Evaluation of Mungbean Germplasm for Genetic Variability

G Roopa Lavanya*

Department of Genetics and Plant Breeding, Allahabad Agricultural Institute–Deemed University, Allahabad (Uttar Pradesh)

In a study conducted during kharif, 2003 and 2004 comprising 132 mungbean genotypes to assess the genetic variability present among the genotypes. Genotypic coefficient of variation was observed high for seed yield per plant^{-1}, number of clusters per plant^{-1}, number of pods per plant^{-1} and number of pods per cluster^{-1}. High estimates of heritability coupled with high genetic advance as per cent of mean was registered for plant height, seed yield per plant^{-1} and number of pods per plant^{-1}, indicating that the genetic variances for these traits are probably owing to their high additive gene effects and thus there is better scope for improvement of these traits through direct selection.

Key words: Genetic variability, Heritability, Genetic advance, Additive gene effect

Pulses are rich sources of protein with two to three times more protein than that in cereals. Mungbean is one of the most important legume crop and ranks third in total production amongst the pulses grown in the country after chickpea and pigeonpea. The genetic reconstruction of a plant type is required for developing high yielding varieties by incorporating and improving the yield component characters. Therefore, evaluation of germplasm for genetic variability is essential for the present as well as future crop improvement programmes. Moreover, proper utilization of germplasm requires testing of genetic potential under local conditions or the target environment for which the breeding programme is aimed. In the view of the above perspectives, the present study was taken up to assess genetic variability in mungbean germplasm to identify genetically diverse and agronomically superior genotypes.

Materials and Methods

The experimental material comprised 132 genotypes of mungbean collected from different geographical regions of India and abroad and grown during *kharif*, 2003 and 2004 at Crop Research Farm of Department of Genetics and Plant Breeding, Allahabad Agricultural Institute-Deemed University, Allahabad. The mungbean germplasm included improved varieties, obsolete varieties, local land races, exotic collections and other species of genus *Vigna*. The experiment was laid out in randomized complete block design replicated thrice in crop geometry of 1 x 1 m^2 with 30 cm and 10 cm inter and intra row spacing, respectively. Recommended cultural practices and plant protection measures were followed to raise a healthy crop. Five plants were selected at random from each block to record observations on 10 characters *viz*., plant height (cm), number of primary branches, number of clusters plant^{-1}, number of pods cluster^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, pod length (cm), 100 seed weight (g), days to maturity and seed yield plant^{-1} (g). The pooled mean values over seasons were subjected to analysis of variance. Genotypic and Phenotypic coefficient of variation (GCV and PCV) were calculated by following the method given Burton (1952). Heritability (broad sense) and expected genetic advance (as per cent of mean) were estimated as per Johnson *et al.* (1955).

Results and Discussion

Analysis of variance revealed significant differences for all 10 characters under study, indicating the presence of substantial genetic variability in the mungbean germplasm (Table 1). The variability among the genotypes, suggested ample scope for improvement through selection. Knowledge of genetic system controlling yield and its components is useful in understanding the prepotency of the parents and thus help to select parents possessing in-built genetic potential. The genotypes like IPRM-90, was identified as a desirable genotype for multiple characters like medium plant height, more number of primary branches plant^{-1}, more number of pods cluster^{-1}, number of pods plant^{-1} and seed yield plant^{-1}. LM-1119 was identified for number of clusters plant^{-1}, number of pods cluster^{-1} and number of pods plant^{-1}. Exotic collections *viz*., EC 393407, EC 398888, EC 398889, MSO-9 were characterized for long pods with more number of seeds

---

**Corresponding Author: Assistant Professor, Allahabad Agricultural Institute–Deemed University, Allahabad-211007*

Indian J. Plant Genet. Resour. 19(1): 104-106 (2006)

Table 1. Analysis of variance for 10 characters in 132 mungbean genotypes

Characters	Mean sum of squares		
	Replication	Treatment	Error
Degree of Freedom	2.00	131.00	262.00
Plant height (cm.)	594.47	361.73**	35.18
No. of primary branches/ plant	2.25	1.91**	0.86
No. of clusters / plant	16.52	72.59**	15.12
No. of pods/ cluster	0.17	2.86**	0.67
No. of pods/ plant	45.47	438.26**	65.37
No. of seeds/ pod	6.86	7.81**	1.17
Pod length (cm.)	2.92	4.26**	0.30
Days to maturity	85.63	177.16**	50.51
100-seed weight (g.)	3.60	15.96**	13.45
Seed yield / plant (g.)	36.88	39.74**	4.07

** Significant at 0.01 level of significance

pod^{-1}. Genotypes like HUM-1, T-44, PDM-54, PS-10, Pusa-9072 and ML-406 were identified as early maturing genotypes. Jyoti, LGG-499, PIMS-11/99, PDM-84-143, LGG-420 and IPRM-90 were recognized for high seed yield plant^{-1} (Table 2).

Higher magnitude of GCV were recorded for seed yield plant^{-1} (31.24%) followed by number of clusters plant^{-1} (28.39%), number of pods plant^{-1} (27.48%) and number of pods cluster^{-1} (25.96%), while plant height (21.99%) and pod length (17.48%) showed moderate GCV values, indicating substantial amount of genetic variability. However, Das *et al.* (1998) recorded high genotypic coefficient of variation for plant height, number of branches plant^{-1}, number of pods plant^{-1}, pod length and seed yield plant^{-1}. A wide range of phenotypic coefficient of variation was observed and ranged form 12.44% for days to maturity to 37.98% for number of clusters plant^{-1}. Seed yield plant^{-1} (36.19%), number of pods cluster^{-1} (35.98 %) and number of pods plant^{-1} (33.95%) registered higher magnitude of PCV values, suggested favourable effect of environment in the expression of these characters (Table 3). However, high magnitudinal differences between PCV and GCV were observed for number of primary branches plant^{-1} followed by number of pods cluster^{-1} and number of clusters plant^{-1}, indicated greater influence of environment, whereas relatively low magnitudinal differences were observed for pod length and plant height. Highest

Table 2. Potential genotypes identified for different attributes in mungbean germplasm

S.No	Characters	Potential genotypes identified
1.	Plant height (55-65 cm)	IPRM-90, LM-497, V-557, ML-287, ML-588, K-1084, JYOTI, ML-131, PS-16, PANT MUNG-1, T-1, EC-398888, LGG-478, LGG-477, VC-3944, MSO-9, PUSA BOLD -2, LGG-491, LGG-476, NM-1
2.	No. of Primary branches plant^{-1}	V-3561, IPRM-90, KM-2197, OBGG-40, LAM-M2, K-2192, LGG-476, LLR-4
3.	No. of clusters plant^{-1}	PUSA-9871, K-1084, WGG-2, PUSA-108, V-4589, PDM-139, LGG-491, LM-1119
4.	No. of pods cluster^{-1}	PUSA BAISAKHI, PS-10, SONAMUNG, UPM-83-1, T1, IPRM-90, OUM-11-5, LM-1119, ML-5, PANT MUNG -1, LGG-478,
5.	No. of pods plant^{-1}	ML-287, V-3561, PS-16, LGG-499, SONAMUNG, PDM-84-143, LM-1119, ML-131, K-1284, IPRM-90
6.	No. of seeds pod^{-1}	EC-393407, K-1310, K-92-200, EC-398888, LGG-477
7.	Pod length (cm)	EC-398888, MSO-8, EC-398889, MSO-9
8.	Days to maturity	EC-398889, PDM-54, PUSA BAISAKHI, HUM-10, ML-406, T-44, HUM-1, PUSA-9072, HUM-14, HUM-7, DPM-60-1, PDM-1, PS-10, PUSA-102
9.	100 – seed weight (g)	EC-398889, K-1282, EC-398888, PUSA BOLD-2, MSO-9, WGG-2, HUM-14
10.	Seed yield plant^{-1} (g)	JYOTI, LGG-499, PIMS-11/ 99, IPRM-90, PDM-84-143, PDM-89-226, LGG-491, LGG-420, PANTMUNG-1

Table 3. Estimates of genetic parameters for 10 characters in 132 mungbean genotypes

Characters	Coefficient of variation (%)		Heritability (%) (broad sense)	Genetic advance	Genetic advance (as percent of mean)
	GCV	PCV			
Plant height (cm.)	21.99	25.29	75.64	18.68	39.36
No. of primary branches/plant	16.18	30.12	28.81	0.65	17.76
No. of clusters/plant	28.39	37.98	55.93	6.74	43.74
No. of pods/cluster	25.96	35.98	52.15	1.27	38.60
No. of pods/plant	27.48	33.95	65.54	18.59	45.82
No. of seeds/pod	15.58	19.27	65.43	2.48	25.97
Pod length (cm.)	17.48	19.36	81.53	2.14	32.57
Days to maturity	8.40	12.44	45.51	9.03	11.67
100-seed weight (g.)	23.96	28.96	35.94	0.46	12.04
Seed yield/plant (g.)	31.24	36.19	74.55	6.13	55.53

genotypic and phenotypic coefficient of variation for seed yield plant^{-1}, number of branches plant^{-1} and number of pods plant^{-1} (Reddy, 1997; Loganathan *et al.*, 2001) and 100-seed weight (Samad and Lavanya, 2005) were reported.

The perusal of the Table 3 revealed the estimates of heritability (%) in broad sense for 10 characters studied, which ranged from 28.81% for number of primary branches plant^{-1} to 81.53% for pod length. Plant height (75.64%), seed yield plant^{-1} (74.55%), number of pods plant^{-1} (65.54%) and number of seeds pod^{-1} (65.43%) recorded high heritability. Burton (1952) suggested that genetic variation along with the heritability estimates would give a better idea about the expected efficiency of selection. Thus, a character possessing high GCV along with the high heritability will be valuable in a selection programme. Seed yield plant^{-1} and number of pods plant^{-1} recorded high estimates of GCV coupled with high heritability.

Maximum genetic advance was recorded for plant height (18.68) followed by number of pods plant^{-1} (18.59). However, high estimates of genetic advance as per cent of mean was registered for seed yield plant^{-1} (55.53%), number of pods plant^{-1} (45.82%), number of clusters plant^{-1} (43.74%) and plant height (39.36%), suggesting that these characters are governed by additive genes and selection will be rewarding for improvement of such traits. Low genetic advance as per cent of mean was observed for days to maturity (11.67%), indicating the involvement of non additive gene action in controlling this trait and heterosis breeding may be useful for further generation of variability for this character.

Heritability estimates along with genetic advance are more useful than heritability alone in predicting the effectiveness of selection. Further, the heritability estimates coupled with expected genetic advance as per cent of mean indicates the mode of gene action in choosing an appropriate breeding methodology. High genetic advance as per cent of mean coupled with high heritability recorded for plant height, seed yield plant^{-1} and number of pods plant^{-1}. This situation indicates that the genetic variances for these traits are probably owing to their high additive gene effects (Johnson *et al.*, 1955) and thus there is better scope for improvement of these traits through direct selection.

High estimates of genetic advance as per cent of mean coupled with high estimates of heritability for number of pods plant^{-1}, seed yield plant^{-1}, plant height, number of seeds pod^{-1} and number of clusters plant^{-1} (Byregowda *et al.*, 1997; Ram *et al.*, 1997; Loganathan *et al.*, 2001; Samad and Lavanya, 2005) were also reported. These characters are likely to provide very high to high selection response, owing to their high transmissibility (Saxena and Singh, 2001). High estimates of genotypic coefficient of variation and heritability and genetic advance as per cent of mean indicate the predominance of additive gene action in controlling these characters and simple directional selection may be effective to improve these characters.

References

Burton GW (1952) Quantitative inheritance of grasses. *Proc. of 6th Inl. Grassland Cong.* **1**: 277-283.

Byregowda M, J Chandraprakash, CS Jagadeesh Babu and P Rudraswamy (1997) Genetic variability and inter-relationships among yield and yield components in greengram (*Vigna radiata* L. Wilczek). *Crop Res.* **13(2)**: 361-368.

Johnson HW, HF Robinson and RE Comstock (1955) Genotypic and phenotypic correlations in soybean and their implications in selection. *Agron. J.* **47**: 477-483.

Lavanya GR and Y Singh (2005) Assessment of genetic variability and character association in mungbean (*Vigna radiata* L. Wilczek). *The Allahabad Farmer* **59(2)**: 70-75.

Loganathan P, K Saravanan and J Ganesan (2001) Genetic variability in greengram. *Res. on Crops* **2(3)**: 396-397.

Ram SG, R Rajkumar, PG Nayagam and R Rathanaswamy (1997) Variability and association analysis yield components in greengram. *Madras Agric. J.* **4(8)**: 469-470.

Reddy KPH (1997) Genetic variability in greengram. *Annals of Agric. Res.* **18(4)**: 554-555.

Samad SS and GR Lavanya (2005) Variability studies for yield parameters in mungbean (*Vigna radiata* L. Wilczek). *J. of Maharastra Agric. Univ.* **30(2)**: 168-170.

Saxena RR and PK Singh (2001) Variability and heritability estimates of post-harvest parameters in greengram (*Vigna radiata* L. Wilczek). *Indian J. of Dryland Agric. Res. and Dev.* **16(1)**: 78-82.