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Sandeep R Kadam
College of Agriculture, Parbhani Vasantrao Naik Marathwada Agriculture University, Parbhani, Maharashtra, India

Jagdish E Jahagirdar
Vilasrao Deshmukh College of Biotechnology, Latur Vasantrao Naik Marathwada Agriculture University, Parbhani, Maharashtra, India

Hirakant V Kalpande
College of Agriculture, Parbhani Vasantrao Naik Marathwada Agriculture University, Parbhani, Maharashtra, India

Shivanand V Kalyankar
College of Agriculture, Parbhani Vasantrao Naik Marathwada Agriculture University, Parbhani, Maharashtra, India

Niranjan R Thakur
(1) College of Agriculture, Parbhani. Vasantrao Naik Marathwada Agriculture University, Parbhani, MS, India
(2) International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Telangana, India

Gajanan H Naik
College of Agriculture, Parbhani Vasantrao Naik Marathwada Agriculture University, Parbhani, MS, India

Corresponding Author:
Sandeep R Kadam
College of Agriculture, Parbhani Vasantrao Naik Marathwada Agriculture University, Parbhani, Maharashtra, India

Assessment of correlation in seed yield and yield contributing characters in mung bean (*Vigna radiata* L.)

Sandeep R Kadam, Jagdish E Jahagirdar, Hirakant V Kalpande, Shivanand V Kalyankar, Niranjan R Thakur and Gajanan H Naik

Abstract
The present investigation entitled 'Assessment studies of correlation in seed yield and yield contributing characters in Mungbean (*Vigna radiata* L.)' was undertaken to study the correlation of yield and yield contributing characters in Mungbean, at Department of Agricultural Botany, College of Agriculture, VNMKV, Parbhani during *Kharif* 2020 and *Kharif* 2021. The experiment arranged in Randomized Block Design (RBD) with two replications. All 34 treatments had four rows of 4.5 meter long with 45 cm distance in between rows and 10 cm in plants. Morphological and yield contributing characters *viz.*, days to 50% flowering, days to maturity, days to shattering, plant height (cm), number of primary branches per plant, number of pods per cluster, number of pods per plant, length of pod (cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g) were recorded. The seed yield character of the study recorded significant positive correlation with number of pods per plant, primary branches number of seeds per pod, 100 seed weight and length of pod (cm). It also observed significant negative correlation with plant height.

Keywords: Correlation, Mung bean, seed yield

1. Introduction
Most people refer to pulses as 'poor man's meat'. It serves as the primary source of dietary protein for a large segment of the world's vegetarian population. Average protein content in pulses ranges from 20 to 30%, which is around 2.5 to 3.0 times the amount typically found in cereals. The world's food supply is made up of 71 million tonnes and 79 million hectares of pulses (Anonymous, 2021) [1]. India ranks third with an area of about 4.5 million ha with total production of 2.5 million tonnes (Anonymous 2021) [1]. The mung bean is a well-known crop in Asian countries, and India is the world's largest producer and consumer of pulses, accounting for 22% of global output and 33% of global production overall. It is the third crucial pulse crop after Red Gram and Chickpea. Particularly in Asia, mungbean is a significant grain legume. It is a warm-season crop that may be grown in the dry and semi-arid tropics and during hot, humid seasons (Kulkarni and Pandey, 1988; Pannu and Singh, 1988) [6, 7]. Mung bean (*Vigna radiata* L. Wilczek) is one of the most important pulse crop in India. Protein from mung beans is added to food, something that cereals cannot possibly offer. The sprouted seed have nutritional value compared with asparagus or mushroom. (USDA and NIH data 2022) [12]. During sprouting, there is an increase in thiamine, niacin and ascorbic acid concentration. The food values of Mung bean lie in its high and easily digestible protein. Saleem *et al.* (1998) [10] reported seed contains total protein, total amino acids, crude fibre and lipids components.
The mutual association between plant characteristics is measured by correlation coefficient analysis, which also identifies the component traits that can be used as the basis for selection to increase yield. If there is a strong positive association between two traits, it will speed up genetic advancement; conversely, a strong negative correlation will slow down genetic improvement following character selection. Thus, the experiment was conducted to study the relationship between seed yield and yield contributing characters.

2. Materials and Methods
The experiment was conducted in two seasons *Kharif* 2020 and *Kharif* 2021 at experimental field, Department of Agricultural Botany, College of Agriculture, VNMKV, Parbhani, MS, India. Randomized Block Design (RBD) was applied with two replications and every treatment has four rows of 4.5 meter long with 45 cm distance in between rows.

All agronomic package of practices were carried out as per recommendation for raising the quality crop.

The experimental material comprised of 34 genotypes including checks were collected from various pulse research stations of Maharashtra. Genotypes and checks involved in the present investigation are presented in Table 1.

Table 1: Experimental Material (genotypes and checks) used in the study

Sr. No.	Genotypes & checks	Sr. No.	Genotypes & checks
1	Phule M 707-5	18	AKM-12-23
2	AKM-12-14	19	Phule M 818-8
3	Phule M 602-9	20	Phule M 809-10
4	AKM-12-24	21	Phule M 402-2-1
5	BM-2019-1	22	Phule M 504-20-27
6	Phule M 702-1	23	AKM-1606
7	AKM-1609	24	AKM-1605
8	AKM-1603	25	AKM-1608
9	AKM-1602	26	BM-4 (C)
10	Phule M 816-10	27	BPMR-145 (C)
11	Phule M 817-13	28	BM-2002-1 (C)
12	TBM-4	29	BM-2003-2 (C)
13	TBM-6	30	PKVM-4 (C)
14	AKM-12-28	31	PKVM-8802 (C)
15	TBM-10	32	PKV-Green Gold (C)
16	TBM-127	33	Vaibhav (C)
17	Phule M 809-12	34	Utkarsh (C)

Morphological traits like days to 50% flowering, days to maturity and days to shattering were recorded on the plot basis, while plant height (cm), number of primary branches per plant, number of pods per cluster, number of pods per plant, length of pod (cm), number of seeds per pod, 100 seed weight (g), seed yield per plant (g) recorded on randomly selected five representative plants. The characters were recorded in the field were subjected for statistical analysis (Table 1).

2.4 Statistical analysis

The statistical analysis of data was carried out as per the standard method suggested by Panse and Sukhatme (1989) [8]. The analysis of variance for each character was carried out and indicated in Table 2. Characters studied in this experiment showed the significance variation among the genotypes.

Table 2: Analysis of variance for experimental design

Source of variation	d. f.	Sum squares	Mean sum of squares	Expected M.S.
Replications	(r–1)	SS_1	M_1	$\sigma^2 e + g\sigma^2 r$
Genotypes	(g–1)	SS_2	M_2	$\sigma^2 e + r\sigma^2 g$
Error	(r–1)(g–1)	SS_3	M_3	$\sigma^2 e$
Total	(rg–l)	--	--	--

where,

r = Number of replications

g = Number of genotypes

σ^2 e = Error variance

σ^2 r = Variance due to replications

σ^2 g = Variance due to genotypes

3. Results and Discussion

The mean values of observations recorded were subjected to analysis of variances for randomized block design in individual season & over pooled (Table 3) revealed that mean squares due to genotypes found significant for all the characters in all environments.

The variations due to genotypes were significant for all the characters under the study at both 5% and 1% probability levels in two seasons. The significant differences in characters indicate the presence of variability in experimental material.

Table 3: Analysis of variance (ANOVA) for randomized block design for different characters in an individual season and over a pooled mean in mungbean

Sr. No.	Characters	Location	Source of variation		
			Replication	Genotypes	Error
			d. f. (1)	d. f. (33)	d. f. (33)
1	Days to 50% flowering	*kh*-2020	3.31	4.92**	1.01
		kh-2021	0.72	6.64**	1.02
		Pool	2.01	5.78**	1.01
2	Days to maturity	*kh*-2020	0.49	9.96**	5.8
		kh-2021	0.53	10.27**	6.35
		Pool	0.51	10.11**	6.08

3	Days to shattering	*kh*-2020	3.31	20.58**	0.85
		kh-2021	3.37	44.14**	0.94
		Pool	3.33	32.36**	0.89
4	Plant height (cm)	*kh*-2020	120.18	260.27**	16.19
		kh-2021	115.25	239.65**	15.57
		Pool	117.71	249.96**	15.88
5	No. of primary branches	*kh*-2020	0.83	1.98**	0.04
		kh-2021	0.92	2.37**	0.03
		Pool	0.42	2.17**	0.05
6	No. of pods/cluster	*kh*-2020	0.17	0.74**	0.06
		kh-2021	0.13	0.71**	0.04
		Pool	0.15	0.72**	0.05
7	No. of pods/plant	*kh*-2020	7.18	64.63**	1.98
		kh-2021	9.94	60.31**	2.44
		Pool	8.56	62.47**	2.21
8	Length of pods (cm)	*kh*-2020	0.12	7.36**	0.09
		kh-2021	0.13	7.37**	0.05
		Pool	0.11	7.36**	0.07
9	No. of seeds/ pod	*kh*-2020	0.08	4.85**	0.45
		kh-2021	0.16	4.96**	0.27
		Pool	0.12	4.9**	0.36
10	100 seed wt. (g)	*kh*-2020	0.01	0.86**	0
		kh-2021	0.01	0.74**	0
		Pool	0.01	0.8**	0
11	Seed yield/plant (g)	*kh*-2020	1.25	12.07**	0.64
		kh-2021	1.17	11.39**	0.87
		Pool	0.71	11.73**	0.75

* Significant at 5 per cent and ** 1 per cent level

Seed yield is a complex and dependant trait and depends on various independent traits. In current study, seed yield shows positive and high significant association with number of pods per plant (0.808), number of primary branches (0.506) and positive and significant association with 100 seed weight (0.288) (Table 4). It reveals that increase in these yield contributing characters reflects increase in a yield. However, it shows negative and high significant association with plant height (-0.453). This indicates increase in height, significantly decrease the yield.

The number of primary branches might be developed into more number of pod clusters which resulted in high seed yield per plant. Similar findings were earlier reported by Kadam *et al.* (2022) [4], Thakur *et al.* (2018) [11], Parihar *et al.* (2018) [9], Ghimire *et al.* (2017) [3], Kritika and Yadav (2017) [5], Das and Barua (2015) [2].

Table 4: Correlation coefficient for yield and yield contributing traits

	Days to 50% flowering	Days to Maturity	Days to Shattering	Plant Height (Cm)	No. of Primary Branches	No. of Pods/Cluster	No. of Pods/Plant	Length of Pods (cm)	No. of Seeds/ Pod	100 Seed Wt. (gm)	Seed Yield/ Plant (gm)
Days to 50% flowering	1										
Days to Maturity	0.360*	1									
Days to Shattering	0.123	0.796**	1								
Plant Height (Cm)	-0.158	0.006	0.216	1							
No. of Primary Branches	0.082	-0.022	-0.144	-0.001	1						
No. of Pods/Cluster	-0.22	-0.19	-0.052	0.062	0.099	1					
No. of Pods/Plant	-0.14	-0.345*	-0.399*	-0.245	0.431*	0.587**	1				
Length of Pods (cm)	0.082	0.238	0.237	0.041	0.396*	-0.147	-0.072	1			
No. of Seeds/ Pod	0.347*	0.261	0.354*	-0.193	0.127	-0.163	-0.081	0.487**	1		
100 Seed Wt. (gm)	0.055	0	0.023	-0.008	0.325	-0.371*	-0.163	0.638**	0.342*	1	
Seed Yield/Plant (gm)	0.022	-0.23	-0.295	-0.453**	0.506**	0.251	0.808**	0.249*	0.280*	0.288*	1

4. Conclusion

Thus, the present study suggests that selection for high seed yield genotypes should be based on number of pods per plant, number of primary branches, 100 seed weight, number of seeds per pod and length of pod (cm).

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