



Research article

Variability, character association and genetic divergence studies in cowpea [*Vigna unguiculata* (L.) Walp] genotypes

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Received: 5th October, 2022

Accepted: 11th September, 2023

Abstract

The present experiment comprised of 46 cowpea genotypes to estimate genetic variability, interrelation among 13 quantitative characters and genetic divergence during *Kharif* 2020. High heritability coupled with high genetic advance as *per cent* of mean was observed for the characters *viz.*, seed yield per plant, number of clusters per plant, number of pods per plant, plant height, days to 50% flowering and days to maturity. High phenotypic and genotypic coefficient of variation, heritability and high genetic advance as *per cent* of mean (GAM) were observed in seed yield per plant, number of clusters per plant, number of pods per plant and plant height. Seed yield per plant was found positively and significantly correlated with pods per plant, seeds per pod, pods per cluster, pod length and 100 seed weight. Path analysis revealed that number of seeds per pod, number of pods per plant and 100 seed weight would be selected as important characters towards seed yield as they showed a high positive direct effect on seed yield. D^2 analysis revealed that all the genotypes were grouped into seven distinct clusters. Cluster V had the maximum intra-cluster distance. The crossing among the genotypes of clusters V and VII, II and V, III and VI would result in novel recombinants as they showed high inter-cluster distance. Increased contribution to the divergence was found for the characters like plant height, seed yield per plant, number of clusters per plant and days to 50% flowering. Cluster V was found to be best performing for agronomic characters, followed by Cluster VI and Cluster III. Cluster II was best performing for nutritional value and earliness.

Keywords: Correlation, D^2 analysis, GCV, Path coefficient, PCV

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is a diploid, self-pollinated annual legume with chromosome number $2n=2x=22$. Cowpea belongs to the family Fabaceae and genus *Vigna*. It is an important grain legume crop in developing countries of the tropics and subtropics (Nguyen *et al.*, 2019b). In India, cowpea is mainly cultivated for fodder, green manure and soil-improving cover crop (Gupta *et al.*, 2019a). The characters having high genotypic and phenotypic coefficient of variation encompass the possibility of significant variation. However, it does not determine the proportion of heritable variation of the total variation present for that character. Heritability and genetic gain together would be more helpful in predicting the effect of selection. Therefore, correctly understanding these parameters is essential for an efficient crop improvement

programme. Yield is a complex character determined by several component characters. Also, the knowledge of the correlation between yield and its component characters is essential for its improvement through selection programs as it helps in simultaneous selection for more than one character of importance at a time. Path analysis splits the correlation coefficients into direct and indirect effects of the component characters of yield based on which an effective crop improvement programme can be formulated. Evaluating and classifying cowpea germplasm into different groups help to assess effective selection among genetically diverse parents, which could be used in a hybridization programme. Keeping these points in view, the study aimed to estimate genetic variability, association among characters and genetic divergence among genotypes to improve cowpea.

Materials and Methods

Experimental material and design: The experimental material consisted of 46 cowpea genotypes whose sources were from different parts of India (Table 1). The material was evaluated in randomized block design (RBD) with three replications at the Dry Land Research Area of the Department of Genetics and Plant Breeding, CCSHAU, Hisar, during *Kharif* 2020. Each genotype was planted in a paired row of 2 m length, following row to row distance of 45 cm and plant-to-plant spacing of 15 cm. Observations were recorded on five randomly selected plants from each replication for 13 quantitative characters viz. plant height (cm), days to 50% flowering, days to maturity, number of branches per plant, number of pods per cluster, number of clusters per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100 seed weight (g), seed yield per plant (g), crude protein content (%) and digestibility (%). The experimental site comprised of a semi-arid climate with hot, dry

summer and severe cold winter. Average annual rainfall was about 450 mm, 75% of which was received in three months (July to September) during the south-west monsoon.

Statistical analysis: Statistical analysis was carried out according to Fisher (1918) for analysis of variance; Burton and De Vane (1953) for estimation of phenotypic and genotypic coefficients of variation, heritability and genetic advance; Al-Jibouri *et al.* (1958) for correlation coefficient, Dewey and Lu (1959) for path analysis and Mahalanobis (1936) for D^2 analysis.

Results and Discussion

Genetic variability: Significant differences among 46 genotypes for all 13 quantitative characters revealed the presence of considerable genetic variability for all the characters under study (Table 2). Arya *et al.* (2021) and Oo *et al.* (2022) also observed substantial genetic variation for different phenological, morphological, yield and yield-

Table 1. List of 46 cowpea genotypes evaluated during the study

S.No.	Genotype	Source	S.No.	Genotype	Source
1.	GC3	SDAU, S.K. Nagar	24.	VCP13001	NPRC, Vamban
2.	RC101	RARI, Durgapura	25.	PTBCP4	RARS, Pattambi
3.	Pant Lobia3	GBPUA&T, Pantnagar	26.	PTBCP5	RARS, Pattambi
4.	Pant Lobia4	GBPUA&T, Pantnagar	27.	GC1612	SDAU, S.K. Nagar
5.	CPD311	RARI, Durgapura	28.	SKAU407	SDAU, S.K. Nagar
6.	KBC13	UAS, Bangalore	29.	TPTC29	ARS, Tirupati
7.	CPD313	RARI, Durgapura	30.	PhuleCP1123	ARS, Pardharpur
8.	PGCP69	GBPUA&T, Pantnagar	31.	VCP12005	NPRC, Vamban
9.	PCP1124-1	ARS, Pardharpur	32.	CPD221	RARI, Durgapura
10.	KBC11	UAS, Bangalore	33.	TC172	BARC, Trombay
11.	GC1602	SDAU, S.K. Nagar	34.	CPD249	RARI, Durgapura
12.	TC901	BARC, Trombay	35.	GC1501	SDAU, S.K. Nagar
13.	GC1712	SDAU, S.K. Nagar	36.	PCP1131	ARS, Pardharpur
14.	PGCP70	GBPUA&T, Pantnagar	37.	PCP1118	ARS, Pardharpur
15.	CPD301	RARI, Durgapura	38.	GC1506	SDAU, S.K. Nagar
16.	VCP12006	NPRC, Vamban	39.	PL7	GBPUA&T, Pantnagar
17.	VCP14005	NPRC, Vamban	40.	GC01802	SDAU, S.K. Nagar
18.	PGCP67	GBPUA&T, Pantnagar	41.	CPD317	RARI, Durgapura
19.	CPD304	RARI, Durgapura	42.	PGCP71	GBPUA&T, Pantnagar
20.	VCP14001	NPRC, Vamban	43.	GC01805	SDAU, S.K. Nagar
21.	GC1601	SDAU, S.K. Nagar	44.	VCP15006	NPRC, Vamban
22.	PCP1122	ARS, Pardharpur	45.	CPD319	RARI, Durgapura
23.	PGCP68	GBPUA&T, Pantnagar	46.	PGCP72	GBPUA&T, Pantnagar

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attributing characters among the cowpea genotypes in their study material. The magnitudes of the phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the characters, indicating that these variations were not only governed by genotypic factors, but there was considerable influence by the environment. There was less difference between PCV and GCV for most of the characters studied except the number of branches per plant, number of pods per cluster, number of seeds per pod and pod length, indicating the strong influence of environment on phenotypic expression of these four characters. The presence of substantial PCV and GCV for seed yield per plant, number of clusters per plant, number of pods per plant, plant height and days to 50% flowering indicated considerable variations for the characters studied. Thus, there is good scope for further improvement through genetic manipulation. Above findings confirmed the results of earlier studies (Sharma *et al.*, 2017; Singh *et al.*, 2018; Baranda *et al.*, 2018; Gupta *et al.*, 2019b; Nguyen *et al.*, 2019b; Sharma *et al.*, 2019; Verma *et al.*, 2019; Chaudhary *et al.*, 2020; Panchta *et al.*, 2020; Purohit *et al.*, 2020; Rai and Sharma, 2020; Thangam *et al.*, 2020; Ugale *et al.*, 2020a; Tambitkar *et al.*, 2021). High heritability coupled with high genetic advance as *per cent* of mean (GAM) for the characters such as seed yield per plant, number of clusters per plant, number of pods per plant, plant height, days to 50% flowering

and days to maturity suggesting that there was predominant additive variation and hence, characters could be improved through direct selection. High PCV, GCV, heritability and GAM were observed in seed yield per plant, number of clusters per plant, number of pods per plant and plant height, indicating these characteristics could be improved through direct selection for high-yielding cowpea breeding. These findings were substantiated by Diwaker *et al.* (2017), Srinivas *et al.* (2017b), Gupta *et al.* (2019a), Nguyen *et al.* (2019b), Bamji *et al.* (2020b), Panchta *et al.* (2020), Purohit *et al.* (2020) and Thangam *et al.* (2020).

Correlation coefficient analysis: The results indicated that the magnitudes of the genotypic correlation coefficient were higher than their phenotypic correlation coefficients, showing an inherent association between different characters having considerably less influence on the environment (Fig 1-2). Seed yield per plant was positively and significantly associated with the pods per plant, seeds per pod, pods per cluster, pod length and 100 seed weight, indicating simultaneous selection based on these characteristics would be effective for seed yield. These results were supported either one or more than one trait indicated as earlier reported by Kumar *et al.* (2016), Srinivas *et al.* (2017a), Tsegaye *et al.* (2018), Gupta *et al.* (2019b), Nguyen *et al.* (2019b), Sharma *et al.* (2019a), Waghmare *et al.* (2019), Bamji *et al.* (2020a),

Table 2. Genetic parameters for thirteen characters in 46 cowpea genotypes

Characters	Mean $\pm$ SEM	Range	Coefficient of variation		Heritability (%)	Genetic Advance as % of mean
			GCV	PCV		
Days to 50% flowering	36.04 $\pm$ 0.91	25.67-56.33	20.61	21.07	95.72	41.54
Days to maturity	72.66 $\pm$ 1.96	59.33-112	15.9	16.57	92.07	31.44
Plant height (cm)	83.21 $\pm$ 1.92	50.00-143.00	25.04	25.35	97.51	50.93
No. of branches per plant	8.95 $\pm$ 0.77	6.00-14.67	17.65	23.04	58.69	27.86
No. of pods per plant	22.93 $\pm$ 1.10	11.67-38.33	25.53	26.85	90.39	49.99
No. of clusters per plant	13.70 $\pm$ 0.68	8.00-25.00	31.34	32.5	93.0	62.26
No. of pods per cluster	1.94 $\pm$ 0.16	1.22-3.11	16.21	21.73	55.6	24.89
No. of seeds per pod	11.43 $\pm$ 0.75	9.00-15.33	10.25	15.27	45.01	14.16
Pod length (cm)	12.85 $\pm$ 0.78	9.11-17.11	11.57	15.59	55.05	17.68
100-seed weight (g)	14.72 $\pm$ 0.60	10.77-20.64	15.42	16.95	82.7	28.88
Crude protein content (%)	22.85 $\pm$ 0.73	18.85-24.97	4.78	7.28	43.14	6.47
Digestibility (%)	68.95 $\pm$ 0.58	63.77-73.70	3.75	4.03	86.8	7.2
Seed yield per plant (g)	33.96 $\pm$ 1.60	14.35-74.34	40.07	40.89	96.01	80.87

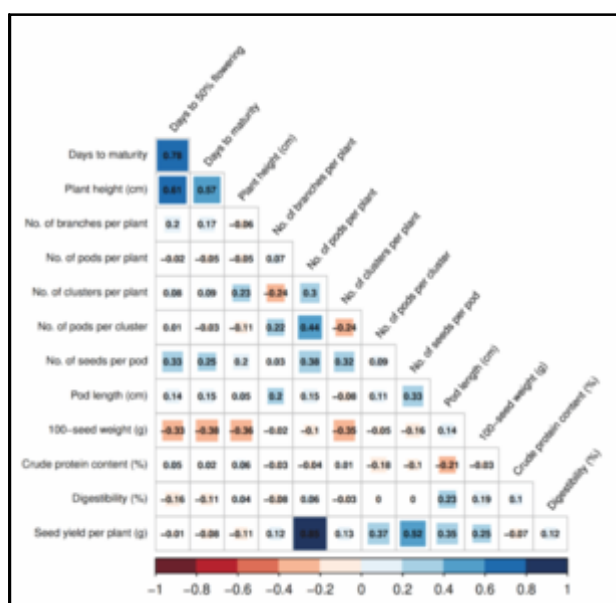


Fig 1. Correlogram showing phenotypic correlation coefficient among 13 quantitative characters in cowpea ($P < 0.01$)

Chaudhary *et al.* (2020), Panchta *et al.* (2020), Ugale *et al.* (2020b) and Snehal *et al.* (2021).

Path coefficient analysis: The value of residual effect in path analysis was 0.0622, showing 93.78% of total variation and the maximum impact of the characters on seed yield per plant (Table 3). The high direct effect of the number of seeds per pod, pods per plant and 100-seed weight on seed yield per plant indicated that these could be selected as necessary for the cowpea improvement programme. The results of these characters were in agreement with the previous reports by Tsegaye *et al.* (2018) and Bamji *et al.* (2020a). Similar findings were recorded earlier by Manisha *et al.* (2018), Sahu (2019) and Snehal *et al.* (2021) for 100 seed weight; by Manggoel *et al.* (2012) for the number of seeds per pod; by Lal *et al.* (2017), Gupta *et al.* (2019a), Panchta *et al.* (2020), Paghadar *et al.* (2019) and Snehal *et al.* (2021) for number of pods per plant; by Kumar *et al.* (2016), Srinivas *et al.* (2017a), Nguyen *et al.* (2019a) and Chaudhary *et al.* (2020) for pods per plant and seeds per pod.

The characters like days to 50% flowering, pod length and clusters per plant showed a negative direct effect on seed yield per plant, indicating that simultaneous selection against these characters would be difficult for seed yield improvement. Similar findings were reported by Kumar *et al.* (2016), Patel *et al.* (2016), Baranda *et al.* (2018), Manisha *et al.* (2018) and Bamji *et al.* (2020a) for clusters per plant; by Khandait *et al.* (2016), Chaudhary *et al.* (2020) and Panchta *et al.* (2020) for days to 50% flowering; by Nguyen *et al.* (2019b) for pod length.

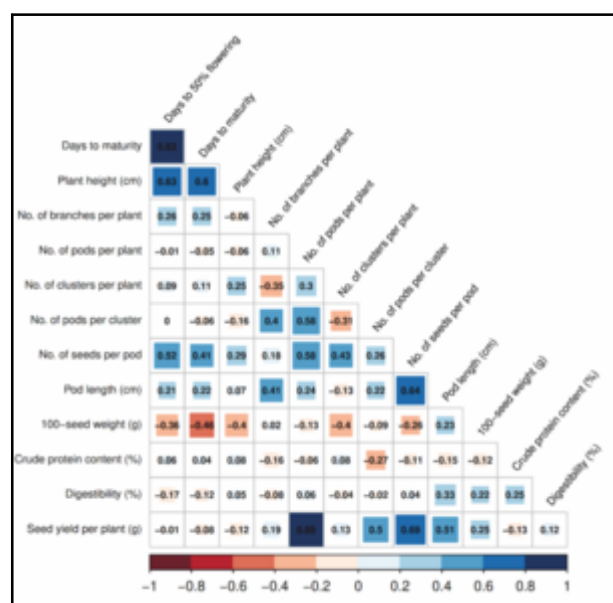


Fig 2. Correlogram showing genotypic correlation coefficient among 13 quantitative characters in cowpea ($P < 0.01$)

A high positive indirect effect on seed yield per plant was shown by the number of seeds per pod, number of pods per cluster, number of clusters per plant, and pod length, through the number of pods per plant, showing direct selection would not be effective based on these traits. This result was in accordance with the previous report of Nguyen *et al.* (2019b) for seed yield. Similar findings were also observed by Walle *et al.* (2018) and Bamji *et al.* (2020a) for number of clusters per plant and pod length; by Lal *et al.* (2018), Paghadar *et al.* (2019), Waghmare *et al.* (2019) and Chaudhary *et al.* (2020) for number of seeds per pod and pod length; by Gupta *et al.* (2019b) for number of pods per cluster and number of clusters per plant.

A high negative indirect effect was shown by days to maturity (-0.237), number of clusters per plant (-0.207), plant height (-0.201) and days to 50% flowering (-0.186) via 100-seed weight. The results were confirmed as reported earlier by Kujur and Sahu (2019) for plant height and by Bamji *et al.* (2020a) for number of clusters per plant. The present study revealed that characters viz., number of pods per plant, number of seeds per pod and 100 seed weight would be selected as important characters towards seed yield for the cowpea improvement programme. The value of residual effect in path analysis was found to be 0.0622, showing 93.78% of total variation and the maximum impact of the traits on seed yield per plant under study.

D² analysis: Results of the clustering pattern among 46 cowpea genotypes revealed that all the genotypes

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Table 3. Direct (diagonal) and indirect effects of various characters on seed yield per plant in cowpea (residual: 0.0622)

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches per plant	No. of pods per plant	No. of clusters per plant	No. of seeds per pod	Pod length (cm)	100-seed weight (g)	Crude protein content (%)	Digestibility (%)	Genetic Correlation Coefficient
Days to 50% flowering	-0.5001	0.1755	0.0758	0.0234	-0.0074	-0.0296	-0.0001	0.5126	-0.0799	-0.1859	0.0039	-0.0060
Days to maturity	-0.4172	0.2103	0.0729	0.0229	-0.0326	-0.0344	0.0038	0.4052	-0.0817	-0.2373	0.0028	-0.0812
Plant height (cm)	-0.3143	0.1271	0.1206	-0.0050	-0.0379	-0.0786	0.0095	0.2862	-0.0250	-0.2088	0.0051	-0.1228
No. of branches per plant	-0.1278	0.0527	-0.0066	0.0915	0.0647	0.1104	-0.0241	0.1767	-0.1556	0.0123	-0.0112	0.1858
No. of pods per plant	0.0062	-0.0114	-0.0076	0.0099	0.6017	-0.0968	-0.0345	0.5791	-0.0903	-0.0675	-0.0044	0.8821
No. of clusters per plant	-0.0467	0.0228	0.0299	-0.0318	0.1833	-0.3175	0.0183	0.4238	0.0484	-0.2073	0.0054	0.1300
No. of pods per cluster	-0.0005	-0.0133	-0.0191	0.0368	0.3474	0.0973	-0.0598	0.2581	-0.0840	-0.0484	-0.0184	0.4967
No. of seeds per pod	-0.2576	0.0856	0.0347	0.0163	0.3501	-0.1352	-0.0155	0.9953	-0.2389	-0.1347	-0.0073	0.6912
Pod length (cm)	-0.1062	0.0457	0.0080	0.0378	0.1443	0.0408	-0.0133	0.6316	-0.3765	0.1203	-0.0101	0.5106
100-seed weight (g)	0.1781	-0.0956	-0.0483	0.0022	-0.0777	0.1261	0.0055	-0.2568	-0.0867	0.5221	-0.0083	0.2529
Crude protein content (%)	-0.0286	0.0086	0.0092	-0.0151	-0.0390	-0.0254	0.0163	-0.1082	0.0563	-0.0643	0.0675	-0.1316
Digestibility (%)	0.0851	-0.0248	0.0061	-0.0073	0.0389	0.0126	0.0010	0.0419	-0.1251	0.1132	0.0168	-0.0354

were grouped into seven distinct clusters (Table 4; Fig 3). It was evident that the existence of high amount of genetic divergence for selecting parents in the hybridization program. Cluster I was the largest group, followed by clusters III, II, IV, V, VII and VI. The present grouping of genotypes revealed that geographical distribution was not as important as genetic diversity in selecting parents for

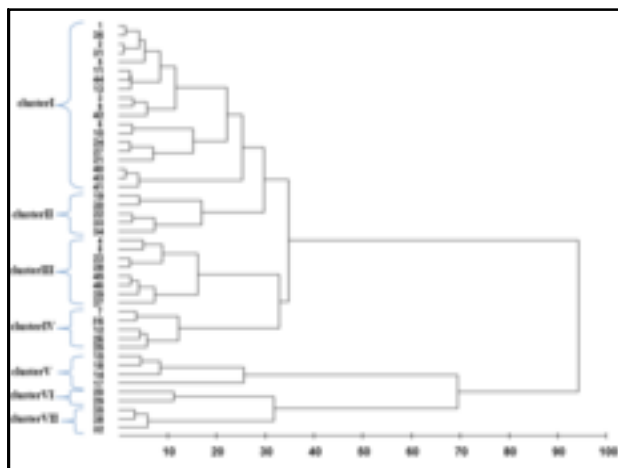


Fig 3. Dendrogram showing the clustering pattern of 46 cowpea genotypes

hybridization, although it was a scale of genetic diversity. Lal *et al.* (2017) demonstrated that parents' choice for hybridization should be based on genetic rather than geographical diversity.

Intra- and inter-cluster distances among different clusters (Table 5) revealed that cluster V had the maximum intra-cluster distance. The involvement of genotypes belonging to Cluster-V and VII, II and V, III and VI in hybridization would help to achieve novel recombinants as they showed maximum inter-cluster distance.

The contribution of an individual character towards variability in terms of the number of times appearing first was recorded (Table 6). High contribution to the divergence by the characters like plant height, seed yield per plant, number of clusters per plant and days to 50% flowering, indicated that selection for divergent parents based on these characters would be useful for successful breeding in cowpea. Similar finding was also observed by Lal *et al.* (2017), Patel *et al.* (2017), Lal *et al.* (2018), Nguyen *et al.* (2019b) and Purohit *et al.* (2020).

The cluster mean for 13 characters was also recorded (Fig 4). Results suggested that cluster V

Table 4. Distribution pattern of 46 cowpea genotypes into 7 clusters

Cluster no.	Number of genotypes	Genotypes
I	19	GC3, PCP1131, RC101, VCP12005, CPD311, GC1602, VCP15006, GC1712, Pant Lobia3, PCP1124-1, PGCP71, KBC13, KBC11, VCP13001, GC1612, GC1601, GC01802, GC01805, CPD317
II	5	CPD304, Phule CP 1123, PCP1122, TC172, CPD249
III	8	Pant Lobia4, PGCP69, PGCP68, SKAU407, CPD319, PGCP72, PL7, PCP1118
IV	5	CPD313, VCP12006, TC901, PTBCP5, PTBCP4
V	4	CPD301, PGCP67, PGCP70, VCP14005
VI	2	VCP14001, TPTC29
VII	3	GC1501, GC1506, CPD221

Table 5. Inter and intra (diagonal) cluster average of D^2 values among different clusters in cowpea

Attributes	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	3.757	4.537	4.322	4.520	6.001	5.886	6.076
Cluster II		3.984	4.766	4.880	7.187	6.028	6.420
Cluster III			3.650	4.668	6.886	7.076	6.874
Cluster IV				3.614	5.900	5.783	6.411
Cluster V					5.094	6.288	7.721
Cluster VI						4.771	5.954
Cluster VII							3.059

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Table 6. Percent contribution of each character towards divergence

S. no.	Characters	Number of times ranked 1 st	Contribution (%)
1	Days to 50% flowering	160	15.46
2	Days to maturity	33	3.19
3	Plant height (cm)	279	26.96
4	No. of branches per plant	3	0.29
5	No. of pods per plant	27	2.61
6	No. of clusters per plant	165	15.94
7	No. of pods per cluster	0	0.00
8	No. of seeds per pod	0	0.00
9	Pod length (cm)	1	0.10
10	100-seed weight (g)	45	4.35
11	Crude protein content (%)	5	0.48
12	Digestibility (%)	95	9.18
13	Seed yield per plant (g)	222	21.45

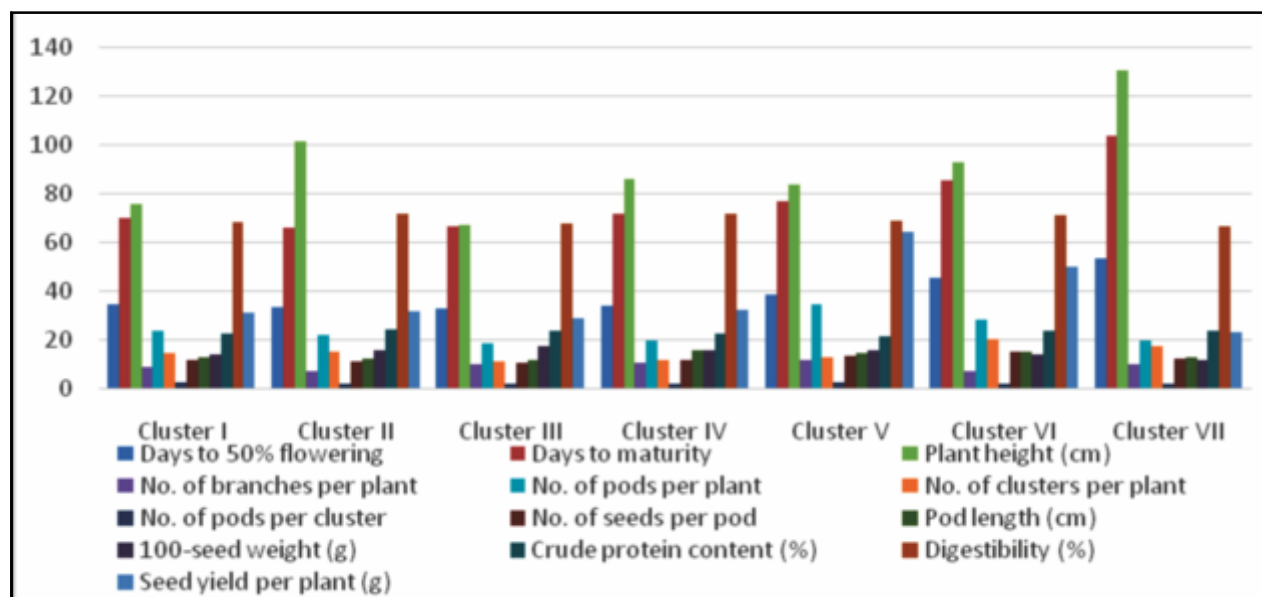


Fig 4. Column chart representing cluster mean for 13 characters of seven clusters

showed the highest mean values for seed yield per plant, number of pods per plant, number of branches per plant and number of pods per cluster. Cluster VI recorded the highest values for the number of clusters per plant and number of seeds per pod, whereas cluster III exhibited the highest values for 100 seed weight but lowest in days to 50% flowering. Cluster II possessed the highest mean values for crude protein content and digestibility with a minimum value of days to maturity. It was evident that Cluster V performed best for agronomic characters, followed by Cluster VI and III, while Cluster II performed best for nutritional values and earliness.

Conclusion

The outcomes of the present study showed substantial variability present in the cowpea germplasm studied of almost all the characters. The high magnitude of heritability coupled with high genetic advance as *per cent* of mean was observed for seed yield per plant, along with other characters and selection could be rewarding for improving seed yield. Association studies revealed that the number of seeds per pod, number of pods per plant and 100 seed weight were important characters towards seed yield as they showed a high positive direct effect. Improvement in these characters could lead to an

increase in seed yield. D² analysis partitioned the germplasm into distinct 7 clusters. Maximum inter-cluster distance was found between clusters V and VII, II and V, III and VI. Recombination among the genotypes belonging to these clusters would result in novel recombinants. The contribution by the characters like plant height, seed yield per plant, number of clusters per plant and days to 50% flowering was high to the divergence. Cluster V was found to be best performing for agronomic characters, while Cluster II contains genotypes that best perform for nutritional value and earliness.

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