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ASSOCIATION OF SEED YIELD AND SOME IMPORTANT MORPHOLOGICAL TRAITS IN MUNGBEAN (*VIGNA RADIATA* L.)

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Abstract

Forty-three mungbean genotypes/accessions were studied for association of seed yield per plant with some important morphological traits i.e., lower node of the pod bearing peduncle, nodes on main stem, average internodal length, pod bearing branches per plant, pod clusters per plant, pod clusters on main stem and pod clusters on branches. Seed yield per plant showed a positive and significant association with pod bearing branches per plant, pod clusters per plant and pod clusters on branches. The pod bearing branches per plant and pod clusters on branches had a negligible and negative direct effect on total correlation respectively, but their indirect contribution through pod clusters per plant towards total correlation was positive and high. The high direct effect and total correlation of pod clusters per plant confirmed its important role in selection for high yielding genotypes. The total variability calculated through multiple correlation in the population for yield improvement accounted for by pod bearing branches per plant, pod clusters per plant and pod clusters on branches was 0.698% compared to 0.793% accounted for by all the traits. The pod clusters per plant showed a significant partial regression coefficient with the seed yield per plant. High heritability was observed for seed yield per plant, node of the first peduncle, pod clusters on branches and pod clusters per plant. The present results revealed that the greater number of pod clusters per plant could be used relatively better selection criterion.

Introduction

Mungbean is the major kharif (July-October) pulse crop of Pakistan. It is mostly grown on marginal lands and matures in a short period. The major crop growing area is located in Punjab but it is also grown in North West Frontier Province (NWFP) as a major pulse crop during the kharif season. The popular mungbean varieties grown in NWFP are NM 92 and NM 98. The provincial mungbean-breeding programme is mainly concentrated on the evaluation of mungbean genotypes in the local environment for yield and adaptability.

Genetic improvement of quantitative traits is dependent upon variable germplasm with a gene for the trait under consideration. Wide spread reservations have been expressed that there is a limited range of genetic variability in the mungbean, but generally these reservations have been based on observations of small and local germplasm collections with narrow genetic backgrounds. The extensive genetic variability for various qualitative and quantitative traits has been reported by studying one hundred local and exotic mungbean genotypes (Khattak *et al*., 1999a). This indicates the potential for breeding progress in numerous traits with existing mungbean germplasm. Seed yield being a complex and multifacet character, it is an ultimate expression of the different factors.

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Table 1. Origin of the accessions included in the study.

S. No.	Genotype	Origin	S. No.	Genotype	Origin
1.	VC 1482E	Thailand	23.	Pak 32	Pakistan
2.	VC 1528C	“	24.	Rc71-27	“
3.	VC 1560A	“	25.	6601	“
4.	VC 1560D	“	26.	NM 28	“
5.	VC 1562A	“	27.	NM 13-1	“
6.	VC 1628A	“	28.	NM 19-19	“
7.	VC 1628C	“	29.	NM 20-21	“
8.	VC 1647B	“	30.	NM121-25	“
9.	VC 1682C	“	31.	NM 51	“
10.	VC 1945	“	32.	NM 54	“
11.	VC 1945A	“	33.	NM 92	“
12.	VC 1968	“	34.	Pant M-3	India
13.	VC 2764B	“	35.	ML-5	“
14.	VC 2768A	“	36.	SML-32	“
15.	VC 2768B	“	37.	Pusa 101	“
16.	VC 2771A	“	38.	Pusa 105	“
17.	VC 2778A	“	39.	ML-131	“
18.	VC 2778B	“	40.	ML-267	“
19.	VC 2802	“	41.	Pusa 9171	“
20.	VC 2802A	“	42.	Pusa 9173	“
21.	Pak 17	Pakistan	43.	Sr. No. 61	Philippines
22.	Pak 22	“			

The knowledge of the interrelationship among various developmental and reproductive traits is necessary for framing an effective breeding programme to exploit the desirable genetic variations and to devise an efficient selection program for the development of high yielding and well adapted genotypes. Selection based on yield components for improving seed yield in mungbean is well documented (Poehlman, 1991; Singh *et al*., 1995; Khattak *et al*., 1995, 1997, 1999a 1999b) but very meager information is available regarding the association of seed yield with the morphological traits in mungbean.

The objectives of the present investigations were to verify the importance of different morphological traits of mungbean through the estimation of the phenotypic and genotypic correlation and path coefficients analysis, so that the suitable selection criterion may be identified for developing ideotypes possessing high yield potential.

Materials and Methods

Forty-three local and exotic mungbean genotypes/accessions from Thailand, Pakistan, India and the Philippines were included in the study (Table 1). These genotypes were planted in a randomized complete block design with three replications at the research farm of the Nuclear Institute for Food and Agriculture (NIFA), Peshawar, Pakistan during July 2004. A plot of a single row, 4 m in length, with 30 cm row-to-row and 10 cm plant-to-plant spacing was kept for each genotype in each replication. Standard cultural practices were followed throughout the season of the crop. Ten plants were randomly selected in each replication at pod maturity and harvested separately. The following data were recorded on each selected plant for the traits, lower node of the pod bearing peduncle, nodes on main stem**,** average internodal length on main stem, pod bearing branches per plant, pod clusters on main stem, pod clusters on branches, pod clusters per plant and seed yield per plant. Average of the 10 plants were calculated.

The analysis of variance, phenotypic and genotypic correlation, path coefficients, multiple correlation, partial regression and heritability (broad sense) were referenced as by Singh & Chaudhry (1985).

Results and Discussion

The genotypes differed significantly for all the traits studied, indicating a considerable range of variability. The phenotypic and genotypic correlation coefficients for seed yield and morphological characters are presented in Table 2. The genotypic correlations were higher than phenotypic correlations. Seed yield per plant was positive and significantly correlated with pod bearing branches per plant, pod clusters per plant and pods clusters on branches. The morphological traits had varying trends of association to each other. The lower node of the pods bearing peduncle and nodes on the main stem exhibited positive and significant phenotypic and genotypic correlation with pod bearing branches per plant. The average internode length had a negative and significant correlation with pod clusters on the main stem but a positive and significant correlation with pod clusters on branches. The pod bearing branches per plant exhibited a positive and significant association with pod clusters per plant and pod clusters on branches. The pod clusters per plant had a positive and significant correlation with pod clusters on branches.

The direct and indirect contribution of the morphological traits towards seed yield per plant estimated through path–coefficient analysis is shown in Table 3. Pod bearing branches per plant, pod clusters per plant and pod clusters on branches showed positive and significant correlation with seed yield per plant. The direct effect of pod bearing branches per plant towards total correlation with seed yield per plant was low but its effect was contributed indirectly through pod clusters per plant. The major portion of the total correlation of pod clusters per plant with seed yield per plant was due to its high direct effect. The genotypic correlation of pod clusters on branches with seed yield per plant was mainly due to the indirect effect through pods clusters per plant whereas its direct effect was negative.

The cumulative effect of all the traits on seed yield per plant estimated through multiple correlations was highly significant (Table 4). The multiple correlations of the three highly correlated traits viz., pod bearing branches per plant, pod clusters per plant and pods clusters on branches was highly significant and found to be close to the multiple correlation of all the traits. The coefficient of determination (R^2) on the basis of all the traits was 0.628, whereas it was 0.600 on the basis of the three traits i.e., pod bearing branches per plant, pod clusters per plant and pod clusters on branches. This indicated that the total genetic variability of seed yield per plant available in the population for selection accounted for by all the traits and the three traits were 62.8% and 60%, respectively.

The partial regression analysis and heritability (broad sense) is presented in Table 5. The partial regression analysis revealed similar trends of association as shown by the correlation coefficient. The pod clusters per plant exhibited a significant partial regression coefficient with the seed yield per plant. The non-significant partial regression coefficient of pod bearing branches per plant and pod clusters on branches with the seed yield per plant showed similar results obtained through the partitioning of the genotypic correlation of the traits. The direct effect on total correlation of pod bearing branches per plant and pod clusters on branches was very low and negative, respectively. The low and negative values of the direct effect on total correlation resulted in the non-significant partial regression coefficient values to pod bearing branches per plant and pod clusters on branches. The high broad sense heritability was estimated for the lower node of the pod bearing peduncle, pods bearing branches per plant, pod clusters on branches and seed yield per plant.

Table 2. Phenotypic (P) and genotypic (G) correlation among the studied traits in mungbeans.

Character	Kind of correlation	Nodes on main stem	Average internodal length	Pod bearing branches per plant	Pod clusters per plant	Pod clusters on main stem	Pod clusters on branches	Seed yield per plant
Lower node of the pods bearing peduncle	P	0.91	0.19	0.52**	0.21	-0.44**	0.29	0.05
	G	0.95**	0.23	0.61**	0.23	-0.50**	0.31*	0.06
Nodes on main stem	P		-0.04	0.60**	0.26	-0.03	0.27	0.09
	G		0.06	0.70**	0.27	-0.19	0.30*	0.08
Average internodal length	P			-0.17	0.23	-0.52**	0.34*	0.18
	G			-0.14	0.30	-0.54**	0.39**	0.15
Pods bearing branches per plant	P				0.42**	0.05	0.40**	0.38**
	G				0.47**	-0.03	0.47**	0.47**
Pods clusters per plant	P					0.05	0.98**	0.68**
	G					0.004	0.98**	0.74**
Pods clusters on main stem	P						-0.17	0.003
	G						-0.18	0.02
Pods clusters on branches	P							0.67**
	G							0.72**

*, ** = Significant at 0.05 and 0.01 levels of probability, respectively

Table 3. Path-coefficient analysis of yield with other metric traits in mungbeans.

Characters	Lower node of the pod bearing peduncle	Nodes on main stem	Average internodal length	Pod bearing branches per plant	Pod clusters per plant	Pod clusters on main stem	Pod clusters on branches	Total correlation
Lower node of the pod bearing peduncle	-1.04	0.49	-0.007	0.24	5.92	2.57	-8.13	0.06
Nodes on main stem	-0.98	0.52	-0.002	0.28	7.21	0.97	-7.91	0.08
Average internodal length	-0.24	0.03	-0.03	-0.05	7.81	2.76	-10.12	0.15
Pod bearing branches per plant	-0.63	0.36	0.004	0.40	12.44	0.16	-12.25	0.47
Pod clusters per plant	-0.23	0.14	-0.009	0.19	26.30	-0.02	-25.63	0.74
Pod clusters on main stem	0.52	-0.09	0.02	-0.01	0.11	-5.15	4.64	0.02
Pod clusters on branches	-0.32	0.16	-0.01	0.19	25.87	0.92	-26.07	0.72

Table 4. Multiple correlation analysis of seed yield per plant on the basis of all yield components (col. 1) and on the basis of branches per plant, clusters per plant and clusters on branches (col. 2).

	Col. 1	Col. 2
Multiple correlation (R)	0.793**	0.698**
R. Square	0.628	0.600
Adjusted R. square	0.554	0.456
Standard error	3.165	3.052

** = Significant at 0.01 levels of probability.

Table 5. Partial regression analysis of seed yields with some important morphological traits and heritability in mungbean.

Morphological traits	Partial regression coefficient (B)	Standard error of partial regression coefficient (S.E. (B)	Calculated student T value (t)	Heritability (Broad sense)
Lower node of the pods bearing peduncle	-2.25	4.74	-0.47	0.93
Nodes on main stem	1.21	4.74	0.26	0.89
Average internodal length	0.29	0.52	0.57	0.87
Pods bearing branches per plant	0.14	0.10	1.44	0.91
Pods clusters per plant	4.36*	1.68	2.60	0.70
Pods clusters on main stem	0.12	0.11	1.05	0.62
Pods clusters on branches	-0.14	0.10	-1.35	0.90
Seed yield per plant	-	-	-	0.95

The pod bearing branches, pod clusters per plant and pods clusters on branches were found to have important morphological factors among the traits in the present findings. Selection on the basis of morphological traits has an advantage over primary yield components as they could be observed and selected during the growing period of the plant, which gives an opportunity to the breeder to select the best ideotype of a genotype along with a highly correlated morphological trait with seed yield. The significant association of branches per plant with seed yield in mungbean has also been reported by Sarwar *et al*., (2004). The partitioning of the genotypic correlation of traits into direct and indirect effect revealed a negligible direct effect of pod bearing branches per plant, a high direct positive effect of pod clusters per plant and a negative direct effect of pod clusters on branches on total correlation. The pod clusters on branches had a negative direct contribution towards total correlation but the indirect effect through pod clusters per plant was positive and very high.

The direct selection is effective in the case where the trait has a high direct effect on total correlation, whereas indirect selection is important where the total correlation is positive and significant but the direct effect is negative or negligible (Singh & Chaudhary 1985). The restricted simultaneous selection model has to be followed in situations where the trait has a negative total correlation but a high positive direct effect (Singh & Kakar 1997). The restricted simultaneous selection model uses the direct effect of the trait towards a dependent variable and imposes restrictions to nullify the undesirable indirect effects. The pod clusters per plant were not only the main direct contributing factor toward seed yield but also indirectly contributed a very high value towards seed yield for pod bearing branches and pod clusters on branches. The greater number of pod clusters per plant may be used as a selection criterion for developing high yielding mungbean genotypes. A pod bearing peduncle initiated at a lower node, more nodes on the main stem and less average internodal length is important to breed lodging resistant mungbean genotypes (Khattak *et al*., 2001, 2002). The current study showed negligible associations of a pod bearing peduncle initiated at a lower node, more nodes on the main stem and less average internodal length, indicating that selection for improving lodging behaviour should not be based on the morphological traits contributing towards seed yield in mungbean.

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