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Assessment of genetic diversity based on principal component analysis in vegetable cowpea (*Vigna unguiculata* (L.) Walp.) germplasm

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Abstract

Data on key flowering, maturity and yield attributes of 87 cowpea accessions including exotic and indigenous accessions were subjected to genotype clustering and principal component analysis (PCA) to identify diverse elite accessions for vegetable purpose. Based on PCA, PC-I, PC-II and PC-III had eigen values more than one, which contributed to 90.87% of total cumulative variability among germplasm. PC-I followed by PC-II and PC-III contributed maximum (46.34%, 28.40% and 15.63%) towards variability. The PC-I exhibited factor loadings in the positive sign for days taken to the happening of first flowering, days required to 50% of plants to flower, days taken to setting of first fruit and days to first harvest, while, except pods per plant and per plant pod yield, all other factors registered were positive towards PC-II. As many as nine traits have contributed positive factor loadings towards PC-III. Cluster analysis grouped 87 vegetable cowpea genotypes into 16 divergent clusters, cluster-II comprised a maximum of 45 genotypes followed by cluster I and XII. As many as 10 out of 16 clusters were solitary with unique genotypes revealing a greater amount of diversity among the germplasm. As confirmed by the D² statistic, the maximum diversity was elucidated by the VI cluster genotypes against those of cluster-XVI and between clusters VII and XVI as well. The maximum uniformity was observed between cluster-IV and cluster-V. Selection of genotypes should be based on the pods formed per plant followed by days taken to 50% flowering of plants, as their contribution for the total divergence of the germplasm was the maximum. Therefore, the investigation suggests that cross combinations between divergent accessions of cluster-V, III, and II, may lead to maximum heterosis in realizing hybrid breeding and isolation of superior breeding lines as well in vegetable cowpea breeding.

1. Introduction

Cowpea (*Vigna unguiculata* (L.) Walp.) is the legume crop. This crop attracted immense importance in cultivation by virtue of it is nitrogen-fixing properties, which fixes 60-70 kg nitrogen per hectare area, high protein content ranging from 20-25% in various cultivars and livestock feed as well (Diouf and Hilu, 2005; Sharmar *et al.* 2013). Compared to other food legumes, cowpea thrives well in drier parts of tropics, hence, established as warm weather and drought-tolerant crop. Due to its shade tolerance, it better fits as an intercrop also (Singh *et al.*, 2003).

Cowpea, though predominantly a pulse crop, initially it's utilized as an underutilized leafy vegetable. In Asia, selection pressure among the introduced unguiculata lines in the process of domestication resulted in the evolution of fleshy, succulent and long pod types. Thus, length of the pod and succulence are the distinguishing features

of cowpea for the vegetable purpose from traditional cowpea (Smart, 1990; Steele and Mehra, 1980). Common cowpea and or African cowpea are generally grain-type (unguiculata), 'yardlong' bean or asparagus bean is vegetable cowpea (*Vigna unguiculata* ssp. *sesquipedalis*). In addition to end-use, thickness and size of the pod and architecture of the plant are the basis for differentiation of two subspecies, at present understanding (Xu *et al.*, 2016, 2010; Timko *et al.*, 2007). The recent investigations revealed further that the cowpea is an excellent vegetable as its tender beans retain a good amount of protein in addition to fibre and other nutrients. To extend the cultivated area, the availability of high yielding varieties, in addition to their biotic and abiotic stress resistance should be ensured.

Several statistical tools, principal component analysis and euclidean clustering as well are employed to study genetic diversity. The PCA technique (Abdi and Williams, 2010) is widely used to assess genetic diversity. Through principal components, this technique helps in maximizing the variance (Jolliffe and Cadima, 2016) and also directs to establish quantitative characters contributing towards genetic divergence (Jindal *et al.*, 2018). Previous studies on divergence in various vegetable crops including cowpea (Kouam *et al.*, 2018 in cowpea, Pidigam *et al.*, 2019 in yard long bean.) highlighted the importance of PCA. The present investigation, therefore, was aimed

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to unravel the genetic divergence among indigenous versus exotic cowpea germplasm based on principal component analysis.

2. Material and Methods

An investigation was performed during *Kharif*, 2019 at College of Horticulture, Sri Konda Laxman Telangana State Horticultural University, Hyderabad, Telangana (India). A total of 87 vegetable cowpea accessions with the inclusion of 59 exotic collections from the International Institute of Tropical Agriculture, Nigeria, along with 24 indigenous germplasm augmented from different states of India and four commercial varieties were evaluated in Randomized Block Design with two replicates. The general packages of practices as recommended were adapted to grow the healthy cowpea crop. Observations were noted with respect to two flowering, two maturities, and six yield attributing traits. The yield per plant and its associate characters were recorded on a plot basis.

2.1 Statistical analysis

WINDOSTAT Software Version 9.2. was used for data analysis. Analysis of variance (ANOVA) was taken us to identification

significant variations among the genotypes. Principal component analysis and cluster analysis were performed following chord distance coefficient, while the average-linkage method of the datasets were as explained by Mazzucato *et al.* (2008).

3. Results

3.1 Analysis of variance (ANOVA)

The values of mean sum of square were significant ($p < 0.05$) for the 87 genotypes based on the ten characters (Table 1), indicating that there is the presence of exercisable and sufficient variation among cowpea accessions under investigation.

Table 1: Analysis of variance of ten key traits in vegetable cowpea genotypes

Source of Variation	Degrees of freedom	Sum of squares	Mean squares
Germplasm	86	3.62E + 16	4.21E + 14**
Error	85	1.97E – 02	2.32E – 04
Total	171	3.62E + 16	2.12E + 14

Table 2: Principal component analysis of ten key traits in vegetable cowpea genotypes

Canonical roots analysis (P.C.A)	1 Vector	2 Vector	3 Vector	4 Vector
Eigen Value (Root)	4.684	2.840	1.563	0.498
% Var. Exp.	46.838	28.401	15.627	4.978
Cum. Var. Exp.	46.838	75.240	90.866	95.844
Eigen vector: Variables				
First flowering (days)	0.417	0.152	0.230	0.046
50% flowering (days)	0.420	0.159	0.213	0.073
1st fruit set (days)	0.415	0.174	0.210	0.028
1st harvest (maturity) (days)	0.420	0.158	0.206	0.052
Pod length in cm	-0.243	0.444	0.171	0.097
Pod width in cm	-0.243	0.428	0.164	-0.468
Mature pod weight in grams	-0.279	0.428	0.202	0.190
Number of pods	-0.161	-0.206	0.633	-0.482
Number of seeds per pod	-0.018	0.521	-0.344	0.078
Pod yield per plant in grams	-0.282	-0.137	0.446	0.697

Analysis based on principal component (PC) revealed that three PCs, out of four generated, serially, I PC, II PC and III PC, had eigen values more than one (ranging from 1.56 to 4.68). Three PCs cumulatively contributed to 90.87% of total variability accounted among accessions studied (Table 2). The PC-I contributed the highest (46.34%) followed by PC-II with 28.40%, while PC-III contributed for 15.63% towards variability. The first PC exhibited factor loadings with +ve sign for first flowering days, 50% flowering days, days taken for setting of first pod and number of days registered to first harvest, while all the factors except for pods set per plant and average pod yield obtained per single plant registered positive factor loading towards PC-II. Towards PC-III, out of ten traits studied, nine traits except for seeds formed per pod have contributed factor loadings in positive sign.

Cluster analysis of genotypes was performed on the basis of ten characters using Tocher's method (Rao, 1952) adapting the D^2 statistic (Mahalanobis's, 1936) and is presented in Table 3. Cluster analysis grouped 87 vegetable cowpea genotypes into 16 clusters. Cluster-II comprised of 45 genotypes followed by I and XII clusters, with 22 and 3 genotypes, respectively. While, three clusters, *i.e.*, cluster VIII, XIII and XVI had two genotypes each. Very interestingly, a large number of clusters (III (EC-390225), IV (EC-390230), V (IC-20645), VI (EC-724547), VII (EC-390231), IX (EC-390264), X (EC-715197), XI (IC-249141), XIV (EC-723987) and XV (EC-390239) were solitary with single genotypes.

With reference to cluster means, the lowest cluster mean values and highest cluster mean values (Table 4) were reported in cluster 7 with

37 days and cluster 10 with 61 days, respectively for first flowering, while cluster 6 and 7 (41.50 days) with early 50% flowering and cluster 10 (69.50 days) had taken more average days to 50% flowering. With respect to days to 1st pod set, cluster 7 exhibited an average

early pod set (44.50), while the late mean fruit set was exhibited by cluster 10. Cluster 7 and 10 were registered with the lowest average days (50.50) and highest (81) average days to first harvest, respectively.

Table 3: Grouping of genotypes into different clusters in vegetable cowpea

Cluster number	Number of genotypes	Genotypes
1.	22 (13 EC and 9 IC)	EC-244018, EC-367694, EC-390204, EC-390207, EC-424872, EC-723784, EC-724296, EC-724319, EC-724416, EC-724552, EC-724805, EC-724907, EC-738119, IC-202796, IC-202824, IC-202924, IC-202931, IC-20720, IC-257449, IC-2574563, IC-259063, IC-97806
2.	45 (36 EC and 9 IC)	EC-101994, EC-343457, EC-390223, EC-723840, EC-390219, EC-724390, EC-724391, EC-724791, EC-734326, EC-390266, EC-724418, IC-202813, EC-367692, EC-724712, EC-724775, EC-738091, IC-219481, EC-202799, EC-202825, EC-202925, IC-257427, IC-333106, IC-91458, IC-202100, IC-202718, IC-202762, EC-725119, EC-725153, EC-725159, EC-725167, EC-734326, EC-738089, EC-724873, EC-724897, EC-724591, EC-724678, EC-724452, EC-724471, EC-724484, EC-724328, EC-724364, EC-390269, EC-390278, EC-390233, EC-390239
3	1 EC	EC-390225
4	1 EC	EC-390230
5	1IC	IC-20645
6	1 EC	EC-724547
7	1 EC	EC-390231
8	2 Check varieties	Kashi Kanchan, Kashi Unnati
9	1 EC	EC-390264
10	1 EC	EC-715197
11	1 IC	IC-249141
12	4 IC	IC-202827, IC-206240, IC-202931, IC-259069
13	2 Check varieties	Arka Samruddi, Arka Suman
14	1 EC	EC-723987
15	1 EC	EC-390239
16	2EC	EC-390210, EC-724374

Table 4: Cluster means of various characters in vegetable cowpea germplasm

Character/Cluster	Days to first flowering	Days to 50% flowering	Days to 1st pod set	Days to 1st harvest (maturity)	Pod length (cm)	Pod width (cm)	Mature pod weight (gm)	No.of Pods	No.of seeds per pod	Pod yield per plant (g)
Cluster 1	47.32	51.27	56.14	62.14	14.55	0.60	4.04	49.72	15.41	195.17
Cluster 2	52.26	56.38	62.32	67.74	14.73	0.45	4.36	14.70	13.83	68.03
Cluster 3	40.00	43.50	47.00	54.50	17.60	1.00	7.76	29.85	17.00	249.68
Cluster 4	43.00	49.00	53.50	59.00	12.75	1.00	3.68	71.13	15.50	262.56
Cluster 5	39.00	42.00	47.50	54.00	15.75	0.55	4.38	74.50	16.00	311.60
Cluster 6	39.50	44.50	47.50	52.00	15.25	0.50	3.31	1.42	10.00	4.26
Cluster 7	37.00	41.50	44.50	50.50	19.60	1.10	9.18	12.63	13.50	118.13
Cluster 8	50.25	49.75	57.00	60.75	20.63	0.64	9.33	61.75	22.25	286.50
Cluster 9	49.00	54.00	61.50	67.00	19.50	0.15	8.26	52.25	14.00	428.75
Cluster 10	61.00	69.50	74.50	81.00	15.25	0.50	2.66	32.13	15.50	85.10
Cluster 11	39.00	43.00	47.00	53.00	12.20	0.45	3.33	87.00	15.50	273.91
Cluster 12	55.13	57.88	64.13	70.13	14.19	0.64	3.44	108.09	15.75	367.15
Cluster 13	38.25	44.50	50.00	54.50	40.75	0.75	18.50	55.25	40.75	299.00
Cluster 14	40.00	44.50	47.50	52.50	18.85	1.05	9.05	54.38	16.50	497.45
Cluster 15	39.00	44.00	47.00	51.50	17.75	0.50	5.36	90.25	16.50	490.00
Cluster 16	47.00	51.25	57.25	61.50	15.38	0.75	5.46	134.63	14.75	743.65

Average pod length of 40.75 cm was exhibited by the genotypes of cluster 13, while the lowest was in cluster 11 (12.20 cm). For pod width, cluster 7 with 1.1 cm pod width was the highest cluster mean, while, two clusters, *i.e.*, cluster 2 and cluster 11 exhibited lowest cluster means (0.45 cm). Cluster 13 had the highest average cluster mean for mature pod weight (18.50 g) and the number of seeds per pod (40.75). Cluster 16 had exhibited the highest mean cluster values for pods formed per plant (134.63) and pod yield obtained per plant (743.63 g), respectively. While the lowest cluster means were recorded for cluster 6 for the number of pods (1.42), the number of seeds per pod (10) and pod yield per plant (4.26 g). For pod width (cm), the

lowest cluster mean was reported with cluster 10 (2.66) (Table 4). Pair-wise Mahalanobis cluster distances (D^2 statistics) are presented in Table 5. Based on inter cluster distances, the maximum diversity of 46082.81 was elucidated between cluster VI and XVI followed by cluster 7 and 16 (40581.15), while lowest inter cluster distance was noticed between cluster-IV and cluster-V (215.49). The intra cluster distances revealed that cluster 12 was most diverse with a distance of 1178.37 followed by cluster 16 (1178.33) and cluster 2 (931.14). While, intra cluster distances of 780.62, 595.56 and 343.54 were reported for cluster 1, cluster 13 and cluster 8, respectively. Ten out of 16 clusters had zero intra cluster distances.

Table 5: Cluster distances (inter and intra) in vegetable cowpea accessions

Cluster number	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	780.62	3864.55	2254.89	1601.78	1995.58	6414.46	5182.63	6128.01
Cluster 2	3864.55	931.14	1888.49	8535.52	9412.33	1559.45	1834.74	11589.43
Cluster 3	2254.89	1888.49	0.00	5385.12	5475.73	2356.28	917.97	7660.89
Cluster 4	1601.78	8535.52	5385.12	0.00	215.49	12343.13	10172.83	4999.14
Cluster 5	1995.58	9412.33	5475.73	215.49	0.00	12864.40	10385.13	5962.39
Cluster 6	6414.46	1559.45	2356.28	12343.13	12864.40	0.00	837.86	15480.14
Cluster 7	5182.63	1834.74	917.97	10172.83	10385.13	837.86	0.00	11317.07
Cluster 8	6128.01	11589.43	7660.89	4999.14	5962.39	15480.14	11317.07	343.54
Cluster 9	1287.24	4641.96	2041.81	2119.60	2152.63	7684.54	5360.01	6157.38
Cluster 10	2024.60	1960.55	3142.69	4762.65	6069.29	4953.14	4951.18	8274.75
Cluster 11	3917.05	13523.60	9245.17	709.69	537.30	17806.47	15225.82	7531.51
Cluster 12	9785.01	22802.75	18431.00	4339.73	4545.21	30019.63	26656.64	11372.52
Cluster 13	14659.41	18034.93	12778.56	14880.85	15590.86	21097.42	14916.65	3902.30
Cluster 14	2077.85	6083.99	1909.79	2501.89	2137.00	8239.79	5216.79	5489.34
Cluster 15	4904.38	15142.90	9624.34	1395.32	847.14	19656.51	16089.06	7575.34
Cluster 16	19794.90	37696.84	29789.93	11395.65	10693.70	46082.81	40581.15	19165.89
Cluster number	Cluster 9	Cluster 10	Cluster 11	Cluster 12	Cluster 13	Cluster 14	Cluster 15	Cluster 16
Cluster 1	1287.24	2024.60	3917.05	9785.01	14659.41	2077.85	4904.38	19794.90
Cluster 2	4641.96	1960.55	13523.60	22802.75	18034.93	6083.99	15142.90	37696.84
Cluster 3	2041.81	3142.69	9245.17	18431.00	12778.56	1909.79	9624.34	29789.93
Cluster 4	2119.60	4762.65	709.69	4339.73	14880.85	2501.89	1395.32	11395.65
Cluster 5	2152.63	6069.29	537.30	4545.21	15590.86	2137.00	847.14	10693.70
Cluster 6	7684.54	4953.14	17806.47	30019.63	21097.42	8239.79	19656.51	46082.81
Cluster 7	5360.01	4951.18	15225.82	26656.64	14916.65	5216.79	16089.06	40581.15
Cluster 8	6157.38	8274.75	7531.51	11372.52	3902.30	5489.34	7575.34	19165.89
Cluster 9	0.00	2964.23	4561.51	9921.47	13514.84	652.89	4184.23	18064.80
Cluster 10	2964.23	0.00	8775.75	14617.45	16658.06	5301.19	10546.70	28165.05
Cluster 11	4561.51	8775.75	0.00	2557.30	18787.04	4630.71	606.74	7618.13
Cluster 12	9921.47	14617.45	2557.30	1178.37	24395.98	11028.86	2864.20	3763.37
Cluster 13	13514.84	16658.06	18787.04	24395.98	595.86	11700.35	17746.82	32796.37
Cluster 14	652.89	5301.19	4630.71	11028.86	11700.35	0.00	3758.11	17846.79
Cluster 15	4184.23	10546.70	606.74	2864.20	17746.82	3758.11	0.00	5956.56
Cluster 16	18064.80	28165.05	7618.13	3763.37	32796.37	17846.79	5956.56	1178.33

From per cent contribution to total divergence, it is evident that pod number per plant contributed maximum (72.89%), which ranked 2727 times followed with days taken to 50% flowering (8.29%), pod width (5.99%), mature pod weight (4.04%), per plant pod yield (3.77%) and number of days genotypes took to first pod set (3.50%) for total genetic divergence reported. While negligible (<1%) contribution was made by days to 1st harvest, pod length and number of seeds per pod. Days to first flowering had no contribution (zero times ranked 1st) towards total genetic divergence in the present study (Table 6).

Table 6: Per cent contribution of various characters towards total divergence in vegetable cowpea germplasm

Source	Number of times Ranked 1 st	Contribution in per cent
First flowering (days)	0	0%
50% flowering (days)	310	8.29%
Days to 1st fruit set	131	3.50%
Days to 1st harvest (maturity)	32	0.86%
Pod length (cm)	13	0.35%
Pod width (cm)	224	5.99%
Mature pod weight (gm)	151	4.04%
No. of pods per plant	2727	72.89%
No. of seeds per pod	12	0.32%
Pod yield per plant (g)	141	3.77%

4. Discussion

From the analysis of variance, the significance of germplasm studied for the ten characters indicated that there is the presence of exercisable and sufficient variation among cowpea accessions under investigation. Genetic variation is the pre-requisite for any crop improvement. Hence, the 87 genotypes investigated can act as the basis for further selection of high yielding vegetable cowpea varieties. More so, the exotic germplasm introduced from IITA, Negeria will further broaden the germplasm pool of Indian vegetable cowpea, if included in crossing programmes. Thangam (2020) and Fatokun *et al.* (2017) studied genetic divergence in cowpea and found high divergence.

Based on principle component analysis, three PCs out of four, *viz.*, I PC, II PC and III PC, cumulatively contributed more than 90 % of total variability, explaining they are the reliable for revealing variability. It is observed that vegetable cowpea flowering (DFF, D50% F) and maturity (DFFS, DFFH) related traits were those with highest contribution to PC-I, whereas pod related traits, number of seeds per pod, pod length, mature pod weight and pod width were the major contributors to II PC. Hence, both I PC and II PC could be named, collectively as a reproductive axis. The PC-III, therefore, can act as the vegetative axis, as the number of pods presented in it contributed maximum share. The study clearly highlighted that principal component (s) analysis is useful for identification of some traits, which can act as basis for executing selections. The similar findings are reported earlier by several investigators (Krsteva and Dimova, 2007; Usha Kumari *et al.*, 2000; Fang *et al.*, 2007; Aremu *et al.*, 2007; Walle *et al.*, 2019). Fatokun *et al.* (2017) reported 22.30% of variation in cowpea with the two principal components. As many

as 115 accessions were included in a single cluster. Recently, Nkhoma *et al.* (2020) evaluated 100 cowpea genotypes and reported wider diversity. The investigation also gave clue that based on the values of principal component analysis, the multivariate analysis aids to place accessions in appropriate clusters.

Cluster analysis grouped 87 vegetable cowpea genotypes into 16 clusters revealing the greater amount of genetic diversity among the germplasm. With 45 genotypes cluster-II was the largest followed by I (22 genotypes) and XIII (4 genotypes) clusters. It is understood that the selection of one or the other genotype from the same cluster would yield similar heterosis. EC-390225, EC-390230, IC-20645, EC-724547, EC-390231, EC-390264, EC-715197, IC-249141, EC-723987 and EC-390239 were the single genotypes placed in different clusters unraveling maximum diversity possessed with them. These genotypes upon crossing among each other may lead pooling of versatile genes into single cultivar by adopting pedigree breeding. The four check varieties were grouped into two clusters, *i.e.*, cluster 8 (Kashi Kanchan, Kashi Unnati) and 13 (Arka Samruddi, Arka Suman), the directional selection for the commercial yield might have contributed to their similarity. Kashi Kanchan and Kashi Unnati are the varieties released for commercial cultivation from the Indian Institute of Vegetable Research, Varanasi. And similarly, from the Indian Institute of Horticulture Research, Bengaluru; Arka Samruddi, Arka Suman were released for cultivation, which has shared the pedigree. So, the study clearly grouped the genotypes based on the centre of origin. This is further evidenced by the grouping of four indigenous collections, IC-202827, IC-206240, IC-202931 and IC-259069 into cluster 12 and two exotic collections, EC-390210 and EC-724374 into cluster 16. The solitary clusters were dominated by EC lines by 80 per cent compared to IC lines (20 per cent). Overall clustering showed that EC lines were more divergent as they were present in 11 clusters versus indigenous clusters, which were grouped into only 4 clusters. However, the grouping of exotic and indigenous lines together into a single cluster indicates that there is no relation between the centre of origin and the centre of diversity. Genetic diversity estimates among lines/accessions is propellant in the improvement and selection of better varieties (Carvalho *et al.*, 2020). Carvalho *et al.* (2020) reported that the accessions of Iberian Peninsula were characterized with little genetic diversity as compared to those of worldwide. Similarly, (Lal *et al.*, 2017; Saini *et al.*, 2004 in cowpea; Pidigam *et al.*, 2019) in yardlong bean and Saidaiah *et al.* (2021) in jack bean also stressed the importance of genetic diversity for breeding new varieties. The improved diverse varieties always have an edge over local cowpea varieties (Manda *et al.*, 2019). From the investigation, very unique genotypes were identified with respect to yield both in exotic and indigenous accessions. Hence, the identified genetically distant genotypes are used in the hybridization programme to further isolate new improved vegetable cowpea varieties.

Varieties with early flowering and maturity are well fit in cropping systems due to their shortest crop duration based on cluster means. EC-390231 of cluster 7 had registered lowest cluster mean value of 37 days was to first flowering and along with EC-724547 of cluster 6 taken 41.50 days for 50% flowering. EC-390231 also early to days to 1st fruit set (44.50) and average days to the first harvest (50.50). The identified genotype could be explored further for breeding early vegetable cowpea varieties in India. As such, multilocation trials of this genotype could also result in establish stability for its

earliness. Two genotypes, *viz.*, Arka Samruddi and Arka Suman of cluster 13 had average pod length (40.75 cm) and with 1.1 cm pod width, were the highest. In addition, the same genotypes had the highest average cluster mean for mature pod weight (18.50 g) and the number of seeds per pod (40.75). The vegetable cowpea clearly differentiated from grain cowpea due to its pod length and width. The cowpea types released for vegetable purpose in India had pod lengths minimum of 25 cms to 50 cm (Pidigam *et al.*, 2019 and Rambabu *et al.*, 2017). The pod length is also main attribute of per plant green pod yield. There is potential for commercial release of those varieties with maximum length. EC-390210 and EC-724374 of cluster 16 had exhibited the highest mean cluster values for green pods formed per plant (134.63) and pod yield obtained per plant (743.63 g), respectively. Economic yield is ultimate objective of any crop breeding programme. In view of the highest average yield realized with EC-390210 and EC-724374 among all the genotypes in investigation. They hold promise for out yield, if tested across seasons and locations as well. These are the EC lines from Nigeria, may exhibit even biotic and abiotic stress resistance with proper plan and execution. The farmers can have wider choice of commercial varieties in vegetable cowpea in India. Nancee *et al.* (2013) concluded that the vegetable cowpea genotypes of cluster II followed by cluster I and V performed better for certain agronomic characters.

The Mahalanobis cluster distances depicted maximum genetic diversity between cluster VI and XVI followed by cluster VII and XVI. To achieve maximum heterosis, a crossing programme needs to be planned between EC-724547 (Cluster VI) with EC-390210 or EC-724374 (Cluster XVI). Similarly, transgressive segregants could be expected in pedigree breeding method of handling of EC-390231 with the genotypes of cluster XVI (EC-390210 or EC-724374). The little inter cluster distance noticed between cluster-IV and cluster-V warrants that poor genetic diversity associated with EC-390210 and IC-20645. Based on the intra cluster distances, the cluster 12 followed by cluster 16 had 4 indigenous collections and 2 exotic collections, respectively. Both these clusters though having less number of genotypes, the variation among the accessions present in clusters were higher in comparison with rest of the 14 clusters genotypes. Interestingly, cluster 2 and cluster 1 had less intra cluster distances in spite possessing 45 and 22 genotypes, respectively. This is possible when the genetic diversity among the genotypes of the clusters is meager and genotypes might share the same pedigree. Presence of solitary genotypes was the reason for ten clusters (Cluster 3, 4, 5, 6, 7, 9, 10, 11, 14 and 15) with zero intra cluster distances. The study established that cluster analysis is regarded as powerful tool to group germplasm, which can act as reliable basis to select material planning breeding strategies. The earlier studies by Patel *et al.* (2017) confirmed the present results. However, several clusters had EC lines in the study. Hence, one must be vigilant of genetic barriers and appropriate breeding strategy to get anticipated improvement of the targeted character.

The pod number per plant followed with days taken to 50% flowering and pod width contributed maximum towards total genetic divergence reported in the study, as pictured from per cent contribution of traits. It implies that 87 genotypes were genetically more variable for pod number per plant and flowering of 50 per cent of plants. Thus, the present study recommends that the genotypes can be selected based on pods set per plant followed by days taken to reach 50% of plants to flowering, which were with maximum

contribution for total divergence of the germplasm under investigation. While, days to first flowering had no contribution followed by negligible (<1%) contribution by days to 1st harvest, pod length and number of seeds per pod towards total genetic divergence in the present study. This indicates the performance of accessions studied for these characters is at par and they do not serve as the basic material for further selections. Certain earlier (Patel *et al.*, 2017; Lal *et al.*, 2017) studies reported similar trend of results. Nancee *et al.* (2013) reported that seeds per pod followed by plant stature registered maximum contribution towards total divergence in vegetable cowpea.

5. Conclusion

It is to conclude that based on principal component analysis and cluster analysis, exotic and indigenous genotypes have greater diversity as there were 16 clusters, which was further confirmed by Mahalanobis D² statistic, which elucidated maximum diversity among the genotypes between clusters. Therefore, the investigation suggests that hybrid combinations between exotic collections (EC-724547, EC-390210, EC-724374, EC-390231, and EC-724374) of genetically diverse clusters could be considered to execute maximum heterosis in hybrid breeding and isolating superior segregant lines useful for vegetable cowpea breeding.

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Conflicts of interest

The authors declare that there are no conflicts of interest relevant to this article.

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