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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN CLUSTER BEAN (*CYAMOPSIS TETRAGONOLOBA* L. TAUB.)

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ABSTRACT

The present investigation was carried out to study the Genetic variability, correlation and path analysis among thirty-six genotypes of cluster bean for seed yield and its attributing traits. The experiment was conducted in a randomized block design with four replications at Agronomy Instructional Farm, C. P. College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *summer* 2020. The analysis of variance revealed that mean sum of squares due to genotypes was found significant for all the thirteen characters studied. A wide range of variation was apparent for all the characters. The genotypes, IC 113275, GAUG 1501, GG 1903 and IC 113661 were found promising for seed yield per plant based on *per se* performance. The high values of genotypic and phenotypic coefficient of variation were observed for number of pods per cluster and seed yield per plant indicated potential variability available for these traits and small difference between them suggesting positive selection in desired direction for improvement of these characters. Path analysis revealed the importance of days to flowering, days to maturity, number of effective branches per plant, pod length, number of pods per plant, protein content and gum content possessed high and positive direct effects towards seed yield per plant. Overall, it could be concluded that variability, heritability, genetic advance, correlation and path coefficient obtained in this study might be useful in future cluster bean improvement programmes.

***Keywords*: Genetic Variability, Correlation and Path Analysis, Cluster Bean (*Cyamopsis Tetragonoloba* L. Taub.)

Introduction

Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.] (2n=2x=14) is commonly known as guar, belongs to family *Leguminaceae*, sub family *papilionaceae* and tribe *galegeae* and also order *Fabales*. Gillette (1958) divided the genus *Cyamopsis* into three races *viz.*, *C. tetragonoloba* (L.) Taub, *C. senegalensis* Guill and Perr. and *C. serrata* Schinz. Africa is probably the center of origin of *Cyamopsis*. Cluster bean possesses potential vegetable cum industrial crop grown for its tender pods for vegetable and for endosperm gum *i.e.*, galactomannan (22-33%) (Gresta *et al.*, 2013) and for guar meal (Singh *et al.*, 2014). Guar seeds are mainly used for extraction endosperm gum (30-35%) having good binding properties and high demand in food, petroleum, varnish, textile, explosive, pharmaceutical, telephone, electricity, juice, paper, dairy, coal industries, nutraceutical, cosmeceutical and paint, oil drilling and mining industries etc.

In India, cluster bean crop is cultivated mainly during Kharif season. It occupied an area of 31.40 lakh hectare with a total production of 15.19 lakh tons of guar seed during 2019-20 in the country (Directorate of Economics and Statistics, DAC&FW). The country exports over 1.17 lakh tons of guar and its derivatives annually, which is comprised by 0.33 lakh tons of refined split guar gum and 0.84 lakh tons of treated and pulverized guar gum. India is the major exporter of guar gum to the world; it exports various forms of Guar products to a large number of countries. The country has exported 234,872 MT of guar gum to the world for the worth of Rs. 1949 Crores during the year 2020-21. [APEDA (Ministry of Commerce and Industry, Govt. of India), Indian stock market].

Guar is a coarse, upright, bushy, drought resistant summer annual plant ranging from 2 to 4 feet in height. Cluster bean produces 8 to 9 mm long purplish pink or white coloured flowers. Cluster bean is completely self-pollinated crop because of its cleistogamous nature. The extent of out crossing has been found to vary from 0.3 to 7.9 % (Ahlawat *et al.* 2012). Cluster bean is grown mainly in the *kharif* season. It is suitable for the areas with light to medium textured soils, with a rainfall range of 250 to 450 mm and temperature range of 25 °C to 40 °C. Guar enhances soil productiveness by fixing atmospheric nitrogen for its own necessitates and also for the succeeding crop (Bewal *et al.*, 2009).

The knowledge of genetic variability in the available germplasm is a pre-requisite for effective selection of superior genotypes. Therefore, there is need for identification or development of cluster bean genotypes suited for vegetable, fodder and gum purpose. The knowledge of nature and magnitude for genetic variability, heritability and genetic advance over mean for pod yield and component characters are useful for an effective selection programme. Therefore, it becomes necessary to partition the observed phenotypic expression of the plant into the genetic makeup of the plant and the environment in which it is growing.

The correlation analysis is a biometrical technique to find out the nature and degree of association between various morphological traits indicating yield. It could be effectively exploited to formulate selection strategies for improving yield and quality. Correlation study does not reveal the direct and indirect contribution of individual character towards yield. In order to have clearer picture of yield components for effective selection programme, it would be desirable to consider the relative magnitude of various characters contributing towards yield. The path coefficient technique developed by Wright (1921) helps in estimating direct and indirect contribution of various components in building-up the correlation towards yield. On the basis of these studies, the quantum importance of individual characters is marked to facilitate the selection programme in cluster bean. Considering the importance of variability & character association in crop improvement programme the present study is formulated.

Materials and Methods

The present investigation was carried out with thirty-six diverse cluster bean genotypes (Table 1) were evaluated with four replications in Randomized Block Design (RBD) during summer 2020 at Agronomy Instructional Farm, S.D. Agricultural University, Sardarkrushinagar, Gujarat. The observations from five randomly selected plants of each genotype in each replication were recorded for 13 characters *viz.,* days to flowering, days to maturity, plant height (cm), pod length (cm), number of effective branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per plant, 100 seed weight (g), seed yield per plant (g), protein content (%) and gum content (%). The analysis was carried out by adopting genetic parameters of variability, estimation of heritability and genetic advance were computed as per Johnson *et al.* (1955). Correlation studies are conducted as per Panse and Sukhatame (1978) whereas, construction of Path coefficient analysis suggested by Dewey and Lu (1959). The formula suggested by Burton (1952) was employed to calculate phenotypic and genotypic coefficient of variation.

Genotypic coefficient of variation (GCV)

$$GCV\ (\%) = \frac{\sqrt{\sigma^2 g}}{\underline{X}} \times 100$$

Phenotypic coefficient of variation (PCV)

$$PCV\ (\%) = \frac{\sqrt{\sigma^2 p}}{\underline{X}} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance

σ^2_p = Phenotypic variance

$\underline{X}$ = Mean value of character

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were classified as suggested by Shivasubramanian and Menon (1973) as follows

< 10 % = Low

10 to 20 % = Moderate

> 20 % = High

Results and Discussions

For any breeding programme the main important parameter is genetic variability which provides the basis for future hybridization & selection programme.

Analysis of variability components

The analysis of variance for all the thirteen characters in thirty-six genotypes was carried out in a randomized block design. The results obtained are presented in Table 3. The result revealed highly significant difference for all the traits *viz.*, days to flowering, days to maturity, plant height (cm), pod length (cm), number of effective branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per plant, 100 seed weight (g), protein content (%), gum content (%) and seed yield per plant (g) which indicated the existence of tremendous variability in the experimental material under study and there may be a scope for improvement of these traits through selection. Similar results were reported by Boghara *et al.* (2016) and Makwana *et al.* (2021).

Variability parameter for cluster bean genotypes

The highest GCV (%) and PCV (%) was recorded for seed yield per plant (29.32 and 31.75) followed by number of pods per cluster (19.15 and 20.45) (Table 3), indicating high variability present in the population and simple selection would be desirable for improving these characters. Similar results were reported by Santhosha *et al.* (2017) and Meghana *et al.* (2019). The degree of inheritance of particular traits from parents to offspring is provided by heritability. In present investigation high heritability coupled with high genetic advance as per cent of mean were recorded for six traits *viz.,* seed yield per plant (85.28 and 55.77), number of clusters per plant (76.07 and 28.55), number of pods per cluster (87.74 and 36.96), pod length(82.47and 27.17), plant height (88.53 and 24.40), and days to flowering (94.75 and 37.19) respectively, which may be due to additive gene effects indicating better scope for the improvement by effective selection (Panchal *et al.*, 2023). Similar results were also reported by Santhosha *et al.* (2017), Makwana *et al.* (2021), Meghana *et al.* (2019), Choyal and Dewangan (2018), Gowd *et al.* (2019) and Depashree *et al.* (2021).

Phenotypic (rp) and Genotypic (rg) correlation

Correlation studies provide the information about degree and direction of trait association with grain yield which is useful for selection of elite genotypes from population. Genotypic and phenotypic correlation coefficient among seed yield per plant and its contributing traits are presented in Table 4. For all traits genotypic correlation values are higher than phenotypic correlation values which indicates little influence of environment. The correlation analysis revealed that seed yield per plant exhibited highly significant and positive association with 100 seed weight ($r_g = 1.031^{**}$ and $r_p = 0.836^{**}$) followed by protein content (%) ($r_g = 1.014^{**}$ and $r_p = 0.931^{**}$), gum content ($r_g = 0.991^{**}$ and $r_P = 0.945^{**}$), pod length (rg = 0.982^{**} and $r_P = 0.970^{**}$) number of pods per plant ($r_g= 0.977^{**}$ and $r_p= 0.931^{**}$), number of pods per cluster ($r_g = 0.971^{**}$ and $r_P = 0.960^{**}$), number of effective branches per plant (r_g 0.879^{**} and $r_P= 0.850^{**}$), number of seeds per pod ($r_g = 0.833^{**}$ and $r_p = 0.727^{**}$) and significant positive correlation number of clusters per plant ($r_g = 0.216^{**}$ and $r_p = 0.181^{**}$) at genotypic and phenotypic levels. Thus, improvement in such characters also leads to increment in seed yield per plant of cluster bean genotypes. Kumar and Ram (2015), Boghara *et al.* (2016), Reddy *et al.* (2018), Patel *et al.* (2018), Panchta and Khatri (2017) and Manivannan *et al.* (2017) also reported similar results.

Path analysis

Path analysis breaks correlation between traits into their direct and indirect effects on the economic product, permitting a critical examination of specific trait contributing individually and collectively to produce the total effect. It also helps to measure the relative importance of each trait. Path analysis, in this study was carried out using the estimates of genotypic coefficients. The analysis of correlation coefficient together with information on path coefficient helps in identification of suitable character for proper weightage to be given to each trait during selection. Such an analysis of genotypes under study provided precise indication of the trait that may contribute towards increased total seed yield and also outlined the possible directions to be followed in the future breeding programme for improvement in these traits. The estimates of direct and indirect effects of various traits on total seed yield per plant are presented in Table 5. The positive direct effect of number of pods per plant and number of effective branches per plant on seed yield per plant were reported by Elshiekh *et al.* (2012), Ramanjaneyulu *et al.* (2018) and Kumar *et al.* (2019).

Table 1: List of genotypes

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1	GAUG 1501	13	IC 113214	25	IC 113443
2	GAUG 1502	14	IC 113215	26	IC 113453
3	GAUG 1507	15	IC 113275	27	IC 113461
4	GG 1802	16	IC 113277	28	IC 113507
5	GG 1901	17	IC 113278	29	IC 113558
6	GG 1903	18	IC 113295	30	IC 113567
7	GG 1907	19	IC 113300	31	IC 113578
8	DRLGG 13-7	20	IC 113320	32	IC 113595
9	DRLGG 13-28	21	IC 113325	33	IC 113660
10	IC 40979	22	IC 113327	34	IC 113661
11	IC 41261	23	IC 113336	35	IC 113587
12	IC 41281	24	IC 113421	36	GG 2

Table 2: Analysis of variance for thirteen quantitative characters in cluster bean

Sr. No.	Characters	Mean sum of square		
		Replication	**Genotypes**	**Error**
Degree of Freedom		**3**	**35**	**105**
1.	Days to flowering	4.08	146.82**	2.00
2.	Days to maturity	1.61	32.01**	8.50
3.	Plant height (cm)	23.35	362.64**	11.36
4.	Number of effective branches per plant	0.29	2.62**	0.28
5.	Pod length	0.21	2.72**	0.13
6.	Number of pods per plant	46.10	199.92**	23.25
7.	Number of seeds per plant	0.60	2.12**	0.63
8.	Number of pods per cluster	0.49	12.34**	0.41
9.	Number of clusters per plant	1.41	22.57**	1.64
10.	100 seed weight (g)	0.47	0.66**	0.21
11.	Protein content (%)	0.88	3.72**	0.54
12.	Gum content (%)	0.53	8.43**	0.58
13.	Seed yield per plant	28.51	272.21**	11.26

Table 3: Genetic parameters of variation for seed yield and its attributing characters in cluster bean

Sr. No.	Characters	Genetic parameters							
		Mean	**Range**		**Variance components**			**Coefficient of variation**	
			Maximum	**Minimum**	**σ2p**	**σ2g**	**σ2e**	**GCV (%)**	**PCV (%)**
1	Days to flowering	32.43	52.50	22.75	38.20	36.20	2.00	18.54	19.05
2	Days to maturity	92.00	95.25	85.50	14.37	5.87	8.50	2.63	4.12
3	Plant height (cm)	74.43	95.06	56.94	99.18	87.81	11.36	12.59	13.38
4	Number of effective branches per plant	7.83	11.07	6.90	0.87	0.58	0.28	9.75	11.91
5	Pod length	5.54	7.00	4.48	0.78	0.64	0.13	14.52	15.99
6	Number of pods per plant	73.74	85.00	58.12	67.42	44.16	23.25	9.01	11.13
7	Number of seeds per pod	10.97	14.45	9.72	1.00	0.37	0.63	5.57	9.13
8	Number of pods per cluster	9.01	12.00	5.80	3.39	2.98	0.41	19.15	20.45
9	Number of clusters per plant	14.39	21.99	11.67	6.87	5.23	1.64	15.89	18.22
10	100 seed weight	7.37	8.07	6.32	0.32	0.11	0.21	4.51	7.76
11	Protein content (%)	24.03	25.88	22.40	1.34	0.79	0.54	3.70	4.81
12	Gum content (%)	25.74	29.00	23.50	2.54	1.96	0.58	5.44	6.20
13	Seed yield per plant	27.54	45.28	16.55	76.50	65.23	11.26	29.32	31.75

Where : σ2g, σ2p and σ2e are the genotypic, phenotypic and environmental variance, respectively; GCV (%) and PCV (%) are genotypic and phenotypic coefficient of variation, respectively

Table 4: Genotypic and phenotypic correlation for thirteen characters in Cluster bean

Sr. No.	Chara-cters	r	DM	DM	PH	NBP	PL	NPP	NSP	NPC	NCP	TW	PC	GC	SYP
1	DM	r_g	1.000	-0.019^{NS}	-0.015^{NS}	-0.047^{NS}	-0.002^{NS}	-0.030^{NS}	-0.027^{NS}	0.012^{NS}	0.115^{NS}	-0.010^{NS}	-0.039^{NS}	-0.004^{NS}	-0.006^{NS}
		r_p	1.000	-0.011^{NS}	-0.018^{NS}	-0.041^{NS}	-0.002^{NS}	-0.017^{NS}	-0.013^{NS}	0.016^{NS}	0.105^{NS}	0.009^{NS}	-0.012^{NS}	0.009^{NS}	-0.002^{NS}
2	DM	r_g		1.000	0.408**	-0.184*	-0.334**	-0.374**	-0.193*	-0.332**	-0.169*	-0.353**	-0.373**	-0.350**	-0.318**
		r_p		1.000	0.261**	-0.076^{NS}	-0.217**	-0.204*	-0.046NS	-0.204*	-0.134^{NS}	-0.146NS	-0.184*	-0.229**	-0.202*
3	PH	r_g			1.000	-0.089^{NS}	0.029^{NS}	0.032^{NS}	0.003^{NS}	0.021^{NS}	-0.299**	0.062^{NS}	0.015^{NS}	-0.069^{NS}	-0.030^{NS}
		r_p			1.000	-0.054^{NS}	0.029^{NS}	0.025^{NS}	0.003^{NS}	0.022^{NS}	-0.264**	0.044^{NS}	-0..001^{NS}	-0.033^{NS}	-0.021^{NS}
4	NBP	r_g				1.000	0.803**	0.774**	0.954**	0.781**	0.276**	0.783**	0.849**	0.852**	0.879**
		r_p				1.000	0.792**	0.778**	0.866**	0.765**	0.210*	0.749**	0.808**	0.792**	0.850**
5	PL	r_g					1.000	0.975**	0.778**	0.973**	0.207*	1.010**	1.008**	0.988**	0.982**
		r_p					1.000	0.930**	0.707**	0.960**	0.169**	0.834**	0.929**	0.938**	0.970**
6	NPP	r_g						1.000	0.746**	1.012**	0.175*	1.055**	1.014**	1.002**	0.977**
		r_p						1.000	0.732**	0.939**	0.110^{NS}	0.905**	0.938**	0.911**	0.931**
7	NSP	r_g							1.000	0.805**	0.089^{NS}	0.737**	0.789**	0.870**	0.833**
		r_p							1.000	0.688**	0.070^{NS}	0.771**	0.757**	0.707**	0.727**
8	NPC	r_g								1.000	0.191*	1.097**	1.017**	0.998**	0.971**
		r_p								1.000	0.165*	0.840**	0.920**	0.941**	0.960**
9	NCP	r_g									1.000	0.152^{NS}	0.213*	0.223**	0.216**
		r_p									1.000	0.074^{NS}	0.133NS	0.163NS	0.181*
10	TW	r_g										1.000	1.023**	1.061**	1.031**
		r_p										1.000	0.900**	0.835**	0.836**
11	PC	r_g											1.000	1.019**	1.014**
		r_p											1.000	0.908**	0.931**
12	GC	r_g												1.000	0.991**
		r_p												1.000	0.945**
13	SYP	r_g													1.000
		r_p													1.000

** and * indicates significance at 1 % and 5 % level of probability, respectively

DF = Days to flowering
DM = Days to maturity
PH = Plant height
NBP = Number of effective branches per plant
PL = Pod length
NPP = Number of pods per plant
NSP = Number of seeds per pod
NPC = Number of pods per cluster
NCP = Number of clusters per plant
TW = 100 seed weight
PC = Protein content
GC = Gum content
SYP = Seed yield per plant

Table 5: Direct (Diagonal) and indirect effects of yield components on seed yield per plant in clusterbean

Sr.No.	Character	DF	DM	PH	NBP	PL	NPP	NSP	NPC	NCP	TW	PC	GC	SYP
1	**DF**	**0.0378**	-0.0007	-0.0006	-0.0018	-0.0001	-0.0011	-0.0010	0.0004	0.0043	-0.0004	-0.0015	-0.0001	-0.006^{NS}
2	**DM**	-0.0007	**0.0348**	0.0142	-0.0064	-0.0116	-0.0130	0.0083	-0.0115	-0.0059	-0.0123	-0.0129	-0.0122	-0.318**
3	**PH**	0.0005	-0.0140	**-0.0343**	0.0031	-0.0010	-0.0011	0.0001	-0.0007	0.0103	-0.0021	-0.0005	0.0024	-0.030^{NS}
4	**NBP**	-0.0188	-0.0738	-0.0358	**0.4005**	0.3214	0.3099	0.9648	0.3128	0.1107	0.3136	0.3399	0.3414	0.879**
5	**PL**	-0.0004	-0.0765	0.0066	0.1835	**0.2286**	0.2228	-0.0006	0.2223	0.0472	0.2309	0.2305	0.2259	0.982**
6	**NPP**	-0.0148	-0.1871	-0.0161	-0.3875	0.4881	**0.5008**	0.0116	0.5070	0.0875	0.5282	0.5079	0.5017	0.977*
7	**NSP**	0.0053	0.0386	-0.0006	-0.1908	-0.1556	-0.1493	**-0.2000**	-0.1610	-0.0178	-0.1474	-0.1578	-0.1740	0.833**
8	**NPC**	-0.0006	0.0183	-0.0012	-0.0431	-0.0537	-0.0559	0.2493	**-0.0552**	-0.0105	-0.0605	-0.0561	-0.0551	0.971**
9	**NCP**	-0.0066	0.0098	0.0173	-0.0160	-0.0119	-0.0101	-0.0090	-0.0110	**-0.0578**	-0.0088	-0.0123	-0.0129	0.216**
10	**TW**	0.0015	0.0538	-0.0095	-0.1193	-0.1539	-0.1607	0.3240	-0.1671	-0.0232	**-0.1524**	-0.1559	-0.1617	1.031**
11	**PC**	-0.0092	-0.0884	0.0037	0.2014	0.2393	0.2407	0.0312	0.2413	0.0506	0.2428	**0.2374**	0.2418	1.014**
12	**GC**	-0.0003	-0.0328	-0.0065	0.0800	0.0927	0.0940	-0.0001	0.0937	0.0210	0.0996	0.0956	**0.0938**	0.991**

Residual effect 0.00059

DF = Days to flowering
DM = Days to maturity
PH = Plant height
NBP = Number of effective branches per plant
PL = Pod length
NPP = Number of pods per plant
NSP = Number of seeds per pod
NPC = Number of pods per cluster
NCP = Number of clusters per plant
TW = 100 seed weight
PC = Protein content
GC = Gum content

Conclusion

The analysis of variance stated that mean square due to genotypes were found highly significant for all the traits *viz.*, days to flowering, days to maturity, plant height (cm), number of effective branches per plant, pod length, number of pods per plant, number of seeds per plant, number of pods per cluster, number of clusters per plant, seed yield per plant, 100 seed weight, protein content (%) and gum content (%) indicating the existence of tremendous variability in the experimental material. There may be a scope for improvement of these traits through selection.

The estimates of genotypic and phenotypic variances revealed higher contribution of genotypic variance to total variance for days to flowering, plant height, number of pods per plant and seed yield per plant. The traits, number of pods per cluster and seed yield per plant exerted high genotypic and phenotypic coefficients of variation while, days to flowering, plant height, number of effective branches per plant, pod length, number of pods per plant, number of clusters per plant were moderate in genotypic and phenotypic coefficients of variation. The characters namely seed yield per plant, number of clusters per plant, number of pods per cluster, pod length, plant height and days to flowering exhibited high heritability coupled with high genetic advance indicated that heritability in genotypes were due to additive gene effects. Thus, selection may be effective for the improvement in such characters of genotypes.

Correlation studies revealed that seed yield per plant had a positive and highly significant and positive association with number of effective branches per plant, pod length, number of pods per plant, number of seeds per pod, number of pods per cluster, 100 seed weight, protein content and gum content and therefore selection for these traits can directly be followed for yield improvement in cluster bean. Path analysis revealed that the traits likes, days to flowering, days to maturity, number of effective branches per plant, pod length, number of pods per plant, protein content and gum content possessed high and positive direct effects towards seed yield per plant and each trait must be given preference in selecting of superior high yielding genotypes.

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