



RESEARCH ARTICLE

COMPONENT APPROACH ANALYSIS IN CORE GERMPLASM OF MUNGBEAN (*VIGNA RADIATA* (L.) WILCZEK)

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ABSTRACT

Character association and path coefficient analysis were carried out in a set of core germplasm lines of mungbean which included 13 promising improved varieties, four popular locally adapted mungbean land races of Odisha (India), one wild form (TCR 20) of mungbean (*Vigna radiata* var. sublobata), one genotype of its closely related species *Vigna mungo*, cv. UG 218 (urdbean) and a popular mungbean variety LGG 460 as standard check. Seeds per plant followed by number of pods per plant, number of clusters per plant and seed weight revealed strong positive significant correlation with seed yield. In contrast, number of primary branches per plant and protein content had negative relationship with seed yield. Among the component traits, number of pods per plant had maximum direct effect on seed yield followed by clusters per plant and 100-seed weight. Seeds per plant though exhibited very high positive correlation with seed yield, it failed to influence seed yield directly at genotypic level. However, seeds per plant contributed indirectly to seed yield through number of clusters and number of pods per plant. Number of clusters per plant and number of pods per plant had shown high inter se indirect effects on seed yield at genotypic level. The merit of these two traits is further ascribed to their positive correlated response through other component traits e.g. seeds per plant, harvest index and seed weight.

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INTRODUCTION

Food legumes are rich source of protein. Mungbean (*Vigna radiata*) harbours high level of lysine rich seed storage protein (17.2-29.9%, average 22.83%) and it is often preferred due to easy digestibility and minimum or traces of flatulence factors in seed (raffinose, stachyose and verbacose) as compared to other legumes (Poehlman, 1991). Being a short duration legume crop, it is best suited for pyrrah cropping and crop rotation. Besides, it adds soil nitrogen status through symbiotic nitrogen fixation (Malik, 1994). Seed yield in mungbean is a complex trait and it is determined by mutual relationship among the component agro-economic traits. Study of the mode and extent of inter-relationship of different component traits and their direct and indirect effects on seed yield can provide the basis for effective selection and successful utilization of germplasm resources in the development of superior mungbean varieties.

Many often unfavorable linkages among the agro-economic traits do exist resulting in genetic slippage and limited genetic advance. Besides, the information for *inter se* association among yield and its component characters is often incomplete and/or varying depending on the composition of the test materials, characters studied, previous selection history and the environment under which the breeding materials are tested. Therefore, an attempt has been made to estimate the correlation and path coefficients of agro-economic traits at both phenotypic and genotypic level to formulate an effective selection strategy in a set of core germplasm of mungbean.

MATERIALS AND METHODS

The experimental materials used in the present investigation consisted of 20 genetically pure genotypes including 13 promising improved varieties, four popular locally adapted mungbean land races of Odisha (India), one wild form (TCR 20) of mungbean (*Vigna radiata* var. sublobata), one genotype of its closely related species *Vigna mungo*, cv. UG 218

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Table 1. Phenotypic (r_p) and genotypic (r_g) correlation co-efficients among 14 characters in 20 selected mungbean genotypes

Characters		DF	PHT	NB	NC	NP/C	NP/P	PL	S/Pod	S/Pl	SW	H.I.	P	SY/P
DM	r_g	0.82**	0.81**	0.53**	0.14	-0.40**	-0.07	0.18	0.34**	0.15	0.09	-0.56**	0.47**	0.19
	r_p	0.81**	0.78**	0.51**	0.12	-0.39**	-0.05	0.18	0.33*	0.13	0.09	-0.54**	0.39**	0.16
DF	r_g		0.84**	0.48**	0.17	-0.29*	0.001	0.37**	0.46**	0.26*	0.09	-0.58**	0.65**	0.30*
	r_p		0.82**	0.47**	0.15	-0.29*	-0.005	0.37**	0.45**	0.25*	0.09	-0.56**	0.58**	0.26*
PHT	r_g			0.26*	0.26*	-0.05	0.21	0.28*	0.36**	0.43**	0.23	-0.32*	0.46**	0.48**
	r_p			0.26*	0.24	-0.04	0.20	0.28*	0.36**	0.40**	0.20	-0.30*	0.38**	0.45**
NB	r_g				-0.18	-0.38**	-0.35	-0.27*	-0.16	-0.42**	0.08	-0.59**	0.65**	-0.27*
	r_p				-0.17	-0.37**	-0.32	-0.27*	-0.16	-0.39**	0.08	-0.56**	0.59**	-0.26*
NC	r_g					0.007	0.89**	-0.19	-0.22	0.72**	0.37**	-0.10	-0.18	0.75**
	r_p					-0.004	0.86**	-0.18	-0.20	0.66**	0.32*	-0.08	-0.15	0.71**
NP/C	r_g						0.48**	0.08	0.06	0.48**	0.12	0.61**	-0.39**	0.43**
	r_p						0.44**	0.08	0.06	0.44**	0.11	0.58**	-0.37**	0.38**
NP/P	r_g							-0.13	-0.18	0.87**	0.39**	0.20	-0.33**	0.86**
	r_p							-0.12	-0.15	0.75**	0.30*	0.17	-0.31*	0.79**
PL	r_g								0.88**	0.37**	-0.30*	0.08	0.05	0.19
	r_p								0.87**	0.34**	-0.29*	0.08	0.05	0.17
S/Pod	r_g									0.38**	-0.23	0.07	0.12	0.21
	r_p									0.37**	-0.23	0.08	0.09	0.23
S/Pl	r_g										0.24	0.22	-0.25*	0.95**
	r_p										0.19	0.24	-0.25*	0.85**
SW	r_g											0.24	-0.25*	0.63**
	r_p											0.20	-0.16	0.50**
H.I.	r_g												-0.73**	0.24
	r_p												-0.66**	0.25*
P	r_g													-0.24
	r_p													-0.26*

*, ** -significant at P 0.05 and P 0.01 respectively.

Table 2. Phenotypic(P) and genotypic(G) path-coefficient analysis showing direct and indirect effects of 13 different traits on seed yield/plant in 20 selected genotypes of mungbean

Characters		DM	DF	PHT	NB	NC	NP/C	NP/P	PL	S/Pod	S/Pl	SW	H.I.	P	r(x,Y)
DM	G	-0.12	-0.01	0.32	-0.13	0.06	-0.13	-0.04	0.06	0.05	-0.03	0.05	-0.09	0.20	0.187
	P	-0.19	-0.02	0.19	0.06	0.03	-0.01	-0.02	-0.01	0.12	0.02	0.03	-0.01	-0.04	0.163
DF	G	0.43	-0.02	-0.34	-0.12	0.07	-0.09	0.003	-0.13	0.07	-0.05	0.05	-0.09	0.27	0.303*
	P	-0.16	-0.02	0.20	0.05	0.03	-0.01	-0.002	-0.01	0.17	0.05	0.03	-0.01	-0.06	0.264*
PHT	G	0.42	-0.02	-0.40	-0.07	0.10	-0.02	0.11	0.10	0.05	-0.09	0.13	-0.05	0.19	0.480**
	P	-0.15	-0.02	0.25	0.03	0.06	-0.001	0.07	-0.01	0.13	0.08	0.06	-0.004	-0.04	0.450**
NB	G	0.28	-0.01	-0.10	-0.25	-0.07	-0.12	-0.18	-0.09	-0.02	0.08	0.04	-0.10	0.27	-0.276*
	P	-0.10	-0.01	0.06	0.11	-0.04	-0.01	-0.11	0.01	-0.06	-0.08	0.02	-0.01	-0.06	-0.262*
NC	G	0.07	-0.003	0.10	0.04	0.41	0.002	0.462	-0.06	-0.03	-0.11	0.21	-0.02	-0.07	0.753**
	P	-0.02	-0.004	0.06	-0.02	0.24	0.000	0.29	0.01	-0.07	0.13	0.09	-0.001	0.016	0.713**
NP/C	G	-0.21	0.006	0.02	0.10	0.003	0.32	0.25	0.03	0.01	-0.10	0.07	0.10	-0.17	0.427*
	P	0.07	0.007	-0.01	-0.04	-0.001	0.02	0.15	-0.003	0.02	0.08	0.03	0.01	0.04	0.386**
NP/P	G	-0.04	0.000	-0.08	0.09	0.36	0.15	0.51	-0.04	-0.03	-0.18	0.22	0.03	-0.14	0.857**
	P	0.01	0.000	0.05	-0.03	0.21	0.01	0.34	0.005	-0.06	0.15	0.09	0.003	0.03	0.796**
PL	G	0.10	-0.01	-0.11	0.07	-0.08	0.02	-0.07	0.34	0.13	-0.07	-0.17	0.01	0.02	0.191
	P	-0.03	-0.01	0.07	-0.03	-0.04	0.002	-0.04	-0.04	0.32	0.07	-0.09	0.001	-0.005	0.173
S/Pod	G	0.18	-0.01	-0.15	0.04	-0.09	0.02	-0.09	0.30	0.15	-0.08	-0.13	0.01	0.05	0.214
	P	-0.06	-0.01	0.09	-0.02	-0.05	0.001	-0.05	-0.03	0.37	0.07	-0.07	0.001	-0.01	0.228
S/Pl	G	0.08	-0.005	-0.17	0.11	0.29	0.15	0.45	0.13	0.06	-0.20	0.13	0.04	-0.10	0.953**
	P	-0.02	-0.006	0.10	-0.04	0.16	0.10	0.25	-0.01	0.14	0.19	0.05	0.004	0.03	0.854**
SW	G	0.05	-0.002	-0.09	-0.02	0.15	0.04	0.20	-0.10	-0.03	-0.05	0.56	0.04	-0.11	0.631**
	P	-0.12	-0.002	0.05	0.01	0.08	0.003	0.10	0.01	-0.09	0.04	0.30	0.003	0.02	0.497**
H.I.	G	-0.29	0.01	0.13	0.15	-0.04	0.20	0.10	0.03	0.01	-0.05	0.13	0.16	-0.30	0.241
	P	0.10	0.01	-0.07	-0.06	-0.02	0.01	0.06	-0.003	0.03	0.05	0.06	0.01	0.07	0.251*
P	G	0.25	-0.01	-0.19	-0.16	-0.07	-0.13	-0.17	0.02	0.02	0.05	-0.14	-0.12	0.42	-0.246
	P	-0.08	-0.01	0.09	0.07	-0.03	-0.01	-0.10	-0.002	0.03	-0.05	-0.05	-0.01	-0.11	-0.259*

Residual : - 0.0527 and 0.0856 at genotypic and phenotypic level respectively.

(urdbean) and a popular mungbean variety LGG 460 as standard check. These genotypes were purposefully selected from a set of 314 germplasm lines based on significant higher seed yield than the best standard checks. The above 20 test genotypes were grown in the field following Randomized Block Design (RBD) with three replications to assess inter-relationship of yield and ancillary traits including protein content. Observations on seed yield and its component traits e.g., days to 50% flowering, days to maturity, plant height (cm), number of primary branches/plant, number of clusters/plant, number of pods/cluster, number of pods/plant, pod length, number of seeds/pod, number of seeds/plant, 100-seed weight (g), harvest index (H.I.%) and seed yield/plant (g) were recorded on randomly chosen ten normal looking competitive plants treatment-wise and replication-wise, and averaged to single plant basis. Protein content (%) of seeds from five single plants of each genotype was analyzed separately in duplicate to minimize experimental error. In order to determine protein in seeds Kjeldahl's digestion and distillation procedure (Jackson, 1973) was followed to determine nitrogen in seeds. Then the protein content of seeds was determined by multiplying the nitrogen content with 6.25. Phenotypic and genotypic correlation coefficients of component traits with seed yield were computed from respective variance and covariance for individual character pairs (Robinson *et al.*, 1951). The estimates of correlation coefficients were tested for their statistical significance using t-test following Singh and Choudhury (1976). Correlation of each component traits with seed yield was partitioned into direct and indirect effects by path coefficient analysis as per Dewey and Lu (1959).

RESULTS AND DISCUSSION

A perusal of Table 1 indicated close correspondence between phenotypic and genotypic correlation co-efficients indicating negligible masking effect of environment on character association and thus, providing reliability of selection at phenotypic level. In general, genotypic correlation coefficient in a pair of agro-economic traits including seed yield was higher than that at phenotypic level indicating the preponderance of genetic variance in expression of characters (Biradar *et al.*, 2007). Days to 50% flowering was estimated to have significant positive association (at 5% level) with seed yield whereas, days to maturity had no such association with seed yield. However, Singh and Bhatnagar (1965) reported that days to flowering and maturity were positively and significantly correlated in mungbean. In the present investigation, seeds per plant followed by number of pods per plant, number of clusters per plant and seed weight exhibited very high and positive significant correlation with seed yield at even 1% level of significance indicating their importance for genetic improvement of productivity in mungbean. Poehlman (1991) and Han-Fen *et al.* (1998) found that number of pods per plant had highest positive correlation with the seed yield. Saxena *et al.* (2007) observed that seed yield per plant had positive association with pods per plant, primary branches per plant and harvest index at both phenotypic and genotypic levels. Harvest index (H.I.) was estimated to have positive correlation with productivity at phenotypic level only. Haritha and Sikhar (2002) and Saxena *et al.* (2007) observed that seed

yield per plant had positive association with pods per plant, primary branches per plant and harvest index at both phenotypic and genotypic levels. In contrast, number of branches per plant and protein content had negative association with seed yield in the present set of materials. Among the traits under study for character association, pod length and seeds per pod had also no appreciable association with seed yield. These results are in partial agreement with Rohman and Hussain (2003). Hence, selection for these characters would likely to have no significant response in improving productivity.

Maturity duration and days to 50% flowering were estimated to have positive *inter se* significant association as well as with traits e.g., plant height, number of primary branches, pod length, seeds per pod, and protein content; whereas number of pods per cluster, number of pods per plant, seeds per plant, harvest index, days to 50% flowering as well as days to maturity were negatively associated with seed yield (Table 1). Singh and Bhatnagar (1965) reported that days to flowering and maturity were positively and significantly correlated in mungbean. Besides, it is noted that days to 50% flowering was only significant and positively correlated with pod length and seeds per plant, but maturity duration had no such strong relationship with these traits. Number of clusters, number of pods per plant and 100-seed weight did not exhibit any appreciable relationship with both days to 50% flowering and maturity duration. Plant height had significant positive correlation with days to 50% flowering, days to maturity, seeds per pod, seeds per plant and protein content at 1% level of significance and with number of primary branches, number of clusters and pod length at 5% level. As expected, harvest index was correlated negatively with plant height among the twenty selected test genotypes in the present investigation. Number of branches correlated negatively with most of the characters. In contrast, days to 50% flowering, days to maturity, plant height and protein content had shown significant positive correlation at even 1% level of significance. Number of clusters was found to have strong positive correlation with number of pods per plant, seeds per plant, and 100-seed weight at genotypic level.

Number of pods per cluster had shown significant positive correlation with pods per plant, seeds per plant and harvest index, while rest of the characters exhibited negative relationship except pod length, seeds per pod and 100-seed weight with feeble positive correlation coefficient. In the present investigation, number of pods per cluster had shown strong negative association with plant height, number of primary branches and protein content. In mungbean, number of pods per plant is regarded as an important yield contributing component trait. Numbers of clusters per plant, number of pods per cluster, number of seeds per plant and 100-seed weight were found to have favourable association with number of pods per plant at even 1% level of significance at both genotypic and phenotypic level. Rest of the traits did not exhibit appreciable association except protein content which had shown significant negative correlation with number of pods per plant at both genotypic and phenotypic level. Pod length was found to have good relationship with days to 50% flowering, number of seeds per pod, and number of seeds per plant only at 1% level of significance and with plant height at 5% level. Number of primary branches and 100-seed weight had adverse affect on

pod length with significant negative correlation at 5% level of significance at both genotypic and phenotypic level. Rest of the characters had shown no appreciable association with pod length. Negative inter-relationships of pod length with number of pods and branches were noted by Singh (1980). As expected, seed number per pod increased significantly with pod length and resulted higher seed number per plant. However, days to maturity, days to 50% flowering and plant height were also found to influence seeds per pod significantly in positive direction at both genotypic and phenotypic level.

Seeds per plant determine seed yield as it had shown significant positive correlation with major yield contributing traits, e.g., days to 50% flowering, plant height, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, and seeds per pod. However, it exhibited significant negative correlation with number of primary branches per plant and protein content. 100-seed weight depends on seed size. In the present investigation, it had feeble relationship with most of the yield contributing traits except number of clusters and number of pods per plant with significant positive correlation. On the other hand, protein content and pod length were found to have unfavourable association with seed size among the component traits under study. However, Patil and Narkhede (1989) through inter-relationship study pointed out that 100-seed weight, pod length, pods per plant and plant height may be successfully used in selection programmes. Harvest index had shown positive significant association with number of pods per cluster only among the major yield contributing traits. A few characters e.g., days to 50% flowering, days to maturity, plant height and number of primary branches per plant which could contribute maximum to total biomass, were estimated to have negative correlation coefficient with harvest index.

Protein content is a nutritionally important quality parameter in mungbean. It had negative association with most of the important yield contributing traits and even with harvest index. In contrast, days to 50% flowering, days to maturity, plant height and number of primary branches per plant showed significant positive association with protein content. In the present investigation, number of clusters per plant, pod length and number of seeds per pod had no appreciable or very feeble relationship with protein content. The correlation coefficients of component traits with grain yield were partitioned into their direct and indirect effects on seed yield following path coefficient analysis to ascertain further conclusive information on choice of characters required for selection of high yielding genotypes. In addition, path co-efficient analysis along with correlation of component traits with seed yield could give more clear picture about relative merit of traits associated with productivity. A perusal of Table 2 indicates direct effects of each of the thirteen independent component traits on seed yield and their indirect influence on seed yield via other component characters. Among the component traits, number of pods per plant had maximum direct effect on seed yield followed by clusters per plant and 100-seed weight. These traits were observed to have strong positive correlation with seed yield at both genotypic as well as phenotypic level. Besides, Makeen *et al.* (2007), Rao *et al.* (2006), Hakim (2008) and Swain *et al.* (2010) stressed the importance of pod number while selection for seed yield. Bhaumik and Jha (1976), Sabaghpour

et al. (1998) and Pundir *et al.* (1992) reported that pods per plant and 100-seed weight had marked positive direct effects on seed yield. Upendra-Kumar *et al.* (2005), however, noted pods per plant and harvest index to have high positive direct effects towards seed yield. In the present investigation, number of pods per cluster had also shown appreciable direct influence on seed yield at phenotypic level only. On the other hand, days to maturity, days to 50% flowering, plant height and number of primary branches per plant exhibited negative direct effects on productivity. Direct negative effect was reported for days to 50% flowering at both genotypic and phenotypic level by Vinay Kumar *et al.* (2010). Obaidullah *et al.* (2006) pointed out the maximum negative direct effect by branches per plant on seed yield in mungbean. Similarly, plant height was reported to have negative direct effect on seed yield (Tabasum *et al.*, 2010). It is worth to note that number of clusters per plant via number of pods per plant and also *vice versa* contributed to seed yield appreciably as revealed from their high *inter se* indirect effects at genotypic level. Similar result was also obtained by Swain *et al.* (2010) in rice bean. Selection for any of these component characters automatically selects the other trait and thus, together could result recovery of high grain yield. The merit of these two traits is further ascribed to their positive correlated response through other component traits e.g. seeds per plant, harvest index and seed weight. Seeds per plant though exhibited very high positive correlation with seed yield, it failed to influence seed yield directly at genotypic level. However, seeds per plant contributed indirectly to seed yield through number of clusters and number of pods per plant. In the present investigation, harvest index had no remarkable direct effect on productivity as also revealed from its non-significant correlation with seed yield at genotypic level, but it had high indirect effect via days to maturity and number of pods per plant at least at genotypic level.

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