	32.0	43.0	11.7	12.1	2.8	58.8
8	PLM-666 × PLM-231	51.0	43.0	20.0	12.4	5.5	40.7
9	PLM-666 × PLM-734	35.3	43.3	5.4	10.1	9.8	46.6
10	PLM-694 × PLM-334	26.0	41.7	10.0	12.5	10.3	73.3
11	PLM-759 × PLM-334	26.0	39.3	3.6	11.1	9.5	55.3
12	PLM-884 × IC-24789	21.3	52.0	1.8	11.1	15.9	36.4

[a] The data from rainy season trials were used for computing realized gain.

basis of any other individual character alone. The estimates of genetic gain and the correlations among characters indicate that in order to realize an effective selection advance in mungbean, cluster number, pods per plant and 100-seed weight should be considered together.

The present demonstration has revealed that enhanced progenies, F_3 bulks and selected F_4 progeny lines may be attractive to plant breeders due to their greater potential for direct use in a breeding programme than the original unimproved/unadapted sources. The core collections are useful instruments to assist germplasm enhancement by providing diverse parents for intercrossing.

Acknowledgements

We thank Dr B. S. Dhillon, Director and Dr Mahendra Singh, Head, Germplasm Evaluation Division, NBPGR, New Delhi for providing facilities for this work. Financial support under the National Agricultural Technology Project on Plant Biodiversity (Indian Council of Agricultural Research) is also gratefully acknowledged.

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