

# ESTIMATES OF GENETIC VARIABILITY AND HERITABILITY FOR YIELD AND YIELD COMPONENT TRAITS IN MUNGBEAN [*VIGNA RADIATA* (L.) WILCZEK]

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## ABSTRACT

Mungbean is an important crop to meet the challenges of food and nutritional security due to its nature of high protein and other micronutrients. Seed yield is a dependent trait, whose manifestation depends entirely on the component traits. With this view, the present investigation was undertaken to estimate the genetic parameters on various quantitative traits with 21 mungbean genotypes in randomized block design with three replications during *kharif* 2010. The results indicated that the traits *viz.*, plant height (95.15, 34.20), number of clusters per plant (95.51, 30.74) and number of pods per plant (99.12, 67.30) exhibited high heritability (>60) coupled with high to moderate genetic advance as percent of mean (>20), which may be improved through simple plant selection methods. While the remaining traits showed high to moderate heritability (30-60) coupled with moderate (10-20) to low (<10) genetic advance as percent of mean, suggesting predominance of non-additive gene action in the expression of the traits, therefore may be potentially utilized in recombination breeding. Furthermore, based on their *per se* performance, the suitable genotypes for these traits could be isolated and utilize for mungbean improvement.

## INTRODUCTION

Mungbean (*Vigna radiata* L.) is an important pulse crop and occupies a good position due to its high seed protein content and ability to store the soil fertility through symbiotic nitrogen fixation (Malik, 1994). Thus, it contributed significantly to enhancing the yield of subsequent crops (Jat *et al.*, 2012). Additionally, it is well suited to both dry areas and irrigated conditions as well. For any crop improvement programme, selection of superior parents is an essential prerequisite especially for the traits showing higher heritability and genetic advance for various traits (Khan *et al.*, 2005). The adequate information on extent of variability parameters may be helpful to improve the yield by selecting the yield component traits because yield is a complex trait, whose manifestation depends on the component traits. Generally, the estimates of heritability ( $h^2$ ) of traits are environment specific (Shimelis and Shiringani, 2010). These estimates should be incorporated and specifically applied only to the population and environment sampled (Duble and Moll, 1969). Thus, selection made on the basis of  $h^2$  alone is likely to be misleading and it becomes necessary to determine the parameters under targeted production environment. Thus, selection of traits based on  $h^2$  and genetic advance as percent of mean is of great importance to the breeder for making criteria for improvement in a

complex character. With these considerations in mind, the present study focuses on assessment of the genetic variability for yield and yield component traits.

## MATERIALS AND METHODS

The present experiment comprised of a set of twenty two mungbean genotypes including check *i.e.* Samrat. The experiment was conducted in randomized block design (RBD) with three replications during *kharif* 2010 at Field Experimentation Centre, Department of Genetics and Plant Breeding, Allahabad School of Agriculture, SHIATS, Allahabad. To record the data on quantitative traits [except days to 50% flowering (DFF) and days to maturity (DM)], *viz.*, plant height (PH), number of primary branches per plant (NPBP), number of clusters per plant (NCP), number of pods per plant (NPP), pod length (PL), number of seeds per pod (NSP), 100 seed weight (100-SW), seed yield per plant (SYP) a total of five plants were selected randomly. These two traits were computed on plot basis. The data were subjected to analysis of variance, genetic parameters by using statistical package WINDOSTAT version 8.6 developed by Indostat Service Hyderabad.

## RESULTS AND DISCUSSION

**Table 1: Analysis of variance (ANOVA) for 10 quantitative characters in mungbean**

S. No.	Characters	Mean sum of square Replications (2)	Treatments (21)	Error (42)
1	Days to 50% flowering	2.33	8.20**	1.60
2	Plant height (cm)	3.52	459.70**	7.30
3	Number of primary branches per Plant	0.48	1.86**	0.53
4	Number of clusters per Plant	0.73	4.96**	0.08
5	Number of pods per plant	4.58	127.30**	0.43
6	Days to maturity	19.63	62.35**	1.98
7	Pod length (cm)	0.50	0.67**	0.27
8	Number of seeds per pod	0.39	5.34**	1.03
9	100 seed weight (g)	0.09	0.65**	0.11
10	Seed yield per plant (g)	0.62	3.18**	0.34

\*\* Significant at 1 % level of significance, df has been given in parenthesis.

**Table 2: Mean performance of mungbean genotypes for 10 quantitative characters**

SN	Characters	#DF	#PH	#PB	#CP	#PP	#DM	#PL	#SP	#SI	#SY
1	KM10-1041	49.33	76.76	2.26	7.80	15.93	73.00	8.03	9.00	3.61	11.26
2	KM10-1042	50.33	84.20	3.43	8.50	12.43	82.00	7.33	9.00	4.10	10.56
3	KM10-1043	48.66	79.20	2.00	9.70	27.67	81.00	6.86	8.66	3.54	10.23
4	KM10-1045	51.00	79.76	3.96	7.00	14.66	82.33	7.23	9.00	3.59	9.10
5	KM10-1046	52.00	82.03	2.43	8.56	29.33	82.00	8.26	9.66	3.11	8.43
6	KM10-1047	53.33	71.33	3.03	6.80	13.00	86.00	7.43	6.00	2.56	8.56
7	KM10-1050	50.66	70.43	2.36	7.33	21.76	82.33	7.50	6.66	3.89	10.26
8	KM10-1051	53.00	53.10	3.43	6.90	14.70	86.00	7.56	10.00	4.036	13.00
9	KM10-1053	50.33	69.40	2.20	10.93	26.80	81.00	8.43	8.66	3.54	9.6
10	KM10-1054	53.00	52.63	2.16	8.56	12.93	84.66	7.83	8.33	2.98	9.20
11	KM10-1057	52.00	59.80	3.83	7.70	23.23	83.66	7.66	7.66	3.56	10.56
12	KM10-1058	48.00	59.30	1.90	6.66	14.10	85.00	7.83	7.00	4.06	10.10
13	KM10-1059	51.00	73.13	4.16	8.70	30.53	81.00	7.56	6.66	4.28	9.36
14	KM10-1062	49.00	50.90	3.10	8.23	15.86	80.66	7.30	8.00	3.70	11.20
15	KM10-1063	48.00	69.73	2.70	7.73	15.40	78.33	7.49	6.66	4.40	10.76
16	KM10-1064	50.66	91.66	2.50	9.83	29.67	82.66	7.13	6.66	3.06	10.83
17	KM10-1068	47.66	95.66	4.63	6.86	13.73	70.33	8.20	5.66	3.60	10.93
18	KM10-1070	49.33	83.66	3.60	8.83	25.10	71.00	8.90	6.33	3.86	10.46
19	KM10-1071	50.66	75.46	3.66	10.66	15.63	74.66	7.46	6.00	4.33	9.50
20	KM10-1074	50.00	75.24	3.33	7.66	16.83	80.66	7.76	8.66	3.67	10.03
21	KM10-1076	50.00	63.50	3.66	9.96	26.53	82.00	7.50	9.00	3.47	10.40
22	SAMRAT (Ch)	41.00	80.36	4.80	6.75	24.67	59.00	6.51	10.17	3.83	9.50
Range	Lowest	47.66	50.90	1.90	6.66	12.43	70.33	6.86	5.66	2.56	8.43
	Highest	53.33	95.66	4.63	10.93	30.53	86.00	8.90	10.00	4.40	13.00
	Mean	50.38	72.23	3.06	8.33	19.80	80.49	7.68	7.77	3.66	10.20
	C.D. 5%	2.08	4.46	1.20	0.48	1.09	2.32	0.86	1.67	0.55	0.96

#Abbreviations of characters are given in materials and methods.

The analysis of variance (ANOVA) showed highly significant differences ( $P < 0.01$ ) among the genotypes for the entire yield and yield component traits studied (Table 1). Similar patterns were also recorded by Khan *et al.* (2004) in which highly significant genetic differences among genotypes were observed for DFF and yield. The success of any breeding programme relies upon the knowledge available on genetically heritable variation with good proportion of selection response of important yield component traits. A wide range of variability was observed among all the traits considered in the present study (Table 2). For example, DFF and DM ranged from 47 to 53 days and 70 to 86 days, respectively. However, none of the genotypes exhibited significant superiority in terms of these traits over check variety (Samrat), whereas all the 21 genotypes showed at par *per se* performance for DFF and poor performance for DM. Similarly, another trait *i.e.* plant height varied from 50.90 to 95.66 cm and more importantly, the three genotypes *viz.*, KM10-1064, KM10-1068, KM10-1070

were found to be superior over the better check (Taller than check). Yimram *et al.* (2009) also suggested the taller plant stature is beneficial for mechanical weeding and mechanical harvesting. None of the genotypes exhibited significant superiority over check for NPBP and SPP. NCP and PL varied from 6 to 10 and 6.86 to 8.90 cm and 16 genotypes exhibited significant superiority over check and rest of the genotypes exhibited at par *per se* performance for these traits (Table 2). Only two genotypes *i.e.* KM10-1051 and KM10-1063 were noted significantly superior than check for SI. Yield is ultimate aim of any crop improvement programme and out of twenty one, nine genotypes showed significant superiority over check for SYP.

The genetic parameters on 10 yield and yield component traits have been presented in Table 3. The coefficient of variation (CV) revealed that the magnitude of phenotypic coefficient of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all

**Table 3: Estimates of genetic parameters for 10 characters in mungbean genotypes**

S. No.	Characters	Coefficient of variation (%)		Heritability (%) (broad sense)	Genetic advance (%)	Genetic advance as % of mean
		Genotypic (GCV)	Phenotypic (PCV)			
1	Days to 50% flowering	2.95	3.87	58.32	2.33	4.62
2	Plant height (cm)	17.00	17.41	95.15	24.71	34.20
3	Number of primary branches per Plant	21.76	32.24	46.26	0.93	30.27
4	Number of clusters per Plant	15.31	15.71	95.51	2.56	30.74
5	Number of pods per plant	32.84	33.01	99.12	13.33	67.30
6	Days to maturity	5.57	5.84	91.14	8.82	10.95
7	Pod length (cm)	4.75	8.33	32.22	0.43	5.57
8	Number of seeds per pod	15.42	20.20	58.03	1.89	24.24
9	100 seed weight (g)	11.61	14.79	62.29	0.69	18.78
10	Seed yield per plant (g)	9.52	11.12	73.42	1.72	16.80

the traits studied which indicates the role of environment in manifestation of these traits. NPBP and NPP showed high magnitude of GCV and PCV suggested that these two traits were less influenced by the environment. Similar finding for NPP has earlier been reported by Singh *et al.* (2009). PH, NCP, NSP and SI exhibited moderate GCV and PCV values, whereas remaining traits *viz.*, DFF, DM and PL had low magnitude of GCV and PCV. Low magnitude of GCV and PCV was indicated the lack of sufficient variability in tested breeding material. Similar finding for DFF has earlier been reported by Venkateshwarlu *et al.* (2001), Biradar *et al.* (2007), Reddy *et al.* (2013). The moderate GCV and PCV values for PH, NCP, SI has earlier been observed by Suresh *et al.* (2010). SY exhibited low magnitude of GCV but moderate magnitude of PCV. This deviation may be noted due to environmental fluctuation on these traits and/ or other traits which having more contribution in manifestation of SY.

Heritability is good index for identification of traits. It is important selection parameter and provides clues on possible improvement (Makeen *et al.*, 2007). Here, the heritability (in broad sense) estimates were recorded to be in the range of 32.22 (PL) and 99.12% (NPP). Interestingly, almost all the traits showed high to moderate heritability estimates. High heritability for PH has earlier been reported by Makeen *et al.*, 2007 and Begume *et al.*, 2013. In addition to heritability, the genetic advance (GA) offers a potential parameter for selection. In the context, in the present study GA estimates ranged from 0.43 (PL) to 24.71% (PH). High heritability coupled with high GAM was recorded for PH, NCP, NPP and DM, indicated the predominance of additive gene action in the expression of the traits which could be easy targets for phenotypic selection and consequently, may be improved genetically *via* simple plant selection methods. The traits with high  $h^2$  coupled high GAM indicating greater role of additive gene effects on the expression of these traits in agreement with Singh *et al.* (2009), Rahim *et al.* (2010) and Baisakh *et al.* (2013). Singh *et al.* (2009) also observed high GAM for NSP and PH. Rest traits showed high to moderate heritability coupled with moderate to low GAM suggesting the existence of non-additive gene action in the expression of the traits and may be exploited better in recombination breeding. Targeting selections based on *per se* performance of genotypes; the superior genotypes for these traits may be isolated and further utilized for mungbean genetic improvement.

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Estimation of Genetic Association of Yield and Quality Traits in Mungbean (*Vigna radiata* L. Wilczek). International journal of tropical agriculture ISSN : 0254-8755. available at <http://www.serialsjournals.com> © Serials Publications Pvt. Ltd. Volume 36 Number 3 2018. of association between yield and its components themselves greatly help in evaluating the contribution of different components towards yield. Yield being a polygenic character is highly influenced by the fluctuations in environment. Hence, selection of plants based directly on yield would not be very reliable. Improvement in yield depends on the nature and extent of genetic variability, heritability and genetic advance in the base population. Genetic variability and interrelationships among yield and yield components in green gram (*Vigna radiata* (L.) Wilczek). Crop. Res., 13: 361-368. Chaudhury, M., M.A. Kalequ Mian and M.M. Rahaman, 1998. Variability and correlation among some yield contribution characters in mung bean. Bangladesh J. Plant Breeding Genetics, Bangladesh, 21: 62-65. Dewey, D.R. and K.H. Lu, 1959. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron. J., 51: 515-518. CrossRef | Direct Link |. Gupta, S.N., S. Lal and R.L. Tomar, 1982. Correlations and path analysis in