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Assessment of genetic variability, correlation and path coefficient for quantitative and biochemical traits of clusterbean [*Cyamopsis tetragonoloba* (L.) taub] accessions

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Abstract

Fifty Clusterbean genotypes were evaluated to estimate variability parameters, association between seed yield and its attributes along with direct indirect effect during kharif 2019 at SDAU, Sardarkrushinagar, Gujarat. The high GCV, PCV as well as high heritability coupled with high genetic advance were recorded for number of fruiting branch per plant, number of cluster on main stem, number of cluster per plant, number of pod on main stem and number of pod per plant indicated additive gene effects. Seed yield exhibited highly significant and positive correlation with plant height, number of cluster per plant, number of pod per plant and 100 seed weight while, non-significant and negative association with days to 50 per cent flowering, pod length, endosperm percentage and protein content. Seed yield possessed high and positive direct effects *via*. days to 50 per cent flowering, number of cluster per plant, number of pod per plant and 100 seed weight and endosperm percentage. Thus, more weightage is given to those genotypes which possess early flowering, more number of cluster on main stem, number of cluster and number of pod per plant and high 100 seed weight for improve the efficiency of selection.

Keywords: Clusterbean, genetic variability, traits interrelationship and path co-efficient

Introduction

Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub] is a deep rooted legumes plant belongs to the family *Leguminosae* and subfamily *Papilionaceae* popularly known as 'guar'. It is settled as a high-valued cash crop mainly cultivated in the arid and semi-arid regions of north western states of India such as Rajasthan, Gujarat, Haryana, Punjab, Uttar Pradesh, Madhya Pradesh and Tamil Nadu during *kharif* and summer season (Rai and Dharmatti, 2014) ^[13]. The haploid and diploid chromosome number of clusterbean is n = 7 and 2n = 14. Clusterbean is completely autogamous crop due to its cleistogamous nature.

Cluster bean can be used for vegetable, high protein cattle feed/fodder or green manure purpose (Rai and Dharmatti, 2014)^[13]. Gum obtained from guar seeds is a biologically produced non-toxic, eco-friendly and safe agro-chemical which is used in paper, food, mining, cosmetics textile and oil across the world. The gum is produced primarily from grind of endosperm after dehusking the seed (Sabahelkheir *et al.*, 2012)^[15].

The success of a particular crop breeding depends on the extent and the magnitude of variability existing in the germplasm. The information on genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance provide an exact picture of variability in the population helps in designing appropriate breeding methodology. The knowledge of association of various quantitative characters would be immense help to breeders in planning and executing breeding programme.

Materials and Methods

The experiment was conducted at Agronomy Instructional Farm, S. D. Agricultural University, Sardarkrushinagar in which fifty clusterbean genotypes were evaluated in randomized block design with four replications during *kharif* – 2019. Each genotype was represented by single row of 45 and 15 cm inter and intra row distances, respectively. Observations were recorded on five randomly selected competitive plants of each genotype from each replication for morphological traits *viz.* plant height, number of fruiting branch per plant, number of cluster on main stem, number of cluster per plant, cluster length, number of pod on main stem,

number of pod per plant, pod length, number of seed per plant, 100 seed weight, seed yield per plant, except days to 50 per cent flowering, days to 80 per cent maturity were visually assessed by a single observation on a group of plants. The biochemical parameters such as endosperm percentage, gum content and protein content were estimated from seed. Method developed by Das et al. (1977)^[4] and Lowry et al. (1951) [8] were used for estimation of Gum and Protein content (%), respectively from guar seed. Phenotypic and genotypic coefficient of variation were calculated as per formula suggested by Burton (1952)^[3]. Heritability and Genetic advance as percentage of mean were computed in per cent using formula given by Allard (1960)^[1]. The phenotypic and genotypic correlations worked out as per procedure suggested by Hazel et al. (1943) [7]. The path coefficient analysis was carried-out according to the method suggested by Wright (1921)^[17].

Results and Discussion

Analysis of variance revealed significant difference among the genotypes for all the traits, which indicating the existence of vast variability in the genotypes and there may be a scope for improvement of these traits through selection (Table 1). Patel et al. (2018) [11], Meghana et al. (2019) [10], Deepashree et al. (2021)^[5] and Makwana et al. (2021)^[9] reported higher genetic variability for yield and its attributing traits in cluster bean genotypes. The magnitude of PCV was higher than the GCV for all the characters indicating the influence of environment on inheritance of these traits. The traits namely, number of fruiting branch per plant, number of cluster on main stem, number of cluster per plant, number of pod on main stem and number of pod per plant were exhibited high GCV and PCV value, while plant height, pod length, 100 seed weight, gum content and protein content showed medium magnitude of GCV and PCV (Table 2).

The heritability estimates were high for the characters *viz.*, days to 50 per cent flowering, plant height, number of fruiting branches per plant, number of cluster on main stem, number of cluster per plant, cluster length, number of pod on main stem, days to 80 per cent maturity, 100 seed weight, endosperm percentage, gum content and protein content stated that not as much environmental effect on expression of these

characters. The characters namely, number of fruiting branch per plant, number of cluster on main stem, number of cluster per plant, cluster length, number of pod on main stem, 100 seed weight, endosperm percentage and gum content exhibited high heritability coupled with high genetic advance indicated that heritability in genotypes were due to additive gene effects (Table 2). Thus, selection may be effective for the improvement in such characters of genotypes. Similar results were observed by Santhosa *et al.* (2017) ^[16], Meghana *et al.* (2019) ^[10], Gowd *et al.* (2019) ^[6], Makwana *et al.* (2021) ^[9] and Deepashree *et al.* (2021) ^[5].

Days to 50 per cent flowering had significant positive association with days to 80 per cent maturity. Hence, earliness in flowering of clusterbean genotypes leads to early maturity. The characters like, plant height, number of cluster on main stem, number of cluster per plant, number of pod on main stem, number of pod per plant and 100 seed weight exhibited highly significant and positive correlation with seed yield per plant. Thus, improvement in such characters also leads to increment in seed yield per plant of clusterbean genotypes. Seed yield per plant showed non-significant and negative association with days to 50 per cent flowering, pod length, endosperm percentage and protein content (Table 3). Biochemical traits like, endosperm percentage and gum content exerted highly significant and positive correlation with each other, while highly significant and negative correlation with protein content.

Path analysis revealed that the traits likes, days to 50 per cent flowering, number of cluster on main stem, number of cluster per plant, number of pod per plant, number of seeds per pod, 100 seed weight and endosperm percentage possessed high and positive direct effects while, Number of pod on main stem, number of fruiting branch per plant and cluster length showed high and negative direct effect towards seed yield per plant (Table 4). Endosperm percentage and gum content exerted negligible and positive indirect effects on seed yield through plant height, number of fruiting branch per plant, number of cluster on main stem, number of cluster per plant and days to 80 per cent maturity. The results are in accordance with these reported earlier by Rai and Dharmati (2014) ^[13], Boghara *et al.* (2016) ^[2], Reddy *et al.* (2018) ^[14], Patel *et al.* (2018) ^[11] and Preeti and Prasad (2018) ^[12].

Sr. No.	Characters	Source of variation							
Sr. No.	Characters	Replications	Genotypes	Error					
1	Days to 50% flowering	4.57	64.29**	2.47					
2	Plant height	20.82	211.07**	8.62					
3	Number of fruiting branch per plant	0.47	11.57**	0.19					
4	Number of cluster on main shoot	1.24	8.21**	0.67					
5	Number of cluster per per plant	3.61	11.74**	1.41					
6	Cluster length	1.75	5.10**	0.61					
7	Number of pod on main shoot	5.51	55.36**	2.48					
8	Number of pod per plant	38.18	60.91**	14.61					
9	Pod length	0.79	1.67**	0.36					
10	Days to 80 per cent maturity	1.57	51.88**	1.81					
11	Number of seed per pod	0.88	1.52**	0.35					
12	100 seed weight	0.05	0.97**	0.02					
13	Seed yield per plant	2.79	4.28**	1.07					
14	Endosperm percentage	5.02	102.49**	1.89					
15	Gum content	1.67	53.31**	0.63					
16	Protein content	0.22	2.81**	0.09					

Table 1: Analysis of variance for different characters in clusterbean

** Significant at 1% level of significance

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Table 2: The genotypic and phenotypic variances and other genetic parameters for different characters in clusterbean

Sr. No.	Characters	Grand Mean	σ^{2} g	σ^{2} p	GCV (%)	PCV (%)	$h^{2}_{bs}(\%)$	GA	GAM (%)
1	DF	44.63	15.45	17.92	8.81	9.49	86.22	7.52	16.85
2	PH	69.66	50.61	59.23	10.21	11.05	85.45	13.55	19.45
3	NFBP	1.80	2.85	3.03	93.91	96.97	93.79	3.37	187.34
4	NCMS	4.60	1.88	2.55	29.85	34.74	73.82	2.43	52.83
5	NCPP	6.22	2.58	3.99	25.85	32.13	64.71	2.66	42.83
6	CL	5.53	1.11	1.78	19.04	24.13	62.26	1.71	30.95
7	NPMS	15.24	13.22	15.70	23.86	26.00	84.23	6.87	45.11
8	NPPP	16.80	11.57	26.19	20.25	30.47	44.20	4.66	27.74
9	PL	4.95	0.33	0.69	11.60	16.73	48.03	0.82	16.56
10	DM	95.76	12.52	14.33	3.69	3.95	87.37	6.81	7.11
12	NSPP	6.49	0.29	0.64	8.35	12.35	45.68	0.75	11.62
13	100 SW	3.12	0.24	0.26	15.65	16.26	92.67	0.97	31.05
14	EP	32.50	25.15	27.04	15.43	16.00	93.00	9.96	30.65
15	GC	22.14	13.17	13.80	16.39	16.78	95.43	7.30	32.99
16	PC	6.01	0.68	0.77	13.70	14.59	88.20	1.59	26.51
17	SYPP	4.63	0.80	1.87	19.35	29.57	42.80	1.21	26.07

DF= Days to 50 per cent flowering, PH= Plant height (cm), NFBP= Number of fruiting branch per plant, NCMS= Number of cluster on main stem, NCPP= Number of cluster per plant, CL= Cluster length (cm), NPMS= Number of pod on main stem, NPPP= Number of pod per plant, PL= Pod length (cm), DM = Days to 80 per cent maturity, NSPP= Number of seed per plant, 100 SW= 100 seed weight (g), SYPP= Seed yield per plant (g), EP= Endosperm percentage, GC= Gum content (%), PC= Protein content (%)

Table 3: Genotypic and phenotypic correlations among different characters in clusterbean

	DF	РН	NFBP	NCMS	NCPP	CL	NPMS	NPPP	PL	DM	NSPP	100 SW	EP	GC	PC	SYPP
	r _n 1	-0.04	0.12	-0.22**	-0.13	0.11	-0.25**	-0.12	-0.17*	0.29**	0.09	-0.09	-0.01	-0.12	0.28**	-0.10
DF	r_{σ} 1	-0.04	0.14	-0.28	-0.20	0.18	-0.33*	-0.26	-0.26	0.32*	0.15	-0.11	-0.01	-0.14	0.32*	-0.26
PH	r _p	1	0.02	0.30**	0.16*	0.14*	0.36**	0.23**	0.04	-0.24**	0.05	0.10	0.12	0.26**	-0.12	0.23**
	rg	1	0.02	0.39**	0.24	0.21	0.39**	0.43**	0.09	-0.29*	0.10	0.11	0.12	0.28*	-0.14	0.42**
NFBP	rp		1.00	-0.35**	0.39**	-0.45**	-0.23**	0.11	-0.05	0.23**	0.14*	0.18**	-0.04	-0.04	0.20**	0.17*
	rg		1.00	-0.38**	0.52**	-0.62**	-0.24	0.22	-0.12	0.25	0.18	0.20	-0.04	-0.04	0.22	0.37*
NCMS r	rp			1.00	0.55**	0.28**	0.76**	0.49**	-0.03	0.05	-0.05	0.12	0.12	0.19**	-0.29**	0.42*
	rg			1.00	0.58**	0.50**	0.96**	0.73**	0.01	0.06	-0.07	0.12	0.14	0.23	-0.35*	0.61*
NCPP	rp				1.00	-0.13	0.60**	0.62**	-0.07	0.21**	0.09	0.19**	0.09	0.15*	-0.16*	0.57**
NCH	rg				1.00	-0.06	0.68**	0.86**	-0.06	0.30*	0.07	0.22	0.12	0.18	-0.18	0.75**
CL	rp					1.00	0.27**	-0.01	-0.01	-0.09	0.12	-0.14*	0.14	0.16	-0.23**	-0.05
CL	rg					1.00	0.39**	0.05	-0.01	-0.12	0.33*	-0.18	0.17	0.22	-0.26	0.13
NPMS	rp						1.00	0.63**	-0.06	0.00	0.01	0.11	0.09	0.21**	-0.32**	0.53*
1011010	rg						1.00	0.83**	-0.07	0.02	-0.04	0.12	0.10	0.24	-0.36**	0.60*
NPPP	rp							1.00	-0.06	0.22**	0.00	0.14	-0.03	0.10	-0.07	0.80**
	rg							1.00	-0.13	0.38**	0.01	0.21	-0.03	0.17	-0.09	0.85**
PL	rp								1.00	-0.05	0.26**	-0.19**	-0.06	0.05	-0.11	-0.03
	rg								1.00	-0.06	0.37**	-0.28*	-0.09	0.08	-0.17	-0.17
DM	r _p									1.00	-0.01	-0.09	-0.02	-0.17*	0.15*	0.11
	rg									1.00	-0.04	-0.11	-0.02	-0.18	0.17	0.18
NSPP	rp										1.00	-0.12	-0.05	0.13	-0.20**	0.22**
	rg										1.00	-0.17	-0.10	0.24	-0.34*	0.27
100 SW	r _p											1.00	-0.02	0.05	0.07	0.48**
	r _g											1.00	-0.03	0.04	0.08	-0.04
EP	r _p												1.00	0.64**	-0.43***	-0.04
	r _g												1.00	1.00	-0.62**	0.14*
GC	r _p r _g													1.00	-0.62**	0.14*
														1.00	1.00	-0.08
PC	r _p rg														1.00	-0.20
	0														1.00	1
SYPP	r _p rg															1
	•g															1

DF= Days to 50 per cent flowering, PH= Plant height (cm), NFBP= Number of fruiting branch per plant, NCMS= Number of cluster on main stem, NCPP= Number of cluster per plant, CL= Cluster length (cm), NPMS= Number of pod on main stem, NPPP= Number of pod per plant, PL= Pod length (cm), DM = Days to 80 per cent maturity, NSPP= Number of seed per plant, 100 SW= 100 seed weight (g), SYPP= Seed yield per plant (g), EP= Endosperm percentage, GC= Gum content (%), PC= Protein content (%)

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Table 4: Direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in clusterbean

	DF	PH	NFBP	NCMS	NCPP	CL	NPMS	NPPP	PL	DM	NSPP	100 SW	EP	GC	PC	R _g (SYPP)
DF	0.05	-0.02	-0.11	-0.20	-0.13	-0.06	0.51	-0.32	0.06	-0.09	0.09	-0.06	-0.00	0.01	0.01	-0.26
PH	-0.02	0.01	-0.02	0.28	0.15	-0.07	-0.61	0.53	-0.02	0.08	0.06	0.06	0.02	-0.03	-0.00	0.42**
NFBP	0.07	0.01	-0.78	-0.28	0.33	0.22	0.37	0.27	0.03	-0.07	0.10	0.10	-0.01	0.00	0.01	0.37*
NCMS	-0.01	0.02	0.30	0.72	0.37	-0.18	-1.49	0.89	-0.00	-0.02	-0.04	0.06	0.02	-0.02	-0.01	0.61**
NCPP	-0.01	0.01	-0.40	0.42	0.64	0.02	-1.06	1.05	0.01	-0.08	0.04	0.12	0.02	-0.02	-0.01	0.75**
CL	0.09	0.01	0.48	0.36	-0.04	-0.35	-0.60	0.06	0.00	0.03	0.19	-0.09	0.02	-0.02	-0.01	0.13
NPMS	-0.01	0.00	0.18	0.69	0.44	-0.14	-1.55	1.01	0.02	-0.05	-0.03	0.06	0.01	-0.02	-0.01	0.60**
NPPP	-0.01	0.02	-0.17	0.53	0.55	-0.02	-1.29	1.22	0.03	-0.10	0.02	0.11	-0.00	-0.02	-0.02	0.85**
PL	-0.05	0.04	0.09	0.01	-0.04	0.00	0.11	-0.15	-0.23	0.02	0.21	-0.15	-0.01	-0.01	-0.01	-0.17
DM	0.01	-0.02	-0.20	0.05	0.19	0.04	-0.03	0.46	0.01	-0.28	-0.02	-0.06	-0.00	0.02	0.01	0.18
NSPP	0.07	0.01	-0.14	-0.05	0.04	-0.12	0.07	0.01	-0.09	0.01	0.59	-0.09	-0.01	-0.02	-0.01	0.27
100 SW	-0.05	0.06	-0.15	0.09	0.14	0.06	-0.19	0.26	0.07	0.03	-0.10	0.53	-0.00	-0.00	0.00	0.75**
EP	-0.05	0.06	0.03	0.10	0.08	-0.06	-0.16	-0.04	0.02	0.04	-0.06	-0.02	0.13	-0.07	-0.01	-0.01
GC	-0.07	0.01	0.03	0.16	0.12	-0.08	-0.37	0.21	-0.02	0.05	0.14	0.02	0.09	-0.10	-0.02	0.17
PC	0.01	-0.07	-0.17	-0.25	-0.12	0.09	0.56	-0.11	0.04	-0.05	-0.20	0.04	-0.07	0.07	0.03	-0.20
							Residu	al effect	= -0.09)						

DF= Days to 50 per cent flowering, PH= Plant height (cm), NFBP= Number of fruiting branch per plant, NCMS= Number of cluster on main stem, NCPP= Number of cluster per plant, CL= Cluster length (cm), NPMS= Number of pod on main stem, NPPP= Number of pod per plant, PL= Pod length (cm), DM = Days to 80 per cent maturity, NSPP= Number of seed per plant, 100 SW= 100 seed weight (g), SYPP= Seed yield per plant (g), EP= Endosperm percentage, GC= Gum content (%), PC= Protein content (%).

Conclusion

Combined results of path analysis and correlation coefficient revealed that the characters *viz.*, number of cluster on main stem, number of cluster per plant, number of pod per plant and 100-seed weight showed positive correlation coefficient and positive direct effect with seed yield should be selected, so that correlation explains its true relationship and a selection for these characters will become effective.

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