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Genetic variability studies in cluster bean [*Cyamopsis* tetragonoloba (L.) Taub.] for growth, yield and quality parameters

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Abstract

The study on genetic parameters of 74 cluster bean genotypes collected from different parts of the country revealed, high estimates of variation for number of branches (90 DAS), number of clusters per plant, number of pods per cluster, pod length, pod weight, vegetable pod yield per plant, pod yield per plot, pod yield per hectare, dry pod yield per plant, weight of ten dry pods, seed yield per plant, seed yield per plot and gum content of seed endosperm The high estimates of heritability coupled with high values of genetic advance over mean (GAM) were noticed for traits like, plant height (cm) (90 DAS), number of branches (90 DAS), number of clusters per plant, pod length, pod weight, pubescence, seed yield per plant, seed yield per plot and seed gum content. These outcomes showed prevalence of additive constituents for these characters and hence for improving these traits by direct selection method would be more effective.

Keywords: cluster bean, genetic variability, GCV, heritability, PCV, genetic advance over mean

Introduction

Cluster bean botanically *Cyamopsis tetragonoloba* (L.) Taub., is a crop of family Leguminaceae, or Fabaceae and sub family Papionaceae, with a chromosome number of 2n = 14. It is familiar as guar, guari, chavalikayi, khutti *etc.* Gillett (1958)^[6] considered *Cyamopsis* as a separate genus with Africa as its probable center of origin and India as the center of its variability (Vavilov, 1951)^[25].

Globally, India ranks first in production as it produces about 75–82 per cent of the world's cluster bean production followed by Pakistan (10–12%). The other major guar producers in the world are USA, South Africa, Zaira, Malawi and Sudan. Total cluster bean vegetable pod production in India is 16.80 lakh tonnes from an area of 23.30 lakh hectares with the productivity of 428 kg per hectare during the year 2017-18 (APEDA, 2018). In India, with 75 per cent of total production, Rajasthan is the top cluster bean producing state followed by Haryana and Gujarat and other states like Punjab, Uttar Pradesh and Madhya Pradesh have small contribution.

Cluster bean is a multipurpose crop as its green pods are used as a vegetable, seed is used as a pulse crop and green plants as fodder/green manure. It adds organic carbon to the soil by shedding its leaves gradually up until maturity thereby rejuvenating soil health. The immature pods are harvested for vegetable purpose, these nutritious tender fruits are rich source of energy (16 kcal), carbohydrate (10.8 g), protein (3.2 g), fat (1.4 g), moisture (81 g), vitamin A (65.3 IU), vitamin C (49 mg), iron (4.5 mg) and calcium (57 mg) for every 100 g of edible part (Kumar and Singh, 2002) ^[12].

The dicotyledonous seed consist of three major fractions in cluster bean *viz.*, the hull or husk (14 to 17%) and germ cell/embryo (35 to 42%) and endosperm (43 to 47%). Seed of cluster bean has preferably a large endosperm unlike most of the other leguminous crops and contains a galactomannan type of gum (23.9 to 34.2%), this gum in cold water form a viscous gel which has diversified industrial applications. The galactomannan gum was found in endosperm normalizes the moisture content of stool in constipation and helps in decreasing the cholesterol content and glucose that is absorbed in the stomach and intestines. This is due to the presence of high soluble fiber content of cluster bean.

The expression of phenotype of the plant is mainly controlled by the plant genetic makeup and environment under which the crop is cultivated. Therefore, it is necessary to divide the phenotypic variability observed into its heritable and nonheritable elements with suitable parameters such as heritability, genetic advance over per cent mean, phenotypic and genotypic coefficient of variations. A comparison of plant phenotype is the simplest approach to the characterization of genotypes and the assessment of genetic diversity; however, phenotypic evaluation is influenced by environment and may not distinguish between closely related accessions. Hence, the use of molecular markers have proven as valuable tools in the characterization and evaluation of genetic diversity within and between species and populations as they are less influenced by the environmental factors.

Material and Methods

The experiment on genetic diversity and molecular characterization in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.] was conducted in vegetable block of department of vegetable science, College of Horticulture, Bagalkote (Karnataka) during *kharif* 2019-20.

The experiment was laid out in Augmented design. Each treatment or genotype in an experiment was represented by three rows of two meter length and one meter breadth plot size with 24 plants.

Cluster bean germplasm contains 74 genotypes collected from the different regions of India formed the experimental material. As per the package of practice suggested by the UHS, Bagalkote, spacing and other intercultural operations were followed.

For recording the various observations, in each experimental genotype block five plants were selected randomly by avoiding border plants. For taking observations selected plants were tagged, and after the picking of tender green pods for vegetable purpose at weekly interval vegetable pod yield parameters were recorded from vegetable purpose block. Similarly five selected plants were tagged and all the pods were left for seed parameters in gum purpose block. The fully matured and dry pods are harvested for recording seed yield and other parameters.

The mean data were subjected to statistical analysis for estimating genetic parameters, phenotypic and genotypic coefficient of variation using formula suggested by Burton and Devane (1953) ^[3], heritability (h2BS) according to Falconer (1989) ^[5] and genetic advance over mean was predicted by formula given by Johnson *et al.* (1955) ^[11].

Results and Discussion

Analysis of variance

The ANOVA for twenty four characters are given in Table 3 revealed that, there was a high significant (both at P = 0.05 and P = 0.01) differences in the group of 74 genotypes of guar bean (Table 1).

The estimates of GCV, PCV, heritability (BS) and GAM for all studied characters are given in Table 2 and Table 3.

In the current research programme, high PCV and GCV were noticed for number of branches (90 DAS), number of clusters per plant, number of pods in a cluster, pod length, pod weight, vegetable pod yield of a plant, pod yield per plot, pod yield per hectare, dry pod yield per plant, weight of ten dry pods, seed yield per plant, seed yield per plot and gum content of a seed endosperm. The identical outcomes were also noticed by Hanchinamani (2004) ^[10], Malaghan (2012) ^[13], Rai *et al.*

(2012)^[17], Santhosha et al. (2017)^[21] and Reddy et al. (2018) ^[18] for number of branches (90 DAS), number of clusters in a plant, fresh pod yield per plant; Prakash et al. (2008) [16] and Santhosha et al. (2017)^[21] for number of pod in an cluster and seed yield per plant; Anandhi and Oommen (2007) [1], Manivannan and Anandakumar (2013) ^[14], Choyal et al. (2018)^[4] and Reddy et al. (2018)^[18] for pod length; Reddy et al. (2018)^[18] for pod weight; Santhosha et al. (2017)^[21] and Rishitha et al. (2019) [19] for pod yield per plot and pod yield per hectare; Choyal et al. (2018)^[4] for weight of ten dry pods and Hanchinamani (2004)^[10], Santhosha et al. (2017)^[21] and Girish et al. (2013)^[7] for gum content of seeds. This indicates the existence of wide genetic variability for these characters. However the traits like number of branches (90 DAS), number of pods per cluster, number of pods per plant, pod yield per plot, pod yield per hectare, dry pod yield per plant, ten dry pod weight, number of seeds per dry pod and seed vield per plot showed the maximum values for PCV than GCV indicating that there is a presence of high environmental influence for these traits. Selections based on phenotypic characters for these traits are not much effective.

Moderate PCV and GCV were noticed for plant height (90 DAS), pubescence and weight of hundred seeds, which indicates there are no much significant differences for these traits henceforth moderate amount of variation is present in these characters. The similar results are in line with Singh *et al.* (2010b) ^[24], Malaghan (2012) ^[13], Girish *et al.* (2013) ^[7], Manivannan and Anandakumar (2013) ^[14], Singh *et al.* (2016) ^[22], Goudar *et al.* (2017) ^[8], Kumar *et al.* (2017) ^[12], Santhosha *et al.* (2017) ^[12], Choyal *et al.* (2018) ^[4] and Rishitha *et al.* (2019) ^[19] for plant height and Singh *et al.* (2010b) ^[24] and Gowd *et al.* (2019) ^[9] for 100 seed weight.

Low PCV and GCV were recorded for germination per cent, pod breadth, days to first commencement of flowering, days to 50 per cent flowering and days taken for first vegetable pod harvest. These results are in compliance with Rishitha et al. (2019) ^[19] for germination; Girish et al. (2013) ^[7] and Santhosha et al. (2017) ^[21] for pod breadth; Girish et al. (2013) ^[7], Goudar et al. (2017), Choyal et al. (2018) ^[4] and Reddy et al. (2018)^[18] for days to 1st flowering; Kumar et al. (2017)^[12], Choyal et al. (2018)^[4], Reddy et al. (2018)^[18] and Rishitha et al. (2019) ^[19] for days to 50 per cent flowering and Singh et al. (2010b) ^[24], Saini et al. (2010) ^[20], Girish et al. (2013)^[7], Manivannan and Anandakumar (2013)^[14], Kumar et al. (2017)^[12], Santhosha et al. (2017)^[21], Choyal et al. (2018)^[4] and Rishitha et al. (2019)^[19] for days taken for first vegetable pod harvest. This showed the presence of narrow genetic base in the traits. Hence, variations has to be created in these parameters either using introduction procedure or hybridization with divergent parents for recovering transgressive segregants or with the help of mutation breeding.

Coefficient of variation designates only the range of variability existing in the germplasm for different traits but for the selection response, prediction and estimates of heritability are useful.

Very high (>80%) heritability was recorded for germination, pod length, pod weight, pubescence, days to first flowering, days to first vegetable pod harvesting, seed yield of a plant and gum content of seeds, indicates the less environmental influence on these characters. Similar findings were also noticed by Anandhi and Oommen (2007) ^[11], Rai *et al.* (2012) ^[17], Malaghan (2012) ^[13], Girish *et al.* (2013) ^[7], Santhosha *et al.* (2017) ^[21], Choyal *et al.* (2018) ^[4], Reddy *et al.* (2018) ^[18] and Gowd *et al.* (2019) ^[9] for pod length; Reddy *et al.* (2018)

^[18] for pod weight: Malaghan (2012), Girish *et al.* (2013) ^[7]. Singh et al. (2016) [22], Goudar et al. (2017) [8] and Santhosha *et al.* (2017)^[21] for days to first commencement of flowering; Prakash *et al.* (2008) ^[16], Singh *et al.* (2010a) ^[23], Singh *et al.* (2010b) ^[24], Manivannan and Anandakumar (2013) ^[14], Singh *et al.* (2016) ^[22], Kumar *et al.* (2017) ^[12], Santhosha *et al.* (2017)^[21], Gowd et al. (2019)^[9] and Rishitha et al. (2019)^[19] for days to first vegetable pod harvesting; Hanchinamani (2004) ^[10], Prakash *et al.* (2008) ^[16], Kumar *et al.* (2017) ^[12] and Choyal *et al.* (2018) ^[4] for seed yield per plant and Prakash *et al.* (2008) ^[16], Malaghan (2012) ^[13], Girish *et al.* (2013) ^[7], Santhosha *et al.* (2017) ^[21] and Reddy *et al.* (2018)^[18] for gum content of seed endosperm. Heritability along with genetic advance as per cent over mean may disclose the prevalence of particular components (non additive and additive) of genetic variance and thus assist in judging the accurate traits by effective selection *i.e.*, high heritability followed with high genetic advance as per cent over mean specifies the predominance of additive gene effect. Hence, selection would be more accurate for such traits. The high approximates of heritability (>60%) with high reading of genetic advance over mean (>20%) were noticed for traits like, plant height (cm) (90 DAS), number of branches (90 DAS), number of clusters in a plant, pod length, pod weight, pubescence, seed yield per plant, seed yield per plot and seed gum content. These outcomes are in comparable with the Hanchinamani (2004) ^[10], Anandhi and Oommen (2007) ^[1], Prakash *et al.* (2008) ^[16], Singh *et al.* (2010b) ^[24], Malaghan (2012) ^[13], Kumar *et al.* (2017) ^[12], Santhosha *et al.* (2017) ^[21], Reddy *et al.* (2018) ^[18] and Gowd *et al.* (2019) ^[9] for number of branches (90 DAS) and number of clusters per plant; Girish et al. (2013) [7], Manivannan and Anandakumar (2013) ^[14], Santhosha *et al.* (2017) ^[21], Reddy *et al.* (2018) ^[18] and Gowd et al. (2019) [9] for pod length; Prakash et al. (2008) ^[16] and Kumar et al. (2017) ^[12] for seed yield of an plant and Malaghan (2012)^[13], Girish et al. (2013)^[7], Santhosha et al. (2017)^[21] and Reddy et al. (2018)^[18] for seed gum content. These outcomes showed prevalence of additive constituents for these characters and hence for improving

these traits by direct selection method would be more effective.

High heritability contemporary with low genetic advance over mean denotes the non-additive gene action importance. High heritability complementary with low to moderate values of GAM were recorded for pod breadth, days to 1st opening of flower, days taken for 50 per cent flower opening and days to 1st harvesting of vegetable pods designates the prevalence of non-additive gene components and there may be a little selection response and these characters can be improved through heterosis breeding. These findings are in resemblance with answers of Rai *et al.* (2012) ^[17] and Choyal *et al.* (2018) ^[4] for pod breadth; Goudar *et al.* (2017) ^[8] and Choyal *et al.* (2018) ^[4] for days to 1st flowering; Kumar *et al.* (2017) ^[12], Choyal *et al.* (2018) ^[4] and Rishitha *et al.* (2019) ^[19] for days to 50 per cent flowering and days taken for first vegetable pod harvest.

Moderate to low heritability with high GAM denotes the importance of effects of additive genes. Moderate to low heritability with high values of GAM was recorded for number of pods in a cluster, number of pods in a plant, pod yield of a plot, pod yield per hectare and dry pod yield of a plant indicates that there is effect of additive genes and low heritability may be due to environmental effect for these characters and there can be better response to selection. Rishitha *et al.* (2019) ^[19] also got the same results for pod yield per plot and pod yield per hectare.

Low GAM with low heritability shows that, the traits have high environmental influence and selections would be ineffective. Moderate to low heritability collateral with low to moderate GAM were detected for traits like number of seeds in a dry pod and protein content in seed. Similar results were also recorded in Hanchinamani (2004) ^[10], Prakash *et al.* (2008) ^[16], Saini *et al.* (2010) ^[20], Manivannan and Anandakumar (2013) ^[14], Girish *et al.* (2013) ^[7] and Santhosha *et al.* (2017) ^[21] for number of seeds in an dry pod; Pathak *et al.* (2011) ^[15] for protein content.

		Mean sum of squares							
Sl. No.	Source of variation	Blocks Entries		(a) Checks	(b) Varieties	(c) Checks Vs Varieties	Error		
	Degrees of freedom	3	73	3	69	1	9		
		P	arameters						
1	Germination (%)	23.08*	74.97**	18.47	68.38**	731.04**	4.95		
2	Plant height (cm) (90 DAS)	133.06*	73.60*	116.48*	73.92*	274.98**	21.73		
3	Number of branches (90 DAS)	6.05*	8.10**	38.78**	6.99**	6.28	1.35		
4	Days to first flowering	3.29**	1.20**	2.08**	1.29**	2.51**	0.13		
5	Days to 50 (%) flowering	2.82**	1.40*	3.56**	1.40**	1.71*	0.28		
6	Days to first vegetable pod harvest	0.25**	0.54**	1.00**	0.54**	0.35**	0.10		
7	Number of clusters per plant	116.71**	41.47*	15.45	46.19**	56.50*	10.01		
8	Number of pods per cluster	28.48**	8.22	0.37	8.20	99.80**	3.27		
9	Number of pods per plant	4827.90**	830.87	3153.75**	910.50	477.24	423.13		
10	Pod length (cm)	7.09**	4.07**	40.18**	2.44**	28.95**	0.23		
11	Pod breadth (mm)	6.24**	0.37	1.67**	0.56*	1.18*	0.13		
12	Pod weight (g)	1.42**	0.55**	4.58**	0.38**	4.44**	0.03		
13	Pod yield per plant (g)	13324.13**	1877.43*	5457.85**	2312.10*	8.12*	519.20		
14	Pod yield per plot (kg)	2.88**	0.44*	0.91	0.50	1.25	0.28		
15	Pod yield per hectare (t/ha)	63.84**	11.09*	22.80	12.25	28.23	7.15		
17	Dry pod yield per plant (g)	107.04	340.90	166.94	342.41	826.93*	126.75		
18	Ten dry pod weight (g)	2.12*	1.97*	12.17**	1.34*	19.46**	0.47		
19	Number of seeds per dry pod	0.16	0.90	0.95	0.90	0.90	0.61		
20	Hundred seed weight (g)	0.45	0.60*	1.58**	0.45*	7.75**	0.15		
20	Seed yield per plant (g)	39.83**	69.46**	215.48**	61.49**	275.67**	2.44		
21	Seed yield per plot (g)	4100.50	9901.74**	52184.05**	8310.71*	6.50	2015.25		

 Table 1: Analysis of variance (ANOVA) for growth, yield and quality parameters in cluster bean

22	Pubescence	0.09**	0.08**	1.00**	0.04**	0.55**	0
23	Gum content (%)	88.57**	52.47**	123.79**	47.35**	426.31**	3.18
24	Protein content (g/100g)	0.02	0.1	0.23	0.09	0.12	0.06

*Significant @ 5% **Significant @ 1%

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SI. No.	Traits	Range		Mean	Co-efficient of Variability		h ² (broad sense)	GAM
		Minimum	Maximum		GCV (%)	PCV (%)	(%)	
		Growth a	nd yield para	meters				
1	Germination (%)	54.16	100.00	91.52	8.10	8.47	91.15	15.96
2	Plant height (cm) (90 DAS)	37.00	77.00	54.41	12.00	14.67	66.90	20.21
3	Number of branches (90 DAS)	0.00	9.00	4.10	54.89	62.21	77.85	99.76
4	Days to first flowering	23.00	27.00	24.23	4.05	4.33	87.47	7.80
5	Days to 50 (%) flowering	28.00	32.00	29.23	3.31	3.78	76.75	5.97
6	Days to first vegetable pod harvest	58.00	60.00	58.88	1.15	1.15	100	2.36
7	Number of clusters per plant	8.33	44.00	20.57	26.36	30.39	75.25	47.10
8	Number of pods per cluster	3.50	17.00	8.80	21.91	29.33	55.81	33.72
9	Number of pods per plant	44.00	174.00	118.72	17.22	24.55	49.22	24.89
10	Pod length (cm)	4.20	13.96	6.48	21.85	23.21	88.61	42.36
11	Pod breadth (mm)	6.00	10.04	7.64	7.90	9.30	72.17	13.82
12	Pod weight (g)	0.60	4.62	1.20	49.36	51.86	90.58	96.77
13	Pod yield per plant (g)	42.00	226.00	121.91	31.83	36.90	74.40	56.55
14	Pod yield per plot (kg)	0.67	3.69	1.97	22.18	35.64	38.73	28.43
15	Pod yield per hectare (t/ha)	3.38	18.47	9.95	21.37	34.91	37.50	26.96

GCV - Genotypic co-efficient variance h^2 – broad sense heritability

PCV - Phenotypic co-efficient of variance GAM - Genetic advance over mean

Table 3: Estimates of genetic parameters in cluster bean genotypes for seed yield and quality components

SI. No.	Traits	Range		Mean	Co-efficient of Variability		h ² (broad sense)	GAM			
		Minimum	Maximum		GCV (%)	PCV (%)	(%)				
Seed yield parameters											
1	Dry pod yield per plant (g)	9.50	67.63	28.58	43.04	56.09	58.87	68.03			
2	Ten dry pod weight (g)	2.31	9.95	3.79	23.90	30.74	60.43	38.26			
3	Number of seeds per dry pod	3.66	8.33	6.55	7.63	14.23	28.79	8.43			
4	Hundred seed weight (g)	2.70	6.22	4.15	12.59	15.88	62.94	20.58			
5	Seed yield per plant (g)	4.32	41.56	17.53	42.19	43.22	95.31	84.85			
6	Seed yield per plot (g)	38.88	519.20	223.76	32.54	38.23	72.44	57.05			
	Quality parameters										
1	Pubescence	0.00	1.00	0.91	19.55	19.55	100	40.27			
2	Gum content (%)	15.50	43.00	26.80	23.65	24.64	92.12	46.75			
3	Protein content (g/100g)	2.11	3.87	2.79	5.08	10.50	23.43	5.06			

GCV - Genotypic co-efficient variance h^2 – broad sense heritability

PCV - Phenotypic co-efficient of variance GAM – Genetic advance over mean

Conclusion

Prevalence of high level of additive constituents of genetic variance, presence of high heritability joint with high GAM and high PCV and GCV for the parameters number of branches at 90 DAS, number of clusters per plant, pod length, pod weight, pod yield per plant, seed yield per plant, seed yield per plot and gum content of cluster bean seed endosperm showed additive gene action therefore by the use of existing germplasm stock higher level of genetic improvement can be achieved for these traits through selection.

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