Research Article



Genetic variability and heritability studies in advanced breeding lines of mungbean

■ HEMANT SAHU, R.K. PANWAR, A.S. JEENA AND JAIRAM AMADABADE

SUMMARY

A study conducted with 35 mungbean [*Vigna radiata* (L.) *Wilezek*] genotypes to estimate for genetic variability, heritability and genetic advance for 19 quantitative characters over two seasons. Significant variations among the genotypes were observed for all the characters. The estimated values of PCV were higher than GCV for all the characters studied. During 2011 highest estimated heritability (broad sense) value was obtained for plant height followed by nodule volume pod per plant, nodule dry weight, pod length, straw protein %, primary branches and yield per plot whereas for 2012, nodule volume followed by straw protein, nitrogen fixation per plant, number of nodule, pod length, seed protein and nodule dry weight had highest estimates of heritability. While estimates for heritability wais lowest for maturity and plant yield in both the season. The highest genetic advance was obtained for yield per plot followed by number of nodules in both the season, whereas nodule dry weight showed lowest genetic advance followed by nitrogen fixation in both the season. High heritability (broad) along with high genetic advance in per cent of mean was observed for yield per plot, plant height and nodule number, suggesting the preponderance of additive gene effect and selection may be effective for these characters.

Key Words : Mungbean, Vigna radiate, Variability, Heritability, Nitrogen fixation, Yield components

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ungbean [Vigna radiata (L.) Wilczek] is an important pulse crop of India grown in an area of 3.55 m ha with 1.80 mt production and productivity 512 kg/ha (Project Coordinator's Report 2011-12). Yield is a complex character associated with various contributing characters which are interrelated among themselves. Genetic improvement in the expression of a quantitative character is dependent upon having germplasm with a range of genetically controlled variability for the trait under consideration. But doubt exists about limited range of genetic variability in

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Address of the Co-authors: P.K. PANWAR, A.S. JEENA AND JAIRAM AMADABADE, Department of Genetics and Plant Breeding, G.B. Pant University of Agriculture and Technology, PANTNAGAR (UTTARAKHAND) INDIA mungbean. For developing suitable selection strategy the knowledge of genetic variability present in the available germplasm for yield and its associated characters is important. Heritability is an index for calculating the influence of environment on the expression of genotypes. Estimates of genetic advance along with heritability would be helpful in assessing the nature of gene action. Therefore, the present investigation was carried out for estimating genetic variability, heritability and predicted genetic gain for various quantitative characters in thirty five genotypes of mungbean over two season.

MATERIAL AND METHODS

The present investigation was carried out at the N. E. Borlaug Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand, India during *Kharif* 2011 and *Kharif* 2012. In the first season, *i.e.*, 2011, 32 advanced breeding lines of mungbean derived from inter-varietal crosses and three checks, PM-4, PM-5 and PM-6 were evaluated for yield and different yield contributing characters. The same set of experimental material was evaluated in 2012 also. Observations were recorded on days to 50 % flowering, nodule number, nodule volume, root length, shoot length, nodule dry weight, days to maturity, plant height, number of primary branches, number of pods per plant, pod length, number of seeds per pod, 100-seed weight, seed yield per plant, harvest index, seed protein %, straw protein %, nitrogen fixation and yield per plot. Plants were harvested when 90% of pods changed to brown color. Analysis of variance (ANOVA) was done to know the variations among the genotypes based on the 19 morphological traits. Phenotypic and genotypic co-efficient of variations was estimated according to Burton and Deyane (1953) Genetic advance was calculated according to formula given by Johnson et al. (1955) and heritability was estimated according to Allard (1962).

RESULTS AND DISCUSSION

The analysis of variance of 2011 and 2012 experiment's data revealed highly significant differences among the mungbean genotypes for all the characters *viz.*, days to 50% flowering, number of root nodules, nodule volume, nodule dry weight, root length, shoot length, days to maturity, plant height, number of primary branches, number of pods per plant, pod length, number of seed per pod, 100-seed weight, harvest index, grain and straw protein, yield per plant, nitrogen fixation and yield per plot except harvest index and straw protein in 2012. The analysis of variance showed significant variability in the mungbean genotypes for most of the characters studied

during both the years. Khairnar *et al.* (2003) observed sufficient variability for plant height, cluster per plant, pods per plant, 100 seed weight and yield per plant. Considerable genetic variability among mungbean genotype was observed by Kapoor *et al.* (2005) and Ghaviami and Rezai (2000) and Sirohi and Kumar (2006) also reported the presence of high genetic variability for yield and other yield components in mungbean.

The estimates of phenotypic co-efficient of variation (PCV) were higher than the corresponding estimates of genotypic co-efficient of variation (GCV) for all the characters (Table 1and 2). Study of GCV help to measure the range of genetic variation existed in the specific environmental site. Comparative study of co-efficient of variation on various characters revealed relatively high contribution of genotypic variation in determining the total phenotypic variation for most of the characters. Root nodule volume, nodule dry weight, nitrogen fixation per plant, nodule number, straw protein %, yield per plot and pod per plant exhibited high value of GCV. Lowest GCV was observed for maturity. A high estimate of PCV was observed for nodule volume, nodule dry weight, nitrogen fixation, nodule number and yield per plot in both the season. Higher PCV value as compared to GCV value for all the character suggest that apparent variation is not entirely due to genotypes but also due to influence of environment and selection for such traits may be sometime misleading. In the present investigation the difference between PCV and GCV were narrow for most of the characters. Indicating the effect of the environment on these traits is low. High difference between GCV and PCV was found in case of yield/plant. A

Table 1 : Range, general mean and standard error mean along with variability parameters for different characters in mungbean during 2011										
Character	Range	GM	$SEM \pm$	PCV %	GCV %	ECV %	$h^{2}(\%)$	GA		
Days to 50 % flowering	38 - 43	40	5.19	2.9	1.83	2.25	40	0.95		
Nodule number	44 - 165.67	80.39	5.9	30.62	27.92	12.72	82.8	42.07		
Nodule volume (ml)	0.07-1.37	0.47	0.052	75.79	73.25	19.11	93.62	0.69		
Root length (cm)	37.67 - 54.67	45.85	1.7	11.08	8.81	6.72	63.19	6.61		
Shoot length (cm)	7.33 - 13.60	11.98	0.56	11.52	8.14	8.16	49.86	1.41		
Nodule dry weight (g)	0.02 - 0.15	0065	0.006	47.67	44.56	16.94	87.36	0.05		
Days to maturity	73.33 - 75.33	74.49	0.41	1.1	0.52	0.97	22.42	0.381		
Plant height (cm)	43.87-88.97	63.13	1.63	18.32	17.76	4.49	93.99	22.39		
Pri. branches	1.07 - 1.93	1.54	0.085	18.32	15.56	9.67	72.14	0.41		
Pod per plant	12.27-31.27	19.63	1.01	27.29	25.77	8.97	89.18	9.84		
Pod length (cm)	5.72 - 8.07	6.94	0.13	8	7.32	3.27	83.33	0.95		
Seed per pod	9.73-12.1	10.97	0.21	5.84	4.78	3.36	66.87	0.88		
100 seed weight (g)	2.91-4.01	3.39	0.13	9.38	6.54	6.72	48.67	0.31		
Yield per plant (g)	4 - 5.67	4.93	0.34	14.33	7.84	11.99	29.95	0.43		
Harvest index (%)	24.07-38.83	32.54	1.03	9.27	7.46	5.51	64.69	4.02		
Seed protein %	25.4 - 29.87	27.28	0.35	3.84	3.12	2.24	65.89	1.42		
Straw protein %	3.89 - 10.65	7.11	0.42	23.65	21.29	10.29	81.04	2.8		
N fixation (g per plant)	0.073 - 0.23	0.148	0.013	35.47	31.84	15.61	80.61	0.087		
Yield per plot (g)	358.33 - 819.37	531.2	47.49	29.33	24.19	15.48	72.12	231.5		

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wide range of phenotypic and genotypic co-efficients of variation (PCV and GCV) was observed among the quantitative traits by Kumar *et al.* (2003) and Gupta *et. al.*, (2004). Whereas Hozayn *et. al.*, (2013) found that the PCV was approximately equal to GCV for most of the traits.

High estimates of heritability (broad sense) value (> 70%) was obtained for plant height, nodule volume, pod per plant, nodule dry weight, pod length, straw protein, primary branches, nitrogen fixation per plant and yield per plot in both the season. But number of primary branches and yield per plot in 2012 showed moderate level (40-70%) of heritability. This indicated that most likely cause of heritability for these characters is due to additive gene action and as such selection for these characters is likely to accumulate more additive genes leading to scope for potential improvement in their performance. According to Panse (1957), the magnitude of heritable value is the most important aspect of genetic constitution of breeding material, which has close bearing on the response to selection. Further, heritability estimates along with genetic advance are normally more useful in predicting the gain under selection than heritability estimates alone (Singh and Narayanan, 1993). Estimates for heritability was low (=40%) for days to maturity, days to 50% flowering and yield per plant in both the season. Harvest index and 100 seed weight in 2012, also exhibited low level of heritability. Gupta et al. (2004) reported high heritability for days to 50% flowering, days to maturity and 100 seed weight; moderate for seeds per pod; and low for plant height, clusters per plant, pods per plant, pods per cluster, pod length and seed yield per plant. Rohman *et al.* (2003), Parameswarappa, (2005) and Prakash (2006) also found similar result. Venkakateswarlu (2001) reported seed yield expressed high genetic advance coupled with high heritability and GCV.

The genetic advance estimates was high for yield/plot, number of nodules, plant height and straw protein. The lowest genetic advance was found in case of nodule dry weight followed by nitrogen fixation. Heritability estimates and genetic advance was high for yield per plot, plant height and nodule number suggests that the high heritability most likely due to additive gene effect and selection may be effective. In the present investigation nodule volume, nodule shoot length, pod length, straw protein and nitrogen fixation exhibited high heritability but low genetic advance which is indicative of non additive gene action (dominance and epistasis) and presence of G x E interaction. It exhibited due to favorable influence of environment rather than genotype, and selection for such traits may not be rewarding. Maturity and yield per plant showed low heritability and low genetic advance, it indicates that the character is highly influenced by environmental effects and selection would be ineffective. Rahim et al. (2010) observed high heritability and genetic advance for plant height, number of pods per plant, number of seeds per pod, 1000-grain weight and grain yield per plant.

Shrivastava and Singh (2012) observed genotypic coefficient of variability, heritability and genetic advance were high for seed yield per plant, 100-seed weight, number of seeds

Table 2: Range, general mean, and standard error mean along with variability parameters for different characters in mungbean during 2012										
Character	Range	GM	SEM±	PCV %	GCV %	ECV %	$h^{2}(\%)$	GA		
Days to 50 % flowering	38.67 - 42.33	40.12	0.47	2.59	1.57	2.06	36.56	0.78		
Nodule number	47.33-129	74.6	4.12	29.16	27.54	9.57	89.22	39.99		
Nodule volume (ml)	0.03- 1.1	0.34	0.37	85.82	83.75	18.74	95.22	0.58		
Root length (cm)	32.67 - 49.47	39.6	1.16	9.73	8.29	5.08	72.68	5.77		
Shoot length (cm)	7.33 – 12.37	8.48	0.18	11.47	10.82	3.80	89.02	1.78		
Nodule dry weight (g)	0.02-0.15	0.06	0.009	49.89	42.68	25.84	73.17	0.047		
Days to maturity	73.33 - 75.67	74.61	0.42	1.12	0.51	0.99	21.37	0.36		
Plant height (cm)	44.83 - 71.47	53.18	1.09	12.39	11.86	3.56	91.70	12.45		
Pri. Branches	1.2 - 2.03C	1.52	0.08	15.94	12.52	9.81	62.06	0.31		
Pod per plant	13.72 - 18.73	15.65	0.64	9.54	6.30	7.15	43.69	1.34		
Pod length (cm)	5.31 - 7.55	6.47	0.19	11.98	10.84	5.10	81.85	1.30		
Seed per pod	8.37 - 11.1	9.8	0.27	7.91	6.18	4.92	61.18	0.98		
100 seed weight (g)	2.64 - 3.95	3.4	0.15	10.27	6.33	8.08	38.06	0.27		
Yield per plant (g)	3.00-4.67	3.72	0.31	17.41	9.4	14.63	29.37	0.39		
Harvest index (%)	23.73C - 34.33	29.32	1.58	11.38	6.50	9.33	32.71	2.24		
Seed protein %	25.65-31.86	28.18	0.40	5.21	4.58	2.47	77.44	2.34		
Straw protein %	4.03 - 13.34	7.68	0.32	26.08	25.06	7.22	92.34	3.81		
N fixation (g per plant)	0.03 - 0.23	0.09	0.008	52.15	49.76	15.58	91.06	0.09		
Yield per plot	236.6-553.33C	410.22	35.32	24.34	19.23	14.91	62.45	128.4		

whereas, GM=General mean, SEM=Standard error of mean, PCV=Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h^2 = Heritability, G_A= Genetic advance

per pod, number of pods per plant and number of nodes on main stem. Rohman *et al.* (2003), Gupta *et al.* (2004) and Kapoor *et al.* (2005) also found similar result.

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