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Extent of Genetic Variability for Quantitative Traits in Indian Clusterbean Germplasm [*Cyamopsis tetragonoloba* (L.) Taub]

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ABSTRACT

Background: Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] (2n=2x=14) is an under exploited legume belonging to the family *Fabaceae*. Clusterbean is a versatile legume crop cultivated mostly as vegetable, for the extraction of guar gum, animal feed cover crop. Clusterbean is a drought tolerant, hardy, deep rooted annual legume. To assess the nature and magnitude for genetic variability, heritability and genetic advance for seed yield and component characters that are useful for an effective selection programme, the present study was under taken.

Methods: A set of 40 clusterbean genotypes were evaluated during *Kharif* 2019 in in randomized complete block design with four replications at Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India.

Result: The highest estimates of genotypic coefficient of variation was observed for the number of branches per plant followed by seed yield per plant, days to flowering and number of clusters per plant indicating the presence of wide genetic variability for these characters. High estimates of heritability coupled with high genetic advance were observed for number of branches per plant, seed yield per plant and days to flowering indicating the presence of additive genes and less environmental influence on the characters and existence of sufficient heritable variation and wider scope for effective selection.

Key words: Clusterbean, Genetic variability, Genetic advance, Heritability.

INTRODUCTION

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] (2n=2x=14) is an under exploited legume belonging to family *Fabaceae*. It is short day self-pollinated crop (Undersander *et al.*, 1991), commonly known as guar, chavli kayi, guari, khutti *etc*. The word "guar" has derivation from the Sanskrit word "Gau-ahaar" which means cow food (Bhosle and Kothekar, 2010). Clusterbean is a versatile legume crop cultivated mostly as animal feed, green manure (Chudzikowski, 1971 and Siddaraju *et al.,* 2010), green leaves as fodder, vegetable and cover crop (Arora and Pahuja, 2008). Clusterbean is a drought resistant, hardy, deep rooted annual arid legume. The powder made from husked clusterbean seeds is known as guar gum which finds use in drilling companies for making high viscosity water to extract shale oil and natural gas. Presently the Shale gas extracting companies are buying large quantity of guar gum from Rajasthan, Gujarat, Haryana and Punjab and it is grown as industrial crop for its endospermic gum (30-35%). Tender pods are nutritionally rich in energy (16 kcal), moisture (81 g), protein (3.2 g), fat (1.4 g), carbohydrate (10.8 g), Vitamin A (65.3 IU), Vitamin 'C' (49 mg), calcium (57 mg) and iron (4.5 mg) for every 100 g of edible portion (Kumar and Singh, 2002).

Vavilov (1951) considered India as the center of diversity for guar, although no wild species was reported in India. A fairly-large number of landforms and cultivars are available in India. The knowledge of genetic variability in the available germplasm is a pre-requisite for effective selection of superior genotypes (Chatale, 2015). It is also necessary to partition the observed phenotypic variability into its heritable and non-heritable components to understand the extent of influence on economically important traits and accordingly apply suitable selection method.

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MATERIALS AND METHODS

The experimental material consisted of 40 clusterbean genotypes were obtained from Pulses Research Station, S.D. Agricultural University, Sardarkrushinagar, Gujarat, India (Table 1).

These germplasm were evaluated in randomized complete block design with four replication at the Agronomy Instructional Farm, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat during *Kharif* 2019. The sowing was done on 5thJuly, 2019. Each genotype was accommodated in a single row of 4 m length with a spacing 45 cm between rows and 15 cm between plants. All the recommended production and protection practices were followed to raise the good crop of clusterbean. The observations on twelve quantitative traits *viz.*, days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), test weight (g), protein content (%), gum content (%) and seed yield per plant(g) were recorded at appropriate crop growth stage as suggested by Curtis *et al*. (2020). Five plants from each genotype were selected at random for recording observations except days to 50% flowering and days to maturity which were recorded on plot basis. After the harvest, 1000 matured and dried seeds were drawn from each germplasm and its test weight was recorded. Protein content (%) was estimated by Instalab 600 NIR analyzer and expressed in percentage whereas, gum estimation involves the extraction and purification of galactomannan, which is then alcohol precipitated, dried and weighted. A rapid and accurate method developed by Pablyana *et al.* (2009) was used. The data recorded for all the characters were subjected to analysis of variance as suggested by Panse and Sukhatme (1978). The coefficient of phenotypic and genotypic variation was calculated using the formula suggested by Burton (1952). Heritability in broad sense (h^2BS) was calculated as per Allard (1961). The expected genetic advance as expressed in per centage of mean was calculated by the method suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The experimental material consisted of 40 clusterbean genotypes were obtained from Pulses Research Station, S.D. Agricultural University, Sardarkrushinagar, Gujarat, India. Among them some are indigenous collection, local collection and released varieties (Table 1).

The analysis of variance (Table 2) revealed highly significant mean square due to genotypes for all the characters studied, suggesting the presence of a sufficient amount of variability in the material used.

The estimates of GCV, PCV, h^2BS, GAM are given in Table 2. The GCV % and PCV % were the highest for number of branches per plant followed by seed yield per plant, days to 50 % flowering and number of clusters per plant and plant height. That was indicating the presence of high variability in the population and therefore more scope for selection. Simple selection based on the phenotypes of these traits would be effective for bringing further improvement. These results are in accordance with the findings of Rishitha *et al.* (2019), Choyal *et al.* (2018) and Meghana *et al.* (2019) for the number of branches per plant, number of clusters per plant, seed yield per plant and Meghana *et al.* (2019) for days to flowering.

Moderate estimates of genotypic and phenotypic coefficient of variation were observed for days to maturity, test weight and number of pods per plant. While the lowest estimates of genotypic and phenotypic coefficient variation were observed for gum content, protein content, pod length and number of seeds per pod, thus indicating lesser variability in the population and lesser scope of selection. These results is in conformity with the findings of Santhosha *et al.* (2017) for test weight, Patel *et al.* (2018) for the number of pods per plant, Rishitha *et al.* (2019) for the number of seeds per pod and Panchta and Khatri (2017) for pod length.

In the present study, the differences between PCV and GCV were relatively low for all the traits indicating the lesser environmental influence on these characters.

In a general sense, heritability specifies the proportion of the total variability that is due to genetic causes or the ratio of genotypic variance to the total variance. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1960). High heritability was recorded for characters such as days to maturity, number of branches per plant, days to flowering, gum content, seed yield per plant, plant height, pod length, protein content, test weight and number of pods per plant (Table 2) suggesting little environmental influence on these characters. These characters also showed lesser difference between PCV and GCV and thus selection based on the phenotype of these traits would be rewarding. The present findings are in accordance with results of Patel *et al.* (2018), Rishitha *et al.* (2019) and Meghana *et al.* (2019) for days to flowering, while Meghana *et al*. (2019) for days to maturity and number of branches per plant, Santhosha *et al.* (2017) for seed yield per plant, pod length and protein content, Shobiya *et al.* (2019) for plant height, Rishitha *et al.* (2019) for the number of pods per plant and test weight, Moderate heritability was found for the characters number of seeds per pod and number of clusters per plant. Similar type of results were reported by Kumar and Ram (2015) and Revathi *et al*. (2017). It indicates that PCV is higher than GCV; there is a little influence of environment on the expression of these characters. Selection for improvement of such characters will be rewarding.

The high heritability coupled with high genetic advance as per centage of mean was observed for traits *viz*., days to maturity, number of branches per plant, days to flowering, seed yield per plant, plant height and test weight, 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 Rai *et al*. (2012), Vir and Singh (2015) and Reddy *et al*. (2019). High heritability coupled with moderate genetic advance was observed for number of pods per plant. As these traits are largely controlled by additive gene action simple selection may be practiced for improving them.

High heritability coupled with low genetic advance was recorded for traits such as gum content, number of seeds per pod and protein content. This could be attributed to lesser magnitudes of genetic variability present in these characters

Table 1: List of germplasm.

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotype
1	IC 41057	11	IC 113537	21	GG 1609	31	GG 1806
2	IC 102828	12	IC 116629	22	GG 1612	32	GG 1807
3	IC 102853	13	IC 116633	23	GG 1702	33	GG 1808
4	IC 113269	14	IC 116645	24	GG 1703	34	GG 1809
5	IC 113289	15	IC 311444	25	GG 1709	35	GG 1810
6	IC 113294	16	IC 319038	26	GG 1710	36	GAUG 1304
7	IC 113298	17	IC 373497	27	GG 1801	37	GAUG1305
8	IC 113427	18	GG 1	28	GG 1803	38	GAUG 1501
9	IC 113432	19	GG 2	29	GG 1804	39	GAUG 1502
10	IC 113498	20	GG 1607	30	GG 1805	40	GAUG 1507

Note: All the genotypes were obtained from Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, India.

Table 2: Genetic parameters of variation for seed yield and its contributing characters in clusterbean.

Character	MSS	Mean	Range	PCV (%)	GCV (%)	h^2(BS) (%)	GA	GAM
	Genotypes							
Days to 50% flowering	187.17**	32.88	22.75-55.25	21.15	20.69	95.73	13.71	41.69
Days to maturity	361.73**	80.15	64.25-112.75	12.00	11.82	96.83	19.19	23.95
Plant height (cm)	490.94**	72.72	51.95-103.43	15.72	15.07	91.91	21.64	29.76
Number of branches per plant	4.83**	3.29	1.10-6.05	33.95	33.24	95.89	2.21	67.06
Number of clusters per plant	2.64**	4.85	2.30-7.35	20.29	15.43	57.82	1.17	24.17
Number of pods per plant	7.31**	13.61	10.70-17.23	11.72	9.16	61.17	2.00	14.77
Pod length(cm)	0.74**	5.04	4.01-5.75	9.06	8.38	85.42	0.80	15.95
Number of seeds per pod	0.62**	7.22	6.30-8.25	6.62	4.99	56.76	0.56	7.74
Test weight (g)	0.37**	2.47	1.95-3.41	13.48	11.88	77.96	0.54	21.64
Protein content (%)	3.39**	23.74	22.41-25.62	4.05	3.82	89.22	1.77	7.43
Gum content (%)	6.69**	26.34	24.35-29.32	4.99	4.88	95.36	2.59	9.81
Seed yield per plant (g)	1.39**	2.51	1.81-4.87	24.28	23.28	91.95	1.15	45.99

MSS is mean sum of square, GCV (%) and PCV (%) are genotypic and phenotypic coefficient of variance, respectively $h^2_{(BS)}$ (%), GA and GAM are broad sense heritability, genetic advance and genetic advance expressed as per cent of mean, respectively.

and therefore, phenotypic selection based on this trait may not yield dividends. However, these traits could be improved by inter-mating superior genotypes followed by selection in the segregating generations.

CONCLUSION

In the present study higher GCV, PCV, heritability coupled with high genetic advance was recorded for the traits such as number of branches per plant, seed yield per plant and days to 50% flowering, indicated the role of additive gene action. Hence, simple phenotypic selection from the existing germplasm is suggested for further improvement.

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