



Assessment of Genetic Variability for Yield, Yield Attributing and Quality Traits of Promising Genotypes of Cluster Bean [*Cyamopsis tetragonoloba* L. Taub.]

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ABSTRACT

The present study was conducted to evaluate twenty four (24) genotypes along with 1 check variety (Pusa Navbahar) of cluster bean during *kharif*, July–September, 2019 at College of Horticulture, Rajendranagar, Sri Konda Laxman Telangana State Horticultural University, Telangana, India to estimate variability, broad sense heritability and genetic advance for pod yield and yield attributing traits. The observations were recorded on various growth, yield and quality parameters. High estimates of GCV and PCV were recorded for plant height, number of branches plant⁻¹, pod length, pod weight and number of pods plant⁻¹. Protein content, gum content and fibre content recorded moderate to high PCV and GCV. High heritability coupled with high genetic advance as % of mean was observed for plant height, number of branches plant⁻¹, number of clusters plant⁻¹, days to maturity, number of pods plant⁻¹, pod length, pod girth, pod weight, number of seeds pod⁻¹, pod yield plant⁻¹, pod yield ha⁻¹, protein content, gum content and fibre content. High variability in conjunction with high genetic advance as % of mean indicating the predominance of additive gene action. These traits could be exploited through manifestation of dominance and epistatic components through heterosis breeding. The overall assessment showed that there was wide variability among cluster bean genotypes which has important implication for selection of cluster bean genotypes for yield and quality attributes.

KEYWORDS: Cluster bean, genetic advance, genetic variability, heritability

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1. INTRODUCTION

Cluster bean (*Cyamopsis tetragonoloba* L. Taub.) with diploid chromosome number $2n=14$, popularly known as guar. It is a self-pollinated crop belongs to the family Fabaceae. Guar originated in India and Pakistan and is characterized as a short day erect or bushy annual plant (Purseglove, 1981). It is a drought tolerant, warm season legume crop with deep and well-developed root system, cultivated mainly as rain fed crop in arid and semi-arid regions during rainy season for vegetable, galactomannan gum, forage and green manure. Guar enhances soil productiveness by fixing atmospheric nitrogen for its own necessities and also for the succeeding crop (Bewal et al., 2009). Guar can be successfully grown in soils where no other crops will survive. It can tolerate saline and moderately alkaline soils with pH ranging between 7.5 and 8.0 (Venkataratnam, 1973). The dicotyledonous seed of cluster bean from outside to interior consists of three major fractions, viz., the husk or hull 14–17%, endosperm 35–42% and germ 43–47%. Germ and hull portion termed as guar meal obtained after the extraction of gum is rich in protein 28.90–46.00%. The endosperm fraction of cluster bean seed is rich in galactomannan (polysaccharide) i.e., 16.80–30.90% (Lee et al., 2004, Rodge, 2008). The seed also contain 30–35% protein, 26.8–32.2% gum, 6.1–7.7% oil and 2.99–3.75% minerals. Seeds having large endosperm that contains galactomannan gum which forms gel in water commonly known as guar gum. Guar gum is commonly used as a stabilizer in many food products like ice-cream fruit beverages, chocolate, milk and milk products, cake toppings etc (Smith, 1976). These qualities have made it the most favoured crop for marginal farmers in the arid areas. Cluster bean gum has emerged as the most important agro-chemical, which is non-toxic, eco-friendly and Generally Recognized as Safe (GRAS) by Food and Drug Administration (FDA).

Due to long history of cultivation, selection and popularity of crops sufficient genetic variability has been generated. Germplasm characterization is essential to utilize and improve plant genetic resources in various breeding programs (Pidigam et al., 2019). Improvement of any crop depends on magnitude of genetic variability and the extent of heritability of economically important characters, though the part played by environment in the expression of such character also needs to be taken into account. Plant breeding programs focus on increasing crop yield in a wide range of growing conditions (Saidaiah et al., 2021a). Hence new genotypes must be characterized to assess the variability and identify promising genotypes which can be used in further breeding programmes (Munshi et al., 2000; Sarma and Roy, 1995, Sreelathakumary and Rajamony, 2004, Pidigam et al., 2021). Therefore, identification and

utilization of diverse genotypes is essential for breeding new cultivars in a desired direction (Aparna et al., 2014). The knowledge of variability provided by principal component analysis is helpful to select genetically and agronomically-important genotypes (Isong et al., 2017). Greater the variability in a population, there will be the greater chance for effective selection for desirable types (Vavilov, 1951). Generally, genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) are measured to study the variability. Heritability estimates give a measure of transmission of characters from one generation to another (Sabri et al., 2020, Saidaiah et al., 2021a, b, c). It helps to improve different characters simultaneously (Santhosha et al., 2017, Praveen et al., 2018, Reddy et al., 2018). After all, the trait improvements that can be made through direct selection are estimated by the availability of heritable variation (Khan et al., 2020). Phenotypic plant expression may not be actual genetic potential of genotypes since environment can affect genotype response, genetic analysis determine the breeding method to achieve maximum genetic advancement with available resources (Manjunathagowda and Anjanappa, 2021). Heritability and genetic advance helps in determining the influence of environment in expression of the characters and the extent to which improvement is possible after selection. Genetic advance provides information on expected gain resulting from selection of superior individuals (Lingaiah et al., 2019). The magnitude of heritable variation is the most important component in any breeding material as it has a close bearing in response to selection. Knowledge of the amount of variability and heritability aids the crop breeder for affecting improvement in any crop by choosing suitable breeding technique. Greater the variability in the available germplasm better would be the chances of selecting superior genotypes (Simmonds, 1962). According to Majumdar et al. (1969), the lowest difference in phenotypic and genotypic coefficients of variation indicates lowest environmental influence, while high difference indicates that environmental variation contributes a major part in the expression of the trait. Efficiency of selection can be determined by using genetic advance (Ashish et al., 2017). In the present study, by comparing phenotypic and genotypic coefficient of variation, most of the characters were low indicating the greater role of genetic factors. This clearly shows that phenotypic values can be used for selection.

2. MATERIALS AND METHODS

A set of 24 genotypes comprising of indigenous collections of cluster bean augmented from the ICAR-National Bureau of Plant Genetic Resources, Regional Station, Jodhpur, Rajasthan along with one check variety of cluster bean (Pusa Navbahar) from IARI, New Delhi



were evaluated in Randomized Block Design with three replications during *kharif*, July–September, 2019 at PG Research Block, College of Horticulture, Rajendranagar, Hyderabad. Hyderabad falls under semi-arid tropical climate, situated at an altitude of 542.3 m above the Mean Sea Level. Mean of Maximum and minimum temperature recorded during crop growing period was 30°C and 17.2°C respectively, mean of relative humidity recorded was 86.8 % in morning and 63.6% in the evening. Geographically, it lies at latitude of 17.19°N and longitude of 79.23°E. Each germplasm line was grown in a plot of 2×1.2 m² with spacing of 30×15 cm². The recommended dosage of N, P and K (10:50:50 kg ha⁻¹) was applied in the form of urea, single super phosphate and murate of potash respectively. Nitrogen was applied in two splits, the first dose as basal application and other split dose at 30 days after planting. The entire dose of phosphorus and potash were applied at the time of sowing as basal dose. Guar plant develops nodules on its roots, in which *Rhizobium* bacteria live and convert the free nitrogen of the atmosphere into a form of fertilizer which is absorbed by the roots of the plant. This symbiotic relation of the bacteria and root nodules is useful in saving cost of nitrogenous fertilizers. Therefore, before sowing the seeds are inoculated with these bacteria so that their population increases in the soil, with the growth of the plant. 10 per cent jaggery solution was prepared in boiling water. This sugar solution was allowed to cool. On cooling 3 to 4 packets of guar bacterial culture (*Rhizobium japonicum*) was mixed with solution to make a thin paste. This paste was coated over to the seed. Seed was dried under shade for 30 to 40 minutes before sowing. The plots were kept free of weeds and irrigated as and when required depending on soil moisture content. Need based plant protection measures were taken up to keep the plot free from pests and diseases. Harvesting was carried out by sickles. The border rows were harvested first and then bulked. The plants from net plot area were then harvested.

Observations were recorded on 5 competitive plants in respect of seventeen characters viz., plant height (cm), plant spread (cm), number of branches plant⁻¹, number of clusters plant⁻¹, number of pods plant⁻¹, days to maturity, pod length (cm), pod girth (mm), pod weight (g), pod yield plant⁻¹ (g), pod yield ha⁻¹ (t ha⁻¹), protein content (%), gum content (%) and crude fibre content (%) whereas days to first flowering and days to 50% flowering were recorded on plot basis. Gum, protein and fibre content were estimated by Association of official Analytical chemists, Kjeldahl method (Subbaiah and Asija, 1956) and Association of official Analytical chemists (1990) respectively. The mean data were subjected to statistical analysis for estimating genetic parameters, phenotypic and genotypic coefficient of variation using formula suggested by Burton (1953),

heritability (h²BS) and genetic advance over mean was predicted by formula given by Johnson et al. (1955).

3. RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed highly significant variation among the genotypes for yield and yield attributing traits in cluster bean, indicates sufficient variability existed for the characters studied and considerable improvement could be achieved.

Plant height exhibited very high phenotypic and genotypic variances (552.20 and 543.50) coupled with high PCV and GCV of 31.53% and 27.80% recorded respectively. High estimates of PCV and GCV recorded for this trait

Table 1: Analysis of variance for 17 characters in 25 cluster bean genotypes

Trait	Replication mean sum of square (df=2)	Treatment mean sum of square (df=24)	Error mean sum of square (df=48)
Plant height (cm)	1.95	1618	8.08
Plant spread (cm) N-S	1.53	42.98	0.71
Plant spread (cm) E-W	0.18	48.33	1.33
No. of branches plant ⁻¹	0.06	21.52	0.076
Days to first flowering	0.84	15.68	0.61
Days to 50% flowering	0.66	19.89	2.01
No. of clusters plant ⁻¹	0.34	27.82	0.25
No. of pods plant ⁻¹	0.42	1137	7.65
Days to maturity	2.25	24.05	0.94
Pod length (cm)	0.01	6.93	0.02
Pod girth (mm)	0.001	5.04	0.034
Pod weight (g)	0.005	0.27	0.018
No. of seeds pod ⁻¹	0.042	3.97	0.041
Pod yield plant ⁻¹ (g)	15.12	4756	34.64
Pod yield ha ⁻¹ (t ha ⁻¹)	16.66	5243.2	38.19
Crude protein content (%)	2.15	16.92	0.37
Gum content (%)	4.17	60.82	0.459
Crude fibre content (%)	0.14	6.03	0.113



indicates the presence of high degree of genetic variability and thus a greater scope for selection on the basis of this character. Similar results were reported in earlier findings of Anandhi and Oomen (2007), Rai et al. (2012) and Vir and Singh (2015). This trait showed high heritability (93.50), high genetic advance (47.50) and high genetic advance as % of mean (GA as % of mean or GAM) (57.8%). High heritability in conjunction with high GAM was observed for this trait which indicates the preponderance of additive gene action governing the inheritance of this character and offers the best possibility of improvement through simple selection procedure. Similar results were reported in earlier findings of Anandhi and Oomen. (2007), Rai et al. (2012), Vir and Singh (2015), Goudar et al. (2017), Santhosha et al. (2017) and Praveen et al. (2018).

High phenotypic and genotypic variances of 7.22 and 7.15 respectively were showed by number of branches plant⁻¹

and also showed high PCV (35.30%) and high GCV (35.10%) values. The results pertaining to this trait were in collaboration with Kapoor (2014), Vir and Singh (2015) and Santosha et al. (2017).

Low phenotypic and genotypic variances (5.60 and 5.02), low PCV (7.30%) and GCV (6.80%) values were recorded in cluster bean genotypes for days to first flowering. Days to first flowering showed high heritability (89.07) but low genetic advance (13.39) and moderate GA as % of mean (13.39%) were also recorded (Table 2). These results were similar with findings of Anandhi and Oomen (2007), Chaudhary et al. (2013) in dolichos bean, Goudar et al. (2017), Santhosha et al. (2017) and Praveen et al. (2018).

Moderate phenotypic and low genotypic variances 7.90 days and 5.90 days respectively and low PCV (6.56%) and GCV (5.67%) along with high heritability (74.72%), low genetic

Table: 2: Estimates of variability, heritability and genetic advance as percentage of mean for seventeen characters in 25 genotypes of cluster bean

Characters	Range		Mean	Variance		PCV (%)	GCV (%)	h ² (%)	Genetic advance	GA as % of mean
	Minimum	Maximum		Phenotypic	Genotypic					
Plant height (cm)	43.90	119.74	86.262	552.20	543.50	31.53	27.80	93.50	47.5	57.8
Plant spread (cm) N-S	15.90	28.59	23.5	14.70	14.10	16.34	15.90	95.17	7.54	32.04
Plant spread (cm) E-W	13.70	26.9	21.14	16.90	15.60	19.49	18.71	92.17	7.82	37.01
No. of branches plant ⁻¹	00	11.20	7.63	7.22	7.15	35.30	35.10	98.95	5.47	72.02
Days to first flowering	28.70	37.50	32.52	5.60	5.02	7.30	6.80	89.07	4.35	13.39
Days to 50% flowering	38.80	48.2	42.90	7.90	5.90	6.56	5.67	74.72	4.34	10.11
No. of clusters plant ⁻¹	9.70	22.30	16.09	9.40	9.14	19.03	18.80	97.35	6.16	38.29
No. of pods plant ⁻¹	43.20	112.60	72.70	384.2	376.5	26.93	26.60	98.01	39.57	54.38
Days to maturity	83.19	92.57	89.66	135.24	126.65	13.36	12.63	92.3	21.26	23.65
Pod length (cm)	6.30	13.70	7.60	2.32	2.30	20.25	20.1	98.76	3.1	40.72
Pod girth (mm)	4.80	10.30	7.90	1.70	1.67	16.42	16.26	97.98	2.63	33.15
Pod weight (g)	1.10	2.54	1.57	0.09	0.091	19.33	19.14	97.9	0.616	39.03
No. of seeds pod ⁻¹	5.60	10.90	7.40	1.32	1.30	15.61	15.37	96.95	2.32	31.17
Pod yield plant ⁻¹ (g)	59.50	208.5	115.60	1608.4	1573.8	34.67	34.3	97.8	80.83	69.89
Pod yield ha ⁻¹ (t ha ⁻¹)	62.40	218.90	121.4	1773.3	1735	34.67	34.30	97.85	84.8	69.89
Crude protein content (%)	15.30	24.10	20.58	5.80	5.50	11.70	11.40	93.6	4.68	22.70
Gum content (%)	18.50	33.16	25.70	20.58	20.12	17.63	17.4	97.7	9.13	35.52
Crude fibre content (%)	4.22	8.86	6.36	2.08	1.97	22.7	22.14	94.58	2.814	44.36

advance (4.34) and moderate GA as % of mean (10.11) estimates were registered by days to 50% flowering. These results were similar to the earlier findings of Singh et al. (2003), Goudar et al. (2017), Santhosha et al. (2017) and Praveen et al. (2018).

With respect to number of clusters plant⁻¹ moderate phenotypic and genotypic variances (9.40 and 9.14) with high PCV (19.03%) and GCV (18.80%) were registered along with high heritability (97.35%), low genetic advance (6.16) and high GA as % of mean (38.29) estimates (Table 2). Similar type of results were reported by and Revathi et al. (2017). High phenotypic (384.2) and genotypic variances (376.2), high PCV (26.93%) and GCV (26.60%) along with high heritability (98.01%), high genetic advance (39.57) and high GA as % of mean (54.38) were registered for number of pods plant⁻¹. These results were in accordance with Anandhi and Oomen (2007), Vir and Singh (2015) and Reddy et al. (2018).

Low phenotypic and genotypic variances of 2.32 and 2.30 respectively along with high PCV (20.25%) and GCV (20.10%) values, high heritability (98.76%), low genetic advance (3.1) and high GA as % of mean (40.72) estimates were observed for pod length. These results were reported in earlier findings of Rai et al. (2012), Chaudhary et al. (2013) in dolichos bean and Reddy et al. (2018).

For pod girth very low phenotypic and genotypic variances of 1.70 and 1.67 respectively with moderate PCV (16.42%) and GCV (16.26%) values. The high heritability (97.98%), low genetic advance (2.63) and high GA as % of mean (33.15) were also recorded. These results are similar reports with Rai et al. (2012), Praveen et al. (2018) and Reddy et al. (2018).

With respect to number of seeds pod⁻¹, low phenotypic (1.32) and genotypic (1.30) variances, moderate PCV (15.61%) and GCV (15.37%) along with high heritability (96.95%), low genetic advance (2.32) and high GA as % of mean (31.17) estimates were observed. These results are consonance with the findings of Rai et al. (2012) and Vir and Singh. (2015), Jitendra et al. (2016), Praveen et al. (2018) and Reddy et al. (2018).

With respect to pod yield plant⁻¹ highest phenotypic (1608.4) and genotypic (1573.8) variances, high PCV (34.67%) and GCV (34.30%) were observed along with high heritability (97.80%), high genetic advance (80.83) and high GA as % of mean (69.83) estimates. These results are similar with the earlier findings of Saini et al. (2010), Rai et al. (2012), Jitender et al. (2014). Whereas high phenotypic (1773.3) and genotypic variances (1735.0) were recorded for pod yield ha⁻¹ with high PCV (34.67%) and GCV (34.30%). This trait also showed high heritability (97.85%), high genetic advance (84.8) and high GA as % mean (69.89).

These results were similar with Rai et al., 2012, Santhosha et al. (2017), Praveen et al. (2018) and Reddy et al. (2018).

Low phenotypic and genotypic variance values were recorded as 5.80 and 5.50 respectively for protein content (%) with moderate PCV (11.70%) and GCV (11.40%). These results are similar with earlier findings of Malaghan et al., 2013. The high heritability (93.6%), low genetic advance (4.68) and high GA as % of mean (22.70) were also recorded. These results were confirmed by Malghan et al. (2013) and Girish et al. (2012). Another quality parameter i.e., gum content in % recorded high phenotypic and genotypic variances of 20.58 and 20.12 respectively with moderate PCV (17.63%) and GCV (17.40%) values along with high heritability (97.7 %), low genetic advance (9.13) and high GA as % of mean (35.52) (Table 2). These results were confirmed by Malaghan et al. (2013), Chaudhary et al. (2013) in dolichos bean, Santhosha et al. (2017), Praveen et al. (2018) and Reddy et al. (2018).

Low phenotypic and genotypic variances were 2.08 and 1.97 respectively with high PCV (22.70%) and GCV (22.14%) were showed by fibre content along with high heritability (94.58%), while low genetic advance 2.814 and high GA as % of mean (44.36) (Table 2). These results are confirmed with Kapoor et al. (2014), Santhosha et al. (2017), Praveen et al. (2018) and Reddy et al. (2018).

High estimates of GCV and PCV were recorded for plant height, number of branches plant⁻¹, pod length, pod weight, number of pods plant⁻¹, pod yield plant⁻¹, pod yield ha⁻¹ and crude fibre content. The magnitude of phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation indicating the influence of environmental factors in their expression.

Moderate estimates of GCV and PCV were recorded for plant spread, number of clusters plant⁻¹, days to maturity, pod girth, number of seeds pod⁻¹, crude protein content and gum content. Low estimates of GCV and PCV were recorded for days to first flowering and days to 50% flowering.

Considering heritability in broad sense along with genetic advance may reveal the prevalence of specific components (additive or non-additive) of genetic variance and thus, helps in judging the effectiveness of selection for the trait more accurately. The high estimates of heritability coupled with high values of genetic advance over mean (GAM) were observed for the characters viz., plant height, plant spread, number of branches plant⁻¹, number of clusters plant⁻¹, days to maturity, number of pods plant⁻¹, pod length, pod girth, pod weight, number of seeds pod⁻¹, pod yield plant⁻¹, pod yield ha⁻¹, protein content, gum content and fibre content indicating that these traits were under the strong influence of additive gene action. Hence, simple selection based on

phenotypic performance of these traits would be more effective.

High heritability coupled with moderate genetic advance as % of mean observed for days to first flowering and days to 50% flowering. Hence, simple selection based on phenotypic performance of these traits would be more effective. High variability in conjunction with high genetic advance as % of mean indicating the predominance of additive gene action. These traits could be exploited through manifestation of dominance and epistatic components through heterosis breeding. Moderate heritability coupled with moderate genetic advance as % of mean observed for days to first flowering. Hence, the breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes, especially in case of cluster bean.

4. CONCLUSION

Higher heritability was recorded by all the traits hence, higher degree of genetic improvement for these traits can be achieved through selection using the existing germplasm stock. These results indicated that these characters were under the influence of additive gene action. The breeder should adopt suitable breeding methodology to utilize both additive and non-additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes, in case of cluster bean.

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