

GENETIC VARIABILITY AND SOWING DATES EFFECT OF CLUSTER BEAN (*CYAMOPSIS TETRAGONOLOBA* L. TAUB) GENOTYPES IN SEMI ARID REGION OF MAHARASHTRA, INDIA

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Abstract

Genotypic and phenotypic variability, heritability, genetic advance, correlation and direct path analysis were studied in cluster bean. Combined analysis of variance in eighteen phenotypic characters indicated significant difference in genotypes, sowing dates and their interaction. The high phenotypic coefficient of variation for branches/plant (43.33) followed by leaf area (37.43), number of clusters/plant (36.69), seed yield/ plant (27.30), dry pod yield/plant (21.55), plant height (20.09), number of pods/cluster (19.71) indicated scope for further improvement in these traits. The genetic advance was above 35 per cent in branches/plant (85.92%), number of clusters/plant (74.60%), leaf area (72.92%), seed yield/ plant (54.86%), dry pod vield/ plant (42.44%), plant height (40.05%) and number of pods/cluster (37.79%). Broad sense heritability (> 90%) was recorded in number of clusters/ plant (98.69%), seed yield/plant (97.56%), plant height (96.77%), dry biomass (96.76%), number of branches/plant (96.24%), dry pod yield/plant (95.59%), leaf area (94.55%), number of pods/cluster (93.06%), days to maturity (92.50%) and days to 50% flowering (91.07) indicated the presence of large number of fixable additive factors and hence these traits could be improved through selection. Low heritability with low genetic advance was recorded in pod length, pod width, number of seeds/ pod, 100-seed weight and days to flower initiation showed lowest share of direct path coefficient effect is indicative of non-additive gene action predominance which could be exploited through heterosis breeding. The positive and significant correlation was observed in seed yield/plant with dry pod yield/plant (0.96**), number of pods/ cluster (0.81**), 100 - seed weight (0.78**), number of clusters/plant (0.75**), branches/plant (0.73**), seed recovery (0.70**), germination (0.67**), number of seeds/pod (0.63**) and dry biomass/plant (0.62**). Whereas negative and significant correlation was recorded in days to flower initiation (-0.66**), plant height (-0.54**), days to maturity (-0.38**) and days to 50% flowering (-0.33**). Plant height, number of seeds/pod, days to 50% flowering, number of clusters/plant, dry pod yield/ plant and dry biomass/plant had direct positive effects on seed yield. Based on high magnitude of heritability, genotypic and phenotypic coefficient variation, genetic advance, correlation and direct path effects, it could be concluded that determinant genetic effects of phenotypic expression of these characters are fundamentally of additive type. The traits like pod length, pod width, number of seeds/pod, 100-seed weight and days to flower initiation are to be improved using heterosis breeding.

Key words : Cyamopsis tetragonoloba, genetic variability, heritability, genetic advance, correlation, path analysis.

Introduction

Cluster bean [*Cyamopsis tetragonoloba* L. Taub., 2n = 14] is self pollinated crop belongs to family *Fabaceae*. The high commercial value of guar seeds are mainly for extraction of endospermic gum (galactomannan). A major share of guar gum goes to petroleum industry for gelling and thickening called as franking. Though, it is export oriented, crop is confined to semi arid region agro-climatic zone of Rajasthan, Haryana, Punjab and Gujarat. Deccan plateau of Maharashtra received rainfall ranged from 250 to 560 mm. The terrain is highly undulating to hilly, rainfed, drought-prone, facing several kinds of abiotic stresses. Yield is a complex character and is known to be associated with a number of yield contributing traits and is highly affected by environmental variances. Researchers namely Dabas *et al.* (1982), Singh *et al.* (2005), Morris (2010) and Sultan *et al.* (2012) worked on cluster bean, but information on genetic variability is limited. Keeping into view its importance as seed guar and its adaptability to arid drought condition, there is need for its improvement

for yield and its components suited to specific agro ecological condition. Hence, the present investigation was formulated to understand genetic variation, heritability, genetic gain, correlation and path coefficient effects. Study helping to establish genotypes, sowing dates and their interaction ($G \times SD$) effects for all studied traits and generate genetic information to develop breeding strategies for future breeding programme in cluster bean.

Materials and Methods

Eight genotypes (RGC-986, RGC-1055, RGC-1038, RGC-1033, RGC-471, RGC-1071, RGC-1031 and RGC-197) were evaluated in the experimental field of School of Drought Stress Management, National Institute of Abiotic Stress Management (NIASM), Indian Council of Agricultural Research, Malegaon Khurd (18°09" 30.62'N by $74^{\circ}30''03.08E$; altitude = 570m amsl), Baramati, Pune district, Maharashtra. The crop was grown during Kharif season in two different sowing dates (2nd and 4th) week of August, 2012 in split plot design with four replications. Six rows of 4m length with plant \times plant distance of 0.20m and ridges of 0.45m/replication/ genotype were maintained. Two split doses of NPK (19:19:19) at the rate of 50 kg/ha were applied by broadcasting method. During crop cycle total 217.10mm rainfall was received. Observations were recorded on individual labeled plant basis. Days to flower initiation was recorded when number of days from seed sowing until 5% of plants have flower in each accession. Number of days from seed sowing until 50% of plants have at least one flower in each accession was considered for days to 50% flowering. Number of days from seed sowing until 80% of plants reaching physiological maturity was treated as days to maturity. Plant height was measured of five random plants from ground level to apex of main stem. Total number of branches originated from main stem was counted. Harvesting of crop was carried out when more than 95 per cent pods in each accession turned brown in colour. The biomass and seed yield potential of individual accessions were estimated from average single plant yield and expressed in t ha⁻¹. Eighteen quantitative traits namely, germination (%), days to flower initiation, days to 50% flowering, days to maturity, plant height (cm), branches/plant, leaf area (cm²), number of clusters/plant, number of pods/cluster, seeds/pod, pod length (cm), pod width (cm), 100-seed weight (g), dry pod yield/plant (g), dry pod husk weight/plant (g), seed recovery (%), dry biomass/plant (g) and seed yield/plant (g) were brought under study. Pooled data of two different sowing dates from mean of five plants/treatment/ replication were used for statistical analysis. On line

statistical programme OPSTAT developed by O.P. Sheoran, Programmer, C.C.S. Haryana Agricultural University, Hisar, Haryana (India) were used for estimation of heritability (h²B), genetic advance (GA), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) estimates, correlation coefficient (r) and path analysis. Broad sense heritability (%) for different traits was computed using the variance components method (Snedecor and Cochran, 1980; Fisher, 1954). The components of variance were computed using observed mean square values of PCV and GCV (Johnson et al., 1955 and Hanson et al., 1956). The collected data were subjected to combined analysis of variance (Gomez and Gomez, 1984). The correlation coefficients were determined for all possible pair wise combinations between characters according to Miller et al. (1958). Path coefficient analysis for partitioning genotypic correlation effects was calculated following procedure suggested by Dewey and Lu (1959). Covariance estimation and residual effect was determined following (Singh and Chaudhary, 1979) by substituting estimated path coefficients and expected genetic advance of these indices was determined according to formula suggested by Robinson et al. (1951).

Results and Discussion

Genotypic and phenotypic coefficient of variation and expected genetic advance

Mean performance of genotypes for 18 traits in two different sowing dated (2nd and 4th week of August) are given in fig. 1. The GCV ranged from 5.97 (seed recovery) to branches/plant (42.51). The highest PCV was for branches/plant (43.33) followed by leaf area (37.43), number of clusters/plant (36.69), seed yield/plant (27.30), dry pod yield/plant (21.55), plant height (20.09), number of pods/cluster (19.71) indicated scope for further improvement in these traits. The estimates of PCV in general were higher than estimates of GCV for all traits that suggested apparent variation is not only due to genotypes, but also due to influence of environment. These partitions were able to quantify genotypic and phenotypic effect due to $G \times SD$ variance effect. The low difference in extent of PCV and GCV indicates low influence of environment on expression as observed in days to 50% flowering, number of clusters/plant, number of pods/ cluster, number of seeds/pod, 100-seed weight, dry pod yield/plant and seed recovery. The improvement in mean genotypic value of selected trait over base population mean (genetic advance) was above 35 per cent in branches/plant (85.92%), number of clusters/plant (74.60%), leaf area (72.92%), seed yield/plant (54.86%),

dry pod yield/plant (42.44%), plant height (40.05%) and number of pods/cluster (37.79%). The high GCV and PCV coupled with high genetic gain expected criteria for traits selection. The traits having low GA over mean indicated involvement of non-additive effects and traits like pod length, pod width 100-seed weight, number of seeds/pod and days to flower initiation can be improved by introgression or incorporation of selected individuals in recurrent breeding programme. These results are in agreement with earlier findings of Dass et al. (1973), Gipson and Balkrishanan (1990), Saini et al. (2010) and Rai et al. (2012) on cluster bean. Exploitation of heterosis for non-additive traits like pod length, pod width, seeds/ pod, 100-seed weight and seed recovery was reported by Patil and Madhusoodanan (2007) and Patil et al. (2007) on small cardamom. Variation was also assessed using heritability (table 1).

Heritability

Broad sense h²B estimate are found to be genetic tool for selection (table 1). The lowest h²B in pod width (9.84%) and the highest h²B in number of clusters/plant (98.69%) were estimated. Very high heritability (> 90%) was recorded in number of clusters/plant (98.69%), seed yield/plant (97.56%), plant height (96.77%), dry biomass (96.76%), number of branches/plant (96.24%), dry pod vield/plant (95.59%), leaf area (94.55%), number of pods/ cluster (93.06%), days to maturity (92.50%) and days to 50% flowering (91.07). High h²B estimates indicated presence of large number of fixable additive factors and hence these traits could be improved by selection. Low h²B was observed in pod length, pod width, 100-seed weight, seeds/pod, days to flower initiation and germination. Johnson et al. (1955) reported that effectiveness of selection depends not only on heritability, but also on genetic advance. Because sometimes high heritability influenced and affected to others characters. High h²B associated with high GA was found in characters like branches/plant, number of clusters/plant, dry pod yield/plant, seed yield/plant, plant height, number of seeds/pod and dry biomass/plant. This indicated that these traits were mostly governed by additive gene action. These results were in harmony with Rai et al. (2012) on same crop. Breeding method based on progeny testing and mass selection could be useful in improving these traits which controlled by additive gene action. High h²B with low GA for days to maturity and seed recovery and lowest h²B with lowest GA was recorded in pod length, pod width, 100-seed weight, seeds/pod, days to flower initiation and germination showed lowest share of direct path coefficient effect is indicative of non-additive gene action predominance which could be exploited through heterosis breeding. To overcome genetic improvement constraints and breaking yield level on cluster bean, maximum amount of heterosis generally expected in cross combinations involving the parents belongs to most diverse genotypes are to be exploited as suggested by Singh et al. (2003) and Pathak et al. (2009) on cluster bean and Patil et al. (2003) on rice. In the present study, high h²B associated with GA was indication of dominance effects. These results are in conformity with those reported by Dass et al. (1973), Dabas et al. (1982) and Saini et al. (2010). High GA for number of pods/plant and branches/plant was reported by Mital and Thomas (1969) and Choudhary and Joshi (1996) in cluster bean confirmed present findings. High heritability supported by high genetic advance coupled with significant and desirable correlation and direct path coefficient effect gives strongest support to present investigation (table 1).

Correlation and direct path coefficient

Correlation coefficient (r) was estimated for 17 morphological traits (table 1). The positive and significant correlation was observed with seed yield/plant and dry pod yield/plant (r = 0.96**), number of pods/cluster (r = 0.81^{**}), 100-seed weight (r = 0.78^{**}), number of clusters/ plant (r = 0.75^{**}), branches/plant (r = 0.73^{**}), seed recovery ($r = 0.70^{**}$), germination ($r = 0.67^{**}$), number seeds/pod (r = 0.63**), dry biomass/plant (r = 0.62**), dry pod husk weight ($r = 0.53^{**}$) and leaf area (0.32^{**}). Whereas, negative and significant correlation was recorded in seed yield/lant with days to flower initiation (r = -0.66**), plant height (r = -0.54**), days to maturity $(r = -0.38^{**})$ and days to 50% flowering $(r = -0.33^{**})$. The association of seed yield/plant with pod length and pod width was found to be non significant. Similar research was conducted on cluster bean crop grown in Pakistan by Sultan et al. (2012). They reported positive and significant correlation of seed yield/plant and branches/plant, number of clusters/plant, pods/cluster, pods/plant and negative and significant correlation with days to flower initiation, days to 50% flowering and days to maturity. The findings obtained for correlation coefficient studies are in strong agreement with Rai et al. (2012) findings, who determined significant and positive correlation of seed yield/plant with plant height, pods/ cluster and pod yield/plant in same crop. Significant and positive correlation of yield/plant with tillers/clump and recovery was reported by Patil et al. (1998) on small cardamom is in support of present findings. Though, fifteen traits has desirable correlation but plant height, days to 50% flowering, number of seeds/pod, number of clusters/ plant and dry pod yield/plant had major share and direct positive effect on seed yield. This is due to correlation



Fig. 1 : Phenotypic performance of 18 traits in two different sowing dates.

Table 1 : Variability, heritability, correlation and direct effect of phenotypic traits with seed yield/ plant.

	Phenotypic traits	GCV	PCV	GA (%)	h ² B	Genotypic correlation (r)	Direct
						with seed yield / plant	path effects
1.	Germination (%)	6.91	7.72	12.74	80.13	0.67**	1.48
2.	Days to flower initiation	14.67	16.48	26.91	79.25	- 0.66**	0.71
3.	Days to 50% flowering	18.09	18.96	35.57	91.07	- 0.33**	14.66
4.	Days to maturity	10.76	11.19	21.33	92.50	- 0.38**	-19.32
5.	Plant height (cm)	19.76	20.09	40.05	96. 77	- 0.54**	23.49
6.	Branches/ plant	42.51	43.33	85.92	96.24	0.73**	-3.96
7.	Leaf area (cm ²)	36.40	37.43	72.92	94.55	0.32**	-17.38
8.	No. of clusters/ plant	36.45	36.69	74.60	98.69	0.75**	11.14
9.	No. of pods/ cluster	19.01	19.71	37.79	93.06	0.81**	14.14
10.	Number of seeds/ pod	8.35	9.18	15.66	82.79	0.63**	14.07
11.	Pod length (cm)	7.27	10.29	10.60	49.99	0.17NS	-7.24
12.	Pod width (cm)	6.24	9.89	4.03	9.84	-0.10NS	2.59
13.	100 – seed weight (g)	6.56	7.31	12.15	80.64	0.78**	-0.18
14.	Dry pod yield/ plant (g)	21.07	21.55	42.44	95.59	0.96**	2.59
15.	Dry pod husk weight (g)	16.78	17.61	32.93	90.75	0.53**	-7.80
16.	Seed recovery (%)	5.97	6.27	11.71	90.65	0.70**	-13.87
17.	Dry biomass/ plant (g)	16.87	17.15	34.20	96.76	0.62**	2.48
18.	Seed yield/ plant (g)	26.96	27.30	54.86	97.56	—	—
	Residual effect						0.22

*P = 0.05, **P = 0.01, NS = Non-significant.

simply measures apparent mutual association between two characters without regard to cause. However, path coefficient specifies causes and measures their relative importance. Study indicated that correlation alone may not give complete information and better measure is to study cause and effects relationship existing between different pairs of characters (Dewey and Lu, 1959; Patil *et al.*, 2003; Singh *et al.*, 2003). Path analysis study partitioned genotypic correlations between seed yield and seventeen its components into direct effects (table 1). The path analysis study indicated that possession of greater plant height, more number of seeds/pod, dry pod yield/plant, number of clusters/plant and early days to 50% flowering had direct positive effect on seed yield, which shares contribution by direct path coefficient values for plant height (23.49), days to 50% flowering (14.66), number of seeds/pod (14.07), number of clusters/plant (11.14) and dry pod yield/plant (2.59). Other traits like germination, pod width and dry biomass/plant also contributed with positive direct effect ranging from 1.48 to 2.48. On the other hand days to maturity (-19.32), leaf area (-17.38), seed recovery (-13.87), dry pod husk weight (-7.80) and pod length (-7.24) exerted negative direct effect on seed yield. Positive direct effect for number of seeds/pod on seed yield/plant was reported by Ibrahim *et al.* (2012) on cluster bean which corroborated the present findings.

Conclusion

Study on genetic variability showed that there is possibility to improve yield and yield contributing traits of cluster bean in semi arid Deccan plateau region of Maharashtra. Based on high magnitude of h²B, GVC, PCV, GA, correlation coefficient and cause and direct effects, it could be concluded that determinant genetic effects of phenotypic expression of these characters are fundamentally of additive type and traits like days to 50% flowering, plant height, branches/plant, clusters/lant, pods/ cluster, dry pod yield, seed recovery, dry biomass and seed yield can be improved through direct selection. The traits like pod length, pod width, seeds/pod, 100-seed weight, seed recovery, dry pod husk weight, number of seeds/pod, days to maturity, days to flower initiation and germination are to be improved using heterosis breeding. Data further is to be analyzed by considering the drought stress factors and study the relationship of genotypes and sowing dates with weather parameters of the given location.

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