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Assessment of Genetic Diversity in Cluster Bean [*Cyamopsis tetragonoloba* (L.) Taub]

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ABSTRACT

Background: Twenty six genotypes of cluster bean [*Cyamopsis tetragonoloba* (L.) Taub] were evaluated under randomized block design with three replications under the field condition to estimate the range of variability and diversity present in cluster bean genotypes for fifteen yield and yield contributing traits.

Methods: The experiment was carried out at Research Farm, Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat in the year 2020 on twenty-six genotypes of cluster bean.

Result: Correlation coefficients of fifteen traits estimates indicated positive and highly significant correlation of seed yield per plant with pods per plant, pods per cluster, pod yield per plant and seeds per plant, so these characters should be considered for selection for increasing yield in cluster bean. Gum content was negatively and significantly correlated with days to 50% flowering, seed yield per plant and 100 seed weight at genotypic level hence, selection for gum content might not be desirable for test seed weight and seed yield. Principal component analysis revealed significant variation among traits evaluated with the five principal components explaining approximately the 75.8% of the total variation with ≥ 1 eigen values. Most of the variation contributed by the pods per cluster, pods per plant, gum content, pod yield per plant and seed yield per plant, these traits should be considered while selecting the cluster bean genotypes. The PCA- biplot revealed GAUG-1305, GG-1801, RGC-936 and RGC-986 as the most diverse genotypes for various traits. Cluster analysis distributed 26 cluster bean genotypes into three different clusters by UPGMA method. In the present investigation, the genotype GAUG-1305 recorded higher pods per plant, while GAUG-1502 for higher pod yield per plant, the genotype RGC-1003 for high pod length and RGC-936 exhibited higher pods per cluster, seeds per pod and seed yield per plant. So, these genotypes could be used in the future breeding programs.

Key words: Cluster analysis, Correlation coefficient, Gum content, PCA-biplot, Principal component, Yield.

INTRODUCTION

Cluster bean [*Cyamopsis tetragonoloba* (L.) Taub] is an annual diploid legume crop, with the chromosome number $2n=2x=14$ belongs to the family *Fabaceace*. It is mainly cultivated for its vegetable, fodder, galactomanan (gum) and for green manure purpose. Cluster bean is commonly known as guar bean, guari, chavlikayi and khutti. Its cultivation dates back from Africa, but now it is widely cultivated in India, Australia, Brazil, Malawi, Pakistan, Sudan, South Africa, USA and Zaire (Bhatt *et al*., 2016). India contributes around 80% of global cluster bean production. It is a climate resilient crop for dry lands with good economic returns to farmers. It is primarily grown for its tender green pods, which contain energy (16 kcal), carbohydrate (10.8 g), protein (3.2 g), fat (1.4 g), calcium (57 mg), vitamin A (65.3 IU), vitamin C (49 mg) and iron (4.5 mg) for 100 g of edible portion. Seeds are rich in protein, vitamins and minerals like Ca, Cu, Fe, K, Mg, Mn, P and Zn and also excellent source of complex carbohydrates (Reddy *et al*., 2019). Like other legumes, cluster bean is an excellent soil-building crop and also used as green manure crop which can fix the atmospheric nitrogen (50-60 kg/ha) and enrich the soil by addition of organic matter (Bhatt *et al*., 2016). The cluster bean endosperm is the important source of gum. It is the prime marketable product owing to its good binding properties and it has high demand in different industries including food, agriculture, varnish, petroleum, pollution control, pharmaceutical, coal and in telephone and electrical (Ambrozek *et al*., 1988). The main objective of breeding programme is mainly oriented towards the improvement of the yield, earliness and quality traits. Since, the yield is dependent trait, it is necessary to understand the nature and association of growth and yield contributing characters through various biometrical tools. So far only limited studies have been reported on this

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underexploited crop. There is a need to improve its yield potential and make it more economical to the farmers. In the present investigation cluster bean genotypes has been screened based of genetic variability and diversity to identify the elite genotypes for future crop improvement programs.

MATERIALS AND METHODS

The experiment was carried out at Research Farm, Department of Genetics and Plant Breeding, N. M. College of Agriculture, Navsari Agricultural University, Navsari, Gujarat in the year 2020 on twenty-six genotypes of cluster bean. These genotypes were collected from Rajasthan Agricultural Research Institute, Jaipur, Rajasthan and Sardarkrushinagar Dantiwada Agricultural University, Banaskantha, Gujarat (Table 1). The experiment was laid out in RBD design (randomized block design) with three replications. Each genotype were grown in a 3m long plot at a spacing of 30 cm between rows and 10 cm between plants. All recommended practices and plant protection measures were timely followed to avoid damage from insect-pests and diseases. Total fifteen yield and yield related traits namely, days to 50% flowering, plant height at 45 days (cm), branches per plant at 45 days, plant height at 90 days (cm), branches per plant at 90 days, pod length (cm), clusters per plant, 100 seed weight (g), pods per cluster, pods per plant, pod yield per plant (g), seeds per pod, seed yield per plant (g), protein content (%) and gum content (%) were observed. The observations were recorded on five randomly selected plants in each plot and in each replication except days to 50% flowering which was recorded on plot basis.

All statistical analyses were carried out in Rstudio software (Rstudio Team, 2020). Various genetic parameters such as genotypic variance, phenotypic variance, heritability in broad sense, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance (GA) and genetic advance as per cent of mean (GAM), correlation and path coefficient analyses were estimated using 'Variability' package of Rstudio (Popat *et al*., 2020). PCA and divergence was performed using the R packages 'biotools' (v4.2; da Silva *et al.,* 2021) and 'FactoMineR' (Le *et al*., 2008).

RESULTS AND DISCUSSION

Mean performance of genotypes

In the present study, a considerable range of variations was found for fifteen quantitative traits among the twenty six cluster bean genotypes were mentioned in the Table 1. Variation of some important traits were explained here, days to 50% flowering ranged from 34.00 days (RGC-986) to 38.33 days (HG-2-20) with the mean of 35.91 days. Clusters per plant exhibited mean of 16.08 with the variation of 9.93 (RGC-1038) to 22.40 (GAUG-1305). 100 seed weight ranged from 2.97 g (RGC-936) to 3.53 g (GG-1609) with the overall mean of 3.27 g. Pods per cluster ranged from 5.20 (RGC-1031) to 11.20 (RGC-936) with the mean of 6.54. Pods per plant exhibited mean of 80.11 and it ranged from 59.73 (GG-2) to 100.37 (GAUG-1305). Pod yield per plant varied from 74.43 g (RGC-986) to 114.33 g (GAUG-1502) and the mean for this trait was 91.72 g. The variation observed for seed yield per plant ranged from 13.20 g (RGC-1055) to 22.50 g (RGC-936) with the overall mean of 16.66 g. Protein content ranged from 28.85% (HGS-563) to 37.87% (CAZG-11-1) with an overall mean of 33.32%. The average value gum content (%) was 23.67% ranging between 19.94% (HGS-563) to 29.17 % (RGC-986). The mean performance of all the studied fifteen traits revealed the presence of sufficient amount of variation so, there is a scope for further improvement of these traits in the future.

Variability analysis

The analysis of variance for all the characters showed significant differences among the genotypes studied, indicating the presence of a considerable amount of variability in the material (Table 1). The genetic parameters range, mean, σ^2_g (genotypic variance), σ^2_p (phenotypic variance), h^2_{bs} (heritability in broad sense), GCV (genotypic coefficient of variation), PCV (phenotypic coefficient of variation), GA (genetic advance) and GAM (genetic advance as per cent of mean) for fifteen characters are presented in the Table 2. The genotypic and phenotypic variances estimated that the characters like days to 50% flowering, branches per plant at 45 days, branches per plant at 90 days, pod length, clusters per plant, 100 seed weight, pods per cluster, seeds per pod, protein content and gum content predominated by genotypic variance in total phenotypic variance, these traits can be improved by direct selection. However, traits like plant height at 45 days, plant height at 90 days, pods per plant, pod yield per plant and seed yield per plant revealed greater influence of environmental factors for their expression. Low GCV values in these characters indicated less variability for these traits in the genotype studied and expressed poor response to selection.

Moderate to high GCV were observed for branches per plant at 45 days, branches per plant at 90 days, clusters per plant, pods per cluster and pod yield per plant indicating the presence of substantial amount of variability, revealed considerable scope for improvement of these traits by selection. The similar findings were reported by Reddy *et al.* (2019) and Kgasudi *et al.* (2020). High heritability was observed for the characters like plant height at 90 days, pods per cluster, seeds per pod, protein content and gum content. High heritability revealed the possibility of effective selection based on the phenotypic expression, the results are in accordance with Vir and Singh (2015); Santhosha *et al.* (2017) and Reddy *et al.* (2019).

The high heritability along with high genetic advance as percent mean showed that heritability in genotypes were due to additive gene effects indicating better opportunity for the improvement in the traits by effective selection. Pods per cluster estimated high heritability coupled with high genetic advance as per cent mean while moderate

Table 1: Mean values of twenty six cluster bean genotypes and analysis of variance for fifteen quantitative traits.

S.no.	Genotype	DFF	PH45	BPP45	PH90	BPP90	PL	CPP	100 SW	PPC	PPP	PYPP	SPP	SYPP	PC	GC
1	GAUG-1501	35.33	37.20	5.17	61.70	7.33	5.64	17.40	3.33	6.37	94.87	113.83	6.93	17.10	35.15	23.23
2	GAUG-1305	35.33	41.97	5.90	66.03	7.17	5.72	22.40	3.40	6.00	100.37	107.60	8.13	19.50	37.56	26.46
3	GG-1808	36.33	38.53	4.60	63.97	6.00	5.75	20.07	3.37	6.53	84.43	113.00	8.30	15.73	34.83	24.91
4	GG-1801	36.67	38.73	2.17	80.57	2.63	5.47	14.10	3.40	8.40	77.73	90.33	7.57	16.50	30.11	25.70
5	GAUG-1502	35.33	40.20	5.47	72.63	6.03	5.55	20.50	3.17	6.40	85.67	114.33	7.93	13.73	32.32	24.92
6	GG-1612	37.00	38.67	5.40	65.07	6.00	5.11	16.43	3.33	6.27	95.37	114.00	7.60	20.07	33.34	21.83
7	GG-1609	34.67	41.93	5.53	65.83	5.90	5.74	15.87	3.53	6.23	77.77	91.10	7.63	17.43	30.98	23.25
8	GG-2	36.00	44.50	4.57	67.53	5.10	5.66	15.57	3.50	6.20	59.73	75.27	7.43	16.10	33.11	20.75
9	RGC-12-1	36.00	39.93	4.73	63.37	5.07	5.67	15.83	3.40	5.70	69.63	80.30	7.87	16.03	29.99	25.02
10	RGC-936	35.67	46.17	4.07	89.37	4.60	5.63	12.17	2.97	11.20	90.67	94.77	8.47	22.50	34.29	24.19
11	RGC-197	36.67	42.30	6.07	78.50	6.90	5.20	20.43	3.13	6.10	75.53	88.23	6.77	15.37	31.95	21.96
12	RGC-986	34.00	39.97	3.90	61.73	4.57	4.93	18.20	3.23	5.73	66.30	74.43	7.23	13.63	33.06	29.17
13	RGC-1003	37.67	40.07	4.07	65.57	4.63	5.86	15.20	3.20	6.23	84.17	86.60	8.27	18.47	33.85	24.31
14	RGC-1017	35.67	38.10	4.90	59.37	5.30	5.11	16.17	3.20	6.17	78.70	84.53	7.33	15.10	29.07	25.68
15	RGC-1002	36.00	41.60	4.00	72.20	4.43	5.63	15.03	3.10	6.37	74.27	87.83	8.10	20.00	33.61	25.10
16	RGC-1031	35.67	40.87	5.23	63.50	5.50	5.37	16.13	3.40	5.20	85.17	99.37	7.00	16.57	31.99	20.04
17	RGC-1033	36.00	41.10	5.13	64.67	5.43	5.31	15.37	3.03	7.17	81.47	86.23	7.23	17.93	35.16	25.01
18	RGC-1038	35.00	44.60	4.53	77.30	5.00	5.56	9.93	3.07	8.43	73.63	87.47	7.67	15.77	32.16	22.47
19	RGC-1066	36.00	43.10	4.60	61.77	4.93	5.43	13.07	3.20	6.60	74.40	89.90	7.80	16.10	35.16	24.80
20	RGC-1055	35.33	40.60	3.87	64.50	4.47	5.54	14.30	3.27	6.20	72.97	76.70	7.03	13.20	35.97	25.94
21	HG-2-20	38.33	39.70	4.60	67.87	5.00	5.48	15.20	3.20	6.07	81.03	87.93	7.43	16.27	36.43	24.14
22	HGS-563	36.33	38.47	4.87	72.90	5.13	5.45	15.63	3.43	6.17	93.60	100.67	7.47	21.53	28.85	19.94
23	CAZG-11-1	36.67	39.23	3.90	65.77	4.40	5.38	13.93	3.33	6.40	79.43	86.30	7.70	16.87	37.87	20.32
24	CAZG-11-3	35.67	40.20	5.07	63.00	5.20	5.45	14.80	3.23	5.63	68.70	76.47	7.63	14.40	35.83	22.64
25	CAZG-82	35.33	39.20	4.60	64.53	5.37	5.47	14.67	3.47	6.23	73.63	87.47	7.57	15.10	29.79	22.63
26	CAZG-824	35.00	40.60	5.00	61.00	5.43	5.13	19.80	3.20	5.97	83.60	90.17	7.40	14.80	33.99	21.04
	Mean	35.91	40.67	4.69	67.70	5.29	5.47	16.08	3.27	6.54	80.11	91.72	7.60	16.66	33.32	23.67
	Minimum	34.00	37.20	2.17	59.37	2.63	4.93	9.93	2.97	5.20	59.73	74.43	6.77	13.20	28.85	19.94
	Maximum	38.33	46.17	6.07	89.37	7.33	5.86	22.40	3.53	11.20	100.37	114.33	8.47	22.50	37.87	29.17
	SEm±	0.56	1.31	0.48	2.93	0.50	0.13	1.24	0.06	0.34	5.96	6.98	0.15	1.68	0.29	0.24
	CD (p≤0.05)	1.60	3.72	1.37	8.31	1.43	0.36	3.53	0.18	0.97	16.93	19.81	0.43	4.77	0.83	0.69
	CV (%)	2.72	5.58	17.75	7.49	16.53	3.99	13.39	3.40	9.07	12.88	13.17	3.46	17.48	1.51	1.77
Mean sum of square	Replications (df: 2)	0.78	0.79	0.79	280.24**	1.16	0.40**	3.57	0.0003	0.73	139.39	125.99	0.08	7.40	0.07	0.05
	Genotypes (df: 25)	2.52**	13.93**	1.90**	151.20**	2.81**	0.16**	23.49**	0.07**	4.22**	281.14**	447.71**	0.57**	14.8*	19.12**	15.17**

Table 1: Continue...

Table 1: Continue...

Error (df: 50)	0.96	5.15	0.69	25.69	0.77	0.05	4.64	0.01	0.35	106.52	145.97	0.07	8.48	0.25	0.18

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP : Clusters per plant; 100SW :100 seed weight (g); BPP90 :Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP : Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% ($p<0.01$) and 1% ($p<0.001$) level, respectively.

heritability with high genetic advance as percent mean revealed by branches per plant at 90 days and clusters per plant which could be effectively improved by selection due to additive gene action. The characters like plant height at 90 days, protein content and gum content exhibited high heritability with moderate genetic advance as percent mean; Branches per plant at 45 days, pods per plant and pod yield per plant observed with moderate heritability and genetic advance as percent mean, moderate to high GAM is proportionate to additive gene action, so selection is effective in improving these traits and eventually we can improve seed yield/plant.

Days to 50% flowering, plant height at 45 days, pod length and 100 seed weight recorded moderate heritability with low genetic advance as percent mean, while seeds per pod and seed yield per plant showed low heritability with low genetic advance as percent mean. The results revealed the involvement of non-additive gene effect *i.e.*, the environmental influence on the expression of these traits. Seed yield in cluster bean is a complex trait, as it is controlled by various component traits, so direct selection is not effective. Hence, selection for various component traits of seed yield is suggesting for the improvement of this trait. Therefore, nature and association of various yield contributing characters were studied further in correlation studies (Reddy *et al*., 2019; Kgasudi *et al*., 2020).

Correlation studies

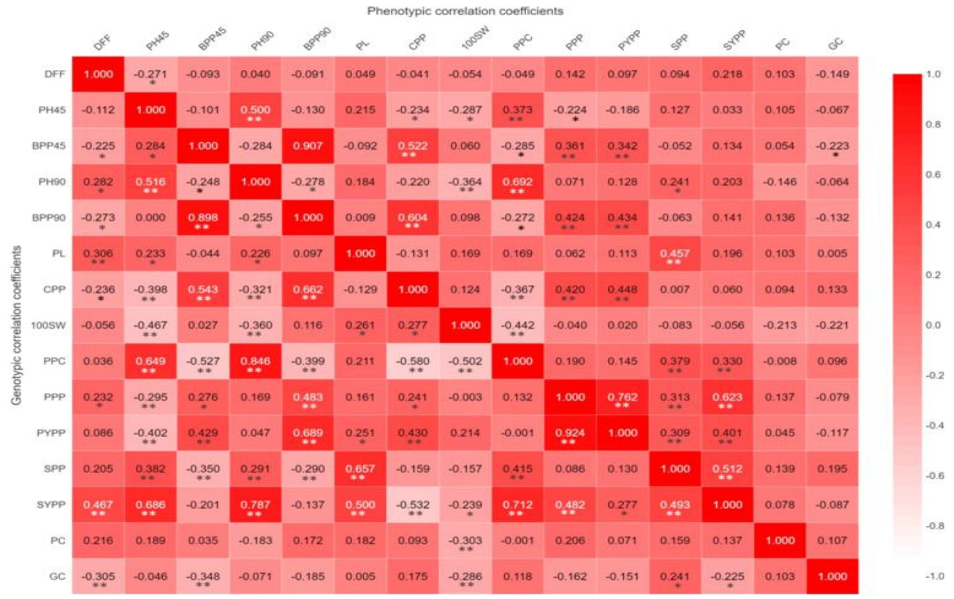
The genotypic correlation coefficients were found to be higher than their corresponding phenotypic correlation coefficient. PH45 had positive significant correlation with PH90 and PPC, on the other hand it had negative significant correlation with CPP, 100SW and PPP. A strong positive correlation of BBP45 found with BBP90, CPP, PPP and PYPP, but it was significantly and negatively correlated with PH90, PPC and GC. PH90 was positively associated with PPC and SPP, negatively associated with BPP90 and 100SW. Similarly, a strong positive correlation of BPP90 was found with CPP, PPP and PYPP, while it was negatively correlated with PPC (Fig 1).

PL showed a strong significant correlation with SPP. CPP positively and significantly correlated with PPP and PYPP but negatively associated with PPC. A strong negative correlation of 100SW was found with PPC. PPC had strong positive association with SPP and SYPP. A similar strong positive correlation of PPP was found with PYPP and SYPP. SYPP showed significant positive correlation with PPC, PPP, PYPP and SPP, so these characters would be given due consideration while selecting for increasing yield in cluster bean. GC showed negative and significant correlation with DFF, 100SW and SYPP at genotypic level. Hence, selection for gum content might not be desirable for test seed weight and seed yield, these findings are in accordance with Manivannan and Anandakumar (2013); Rai and Dharmatti (2014); Singh *et al*. (2016) and Patel *et al*. (2018).

Table 2: Estimates of genetic parameters for fifteen quantitative characters.

Trait	Range		σ^2_g	σ^2_p	GCV (%)	PCV (%)	h^2_{bs}(%)	GA	GAM (%)
	Min.	Max.							
DFF	34.00	38.33	0.52	1.48	2.01	3.39	35.34	0.89	2.46
PH45	37.20	46.17	2.93	8.08	4.21	6.99	36.27	2.12	5.22
BPP45	2.17	6.07	0.40	1.10	13.52	22.32	36.73	0.79	16.88
PH90	59.37	89.37	41.84	67.53	9.55	12.14	61.96	10.49	15.49
BPP90	2.63	7.33	0.68	1.45	15.61	22.74	47.15	1.17	22.08
PL	4.93	5.86	0.04	0.09	3.53	5.32	43.94	0.26	4.82
CPP	9.93	22.40	6.28	10.92	15.59	20.55	57.53	3.92	24.35
100SW	2.97	3.53	0.02	0.03	4.09	5.32	59.13	0.21	6.48
PPC	5.20	11.20	1.29	1.64	17.36	19.59	78.56	2.07	31.70
PPP	59.73	100.37	58.21	164.72	9.52	16.02	35.34	9.34	11.66
PYPP	74.43	114.33	100.58	246.55	10.93	17.12	40.79	13.2	14.39
SPP	6.77	8.47	0.17	0.24	5.37	6.39	70.67	0.71	9.30
SYPP	13.20	22.50	2.11	10.59	8.71	19.53	19.91	1.34	8.01
PC	28.85	37.87	6.29	6.54	7.53	7.68	96.13	5.07	15.20
GC	19.94	29.17	5.00	5.17	9.44	9.61	96.60	4.53	19.12

σ^2_g : Genotypic variance; σ^2_p : Phenotypic variance; h^2_{bs} : Heritability (Broad sense); GCV : Genotypic coefficient of variation; PCV : Phenotypic coefficient of variation; GA : Genetic advance; GAM : GA as per cent of mean. DFF: Days to 50 % flowering; PH45: Plant height at 45 days (cm); BPP45: Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL: Pod length (cm); CPP: Clusters per plant; 100SW: 100 seed weight (g); BPP90: Branches per plant at 90 days; PPC: Pods per cluster; PPP : Pods per plant; PYPP: Pod yield per plant (g); SPP: Seeds per pod; SYPP: Seed yield per plant (g); GC: Gum content (%); PC: Protein content (%). Note: * and ** indicate significant at 5% ($p<0.01$) and 1% ($p<0.001$) level, respectively.



	DFF	PH45	BPP45	PH90	BPP90	PL	CPP	100SW	PPC	PPP	PYPP	SPP	SYPP	PC	GC
DFF	1.000	-0.271 *	-0.093	0.040	-0.091	0.049	-0.041	-0.054	-0.049	0.142	0.097	0.094	0.218	0.103	-0.149
PH45	-0.112	1.000	-0.101	0.500 **	-0.130	0.215	-0.234 *	-0.287 *	0.373 **	-0.224 *	-0.186	0.127	0.033	0.105	-0.067
BPP45	-0.225 *	0.284 *	1.000	-0.284	0.907	-0.092	0.522 **	0.060	-0.285 *	0.361 **	0.342 **	-0.052	0.134	0.054	-0.223 *
PH90	0.282 *	0.516 **	-0.248 *	1.000	-0.278 *	0.184	-0.220	-0.364 **	0.692 **	0.071	0.128	0.241 *	0.203	-0.146	-0.064
BPP90	-0.273 *	0.000	0.898 **	-0.255 *	1.000	0.009	0.604 **	0.098	-0.272 *	0.424 **	0.434 **	-0.063	0.141	0.136	-0.132
PL	0.306 **	0.233 *	-0.044	0.226 *	0.097	1.000	-0.131	0.169	0.169	0.062	0.113	0.457 **	0.196	0.103	0.005
CPP	-0.236 *	-0.398 **	0.543 **	-0.321 **	0.662 **	-0.129	1.000	0.124	-0.367 **	0.420 **	0.448 **	0.007	0.060	0.094	0.133
100SW	-0.056	-0.467 **	0.027	-0.360 **	0.116	0.261 *	0.277 *	1.000	-0.442 **	-0.040	0.020	-0.083	-0.056	-0.213	-0.221
PPC	0.036	0.649 **	-0.527 **	0.846 **	-0.399 **	0.211	-0.580 **	-0.502 **	1.000	0.190	0.145	0.379 **	0.330 **	-0.008	0.096
PPP	0.232 *	-0.295 **	0.276 *	0.169	0.483 **	0.161	0.241 *	-0.003	0.132	1.000	0.762 **	0.313 **	0.623 **	0.137	-0.079
PYPP	0.086	-0.402 **	0.429 **	0.047	0.689 **	0.251 *	0.430 **	0.214	-0.001	0.924 **	1.000	0.309 **	0.401 **	0.045	-0.117
SPP	0.205	0.382 **	-0.350 **	0.291 **	-0.290 **	0.657 **	-0.159	-0.157	0.415 **	0.086	0.130	1.000	0.512 **	0.139	0.195
SYPP	0.467 **	0.686 **	-0.201	0.787 **	-0.137	0.500 **	-0.532 **	-0.239 *	0.712 **	0.482 **	0.277 *	0.493 **	1.000	0.078	-0.087
PC	0.216	0.189	0.035	-0.183	0.172	0.182	0.093	-0.303 **	-0.001	0.206	0.071	0.159	0.137	1.000	0.107
GC	-0.305 **	-0.046	-0.348 **	-0.071	-0.185	0.005	0.175	-0.286 **	0.118	-0.162	-0.151	0.241 *	-0.225 *	0.103	1.000

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP : Clusters per plant; 100SW : 100 seed weight (g); BPP90 : Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP : Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% ($p<0.01$) and 1% ($p<0.001$) level, respectively.

**Significant at $p < 0.01$; *Significant at $p<0.05$.

Fig 1: Estimates of correlation coefficient among 15 quantitative traits in 26 cluster bean genotypes (phenotypic above the diagonal and genotypic correlation coefficient below the diagonal).

Path coefficient analysis

Path analysis effectively partition the correlation coefficients into direct and indirect effects, also it determines the direct and indirect contribution of various characters towards yield. Path coefficient analysis (Table 3) revealed that pods per plant, pods per cluster, days to 50 % flowering, pod length and pod yield per plant exhibited high positive direct effect and significant association with seed yield per plant in favorable direction. So, it would be rewarding to lay emphasis on these characters while developing selection strategies in cluster bean. 100 seed weight had positive direct effect on seed yield but its negative contribution *via* other contributes resulted into negative and significant association. Branches per plant at 45 days reported positive direct effect but its negative contribution is high through other characters and it had negative and non-significant correlation with seed yield. Other traits like plant height at 90 days, branches per plant at 90 days and seeds per pod had high to moderate negative direct effect on seed yield, they also showed positive indirect effect *via* other characters. Hence, selection is less effective through these characters for genetic improvement of seed yield in cluster bean. In this study the residual effect was 0.238 at genotypic level which indicated that there might be few more component traits responsible to influence the seed yield per plant than those studied by Patil (2014); Singh *et al*. (2016); Patel *et al;* (2018) and Reddy *et al.* (2019).

Overall picture of path coefficient analysis showed that for improving seed yield in cluster bean, selection advantage should be given to pods per cluster, pods per plant, pod length, days to 50% flowering and pod yield per plant.

Principal component analysis (PCA)

PCA is widely used multivariate statistical tool to analyze the genetic diversity and to determine the most important variables contributing to the total variation. In this present study first five principal components contributed the 75.8% of the total variability with eigen values ≥1 (Table 4). The first principal component is the highest contributor to the total variation it contributes 25.34% of variation. The eigen vectors which were positively influenced the PC 1 were PPC and PH90 but negatively influenced by BPP90, CPP and BPP45. PC 2 was positively influenced by PPP, PYPP and SYPP and contributed 21.08% of total variance. Third principal component accounted 11.14% of variation, it was positively influenced by PH45 and negatively influenced by 100SW and DFF. GC and PC had contributed about 9.69% of total variance in PC 4. Fifth principal component (PC 5) attributed 8.56% of total variance by the major contributor PL. Similarly, first three principal components contributed more than 75% of the total variation with eigen value greater than one in Khatoon *et al.* (2023). The cos^2 (squared cosines or squared coordinates) values are used to estimate the quality of representation of the variables on factor map. A high cos^2 value indicated the good representation of the variable on the principal component whereas low cos^2 indicated that the variable is not perfectly represented by the PCs (Fig 2). The percentage contribution of traits to the principal components are presented in Table 5. An average percentage contribution of traits to the first two principal components represented in the Table 5 and Fig 3. The red dashed line indicates the average expected contribution of variables to both principal components assuming a similar contribution to each PC ($1/15 \times 100 = 6.667\%$). The average contribution to PC-1 and PC-2 is obtained by ($6.667 \times$Eigen1) + ($6.667 \times$Eigen2) / Eigen1 + Eigen2 (Kassambara, 2017). PPC, BPP90, PPP, PYPP, SYPP, BPP45, PH90 and CPP contributed more than expected values (>6.667) to the PC-1 and PC-2.

The variability of traits, correlation between different traits and the dispersion pattern of genotypes represented in the PC-1-2 biplot (Fig 4). All the traits had considerable higher vector length expect DFF, PC and GC indicated the presences of large variability. The acute angle (<90°) between the vectors explains the strong positive correlation between the traits. So, the traits like SYPP, SPP, PPC, PL, PYPP and PH90 were positively correlated with each other. Similarly, BPP45, BPP90 and CPP showed positive correlation among themselves. On the other hand, obtuse angle (>90°) between the vectors indicates the negative correlation. Thus, the trait SYPP had negative correlation with 100SW and GC. Similarly the traits 100SW, PC and GC were negatively correlated among themselves. The trait PH45 had negative correlation with 100SW (had nearly 180°). The genotypes 2 (GAUG-1305), 4 (GG-1801), 10 (RGC-936) and 12 (RGC-986) were the most diverse genotypes for various traits as they were far from the origin. Thus these genotypes may be used in the future hybridization programme to get diverse sergeants in the improvement of cluster bean genotypes. These findings were supported by Padmavathi *et al.* (2021) and Khatoon *et al.* (2023).

Cluster analysis

Cluster analysis is a commonly used biometrical method for grouping of genotypes based on similarity and dissimilarity. The unweighted pair group method with arithmetic mean (UPGMA) dendrogram represented the distribution of 26 cluster bean genotypes in three different clusters (Fig 5). Among all these clusters, cluster-III had the highest number of genotypes (16, 61.54%) followed by both cluster-I (5, 19.23%) and cluster-II (5, 19.23%). In a similar study fifty-five diverse genotypes of cluster bean were grouped into 8 clusters by Wankhade *et al.* (2017), eighteen genotypes into 3 clusters by Gowd *et al.* (2019), Mishra *et al.* (2019) grouped thirty-eight genotypes into 4 different clusters and Khatoon *et al.* (2023) grouped 219 accessions into nine clusters. The mean values of cluster III recorded the highest SYPP with late DFF, high PH45, PH90 and PPC (because of positive correlation of SYPP with all these traits) and lowest mean values for BPP45, BPP90, CPP and 100SW (Fig 6). The genotypes present in the cluster II showed the

Table 3: Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of component characters towards seed yield per plant.

	DFF	PH45	BPP45	PH90	BPP90	PL	CPP	100SW	PPC	PPP	PYPP	SPP	PC	GC	Correlation with SYPP
DFF	0.395	-0.030	-0.301	-0.134	0.422	0.115	-0.046	-0.018	0.046	0.090	0.028	-0.073	0.018	-0.044	0.467**
PH45	-0.044	0.270	0.381	-0.245	0.001	0.088	-0.078	-0.149	0.837	-0.114	-0.132	-0.137	0.016	-0.007	0.686**
BPP45	-0.089	0.077	1.342	0.118	-1.392	-0.016	0.107	0.008	-0.679	0.106	0.141	0.125	0.003	-0.051	-0.201
PH90	0.111	0.139	-0.333	-0.475	0.396	0.085	-0.063	-0.115	1.090	0.065	0.016	-0.104	-0.015	-0.010	0.787**
BPP90	-0.108	0.0001	1.205	0.121	-1.550	0.036	0.130	0.037	-0.514	0.186	0.226	0.104	0.014	-0.027	-0.137
PL	0.121	0.063	-0.059	-0.108	-0.150	0.377	-0.025	0.083	0.272	0.062	0.082	-0.235	0.015	0.001	0.500**
CPP	-0.093	-0.108	0.728	0.153	-1.026	-0.048	0.197	0.088	-0.747	0.093	0.141	0.057	0.008	0.026	-0.532**
100SW	-0.022	-0.126	0.036	0.171	-0.180	0.098	0.054	0.318	-0.647	-0.001	0.070	0.056	-0.025	-0.042	-0.239*
PPC	0.014	0.175	-0.707	-0.402	0.618	0.080	-0.114	-0.160	1.289	0.051	0.000	-0.148	0.0001	0.017	0.712**
PPP	0.092	-0.080	0.370	-0.080	-0.749	0.061	0.047	-0.001	0.170	0.386	0.303	-0.031	0.017	-0.024	0.482**
PYPP	0.034	-0.109	0.575	-0.023	-1.069	0.094	0.085	0.068	-0.001	0.356	0.328	-0.046	0.006	-0.022	0.277*
SPP	0.081	0.103	-0.470	-0.138	0.450	0.247	-0.031	-0.050	0.535	0.033	0.043	-0.358	0.013	0.035	0.493**
PC	0.085	0.051	0.047	0.087	-0.267	0.068	0.018	-0.096	-0.001	0.079	0.023	-0.057	0.084	0.015	0.137
GC	-0.120	-0.013	-0.467	0.034	0.286	0.002	0.034	-0.091	0.153	-0.062	-0.050	-0.086	0.009	0.146	-0.225*

(Residual effect = 0.238) *, **Significant at 5% and 1% levels, respectively.

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP : Clusters per plant; 100SW :100 seed weight (g); BPP90 :Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP: Pod yield per plant (g); SPP : Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% (p<0.01) and 1% (p<0.001) level, respectively.

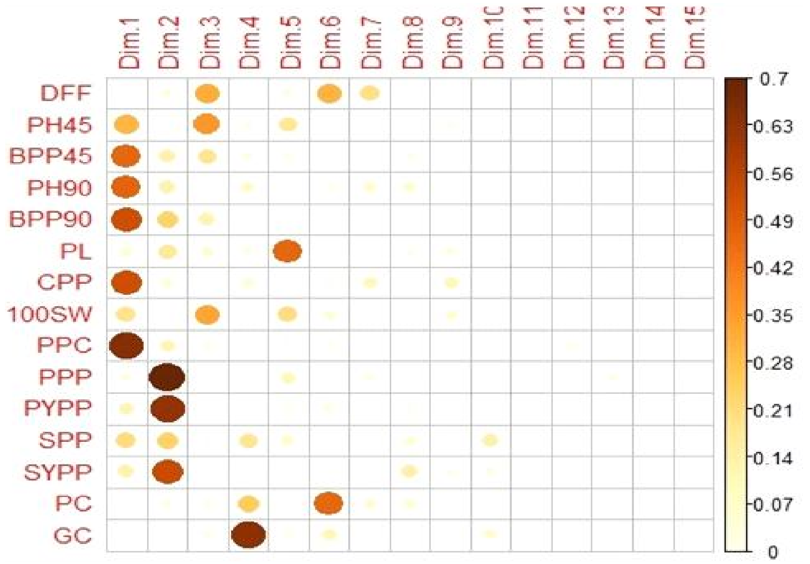
Table 4: Eigen value, cumulative variance and scores of the six major factors obtained from the PCA of fifteen quantitative traits.

Variable	PC1	PC2	PC3	PC4	PC5
Eigen value	3.80	3.16	1.67	1.45	1.28
% Variance	25.34	21.08	11.14	9.69	8.56
% Cumulative variance	25.34	46.42	57.55	67.25	75.80
DFF	0.16	0.24	-0.57**	-0.06	-0.23
PH45	0.55	0.13	0.61**	-0.18	0.42
BPP45	-0.69**	0.38	0.43	-0.24	0.20
PH90	0.69**	0.37	0.14	-0.31	-0.12
BPP90	-0.73**	0.48	0.36	-0.07	0.16
PL	0.26	0.42	-0.29	0.22	0.68**
CPP	-0.73**	0.25	0.15	0.28	-0.06
100SW	-0.44	-0.12	-0.58**	-0.15	0.46
PPC	0.81**	0.35	0.20	-0.09	-0.17
PPP	-0.24	0.84**	-0.13	0.01	-0.34
PYPP	-0.36	0.79**	-0.14	0.01	-0.18
SPP	0.46	0.49**	-0.17	0.44	0.29
SYPP	0.37	0.74**	-0.14	-0.13	-0.02
PC	0.00	0.24	0.19	0.51**	0.03
GC	0.15	-0.16	0.20	0.80**	-0.18

Significant factor loading was observed above 0.490.

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP :Clusters per plant; 100SW :100 seed weight (g); BPP90 :Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP :Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% (p<0.01) and 1% (p<0.001) level, respectively.



Dimensions represents the Principal components. Colour represents quality of representation of variables to the principal components.

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP : Clusters per plant; 100SW : 100 seed weight (g); BPP90 : Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP : Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% (p<0.01) and 1% (p<0.001) level, respectively.

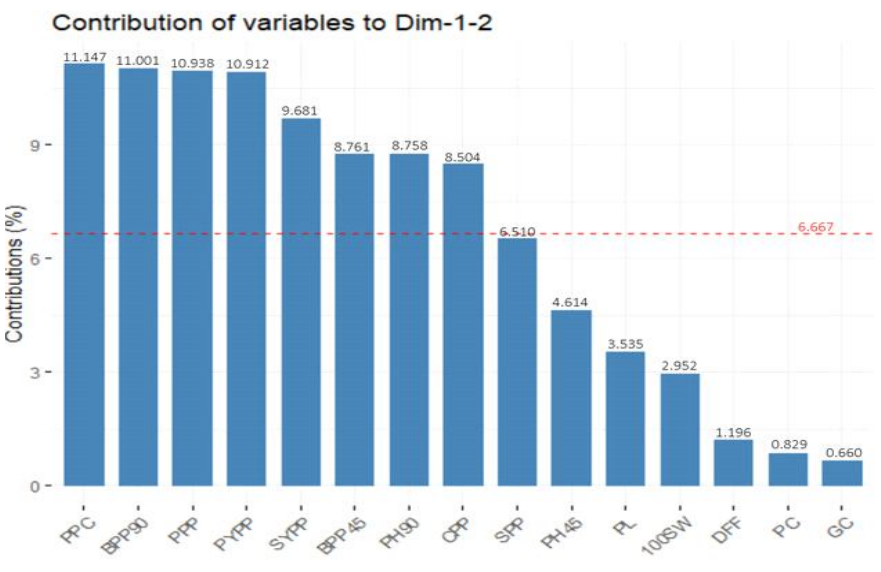
Fig 2: Quality of representation of different traits (cos^2).

Table 5: Contribution of different traits to the principal components.

Trait	PC1	PC2	PC3	PC4	PC5	PC6	Average contribution to PC-1 and PC-2
DFF	0.640	1.864	19.173	0.247	3.981	26.279	1.196
PH45	8.001	0.544	22.045	2.190	13.998	1.211	4.614
BPP45	12.344	4.455	11.232	3.881	2.961	1.197	8.761
PH90	12.502	4.257	1.238	6.800	1.177	3.481	8.758
BPP90	13.934	7.475	7.899	0.331	1.956	0.088	11.001
PL	1.807	5.612	4.851	3.230	36.455	0.031	3.535
CPP	13.931	1.980	1.336	5.399	0.297	2.625	8.504
100SW	5.043	0.439	20.260	1.489	16.268	5.910	2.952
PPC	17.182	3.894	2.381	0.548	2.218	3.447	11.147
PPP	1.533	22.243	1.056	0.003	8.750	0.470	10.938
PYPP	3.388	19.956	1.142	0.003	2.627	4.548	10.912
SPP	5.581	7.628	1.691	13.017	6.759	1.215	6.510
SYPP	3.536	17.068	1.130	1.136	0.046	0.303	9.681
PC	0.000	1.826	2.152	17.827	0.072	39.639	0.829
GC	0.578	0.758	2.415	43.898	2.435	9.557	0.660

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP :Clusters per plant; 100SW :100 seed weight (g); BPP90 :Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP :Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% (p<0.01) and 1% (p<0.001) level, respectively.



Red line indicates average expected contribution of traits assuming similar contribution from all the traits.

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP : Clusters per plant; 100SW : 100 seed weight (g); BPP90 : Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP : Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

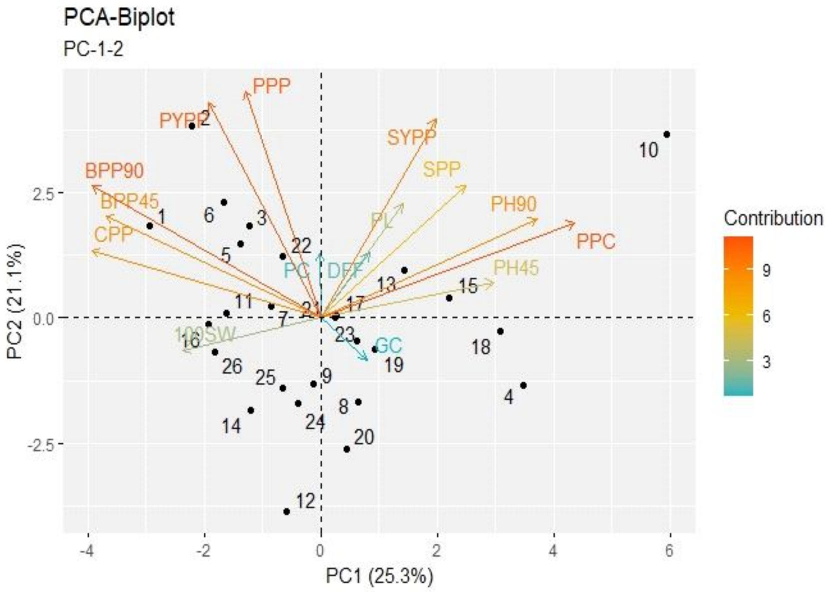
Note: * and ** indicate significant at 5% (p<0.01) and 1% (p<0.001) level, respectively.

Fig 3: An average percentage contribution of traits to the first two principal components.

lowest mean value for SYPP with early DFF and low mean value for other yield related traits PL, PPP, PYPP and SPP was due to its highest mean value for GC and PC. The mean values for the cluster I recorded good performance for yield and other yield related characters. So, the genotypes present in the cluster I and III can be utilized to get the desirable transgressive segregants for the maximum yield. On the

Table 6: Average intra (Bold) and inter cluster distance (D^2) of 26 cluster bean genotypes.

	Cluster 1	Cluster 2	Cluster 3
Cluster 1	**15.815**		
Cluster 2	32.146	**14.086**	
Cluster 3	31.006	22.807	**16.859**



Scattered numbers across the plot indicates serial number of genotypes enlisted in materials and methods.

DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP : Clusters per plant; 100SW : 100 seed weight (g); BPP90 : Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP : Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% (p<0.01) and 1% (p<0.001) level, respectively.

Fig 4: PCA Biplot of PC 1 and PC 2 representing distribution of 26 cluster bean genotypes and 15 quantitative traits.

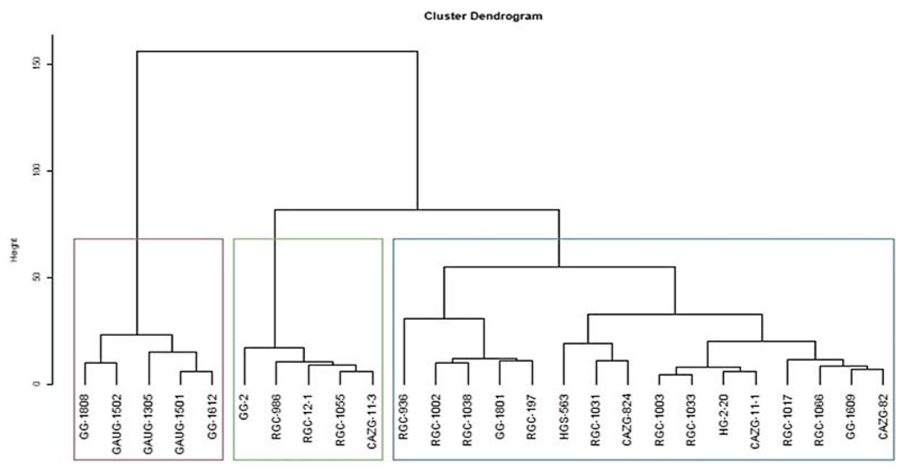
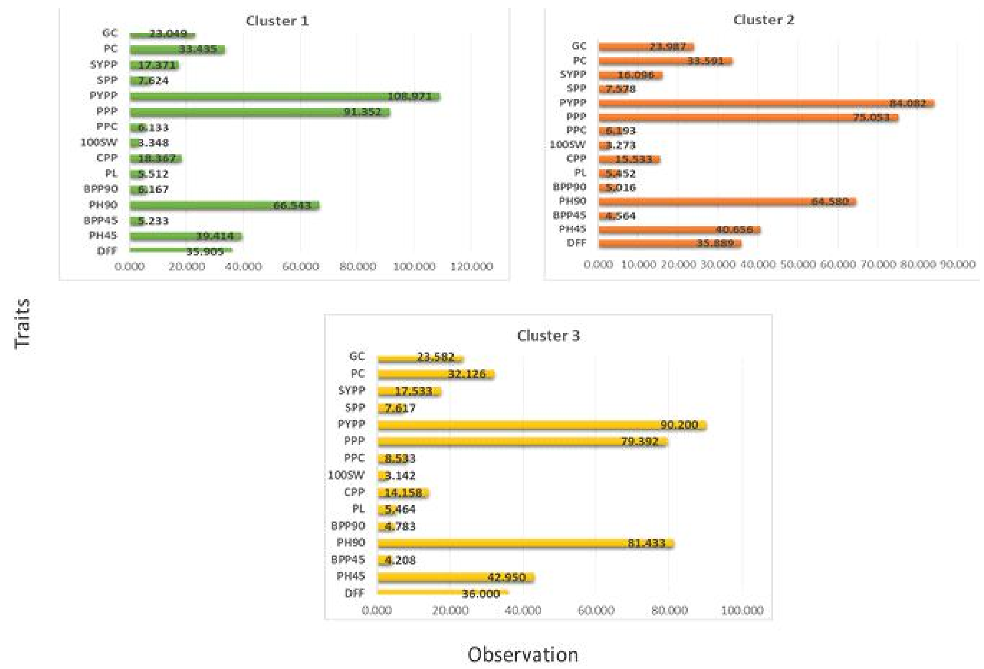


Fig 5: Dendrogram showing clustering pattern of 26 cluster bean genotypes (Ward method).



DFF : Days to 50 % flowering; PH45 : Plant height at 45 days (cm); BPP45 : Branches per plant at 45 days; PH90 : Plant height at 90 days (cm); PL : Pod length (cm); CPP : Clusters per plant; 100SW : 100 seed weight (g); BPP90 : Branches per plant at 90 days; PPC : Pods per cluster; PPP : Pods per plant; PYPP : Pod yield per plant (g); SPP : Seeds per pod; SYPP : Seed yield per plant (g); GC : Gum content (%); PC : Protein content (%).

Note: * and ** indicate significant at 5% (p<0.01) and 1% (p<0.001) level, respectively.

Fig 6: Cluster means for fifteen quantitative characters in 26 cluster bean genotypes.

other hand cluster I or cluster III genotypes could be crossed with the genotypes present in the cluster II to obtain the desirable transgressive segregants with maximum yield along with earliness, good protein and gum content. Genetic divergence estimated through intra and inter distance (D^2) values among the genotypes present in the clusters (Table 6). In all the cases inter cluster distances were more than intra cluster distance, indicating the presence of wide range of genetic diversity among the genotypic groups. On the other hand, the genotypes present within the clusters estimated less divergence among themselves. The inter cluster distance estimated highest between cluster I and II (32.146), followed by between cluster I and III (31.006) and between cluster II and III (22.807), indicating the presence of broad divergence among the genotypes present in these clusters, therefore genotypes present in these cluster could be utilized as a parent for varietal development. These findings were supported by (Khatoon *et al.,* 2023).

CONCLUSION

In essence, the genotype GAUG-1305 recoded higher pods per plant, while GAUG-1502 for higher pod yield per plant, the genotype RGC-1003 for high pod length and RGC-936 exhibited higher pods per cluster, seeds per pod and seed yield per plant; these genotypes could be further improved for the development of high yielding clusterbean cultivars. The genotypic variance was predominated by days to 50 % flowering, branches per plant at 45 days, branches per plant at 90 days, pod length, clusters per plant, 100 seed weight, pods per cluster, seeds per pod, protein content and gum content, so these traits can be improved by selection. High heritability with high genetic advance as percent mean represented by pods per cluster; branches per plant at 90 days and clusters per plant showed high genetic advance as percent mean, these traits effectively improved by selection due to additive gene action.The PCA- biplot revealed GAUG-1305, GG-1801, RGC-936 and RGC-986 as the most diverse genotypes for various traits. So, these genotypes could be utilized in the future breeding programs.

Conflict of interest

No conflict of interest.

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