Genetic association and path coefficient analysis in mung bean *Vigna radiata* (L.) Wilczek

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Abstract. Genetic variability and character association in 23 genotypes of mung bean for different quantitative characters were studied in *kharif* (summer or monsoon crop) 2007. The analysis of variance revealed highly significant difference for all characters, under study among the genotypes, indicating the presence of sufficient amount of variability in the varieties. Thus there is ample scope for selection of different quantitative characters for crop improvement. The highest GCV and PCV were observed for harvest index and pods per plant respectively. High estimates of genetic advance as percent of mean were observed for 100 seed weight and harvest index. High significant correlation was recorded for pods per plant and harvest index at both genotypic and phenotypic levels with seed yield per plant and plant height, primary branch per plant, clusters per branch and days to maturity had direct positive effect on seed yield.
Key words: mungbean, GCV, PCV, heritability, genetic advance, correlation and path analysis.

Introduction. Mungbean (*Vigna radiata* (L.) R. Wilczek) syn. *Phaseolus aureus* (Roxb.) is one of the leading pulse crop widely grown in India. The crop is often preferred to other pulse crop because of its better digestibility and less flatulence problem owing to lower content of raffinose, stachyose and verbacose (Poehlman 1991). In this crop the earlier hybridization did not raise attention, as native cultivars or selection from native cultivars were grown. Now practically all new varieties originated by hybridization as a result of favorable characteristics of new lines being identified more fully so that breeder can choose desirable parental combination with greater precession and crossing procedure being improved and standardized so that a higher percent of seed yield obtained.

Genetic improvement of crop is largely depending on the magnitude of genetic variability and the extent to which desirable traits are heritable. Genetic variability studies about the presence of difference in their genetic constitution. It is of outmost important as it provide the basis for effective selection. Therefore an attempt was made in the present studies to estimate the extent of variability, heritability, genetic advance, correlation and path analysis by utilizing 23 genotypes. Infect this study is the prerequisite for any crop improvement programme. The correlation and path coefficient analysis provide information about importance of various yield components in formulation of appropriate selection strategies. Studies on above aspects on available germplasm under the environment where it is to be explained are essential for successful utilization of germplasm resources for the development of superior mung bean varieties.

Material and Methods. The experimental material for the present study consisted of 23 mungbean genotypes viz. KM-7-173, KM-7-174, KM-7-178, KM-7-179, KM-7-180, KM-7-

181, KM-7-182, KM-7-184, KM-7-187, KM-7-189, KM-7-190, KM-7-191, KM-7-192, KM-7-193, KM-7-194, KM-7-198, KM-7-200, KM-7-202, KM-7-203, KM-7-207, KM-7-211, KM-7-212, and KM-7-176 received from Indian Institute of Pulses Research, Kanpur. The experiment was carried out at experimental farm of the Department of Genetics and Plant Breeding, Allahabad Agricultural Institute-Deemed University, Allahabad during *kharif* (summer or monsoon crop) 2007 in randomized block design in two replications. Each genotype was grown in a plot size of 4 m^2 area with 30x10 cm spacing. The recommended cultural practices were adopted for the proper growth and stand of the crop. The data were recorded 10 randomly selected plants from each replication for plant height, number of pods per plant, number of cluster per plant, number of branch per plant, number of primary branches per plants, pod length, number of seeds per pod, 100 seeds wt. (g), seed yield per plant (g) and seed yield per plot(g). The mean value were used to obtained analysis of variance was carried out as per methodology advocated by Panse & Sukhatme (1967). PCV and GCV were calculated by the formula given by Burton (1952), Heritability in broad sense (h^2) by Burton (1952), Burton & De Vane (1953), and genetic advance i.e. the expected genetic gain were calculated by using the procedure given by Johnson et al (1955). Correlation coefficient and path coefficient was worked out as method suggested by Jibouri et al (1958); Deway and Lu (1959) respectively.

Results and Discussion. The analysis of variance revealed highly significant difference for all characters, under study among the genotypes, indicating the presence of sufficient variability in the varieties. The mean range, GCV, PCV, h^2, genetic advance and genetic advance% of mean are given in Table 1. The highest range of variation was recorded for number of pods per plant, plant height and harvest index seed yield per plant (g) indicating maximum scope for the selection of these characters for effective improvement. Primary branches per plant and cluster per plant have not shown significant difference among the genotypes. Similar finding were also reported by Choudhary et al 1988 and Ilhamuddin et al 1989.

The character possessing high genotypic coefficient of variation value has better scope of improvement through selection. The influence of environment on each trade could be determined on the basis of difference between phenotypic coefficient of variation and genotypic coefficient of variation. A perusal of GCV revealed that maximum value of genetic coefficient of variation was recorded for harvest index (32.95), 100 seed weight (40.67) and cluster per plant (14.99). Lowest GCV was observed for number of seed per pod (5.26), days to 50% flowering (5.99),cluster per branch (7.32) and days to maturity (9.04) (Table 2). The PCV for pods per plant exhibited value of (34.90) followed by harvest index (34.79) and primary branches per plant (20.82) while estimates of PCV were low for days to 50% flowering (6.10) and number of seeds per pod (7.71). The high difference between phenotypic coefficient of variation and genotypic coefficient of variation pods per plant, primary branches per plant, cluster per branch and cluster per plant indicates these characters were highly influenced by environment.

On the basis of genotypic coefficient of variation alone, it is not possible to determine the amount of heritable variation. It can be find out with greater degree of accuracy when heritability in conjunction with genetic advance is studied Dudley and Moll (1969). The high heritability in broad sense was recorded for 100 seed weight (59.9), harvest index (89.7), length (88.2), and days to maturity (83.1). The moderate heritability was recorded for plant height (75.2), days to 50% flowering (73.3), and cluster per plant (61.9). Low heritability was recorded for cluster per branch (26.4), primary branches per plant (37.5), and number of seeds per pod (46.4). The characters with exhibited high heritability, suggested that the selection will be more effective whereas the characters showing low heritability indicated that the selection will be effected by the environment factors.

Similar findings were recorded by Choudhary et al (1988). The heritability estimates were of high magnitude for 100 seed weight, harvest index and days to maturity. According

to Panse (1958, 1967) such characters governed predominantly by additive gene action and could be improved through individual plant selection. Similar results have been reported by Anwari & Sochendi (1999). Low heritability observed for the characters viz, number of primary branches per plant cluster per branch, number of seeds per pod revealed that the characters were highly influenced by environmental effect and genetic improvement through selection will be difficult due to effect of genotypes.

The estimate of genetic advance expressed and percentage of mean showed a wide range for 7.37 for number of seeds per pods and 56.35 for pods per plant. Thus genetic advance coupled with high heritability recorded for the character of harvest index. Low genetic advance coupled with low heritability for the character number of seeds per pod and primary branches per plant. Low genetic advance coupled with high heritability for the character 100 seed weight. The high heritability coupled with moderate genetic advance was observed for plant height, harvest index and days to maturity.

Correlation coefficient analysis measures the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield. A positive value of correlation shows that the changes of two variables are in the same direction, i.e., high value of one variable are associated with high values of other and vice-versa. When correlation is negative the movements are in opposite directions, i.e., high values of one variable are associated with low values of other. The breeder is always concerned for the selection of superior genotypes on the basis of phenotypic expression. However for the quantitative characters, genotypes are influenced by environment, thereby affecting the phenotypic expression. Information regarding the nature and extent of association of morphological characters would be helpful in developing imitable plant type, in addition to the improvement of yield a complex character for which, direct selection is not effective. The correlation coefficient between seed yield per plant and other quantitative attributing to yield showed that seed yield per plant was significantly and positively associated with pods per plant and harvest index at both genotypic and phenotypic levels (Kasundra et al 1995). Thus selection for higher yield on the basis of above two characters would be reliable. The findings of Zabet et al (2004) and Rao et al (2006) were also similar (Table 2).

A negative non significant correlation was found between plant height and days to maturity at both genotypic and phenotypic levels. It indicates that an association of two characters is not only due to genes but also due to their influence of the environment. Mittal (2007) also reported that the seed yield per plant was positively correlated with pods per plant and 100 seed weight but it was negatively correlated with days to maturity and plant height. The days to 50% flowering expressed strong positive association with days to maturity and cluster per plant with seeds per pod, pods per plant and seed per pod contributed positive association at both genotypic and phenotypic levels. These findings are also similar to Sridevi & Sekhar (2004) findings. If relationship is due to manifold effect of gene (s) it is difficult to separate these effects by selecting particular character so related (Das et al 1988). If correlation is due to genetic linkage, it is possible to reserve the association provided the linkage is not very close. It is therefore important to establish the genetic basis of correlation before launching any breeding programme. Information obtained from correlation study does not give a complete idea about the contributions of each component character. Path coefficient analysis is useful for partially direct and indirect causes of correlation and also enables us to compare the causal factors on the basis of their relative contributions. As the correlation coefficient it is not sufficient to explain true relationship for an effective manipulation of the character, path coefficient was worked out.

Path coefficient at phenotypic level revealed that harvest index (0.3781), pods/plant (0.3491), cluster per branch (0.1271), seeds per pod (0.1751), plant height (0.0335), days to maturity (0.03376), and pod length (0.0062) had highest positive direct effect on seed yield per plant, indicating there are main contributors to yield (Table 3). Plant height, primary branches per plant, seeds per pod, and days to maturity had direct positive effect

at genotypic level and phenotypic level. The findings are in agreement with the findings of Kumar et al (2004). Direct negative effect was observed for days to 50% flowering, and clusters per plant at genotypic level and phenotypic level.

Table 1

Estimate of variance and genetic parameters for 12 quantitative characters in 23 mung bean genotypes

S. No.	Characters	GCV	PCV	ECV	H(bs)%	GA	GG
1.	Days to 50% flowering	05.99	06.10	03.61	73.3	03.84	10.57
2.	Plant height	10.12	11.67	05.81	75.2	11.68	18.07
3.	Primary branches per plant	12.75	20.82	16.46	37.5	00.46	16.09
4.	Cluster per branch	07.32	14.26	12.23	26.4	00.28	07.75
5.	Cluster per plant	14.99	19.16	11.93	61.2	02.91	24.16
6.	Pod per plant	13.90	34.90	16.23	78.4	15.02	56.35
7.	Pod length	13.32	14.19	04.88	88.2	02.08	25.76
8.	No. of seed per pod	05.26	07.71	05.65	46.4	00.83	07.37
9.	Days to maturity	09.04	09.91	04.07	33.1	12.45	16.98
10.	100 seed weight	14.67	15.47	04.92	89.9	01.25	28.64
11.	Harvest index	32.95	34.79	11.18	89.7	24.07	64.28
12.	Seed yield per plant	12.73	17.41	11.88	53.5	02.06	09.18

GCV = Genotypic coefficient of variance
PCV = phenotypic coefficient of variance
ECV = Environment coefficient of variance
H (bs) = Heritability broad sense
GA = Genetic advance,
GG = Genetic gain

Table 2

Estimates of correlation coefficient value at genotypic and phenotypic level for 11 component characters and with seed yield

Characters		Plant height	Primary branches per plant	Cluster per branch	Cluster per plant	Pod per plant	Pod length	No. of seeds per pod	Days to maturity	100 seed weight	Harvest index	Seed yield per plant
Days to 50% flowering	rg	-0.0778	-0.4833**	0.4504*	0.0665	-0.1998	-0.2608	0.5538**	0.1243	-0.1431	-0.1431	-0.5186**
	pg	-0.2530	-0.1847	0.2310	0.0985	-0.0650	0.1554	-0.1413	0.4201**	0.0860	-0.0732	0.2827
Plant height	rg	1.0000	0.4441*	-0.2121	0.1899	-0.6907**	-0.1836	-0.1690	0.1085	-0.3019	-0.4408*	-0.3479*
	pg		0.3569**	-0.0022	0.2718	-0.4694**	-0.1378	-0.1495	0.1352	0.2113	-0.3519*	-0.2725
Primary branches per plant	rg		1.0000	0.4192*	0.8184**	-0.1482	0.4685**	-0.0432	-0.3542*	-0.0806	-0.0713	0.0256
	pg			0.1837	0.6446**	-0.0830	-0.2872	0.0405	-0.2291	0.0043	-0.0350	0.0399
Cluster per branch	rg			1.0000	0.7546**	0.4612*	0.3231	0.2999	0.2308	0.2790	0.2654	0.1611
	pg				0.5712**	0.2568	0.1794	0.1951	0.1622	2.1793	0.0636	0.1568
Cluster per plant	rg				1.0000	0.0982	-0.1748	0.2119	0.0703	-0.1503	-0.0784	-0.0446
	pg					0.1070	-0.1365	0.0973	0.0555	-0.0618	-0.0725	0.0096
Pod per plant	rg					1.0000	0.0646	0.2464	-0.1863	0.2025	0.4979**	0.8606**
	pg						0.0902	0.1931	-0.1749	0.1815	0.4455*	0.5419**
Pod length	rg						1.0000	0.5303**	0.1994	0.6970**	0.1572	0.1459
	pg							0.4742**	0.1816	0.6247**	0.1343	0.1222
No. of seed per pod	rg							1.0000	-0.3775	0.5351**	0.1076	0.3556
	pg								-0.2404	0.3684*	0.0736	0.2855
Days to maturity	rg								1.0000	-0.1241	-0.1684	-0.3217
	pg									-0.1092	-0.1759	-0.2234
100 seed weight	rg									1.0000	0.1015	0.2161
	pg										0.1948	0.1214
Seed yield per plant	rg										1.0000	0.7635**
	pg											0.5553**

**and * significant at 1% and 5% level, respectively;
rg= Genotypic correlation, pg= phenotypic correlation.

Path coefficient at phenotypic level for 11 yield component characters in mung bean genotypes

Characters	Days to 50% flowering	Plant height	Primary branches per plant	Cluster per branch	Cluster per plant	Pod per plant	Pod length	No. of seeds per pod	Days to maturity	100 seed weight	Harvest index	Correlation Coefficient with Seed yield per plant
Days to 50% flowering	-0.2133	0.0054	0.0400	-0.0493	-0.210	0.0139	-0.0331	0.0301	-0.0896	-0.183	0.0156	-0.2827
Plant height	-0.0008	0.0335	0.0120	-0.0001	0.0091	-0.0157	-0.0046	-0.0050	0.0045	-0.0071	-0.0118	-0.2725
Primary branches per plant	-0.203	0.0387	0.1085	0.0199	0.0699	-0.0090	-0.0312	0.0044	-0.00249	0.0005	-0.0038	0.0399
Cluster per branch	0.0294	-0.0003	0.0234	0.1271	0.0726	0.0326	0.0228	0.0248	0.0206	0.0228	0.0081	0.1568
Cluster per plant	-0.0150	-0.0414	-0.0982	-0.0870	-0.1524	-0.0163	0.0208	-0.0148	-0.0084	0.0094	0.0110	0.0096
Pod per plant	-0.0227	-0.1639	-0.0290	0.0896	0.0373	0.3491	0.0315	0.0674	-0.0611	0.0634	0.1555	0.5419**
Pod length	0.0010	0.0009	-0.0018	0.0011	-0.0008	0.0006	0.0062	0.0029	0.0011	0.0039	0.00008	0.1222
No. of seed per pod	-0.0247	-0.0262	0.0071	0.0342	0.0170	0.0338	0.0830	0.1751	-0.0421	0.0645	0.0129	0.2855
Days to maturity	0.0158	0.0051	-0.0086	0.0061	0.0021	-0.0066	0.0068	-0.0091	0.03376	-0.0041	-0.0066	-0.2234
100 seed weight	0.0042	0.0104	-0.0002	-0.0088	0.0030	-0.0089	-0.0308	-0.0182	0.0054	-0.0493	-0.0047	0.1214
Harvest index	0.0277	-0.1331	-0.0132	0.0241	-0.0274	0.1685	0.0508	0.0278	-0.0665	0.0358	0.3781	0.5553**

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