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## Studies on genetic variability, character association for yield and yield components in green gram (*Vigna radiata* L. Wilczek)

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### Abstract

Twenty Mungbean (*Vigna radiata* L. Wilczek) genotypes were evaluated for the estimation of genetic variability parameters, correlation coefficient, Heritability and Genetic advance. The genotypes differed significantly for all characters. Higher GCV and PCV was observed for number of branches per plant (42.09%;62.27%) followed by number of clusters per plant (24.44%;30.08%), number of pods per plant (19.15%;25.36%), plant height (15.92%;17.59%), harvest index (11.14%;11.94%), seed yield per plant (9.72%;10.32%), seeds per pod (8.33%;12.44). High heritability observed for the biological yield per plant (97.96%) followed by harvest index (91.69%), seed yield per plant (88.73%), plant height (81.97%) and 100 seed weight (70.09%) indicating the impact of additive gene expression. The plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100 seed weight had highly significant and positive correlations with seed yield at both genotypic and phenotypic levels.

**Keywords:** Greengram, Genetic variability, Correlation Coefficient, Heritability, Genetic advance.

### 1. Introduction

Mungbean (*Vigna radiata* (L.) Wilczek) is one of the major pulse crop of India, which is cultivated from humid tropic to arid and semi-arid regions. Mungbean is cultivated in Bangladesh, China, India, Pakistan, Srilanka, Thailand, Philippines, Myanmar, Indonesia, East Africa, Nepal and Bhutan. Mungbean was originated in India from where it spread to Java, Eastern and Central Africa, West Indies, Warmer parts of China and U.S. The genus *Vigna* belongs to Fabaceae family, species *Vigna radiata* with diploid chromosome number  $2n=22$ . It is an annual plant with erect to semi erect plant type. India is the largest producer and consumer of pulses in the world contributing around 25-28% of the total global production. The country grows a variety of pulse crops, such as chickpea, Pigeonpea, Greengram, Blackgram, dry peas and lentils under a wide range of agro-climate conditions. The total pulse production is 17.2 million tonnes from 24.8 million ha area (Anonymous, 2012) [2] which is all times high and is the only exception. Pulses are least preferred by farmers because of high risk and less remunerative than cereals; consequently, the production of the pulses is significantly low to meet the demand of pulses. Majority of Indian population is vegetarian, pulses are cheap and best source of protein for Indian diet. It contains 20-25 per cent protein, which is more than two times of cereals. India importing about 3 million tonnes and the future demand of pulses by 2015 will be 27.0 million tonnes (Singh, 2011) [17].

Greengram occupies an area of 2.89 million hectare with the production of 1.10 million tonnes and productivity of 381 kg ha<sup>-1</sup>. Farmers grow this crop not as a principal crop but as a bonus crop, mixed with other crops on marginal lands and that too without manuring. The entire success of plant breeding programme of any crop largely depends on the wide range of variability present in that crop. It is the range of genetic variability in respect of important economic characters present in the population upon which is based on the effectiveness of selection. Environment has a profound influence upon the economically important characters, which are quantitatively inherited. Hence, it is difficult to decide upon whether the observed variability is heritable or due to environment and it is therefore, necessary to partition the same into its heritable and non-heritable components. Selection procedure is more difficult in a trait, where heritability is low or is not precisely measurable. Indirect selection in such a situation is more effective and study of correlation among different economic traits are therefore, essential for an effective selection programme because selection for one or more trait results in correlated response for several other traits and sequence of variation will also be influenced. Hence, the knowledge of genotypic and phenotypic correlation between yield and its contributing

characters is very essential. Correlation studies measure only mutual association between two traits and it does not imply the cause and effect of relationship.

### Materials and Methods

The present investigation was carried out at the Field Experimentation Centre, Department of Genetics and Plant Breeding, SHUATS, Allahabad (U.P.) during *Kharif-2016*. The experimental materials for the present study was obtained from the Rajasthan Agriculture Research Institute, Durgapura, Jaipur (Rajasthan). The experiment was conducted in Randomized Block Design with 20 treatments. The treatments were replicated three times. Treatments were randomly arranged in each replication divided into 60 plots. The gross area of experiment was 152.54 m<sup>2</sup> and cash plot size was 1 x 1 m. The row to row spacing was 30 cm and plant to plant distance was 10 cm. The five competitive plants from each of the replication were tagged and observations were taken from these tagged plants at various stages of the crop plant growth. Data were recorded from twelve characters viz., days to 50% flowering, plant height, Number of branches, days to maturity, number of clusters per plant, number of pod per plant, pod length, number of seed per pod, biological yield, 100 seed weight (g), harvest index and seed yield per plant (g). Mean values were computed and data were analysed for analysis of variance as suggested by (Fisher, 1936) [5] and coefficient of variances as well as heritability (in broad sense), as suggested by Burton and Devane (1953) [3]. The estimates of genetic advance were obtained by the formula suggested by Lush (1949) [10] and Johnson *et al.* (1955) [7].

### Results and Discussion

The genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent over mean for each of the characters are presented in Table-1. Considerable range in variation was observed for all characters. Phenotypic coefficients of variation values were relatively higher than corresponding genotypic coefficient of variation for all traits under study. It indicated the effect of environment in the expression of the traits. The PCV which gives the extent of phenotypic variability ranged from 3.39 to 67.27 percent for various traits. The PCV was high for number of primary branches per plant (67.27), followed by number of clusters per plant (30.08) and number of pods per plant (25.36). Genotypic coefficient of variation which gives the extent of genetic variability in the population, ranged from 2.50 to 42.09 per cent. Maximum genotypic coefficient of variation was observed for number of branches per plant (42.09) followed by number of clusters per plant (24.44), while moderate GCV were recorded for pods per plant (19.15), plant height (15.92), harvest index (11.44), seed yield per plant (9.72) and seeds per pod (8.33) showed low genotypic coefficient of variation (GCV) indicating large variation in the population for this trait. High phenotypic coefficient of variation and genotypic coefficient of variation were observed for seed yield per plant followed by number of clusters per plant, 100- seed weight, number of pods per plant, number of primary branches per plant and number of pods per cluster. Similar findings were reported by Patel (2000), Makeen *et al.* (2007) [11] and Saxesena *et al.* (2014). Less differences

observed between phenotypic and genotypic coefficient of variation in certain cases indicated that these characters were less influenced by the environment. The highest heritability value was registered by biological yield per plant (97.96%) followed by harvest index (91.69%), seed yield per plant (88.73%), plant height (81.97 %) and 100 seed weight (70.09%) indicating preponderance of additive gene action in expression of these traits and they can be improved through individual plant selection. These results are in conformity with the findings of Patel (2000), Reddy *et al.* (2003) [15] and Makeen *et al.* (2007) [11]. The high genetic advance was observed for a similar result for high genetic advance was observed by Patel (2000) and Reddy *et al.* (2011) [14]. Johnson *et al.* (1955) [7] suggested that the heritability and genetic advance when calculated together would be more useful in predicting the resultant effects of selection, because the characters which show high heritability along with high genetic advance probably due to additive gene effects and it was observed for seed yield per plant (g). But, High heritability estimates with moderate to low genetic advance were found for days to 50% flowering and days to maturity, which indicated that these characters were highly influenced by the environmental effects and direct selection for this character would be ineffective. Correlation coefficient analysis among Seed yield and its contributing characters are shown in Table 3. There was positive, significant and strong correlation of this trait with plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, 100-seed weight at both genotypic and phenotypic levels. Days to 50% flowering, days to maturity and 100 seed weight showed negative and highly significant correlation with seed yield per plant at both the levels. Similar results were reported by Venkateswarlu (2001) [20], Haritha and Reddy (2002) [6], Nazir *et al.* (2005) [13], Tejbir Singh *et al.* (2009) [18] and Reddy *et al.* (2011) [14] for seed yield with number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod. Ahmad *et al.* (2013) [11] also observed positive genotypic association of seed yield with plant height, number of primary branches per plant, number of cluster per plant, number of pods per plant and 100- seed weight. Kumar *et al.* (2013) [9] and Narasimhulu *et al.* (2013) [12] also found with number of clusters per plant and number of seeds per pod. Khan *et al.* (2001), Peerajade *et al.* (2009), Saxena *et al.* (2007) [16] and Ahmad *et al.* (2013) [11] had also observed with number of primary branches per plant. Days to maturity, days to 50% flowering and pod length showed negative and highly significant correlation with seed yield per plant at both the levels. Similar results were also reported by Ved Prakash *et al.* (2007) [19] and Verma and Garg (2007) [21]. While Ahmed *et al.* (2013) also reported for days to maturity. The results thus, revealed that seed yield per plant, 100-seed weight, number of primary branches per plant, number of pods per cluster, number of pods per plant and number of seeds per pod were the important attributes, which contributed towards higher yield. Therefore, more emphasis should be given to these components during selection for higher yield. The interrelationship among yield components would help in increasing the yield levels.

**Table 1:** Coefficient of Variation, Heritability and Genetic Advance for 12 yield contributing characters of 20 mungbean genotypes.

Parameters Characters	$\sigma^2g$	$\sigma^2p$	Coefficient of variation		Heritability (h <sup>2</sup> ) (BS)	Genetic advance 5 %	Genetic advance as % of mean 5%
			GCV	PCV			
Days of 50% flowering	2.65	4.57	3.90	5.11	58.04	2.56	6.12
Plant height	123.01	150.06	15.92	17.59	81.97	20.69	29.70
Number Of branches per plant	0.68	1.74	42.09	67.27	39.15	1.07	54.26
Number Of clusters per plant	2.02	3.07	24.44	30.08	66.02	2.38	40.90
Number Of pods per plant	16.60	29.11	19.15	25.36	57.03	6.34	29.80
Days of 50% maturity	2.00	3.68	2.50	3.39	54.29	2.15	3.79
Pod length	0.14	0.25	5.15	6.76	57.89	0.59	8.07
Number of seeds per pod	0.78	1.75	8.33	12.44	44.81	1.22	11.49
100 seed weight	0.02	0.03	4.29	5.12	70.09	0.24	7.39
Biological yield per plant	12.07	12.32	6.58	6.65	97.96	7.08	13.42
Harvest index	5.04	5.49	11.44	11.94	91.69	4.43	22.56
Seed yield per plant	1.01	1.13	9.72	10.32	88.73	1.95	18.86

$\sigma^2g$  = Genotypic variance,  $\sigma^2p$  = Phenotypic variance,  $h^2$  = Heritability (broad sense), GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation.

**Table 2:** Genotypic and phenotypic correlation coefficients of different yield components with seed yield per plant in green gram.

Characters		Days of 50% flowering	Plant Height	Number Of branches per plant	Number Of clusters per plant	Number Of pods per plant	Days of 50% maturity	Pod length	Number of seeds per pod	100 seed weight	Biological yield per plant	Harvest index	Seed yield per plant
Days of 50% flowering	g	1.00	0.065	-0.055	-0.158	0.349**	0.968**	0.312*	0.482**	0.381**	0.010	-0.180	-0.183
	p	1.00	0.032	0.259*	-0.121	0.132	0.918**	0.126	0.233	-0.198	0.000	-0.136	-0.145
Plant height	g		1.00	0.206	0.455**	0.356**	0.172	0.156	-0.022	0.288*	-0.007	0.158	0.167
	p		1.00	0.159	0.445**	0.338**	0.100	0.069	-0.056	0.243	0.010	0.121	0.133
Number Of branches per plant	g			1.00	-0.006	0.094	0.018	0.301*	0.516**	-0.155	0.306*	-0.082	0.069
	p			1.00	0.056	0.102	0.323*	-0.040	0.006	-0.004	0.190	-0.115	-0.042
Number Of clusters per plant	g				1.00	0.725**	-0.028	0.390**	0.191	0.184	0.413**	0.104	0.383**
	p				1.00	0.656**	-0.087	0.270*	-0.074	0.169	0.351**	0.041	0.261*
Number Of pods per plant	g					1.00	0.357**	0.598**	0.717**	-0.245	0.140	0.386**	0.553**
	p					1.00	0.101	0.280*	0.241	-0.067	0.109	0.232	0.345**
Days of 50% maturity	g						1.00	0.336**	0.382**	0.369**	0.024	-0.182	-0.183
	p						1.00	0.191	0.207	-0.152	0.007	-0.108	-0.113
Pod length	g							1.00	-0.028	0.334**	-0.235	0.559**	0.522**
	p							1.00	-0.077	-0.230	-0.173	0.380**	0.344**
Number of seeds per pod	g								1.00	0.388**	0.007	0.230	0.285*
	p								1.00	-0.171	-0.013	0.174	0.204
100 seed weight	g									1.00	0.319*	-0.253	-0.114
	p									1.00	0.265*	-0.200	-0.086
Biological yield per plant	g										1.00	-0.516**	0.025
	p										1.00	-0.493**	0.031
Harvest index	g											1.00	0.842**
	p											1.00	0.853**
Seed yield per plant	g												1.00
	p												1.00

\*\*1% and \* 5% level of significance respectively

## Conclusion

The experimental results concluded that high yield was recorded by RMG-1079 (12.49) followed by ML-1299 (11.66), PUSA-672 (11.60), RMG-1041 (11.30) and RMG-1045 (11.27) identified as desirable genotypes with seed yield per plant as compared with JYOTI (check) (8.83). High magnitude of GCV and PCV were recorded for pods per plant, branches per plant, and clusters per plant, heritability and genetic advance also showed positive significant association with seed yield. Seed yield per plant showed positive significant association with number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and harvest index. Thus, priority should be given to these characters for yield improvement in Mungbean.

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