

## Research Note

# The interrelationship of various traits with seed yield in mungbean (*Vigna radiata* (L.) Wilczek)

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### Abstract

The experimental material consisted of 58 diverse genotypes and 12 traits. Analysis of variance showed that these traits differ to each other. The seed yield per plant had highly significant and positive correlations both at genotypic and phenotypic levels with number of pods per plant, number of pods per cluster, number of cluster per plant and number of seeds per pod. Days to maturity showed negative and highly significant correlation with seed yield per plant at phenotypic and genotypic levels and days to 50% flowering at only genotypic level. The seed yield per plant did not show any significant association with protein content and other traits including number of branches per plant, number of pods per cluster and 100-seed weight that showed positive and significant correlation to protein content. So it can be concluded that selection for these traits enhance the seed yield and protein content in Mungbean.

### Key Words:

Mungbean, correlation, protein, seed yield.

Mungbean (*Vigna radiata* (L.) Wilczek) is one of the major pulse crops of India which is cultivated from humid tropic to arid and semi arid regions. India accounts for about 45 per cent of the total world mungbean production among pulse crops. Mungbean is cultivated in Bangladesh, Pakistan, Sri Lanka, Thailand, China, Philippines, Myanmar, Indonesia, East Africa, Nepal and Butan. The origin of the crop is considered in India from where it spread in Indochina, Java, Eastern and Central Africa, West Indies, Warmer parts of China and U.S.A. (Janoria *et al.* 1984). Mungbean belongs to family *Fabaceae* with diploid chromosome number  $2n=22$ . It contains about 24 per cent protein which is nearly two and half times the amount of storage protein found in the cereals. It is also used for preparing the variety of savoury and sweet dishes (Mishra, 2003).

Correlation among traits may result from pleiotropy, linkage or physiological associations among characters. The linkage is a cause of transit correlations particularly in a population derived from crosses between divergent strains. The correlation is the overall or net effect of the segregating genes; some of the genes may increase both the characters causing the positive correlation, while the others may increase the one and decrease the other causing the negative correlation (Falconer, 1981). Thus, to accumulate optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the interrelationship of various characters.

Seed yield in mung bean is a complex character like other crops, and is determined by various components and influenced by many other important yield contributing characters controlled by polygenes and also environmental factors. Selection is an integral part of a breeding program by which genotypes with high productivity in a given environment could be developed. However, selection for high yield is made difficult because of its complex nature. Therefore, only little progress could be made over a long span of time through direct selection for yield. Indirect selection through yield components has been proved more effective. This selection criterion takes into account the information on interrelationship among agronomic characters, their relationship with grain yield as well as their direct influence on grain yield. Nevertheless, selection for yield *via* highly correlated characters becomes easy if the contribution of different characters to yield is quantified using path coefficient analysis.

The present investigation was carried on Mungbean (*Vigna radiata* (L.) Wilczek) and conducted at Instructional Farm, Department of Agronomy, Junagadh Agricultural University, Junagadh during *kharif* 2010. The experimental material consisted of 58 diverse genotypes of mungbean (*Vigna radiata* (L.) Wilczek) representing various sources (Table 1). The pure seeds of these genotypes were provided by the Research Scientist, Pulses Research Station, Junagadh Agricultural University, Junagadh. These genotypes of mungbean were sown during *kharif*, 2010 in a

randomized block design with three replications under rainfed condition. Each entry was sown in a single row of three meter length spaced at 30 x 10 cm distance. The genotypes were randomly allotted to the different lines in each replication. The observation has been taken on 12 different traits namely, 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 clusters, number of pods per plant, pod length (cm), number of seeds per pod, 100-seeds weight (g), seed yield per plant (g) and protein content (%).

Correlation coefficient measures, the relationship between two or more series of variables. The genotypic correlation coefficient provides a measure of genotypic association between different characters while phenotypic correlation includes both genotypic as well as environmental influences. The phenotypic and genotypic correlation coefficients for all the characters were worked out for different germplasm lines through covariance analysis as per AI-Jibouri *et al.* (1958).

The analysis of variance (Table 2) revealed significant differences among the genotypes for all the characters studied. It indicates the presence of sufficient variability in material investigated in the present study. Availability of sufficient variability in the material handled by the breeder is of immense importance for the success of any breeding programme.

The study of genotypic correlation gives an idea of the extent of relationship between different variables (Table 3). This relationship among yield contributing characters as well as their association with yield provides information for exercising selection pressure for bringing genetic improvement in seed yield. In the present study, seed yield per plant was found to be significantly and positively correlated with number of pods per plant, number of pods per cluster, number of clusters per plant and number of seeds per pod at both the genotypic and phenotypic levels. Such positive interrelationship between seed yield and these attributes has also been reported in mungbean by several researchers. The positive genotypic association has been reported between seed yield per plant and pods per cluster and number of pods per plant and 100 seed weight. The same trend was recorded by Rajan *et al.* (2000), Venkateswarlu (2001), Haritha and Reddy (2002), Asifa Nazir *et al.* (2005) and Tejbir Singh *et al.* (2009). These character can serve as marker/indicator characters for improvement in seed yield. Days to maturity showed negative and highly significant correlation with seed yield per plant at both the levels and days to 50% flowering at only genotypic level. Similar

results obtained by Ved Prakash *et al.* (2007) and Verma and Garg (2007). But contrary to this, Yaqoob *et al.* (1997) and Kumar *et al.* (2005) noticed positive significant relationship with days to 50% flowering.

Days to flowering had positive and significant association with days to maturity at both levels is of an important component in identifying and deciding the duration of the crop. Thus, it indicated that flowering time was an important indicator of maturity. Both these traits i.e. days to flowering and days to maturity were also found to have positive and significant correlations with number of branches per plant and negative associations with number of pods per cluster and number of pods per plant at genotypic levels only. These results are in line with the earlier findings of Vikas *et al.* (1999) and Sirohi *et al.* (2007). In contrast Haritha and Reddy (2002), reported significant and positive correlation of days to flowering with number of clusters per plant and number of pods per plant.

The relationship of plant height with number of branches per plant, pod length and 100-seed weight were positive and highly significant at both levels. Similar results were recorded by Pundir *et al.* (1992) and Arshad *et al.* (2009) this found only for number of branches per plant. Number of branches per plant exhibited positive and highly significant associations with 100-seed weight followed by number of seeds per pod at both genotypic as well as phenotypic levels, while number of pods per cluster at genotypic level only. Number of branches per plant was significantly and positively associated with protein content, which was confirmed by Naik *et al.* (2000).

The significant and positive association was observed between number of pods per cluster and number of pods per plant. Pathak and Patel (1993), Reddy *et al.* (1994), and Haritha and Reddy (2002) also reported positive and significant association of number of pods per cluster and number of pods per plant. The correlations of pod length with number of seeds per pod and 100-seed weight were positive and significant. These results are in conformity with the findings of Kumar *et al.* (1995), Vikas *et al.* (1999) and Haritha and Reddy (2002).

The results thus, revealed that number of pods per plant, number of pods per cluster, number of clusters per plant, number of seeds per pod and days to maturity 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.

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**Table 1. List of genotypes and their source**

Sr. No.	Name of genotypes	Source
1	AKM-8803	PDKV, Akola
2	EC-501569	NBPGR, New Delhi
3	AKM-6802	PDKV, Akola
4	Pant-M-2	GPUA and T, Pantnagar
5	Pant-M-4	GPUA and T, Pantnagar
6	TARM-18	BARC, Trombay, Maharashtra
7	PM-2	MPKV, Rahuri
8	IC-73536	NBPGR, New Delhi
9	KO-Pergaon	Nagpur, Maharashtra
10	J-781	Jalgaon, Maharashtra
11	TARM-1	BARC, Trombay, Maharashtra
12	TARM-2	BARC, Trombay, Maharashtra
13	Pant-M-3	GPUA and T, Pantnagar
14	GM-02-16	SDAU, S.K. Nagar
15	GM-02-15	SDAU, S.K. Nagar
16	BPMR-145	Badnapur, Maharashtra
17	GM-2K3	SDAU, S.K. Nagar
18	GM-02-12	SDAU, S.K. Nagar
19	GM-9925	SDAU, S.K. Nagar
20	EC-482909	NBPGR, New Delhi
21	EC-482908	NBPGR, New Delhi
22	GM-02-13	SDAU, S.K. Nagar
23	K-851	CSAU A and T Kanpur
24	GM-9926	SDAU, S.K. Nagar
25	EC-314286	NBPGR, New Delhi
26	EC-450450	NBPGR, New Delhi
27	GM-02-14	SDAU, S.K. Nagar
28	EC-396523	NBPGR, New Delhi
29	EC-501566	NBPGR, New Delhi
30	EC-496839	NBPGR, New Delhi
31	RMG-62	ARS Durgapur, Rajasthan
32	EC-450446	NBPGR, New Delhi
33	EC-251557A	NBPGR, New Delhi
34	Local Collection	Navasari, Gujarat
35	EC-482907	NBPGR, New Delhi
36	GM-05-05	SDAU, S.K. Nagar
37	GM-05-08	SDAU, S.K. Nagar
38	Vaibhav	MPKV Rhuri
39	IC-8961-5	NBPGR, New Delhi
40	Yellow mungbean Local Collection	-
41	GM-9918	SDAU, S.K. Nagar
42	Asha	Hissar, Haryana
43	GM-06-08	SDAU, S.K. Nagar
44	EC-496841	NBPGR, New Delhi
45	GM-4	SDAU, S.K. Nagar
46	CO-6	TNAU, Coimbatore
47	GM-3	SDAU, S.K. Nagar
48	GM-04-04	SDAU, S.K. Nagar
49	GM-04-02	SDAU, S.K. Nagar
50	Pant-M-5	GPUA and T, Pantnagar
51	IC-24789	NBPGR, New Delhi
52	IC-12434	NBPGR, New Delhi
53	OUM-11-5	Behrampur, Orissa
54	EC-251810	NBPGR, New Delhi
55	CO-5	TNAU, Coimbatore
56	GM-2K-J	SDAU, S.K. Nagar
57	RMG-268	Durgapur, Rajasthan
58	COGG-912	TNAU, Coimbatore



**Table 2. Analysis of variance 12 characters in 58 genotypes of mungbean**

Source	Df	Seed yield per plant (g)	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of cluster per plant	Number of pods per cluster
Replications	2	2.042**	11.844*	3.195	32.949*	0.148	0.104	0.054**
Genotypes	57	5.086**	10.048**	9.907**	27.724**	0.432**	0.501**	0.614**
Error	114	0.386	3.202	2.511	10.224	0.109	0.072	0.125

**Table 2. Contd..**

Source	Df	Number of Pods per plant	Pod length (cm)	Number of seeds per pod	100-seed weight (g)	Protein content (%)
Replications	2	1.519**	0.882	1.641*	79.437**	4.306*
Genotypes	57	5.200**	1.042**	2.205**	72.987**	11.909**
Error	114	0.306	0.583	0.485	1.036	3.202

\*, \*\* Significant at 5% and 1% levels, respectively



**Table 3. Genotypic ( $r_g$ ) and phenotypic ( $r_p$ ) correlation coefficients among 12 characters in mungbean**

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of 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)	$r_g$	-0.350**	-0.326**	0.015	0.043	0.662**	0.795**	0.994**	-0.240	0.312**	0.043	0.078
	$r_p$	-0.141	-0.154*	0.081	0.065	0.547**	0.640**	0.972**	-0.114	0.202**	0.059	0.083
Days to 50% flowering	$r_g$		1.000**	0.340**	0.454**	0.035	-0.454**	-0.324**	0.179*	0.068	0.130	-0.179*
	$r_p$		0.955**	0.221**	0.300**	-0.016	-0.133	-0.134	0.099	0.017	0.104	-0.035
Days to maturity	$r_g$			0.327**	0.446**	0.026	-0.408**	-0.299**	0.215**	0.070	0.126	-0.172*
	$r_p$			0.234**	0.306**	0.000	-0.170*	-0.151*	0.078	0.010	0.107	-0.041
Plant height (cm)	$r_g$				0.654**	0.153*	-0.066	0.048	0.580**	0.147	0.310**	0.027
	$r_p$				0.399**	0.088	0.013	0.081	0.274**	0.104	0.181*	0.044
Number of branches per plant	$r_g$					-0.126	0.230**	0.074	0.118	0.372**	0.308**	0.188*
	$r_p$					-0.057	0.141	0.087	0.180*	0.175*	0.235**	0.168*
Number of cluster per plant	$r_g$						0.119	0.669**	-0.302**	0.081	-0.070	0.005
	$r_p$						-0.210**	0.522**	-0.149*	0.079	-0.053	-0.008
Number of pods per cluster	$r_g$							0.807**	-0.139	0.277**	0.167*	0.228**
	$r_p$							0.703**	-0.032	0.159*	0.144	0.182*
Number of pods per plant	$r_g$								-0.239**	0.282**	0.066	0.131
	$r_p$								-0.101	0.209**	0.083	0.130
Pod length (cm)	$r_g$									0.453**	0.091	-0.053
	$r_p$									0.028	0.060	0.044
Number of seeds per pod	$r_g$										0.080	0.070
	$r_p$										0.059	0.038
100-seed weight (g)	$r_g$											0.684**
	$r_p$											0.627**

\*, \*\* Significant at 5% and 1% levels, respectively

Where,  $r_g$  genotypic correlation and  $r_p$  phenotypic correlation