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Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mung bean [*Vigna radiata* (L.) Wilczek]

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Abstract

Forty-four mung bean [*Vigna radiata* (L.) Wilczek] genotypes were studied to assess the genetic variability parameters, heritability, genetic advance, correlation and path coefficient analysis for yield and yield contributing characters. The genotypes differed significantly for all twelve characters studied. High GCV and PCV observed for primary branches per plant, pods per plant, seed yield per plant and clusters per plant. High heritability along with high genetic advance as percent of mean was observed for plant height, primary branches per plant, clusters per plant, pods per plant and seed yield indicating preponderance of additive gene action. The characters, clusters per plant and pods per plant showed positive and high significant correlation with seed yield per plant. Among the characters studied, days to 50% flowering had high positive direct effect on seed yield per plant while, test weight, clusters per plant, pods per plant and primary branches per plant had low positive direct effect on seed yield per plant. Therefore, more emphasis should be given on these characters while selection for high yielding mung bean cultivar.

Keywords: GCV, PCV, *Vigna radiata* (L.) wilczek, correlation, path coefficient

Introduction

Mung bean [*Vigna radiata* (L.) Wilczek] is a legume cultivated for its edible seeds and sprouts across Asia. It belongs to family Fabaceae and sub family papilionaceae with diploid chromosome number $2n = 2x = 22$. There are three subgroups of *Vigna radiata*: one is cultivated (*Vigna radiata* subsp. *radiata*), and two are wild (*Vigna radiata* subsp. *sublobata* and *Vigna radiata* subsp. *glabara*). Mung bean (*Vigna radiata* var. *radiata*) is believed to have originated in Indian subcontinent (deCandolle, 1884; Vavilov, 1926; Zukovskij, 1962) [28, 1, 2]. Since India has a wide range of genetic diversity of cultivated, as well as of weedy wild types of mung bean, it is considered as the region of its first domestication (Baudoin and Marechal, 1988) [4].

Mung bean is a rich source of nutrient and is considered a healthy food. It constitutes an important place in vegetarian diets. Mung bean seeds are a good source of dietary protein and contain higher levels of folate and iron than most other legumes (Keatinge *et al.*, 2011) [5]. Sprouted seeds of mung bean is equivalent to fresh fruit in respect of nutrient content as it contains vitamins A, B, C, E and minerals, such as, iron, calcium and phosphorus. Besides, there is an increase in the thiamine, niacin and ascorbic acid content with sprouting. On dry weight basis, it contains 22-28 percent protein, 1.0-1.5 per cent fat, 3.5-4.5 percent fiber, 4.5-5.5 per cent ash and 60-65 percent carbohydrate. It is also a rich source of essential amino acids like isoleucine, leucine, lysine and phenylalanine (Lambrides and Godwin, 2007). The character yield is governed by many genes and their interactions. The study of correlations between pair of these characters provides basics for selection of traits. Path coefficient analysis helps to study the direct and indirect effect of traits on yield.

Materials and Methods

The experiment was conducted at Agricultural Research Station, Anand Agricultural University, Sansoli during *kharif* 2017. The experimental material comprised of forty four diverse genotypes of mung bean (listed in Table 1) obtained from Pulse Research Station, Anand Agricultural University, Vadodara. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications.

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Each entry was accommodated in two rows of 4.0 m length with a spacing of 45 × 10 cm. All the recommended package of practices was adopted to raise a good crop. Observations were recorded on five randomly selected plants from each entry for twelve traits viz. days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, clusters per plant, pods per cluster, pods per plant, pod length (cm), seeds per pod, test weight (g), seed yield per plant (g) and protein content. The mean values were used for estimation of analysis of variance (Panse and Sukhatme, 1978) ^[6], genotypic and phenotypic coefficient of variation (Burton, 1952) ^[7], heritability in broad sense (Allard, 1960) ^[8] and genetic advance expressed as percent of mean (Johnson *et al.*, 1955) ^[9]. The genotypic and phenotypic correlation coefficients were computed using genotypic and phenotypic variances and covariances. The path coefficient analysis was carried out as per the method suggested by Dewey and Lu (1959) ^[10].

Results and Discussion

The analysis of variance (Table 2) indicated significant amount of variability present among the genotypes for all the characters studied. Therefore, there is a lot of scope for selection for majority of the traits in the genotypes.

Genetic variability studies

The extent of variability as measured by GCV and PCV provides information regarding the relative amount of variation in different characters. Differences between phenotypic coefficient of variation and genotypic coefficient of variation were narrow for all the characters under investigation, suggesting that these traits studied have low environmental influence. High genotypic and phenotypic coefficient of variation was observed for primary branches per plant, pods per plant, seed yield per plant and clusters per plant indicated that there is greater diversity for these traits in mung bean. Hence direct selection for these traits would be effective for the improvement of this crop, whereas, plant height, test weight, pods per cluster, seeds per pod and pod length had moderate genotypic and phenotypic coefficient of variation expressed moderate variability in the material under investigation. Low values of genotypic and phenotypic coefficient of variation were noted for protein content, days to maturity and days to 50% flowering which indicated low range of variation for these characters in the genotypes, thus offering little scope for further improvement of these characters through simple selection. The results are in accordance with that of Ahmad *et al.* (2015), Patel *et al.* (2014) ^[11, 12] for high GCV and PCV of pods per plant, seed yield per plant and cluster per plant, Mehandi *et al.* (2013) ^[13] for primary branches per plant and pods per plant, Garg *et al.* (2017), Hemavathy *et al.* (2015), Suresh Babu *et al.* (2012) ^[14, 15, 16] for seed yield per plant and pods per plant.

Selection of traits based on heritability and genetic advance as percent of mean is of great importance to the breeder for making criteria for improvement in a complex character. High heritability along with high genetic advance as percent of mean was observed for plant height, primary branches per plant, clusters per plant, pods per plant and seed yield indicating the preponderance of additive gene action and hence simple selection would be more effective for improvement of these characters (table 3). Similar results were reported by Shiv *et al.* (2017), Ramakrishnan *et al.* (2018), Jagdhane *et al.* (2017) ^[17, 18, 19] for primary branches per plant and pods per plant, Sana *et al.* (2017) and Katiyar *et al.* (2015a) ^[20, 21] for pods per plant and seed yield per plant.

Correlation coefficient analysis

As yield is the resultant of combined effect of several component characters and environment, understanding the interaction of characters among themselves and with environment has been of great use in the plant breeding. Seed yield per plant showed positive and highly significant correlation with clusters per plant and pods per plant (table 4). Hence, these characters should be given due consideration while selecting for increased yield. Seeds per pod, test weight, plant height and protein content showed positive and non-significant correlation at both genotypic and phenotypic levels except test weight which showed positive and significant correlation at phenotypic level only. Days to 50% flowering and days to maturity showed negative and highly significant correlation with seed yield per plant at both genotypic and phenotypic levels which indicated that selection for high yield and early maturity variety is possible. Negative and non-significant correlation was found for pods per cluster and pod length. Similar findings were reported by Makeen *et al.* (2007) ^[22] for pods per plant, seeds per pod (genotypic correlation only) and test weight, Parihar *et al.* (2018) ^[23] for days to maturity, seeds per pod and test weight, Ramakrishnan *et al.* (2018) ^[18] for clusters per plant, pods per plant and seeds per pod.

Path coefficient analysis

A polygenic trait like seed yield is influenced by its various components directly as well as indirectly via other traits, which create a complex situation before a breeder for making selection. Therefore, path coefficient analysis could provide a more realistic picture of the interrelationship by partitioning it into direct and indirect effects of the variables. In the present study, days to 50% flowering had high and positive direct effect on seed yield per plant followed by low and positive effect exerted by test weight, clusters per plant, pods per plant and primary branches per plant (table 5). The direct effect of days to maturity on seed yield was very high and negative. High and positive direct effect of days to 50% flowering on seed yield per plant was also reported by Ghimire *et al.* (2017), Ghimire *et al.* (2018) and Parihar *et al.* (2018) ^[24, 25, 23]. Similar results were reported by Ramakrishnan *et al.* (2018) ^[18] for test weight, Suresh and Malathi (2016) ^[26] for clusters per plant and pods per plant, Srivastava and Singh (2012) ^[27] for primary branches per plant.

The residual effect determines how best the causal factors accounts for the variability in seed yield. In the present study the residual effect was found low and positive (0.0324). The residual effect indicates that the characters included in the study are enough to explain the variability in mung bean.

Conclusion

All the characters recorded high heritability indicating the high influence of genetic components. Traits plant height, primary branches per plant, clusters per plant, pods per plant and seed yield per plant were governed by additive gene action as they possessed high heritability along with high genetic advance. Cluster per plant and pods per plant were significant and positively correlated with seed yield per plant. Hence, these traits should be given consideration while selecting for increasing yield. Path analysis for seed yield revealed that days to 50% flowering, test weight, clusters per plant, pods per plant and primary branches per plant had positive direct effect. Hence direct selection for yield improvement through these traits would be rewarding.

Table 1: List of genotypes

Sr. no.	Genotypes	Sr. no.	Genotypes	Sr. no.	Genotypes
1	VMG-3	16	VMG-50	31	VMG-70
2	VMG-12	17	VMG-51	32	VMG-71
3	VMG-13	18	VMG-52	33	VMG-72
4	VMG-28	19	VMG-55	34	VMG-73
5	VMG-29	20	VMG-56	35	VMG-74
6	VMG-34	21	VMG-57	36	VMG-75
7	VMG-36	22	VMG-58	37	VMG-76
8	VMG-38	23	VMG-59	38	VMG-81
9	VMG-40	24	VMG-60	39	VMG-82
10	VMG-42	25	VMG-62	40	VMG-83
11	VMG-44	26	VMG-63	41	VMG-84
12	VMG-45	27	VMG-65	42	VMG-85
13	VMG-46	28	VMG-66	43	VMG-86
14	VMG-47	29	VMG-68	44	VMG-87
15	VMG-49	30	VMG-69		

Table 2: Analysis of variance (mean sum of squares) for various characters in mung bean

Sr. No.	Source of variation	Mean sum of square		
		Replication	Genotypes	Error
	Degree of freedom	2	43**	86
1	Days to 50% flowering	12.94	16.39**	1.13
2	Days to maturity	3.23	37.38**	1.48
3	Plant height	46.72	127.74**	11.22
4	Primary branches per plant	0.09	1.25**	0.04
5	Clusters per plant	2.23	9.01**	0.46
6	Pods per cluster	0.09	0.24**	0.04
7	Pods per plant	17.70	73.51**	3.64
8	Pod length	0.11	1.76**	0.03
9	Seeds per pod	1.00	3.01**	0.29
10	Test weight	0.18	1.13**	0.07
11	Seed yield per plant	2.37	7.50**	0.30
12	Protein content	1.40	10.26**	0.12

* Significant at 5% level; ** Significant at 1% level

Table 3: The estimate of GCV and PCV and other genetic parameters for different characters in mung bean

Character	σ^2_g	σ^2_p	GCV (%)	PCV (%)	H _b (%)	GA	GA (%)
Days to 50% flowering	5.09	6.22	6.15	6.8	82	4.2	11.46
Days to maturity	11.92	13.35	5.15	5.45	89	6.72	10.03
Plant height	38.84	50.05	16.58	18.82	78	11.31	30.09
Primary branches per plant	0.40	0.45	32.16	33.91	90	1.24	62.83
Clusters per plant	2.85	3.31	25.42	27.38	86	3.23	48.62
Pods per cluster	0.07	0.11	10.12	13.07	60	0.41	16.14
Pods per plant	23.28	26.92	28.77	30.94	86	9.24	55.11
Pod length	0.58	0.61	9.89	10.12	96	1.53	19.91
Seeds per pod	0.91	1.20	9.42	10.82	76	1.71	16.89
Test weight	0.35	0.42	12.88	14.09	84	1.12	24.25
Seed yield per plant	2.40	2.70	28.64	30.35	89	3.01	55.67
Protein content	3.38	3.50	7.64	7.77	97	3.72	15.48

Table 4: Genotypic and phenotypic correlation coefficient for different characters in mung bean

Characters		Days to maturity	Plant height	Primary branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	Test weight	Seed yield per plant	Protein content
Days to 50% flowering	rg	1.007**	0.017	-0.185	-	0.297*	-	0.025	-0.139	-0.186	-0.983**	0.023
	rp	0.877**	0.034	-0.140	0.860**	0.260**	0.538**	0.022	-0.116	-0.154	-0.846**	0.013
Days to maturity	rg		-0.035	-0.145	-	0.282*	-	0.035	-0.075	-0.199	-0.962**	0.041
	rp		-0.042	-0.149	0.861**	0.237**	0.652**	0.034	-0.119	-0.183*	-0.841**	0.036
Plant height	rg			0.212	0.172	0.01	0.147	-0.083	-0.125	-0.223	0.025	0.038
	rp			0.172*	0.148	0.016	0.121	-0.075	-0.052	-0.152	0.017	0.042
Primary	rg				0.326*	0.520**	0.489**	-0.226	0.054	-0.260	0.260	0.165

Branches	rp				0.296**	0.345**	0.420**	-0.208*	0.066	-0.210*	0.231**	0.147
Clusters per plant	rg					0.036	0.934**	-0.354*	-0.036	-0.149	0.872**	0.017
	rp					0.018	0.871**	-0.313**	-0.065	-0.120	0.837**	0.016
Pods per cluster	rg						0.388**	-0.522**	0.053	-0.660**	-0.219	-0.113
	rp						0.456**	-0.396**	0.003	-0.438**	-0.161	-0.106
Pods per plant	rg							-0.524**	-0.058	-0.377*	0.697**	-0.009
	rp							-0.466**	-0.094	-0.305**	0.661**	-0.013
Pod length	rg								0.369*	0.748**	-0.004	0.045
	rp								0.308**	0.662**	0.000	0.046
Seeds per pod	rg									0.001	0.043	-0.181
	rp									0.011	0.005	-0.152
Test weight	rg										0.262	0.138
	rp										0.211*	0.125
Seed yield per plant	rg											0.063
	rp											0.062

* = significant at 5% and ** = significant at 1% level of significance

Table 5: Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in mung bean

Characters	Days to 50% flowering	Days to maturity	Plant height	Primary branches per plant	Clusters per plant	Pods per cluster	Pods per plant	Pod length	Seeds per pod	Test weight	Protein content	Correlation coefficient with seed yield per plant (r _g)
Days to 50% flowering	0.505	-1.195	-0.001	-0.024	-0.129	-0.01	-0.094	0.000	-0.004	-0.033	0.001	-0.983**
Days to maturity	0.509	-1.186	0.002	-0.019	-0.129	-0.009	-0.095	0.001	-0.002	-0.035	0.002	-0.962**
Plant height	0.009	0.042	-0.057	0.027	0.026	0.000	0.021	-0.001	-0.004	-0.039	0.002	0.025
Primary branches per plant	-0.093	0.172	-0.012	0.130	0.049	-0.017	0.071	-0.004	0.002	-0.046	0.009	0.260
Clusters per plant	-0.434	1.021	-0.01	0.042	0.150	-0.001	0.136	-0.006	-0.001	-0.026	0.001	0.872**
Pods per cluster	0.15	-0.335	-0.001	0.067	0.005	-0.033	0.056	-0.008	0.002	-0.117	-0.006	-0.219
Pods per plant	-0.326	0.773	-0.008	0.063	0.14	-0.013	0.146	-0.008	-0.002	-0.067	0.000	0.697**
Pod length	0.012	-0.042	0.005	-0.029	-0.053	0.017	-0.076	0.016	0.011	0.132	0.003	-0.004
Seeds per pod	-0.07	0.089	0.007	0.007	-0.005	-0.002	-0.009	0.006	0.029	0.000	-0.01	0.043
Test weight	-0.094	0.236	0.013	-0.034	-0.022	0.022	-0.055	0.012	0.000	0.177	0.008	0.262
Protein content	0.012	-0.048	-0.002	0.021	0.003	0.004	-0.001	0.001	-0.005	0.024	0.055	0.063

Residual effect = 0.0324, ** = significant at 1% level of significance

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