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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS FOR SEED YIELD AND ITS COMPONENTS IN GREEN GRAM [*VIGNA RADIATA* (L.) WILCZEK]

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ABSTRACT

Forty diverse mungbean (*Vigna radiata* L. Wilczek) genotypes were evaluated for the estimation of genetic variability parameters, correlation coefficient and path coefficient analysis. The genotypes differed significantly for all characters. Higher GCV and PCV was observed for seed yield per plant (31.76%; 31.45%) followed by number of clusters per plant (21.59%; 21.03%), 100- seed weight (20.75%; 18.68%), number of pods per plant (19.885%; 19.33%), number of primary branches per plant (19.14%; 17.93%) and number of pods per cluster (18.78%; 17.55%). High heritability coupled with high expected genetic advance was observed in seed yield per plant (98.1%; 64.20%) 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 and protein content had highly significant and positive correlations with seed yield at both genotypic and phenotypic levels. Maximum direct effect of number of seeds per pod (0.642) and number of pods per cluster (0.432) on seed yield was observed.

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 Butan. 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 semierect 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) 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). Greengram occupies an area of 2.89 million hectare with the production of 1.10 million tonnes and productivity of 381 kg ha^{-1}. 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. Path analysis is a standardized partial regression analysis, which further permits the partitioning of correlation coefficient in to components of direct and indirect effects of independent variable on the dependent variable (Wright, 1921).

MATERIALS AND METHODS

The experiment was conducted at Muvaliya Farm, Hill Millets Research Station, Anand Agricultural University, Dahod during *Kharif* 2012. The experimental material comprised of forty genotypes of mungbean representing different geographic origin. The experiment was laid out in randomized block design with three replications, and the crop was raised as per the recommended package of practices. Seeds were sown with row to row spacing of 45 cm and plant to plant spacing of 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 for twelve characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g), seed yield per plant (g) and protein content (%).

Mean values were computed and data were analyzed for analysis of variance as suggested by Panse and Sukhatme (1985) and coefficient of variances as well as heritability (in broad sense), as suggested by Burton (1952), Genotypic and phenotypic correlation coefficients analysis were estimated adopting the procedure suggested by Comstock and Robinson (1952). Path coefficient analysis as suggested by Wright (1921) was used to partition the genotypic correlation coefficients of seed yield into direct and indirect effects.

RESULTS AND DISCUSSION

The mean sums of squares due to various sources for different traits are presented in Table 1. The analysis of variance indicated highly significant differences for all characters among 40 accessions for all the traits indicating presence of wide genetic variation for different characters among the genotypes of mungbean. The genotypic and phenotypic coefficient of variation, heritability and genetic advance as percent over mean for each of the characters are presented in Table 2. 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 4.97 to 31.76 per cent for various traits. The PCV was high for seed yield per plant (31.76 %), number of clusters per plant (21.59 %) and 100-seed weight (20.75 %).

Genotypic coefficient of variation which gives the extent of genetic variability in the population, ranged from 4.00 to 31.45 per cent. Maximum genotypic coefficient of variation was observed for seed yield per plant (31.45 %) followed by number of clusters per plant (21.03 %), number of pods per plant (19.33 %) and 100-seed weight (18.68 %) 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) 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 seed yield per plant (98.1 %), followed by number of seeds per pod (97.4 %), protein content (96.1 %), number of clusters per plant (94.9 %), number of pods per plant (94.7 %), days to 50% flowering (94.6 %), plant height (94.1 %), pod length (90.2%), number of primary branches per plant (87.8 %), number of pods per cluster (87.4 %), 100 seed weight (81.1 %) and days to maturity (64.6 %) 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) and Makeen *et al.* (2007). The high genetic advance was observed for plant height (11.77) followed by number of pods per plant (5.54),

Table 1: Analysis of variance (mean sum of squares) for various characters in mungbean

Source	Mean Squares Replications	Genotypes	Error
d.f	2	39	78
Seed yield per plant	0.18	17.77**	0.11
Days to 50% flowering	5.26	19.46**	0.36
Days to maturity	7.78	25.14**	3.88
Plant height	0.78	106.33**	2.17
Number of primary branches per plant	0.00	0.86**	0.03
Number of cluster per plant	0.04	4.14**	0.07
Number of pods per cluster	0.18	1.49**	0.06
Number of Pods per plant	0.34	23.37**	0.42
Pod length	0.68	2.95**	0.08
Number of seeds per pod	0.01	7.00**	0.06
100-seed weight	0.03	1.73**	0.11
Protein content	0.03	6.32**	0.12

*, ** Significant at 5% and 1% levels of probability, respectively

Table 2: Phenotypic and genotypic coefficients of variation, heritability (b. s.), genetic advance and genetic advance expressed as per cent of mean for twelve characters of mungbean genotypes

Characters	σ^2_g	σ^2_p	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability in broad sense (%)	Genetic advance	Genetic advance expressed as per cent of mean
Days to 50% flowering	6.36	6.72	7.10	6.91	94.6	5.06	13.85
Days to maturity	7.08	10.97	4.97	4.00	64.6	4.41	6.62
Plant height	34.72	36.89	17.67	17.14	94.1	11.77	34.23
Number of primary branches per plant	0.27	0.31	19.14	17.93	87.8	1.02	34.77
Number of cluster per plant	1.35	1.43	21.59	21.03	94.9	2.34	42.23
Number of pods per cluster	0.47	0.54	18.78	17.55	87.4	1.33	33.84
Number of pods per plant	7.65	8.07	19.88	19.33	94.7	5.54	38.76
Pod length	0.95	1.04	16.06	15.37	90.2	1.93	30.32
Number of seeds per pod	2.31	2.37	15.37	15.17	97.4	3.09	30.81
100-seed weight	1.00	1.11	20.75	18.68	81.1	1.36	34.69
Seed yield per plant	5.70	5.81	31.76	31.45	98.1	4.95	64.20
Protein content	2.02	2.06	5.85	5.08	96.1	2.91	11.85

days to 50% flowering (5.06), seed yield per plant (4.95), days to maturity (4.41) and number of seeds per pod (3.09). A similar result for high genetic advance was observed by Patel (2000) and Reddy *et al.* (2011). Johnson *et al.* (1955) 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, protein content 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 and protein content at both genotypic and phenotypic levels. Days to 50% flowering, days to maturity and pod length showed negative and highly significant correlation with seed yield per plant at both the levels. Similar results were reported by Venkateswarlu (2001), Haritha and Reddy (2002), Nazir *et al.* (2005), Tejbir Singh *et al.* (2009) and Reddy *et al.* (2011)for seed yield with number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod and protein content. Ahmad *et al.* (2013) 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) and Narasimhulu *et al.* (2013) 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) and Ahmad *et al.* (2013) 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) and Verma and Garg (2007). 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.

The path coefficient analysis revealed that the highest direct and positive effect on seed yield was exhibited by number of seeds per pod and number of pods per cluster. Thus, these characters turned out to be the major components of seed yield. Such positive and high direct effects of these variables had also been reported by Khan and Ahmed (1989), Byregowda *et al.* (1997), Venkateswarlu (2001), Ved Prakash *et al.* (2007), Tnippani *et al.* (2013), Rajanna *et al.* (2014) and Shekhawat *et al.* (2014). Other characters like number of primary branches per plant, number of pods per plant and 100-seed weight showed moderate positive effect on seed yield. The direct effect of number of clusters per plant, pod length was negative. Negative direct effect of pod length contributed negative correlation with seed yield per plant and its direct effect on seed yield per plant was also negative. While, days to 50% flowering and days to maturity showed negative and significant association with seed yield per plant but its direct effect on seed yield per plant was moderate and positive.

Hence, selection based on characters number of seeds per pod and number of pods per cluster with high direct effects and number of primary branches per plant, number of pods per plant and 100-seed weight with moderate indirect effects may be useful for improving the seed yield per plant of mungbean.

It is evident from the foregoing discussion that the economic character, seed yield per plant showed genetic variability, heritability and genetic advance of high magnitude. The correlation study revealed that the number of seeds per pod and number of pods per plant were important characters for increasing seed yield. Genotypic path coefficient analysis indicated that the predominance of direct effects of number of

Table 3: Genotypic (r_g) and phenotypic (r_p) correlation coefficients among twelve characters in mungbean

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of cluster per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Protein content (%)
Seed yield per plant (g)	r_g	-0.924**	-0.900**	0.809**	0.868**	0.924**	0.898**	0.925**	-0.880**	0.930**	0.826**	0.809**
	r_p	-0.890**	-0.730**	0.778**	0.810**	0.893**	0.846**	0.892**	-0.828**	0.911**	0.729**	0.784**
Days to 50% flowering	r_g		0.955**	-0.732**	-0.125	-0.897**	-0.861**	-0.924**	0.862**	-0.930**	-0.761**	-0.851**
	r_p		0.755**	-0.690**	-0.213	-0.854**	-0.778**	-0.883**	0.793**	-0.886**	-0.660**	-0.810**
Days to maturity	r_g			-0.767**	-0.938**	-0.975**	-0.911**	-0.911**	0.796**	-0.864**	-0.754**	-0.874**
	r_p			-0.608**	-0.716**	-0.740**	-0.693**	-0.729**	0.621**	-0.677**	-0.530**	-0.683**
Plant height (cm)	r_g				0.737**	0.807**	0.846**	0.827**	-0.701**	0.762**	0.653**	0.248
	r_p				0.682**	0.760**	0.766**	0.787**	-0.626**	0.726**	0.559**	0.187
Number of primary branches per plant	r_g					0.847**	0.859**	0.812**	-0.734**	0.763**	0.317*	0.096
	r_p					0.780**	0.755**	0.759**	-0.671**	0.703**	0.232	0.068
Number of cluster per plant	r_g						0.932**	0.920**	-0.833**	0.908**	0.755**	0.870**
	r_p						0.840**	0.872**	-0.778**	0.874**	0.616**	0.830**
Number of pods per cluster	r_g							0.866**	-0.802**	0.810**	0.721**	0.830**
	r_p							0.788**	-0.698**	0.754**	0.616**	0.767**
Number of pods per plant	r_g								-0.842**	0.880**	0.204	0.841**
	r_p								-0.775**	0.847**	0.113	0.802**
Pod length (cm)	r_g									-0.866**	-0.250	-0.765**
	r_p									-0.847**	-0.178	-0.706**
Number of seeds per pod	r_g										0.756**	0.321*
	r_p										0.674**	0.216
100-seed weight (g)	r_g											0.861**
	r_p											0.805**

*, ** significant at 5% and 1% levels, respectively

Table 4: Genotypic path coefficient analysis showing direct and indirect effects of different characters on seed yield in mungbean

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of cluster per plant	Number of pods per cluster	Number of pods per plant	Pod length (cm)	Number of seeds per pod	100 seed weight (g)	Protein content (%)	Genotypic correlation with seed yield
Days to 50% flowering	0.126	0.208	0.112	-0.188	0.087	-0.372	-0.257	-0.015	-0.596	-0.193	0.165	-0.924**
Days to maturity	0.120	0.218	0.118	-0.213	0.095	-0.394	-0.254	-0.014	-0.555	-0.191	0.169	-0.900**
Plant height (cm)	-0.092	-0.167	-0.153	0.168	-0.078	0.365	0.230	0.012	0.489	0.165	-0.130	0.809**
Number of primary branches per plant	-0.104	-0.204	-0.113	0.228	-0.082	0.371	0.226	0.013	0.489	0.196	-0.151	0.868**
Number of cluster per plant	-0.113	-0.213	-0.124	0.193	-0.097	0.403	0.256	0.014	0.583	0.191	-0.169	0.924**
Number of pods per cluster	-0.109	-0.199	-0.130	0.195	-0.091	0.432	0.241	0.014	0.520	0.183	-0.160	0.898**
Number of pods per plant	-0.117	-0.199	-0.127	0.185	-0.089	0.374	0.278	0.015	0.564	0.204	-0.164	0.925**
Pod length (cm)	0.109	0.170	0.104	-0.165	0.078	-0.335	-0.231	-0.018	-0.556	-0.165	0.142	-0.880**
Number of seeds per pod	-0.117	-0.188	-0.117	0.174	-0.088	0.350	0.245	0.015	0.642	0.171	-0.155	0.930**
100-seed weight (g)	-0.096	-0.165	-0.100	0.176	-0.073	0.312	0.224	0.011	0.432	0.253	-0.148	0.826**
Protein content (%)	-0.107	-0.190	-0.103	0.177	-0.085	0.356	0.235	0.013	0.513	0.194	-0.194	0.809**

Residual effect, R = 0.0190

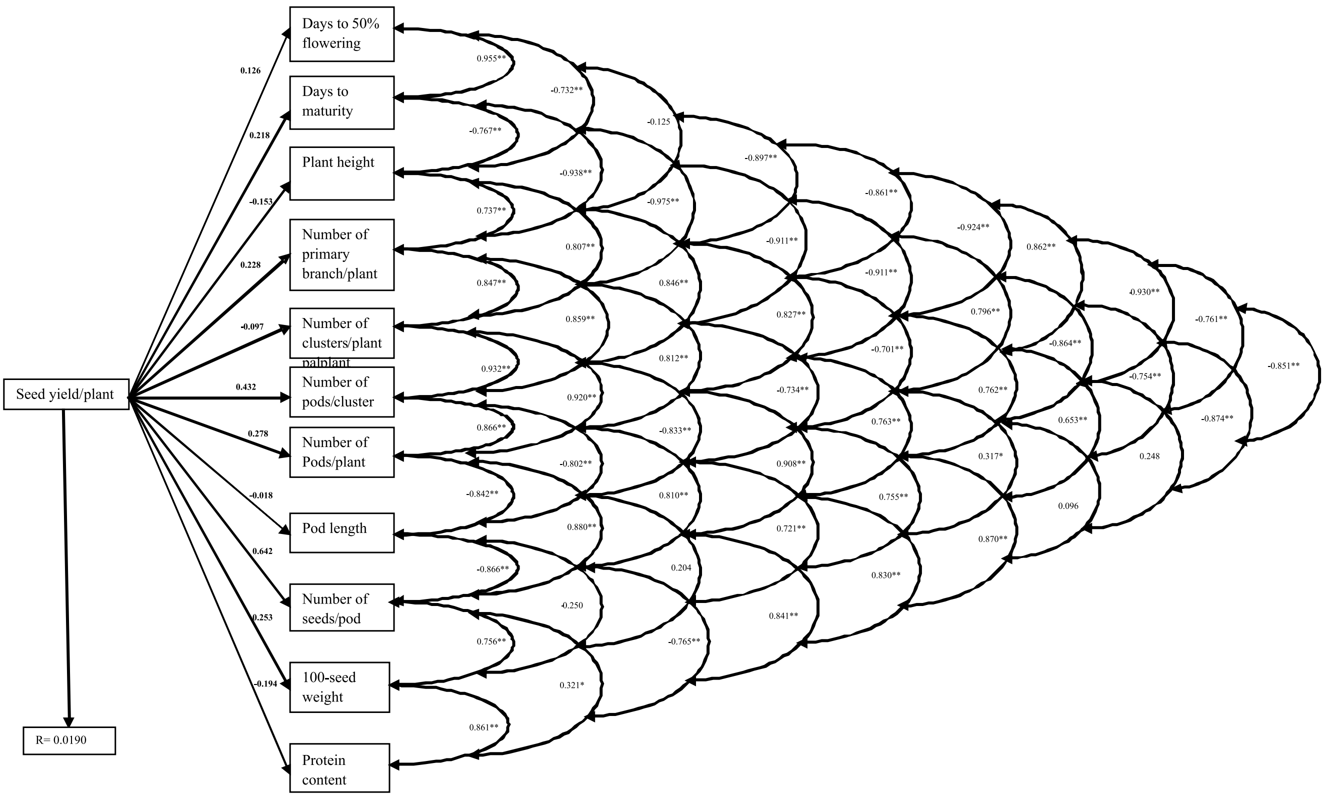

Figure 1: Path diagram showing direct and indirect effect of various traits on seed yield

seeds per pod and number of pods per cluster.

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