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Studies on genetic diversity for yield and yield attributing traits in pigeonpea [*Cajanus Cajan* (L.) Millsp] germplasm

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Abstract
Pigeonpea (*Cajanus cajan* (L). Millsp.) is one of major food legume crop after chickpea in India. Assessment of genetic diversity for yield and yield characters and its application for pigeonpea breeding results in enhanced and sustainable nutritional security. In this study 100 germplasm and 4 checks (CGA2, CGA1, RJLN, ASHA) are characterized which was conducted in Augmented Randomized Complete Block Design (RBD) with 4 blocks during kharif 2020-21 and kharif 2021-22 at College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh for 13 characters *Viz*., days to 50% flowering, days to maturity, plant height, primary branching per plant, secondary branching per plant, pods per plant, pod length, pod width, number of seed per pod, 1000 seed weight, seed yield per plant, biological yield and harvest index. In this study out of 18, four principal components (PCs) exhibited more than 1.00 eigenvalue and showed about 5% variability among the traits studied. So, these 4 PCs were given importance for further explanation. The PC1 showed 32.74% whereas, PC2, PC3 and PC4 revealed 19.51%, 12.58% and 8.19% variability correspondingly between the genotypes for the characters under study. Cluster analysis result showed existence of considerable diversity in pigeonpea germplasm accession. The inter cluster distance was extreme between cluster III and VIII (75.207) and inter cluster distance was least detected between cluster I and cluster IV (18.454).

Keywords: Principal component analysis, augmented design, scree plot, clustering, pigeonpea, germplasm

Introduction
Pigeonpea [*Cajanus cajan* (L.) Millsp] (2n =22)] is an important pulse crop which occupies a major place in Indian agriculture. Pigeonpea is an often cross-pollinated (20-70%) crop (Saxena, 2006) belongs to the family of '*Fabaceae*' and is also recognized as '*Arhar*' or '*Tur*', usually consumed as *dal* and with rich in dietary protein and nourishment minerals and consumed by almost all Indians. The stem of pigeonpea is used for making local brooms (*Kharhara*) and baskets. The dry stem of pigeonpea is used as firewood, hedge (*badi*) and *chhani* (roof of the hut) in tribal villages. Pigeonpea has an inimitable venue in Indian rural agriculture and India grosses for around 90% of total cultivation. Pigeonpea is one of the most essential legume crops following to chickpea in India, Globally; it is cultivated in a total area of 4.92 million ha. (mha), with an annual production of 3.65 million tonnes (mt) and productivity is around 900 kg/ha. India has ~80% of world acreage (3.90 mha) with a total production and productivity of 2.89 mt (~79% of world acreage) and around 750 kg/ha respectively (http:// www.faostat.fao.org). In any crop improvement programme genetic diversity is an essential pre-requisite for hybridization. Divergence studies indicated that geographical diversity is always not necessarily associated with the genetic diversity. The divergence analysis by means of principal component analysis and hierarchical cluster analysis have been shown to be useful in selecting genetically distant parents for hybridization. Principal component analysis is used to confirm the diversity pattern brought about by cluster analysis. Hence the present study was planned to estimate diversity through classification of genotypes by principal component analysis and hierarchical cluster analysis. Assessment of genetic diversity for yield and yield characters and its application for Pigeonpea breeding results in enhanced and sustainable nutritional security.

Method and Materials
Experimental site and period of experiment
The research was carried out at Research together with Instructional Training Farm, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh throughout

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Kharif 2020-21 and kharif 2021-22.

Experimental season and climatic condition
The area falls underneath central India Hill region and Eastern Plateau (Agro-climatic zone-7) of Chhattisgarh state. It is categorize into three parts, where Raipur comes under the Chhattisgarh Plains Zone. Climatic condition of Raipur has a dry sub-humid to semi-dry with 1200-1400 mm average annual rainfall, from the total nearly 85 percent occurs during rainy season (June to September) and 7-8 per cent remaining received post monsoon duration (October to February). During summer month maximum temperature about high as 48.1ºC and during winter (December) minimum occurs at 6ºC low temperature. The statistics regarding to minimum and maximum temperatures, evaporation, weekly rainfall, relative humidity, wind velocity and bright sunshine hours during complete crop rises.

Experimental Approaches
The research was conducted in Augmented Randomized Complete Block Design (RBD) with 4 blocks. Pigeonpea germplasm were sown in single lines whereas four checks were replicated in all the blocks to calculate the error and get estimation of blocking effects. The trial seed was sown in 4 blocks and each block included of 25 genotypes and four checks. Spacing of 60 cm between rows and 20 cm between plants were kept. Dose of fertilizer are applied with rate of 20N: 50P: 20K kg/ha. Within the block checks were randomized. For normal growth thinning and gap filling were done that does also maintain plant population in uniform. The regular agronomic performs were implemented for normal crop cultivation.

Observations recorded
During observations time several agro-morphological and quantitative characters were noted to fulfil the purposes of the study. Random 5 plants from each of pigeonpea genotypes row were observed for remarking data of various characters at guided plant growth stage from guidance of UPOV DUS guidance and the average of these samples constituted the mean data of 1st season and 2nd season was recorded and pooled data of both seasons were obtained.

Experimental material
The plant material total of 100 germplasm of pigeonpea collected from different parts of Chhattisgarh and 4 checks were used in present study.

Table 1: List of germplasm accessions of Pigeonpea and standard checks used in the present study.

Entry No.	Genotype	Entry No.	Genotype	Entry No.	Genotype
CH1	CGA2	T32	RP-161	T67	RP-197
CH2	CGA1	T33	RP-162	T68	RP-198
CH3	RJLN	T34	RP-163	T69	RP-199
CH4	ASHA	T35	RP-164	T70	RP-200
T1	RP-124	T36	RP-165	T71	ICP-6993
T2	RP-126	T37	RP-166	T72	ICP-6994
T3	RP-127	T38	RP-167	T73	ICP-6995
T4	RP-128	T39	RP-169	T74	ICP-6996
T5	RP-129	T40	RP-170	T75	ICP-6997
T6	RP-130	T41	RP-171	T76	ICP-6998
T7	RP-131	T42	RP-172	T77	ICP-7000
T8	RP-132	T43	RP-173	T78	ICP-7001
T9	RP-133	T44	RP-174	T79	ICP-7002
T10	RP-134	T45	RP-175	T80	ICP-7003
T11	RP-135	T46	RP-176	T81	ICP-7004
T12	RP-136	T47	RP-177	T82	ICP-7005
T13	RP-137	T48	RP-178	T83	ICP-7349
T14	RP-138	T49	RP-179	T84	ICP-7358
T15	RP-139	T50	RP-180	T85	ICP-7359
T16	RP-140	T51	RP-181	T86	ICP-7362
T17	RP-141	T52	RP-182	T87	ICP-7363
T18	RP-142	T53	RP-183	T88	ICP-7364
T19	RP-143	T54	RP-184	T89	ICP-7366
T20	RP-144	T55	RP-185	T90	ICP-7367
T21	RP-145	T56	RP-186	T91	ICP-7373
T22	RP-146	T57	RP-187	T92	ICP-7376
T23	RP-149	T58	RP-188	T93	ICP-7379
T24	RP-150	T59	RP-189	T94	ICP-7382
T25	RP-152	T60	RP-190	T95	ICP-7384
T26	RP-155	T61	RP-191	T96	ICP-7389
T27	RP-156	T62	RP-192	T97	ICP-7391
T28	RP-157	T63	RP-193	T98	ICP-7392
T29	RP-158	T64	RP-194	T99	ICP-7393
T30	RP-159	T65	RP-195	T100	ICP-7397
T31	RP-160	T66	RP-196		

Note: CH=check variety, T=new treatment entry

Result and Discussion
Principal Component Analysis
It is a manifold variable statistical analysis to short the data with huge number of connected variables into a significantly lesser set of unique variables through linear grouping of the variables that accounts greatest of the variation existing in the original variables. In the current exploration, PCA was accomplished for 13 quantitative characters of Pigeonpea and presented in (Table 2). As per the criteria set by Brejda *et al.* (2000), the PC with Eigenvalues more than 1 and which explained at least 5% of the variation in the data was considered in the present study. The PC with higher eigenvalues and variables which had high factor loading was considered as the best representative of system attributes. Out of 18, only four principal components (PCs) exhibited more than 1.00 eigenvalue and showed about 5% variability among the traits studied. So, these 4 PCs were given due importance for further explanation. The PC1 showed 32.74% whereas, PC2, PC3 and PC4 revealed 19.51%, 12.58% and 8.19% variability correspondingly between the genotypes for the characters under study (Table 2.1). The first PC accounts for as much of the variability in the data as possible, and each following component accounts for as much of the remaining variability as possible. These results are validation within the findings of earlier workers (Hemavathy *et al.*, 2017; Bhavana *et al.*, 2019; Alagupalamuthirsolai and Vijayabharathi, 2020; Tharageshwari *et al.*, 2020; Kimaro *et al.*, 2021) [3, 2, 1, 4, 5].

Scree plot explained the percentage of variation associated with each principal component obtained by drawing a graph between Eigen values and principal component numbers. The PC1 showed 32.74% variability with Eigen value 4.9 which

then declined gradually. Elbow form line is got which after 4th PC tended to straight with little variance observed in each PC. From the graph, it is clear that the maximum variation was observed in PC1 (Fig. 1).

Table 2: Principal component analysis of 13 agro-morphological characters of 104 genotypes of pigeonpea.

Characters	PC1	PC2	PC3	PC4
DTF	0.662	0.084	0.041	0.009
DTM	0.805	0.000	0.013	0.025
PH	0.002	0.723	0.051	0.002
PB	0.234	0.001	0.106	0.048
SB	0.049	0.409	0.026	0.150
PPP	0.004	0.037	0.658	0.000
PL	0.740	0.000	0.049	0.002
PW	0.486	0.230	0.031	0.014
NSPP	0.004	0.434	0.004	0.342
TSW	0.665	0.122	0.015	0.000
SYPP	0.468	0.012	0.320	0.020
BY	0.000	0.588	0.045	0.127
HI	0.130	0.009	0.508	0.000
Eigenvalue	4.911	2.927	1.888	1.230
Variability (%)	32.741	19.514	12.586	8.199
Cumulative%	32.741	52.255	64.841	73.040

Days to 50% Flowering = DTF, Days to Maturity = DTM, Plant Height (cm) = PH, No of Primary Branches = NPB, No of Secondary Branches = NSB, No of Pods/plant = NPP, No of Seeds/Pod = NSP, Pods Length (cm) = PL, Pod Width (cm) = PW, 1000 Seed Weight (gm) = TSW, Seed Yield (gm/plant) Seed yield per plant = SYPP, Biological Yield (gm/plant) = BY, Harvest Index = HI
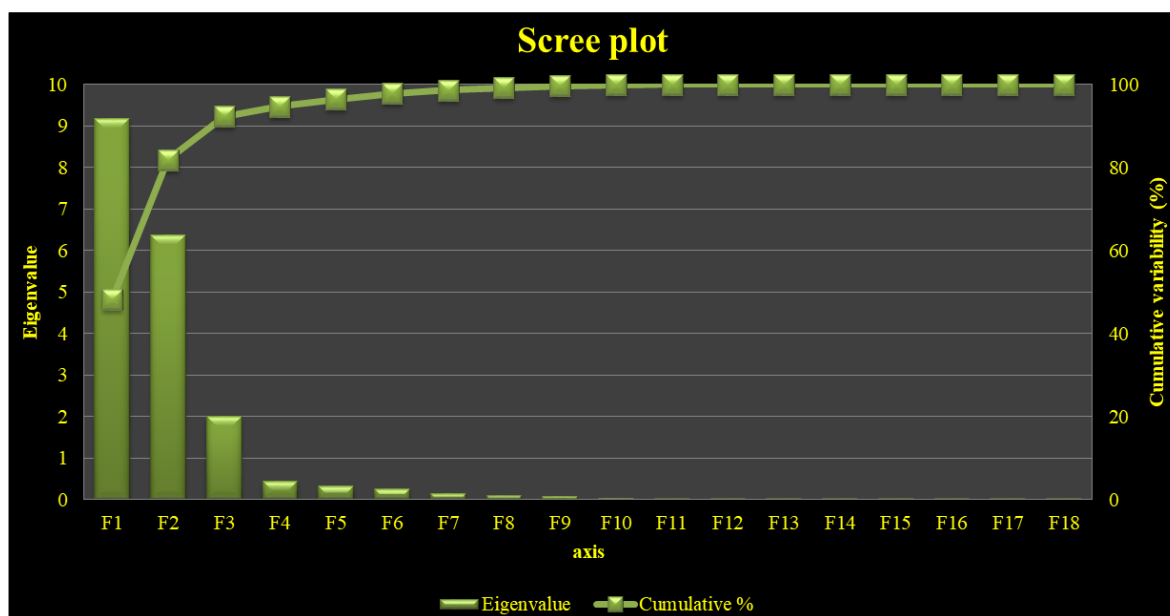

Fig 1: Scree plot showing eigenvalue and percentage of cumulative variability

Study of the PCA result clarified that genetic diversity of the native landraces of Pigeonpea. Within each PC, only highly loaded factors or traits were retained for further explanation. Component matrix revealed that the PC1 which accounted for the highest variability (32.74%) was mostly related with traits such as days to 50% flowering (0.662), days to maturity (0.805), pods length (cm) (0.740), pod width (cm) (0.468), 100 seed weight (g) (0.665) and seed yield (g) per plant

(0.468). As an outcome, the first component hence recognized the traits responsible for direct seed yield characterization. The second principal component accounted for 19.51% of the total variance. Variables highly and positively correlated were plant height (0.723), harvest index (%) (0.409), number of seed per pod (0.434) and biological yield (g) (0.588). The second component thus acknowledged traits responsible for plant physiological growth. The third principal component

accounted for 12.58% of the variability and was decidedly loaded with number of pods per plant (0.658) and harvest index (%) (0.508). The fourth principal component accounted for 8.19% of the variability. Thus, the manifest characters coming composed in different principal components and causative towards expounding the variability tend to remain together which may be reserved into helpfulness throughout the application of these traits in the breeding program. From the first four PCs, it was shown that the PC1 was mostly related to yield-related traits while PC2, PC3 and PC4 were mostly associated with plant physiological growth and quality traits respectively. So, a good breeding programme can be started by choosing the genotypes from PC1 for yield aspect and plant physiological growth and quality traits genotypes from PC2, PC3 and PC4 can be nominated. These results are

validation within the findings of earlier workers (Shreelaskmi and Shivani, 2015; Hemavathy *et al.*, 2017; Alagupalamuthir solai and Vijayabharathi, 2020; Yohane *et al.*, 2020) [6, 3, 1, 7].

Top 10 principal component scores (PC scores) for all the Genotype were estimated in four principal components and presented in (Table 2.1). These scores can be utilized to propose precise selection indices whose intensity can be decided by variability explained by each of the principal components. A high PC score for a particular genotype in a particular component denotes high values for the variables in that particular genotype. On the basis of top 10 PC scores in each principal component genotypes are selected. These results are validation within the findings of earlier workers (Shreelaskmi and Shivani, 2015) [6]

Table 3: List of selected genotype in each principal component on the basis of top 10 PC score

S. No.	Genotype	PC1	Genotype	PC2	Genotype	PC3	Genotype	PC4
1	RP-126	4.367	RP-142	3.648	RP-169	4.486	RP-131	2.894
2	RP-133	4.068	RP-157	3.217	RP-138	3.589	RP-163	2.778
3	RP-140	3.497	RP-143	3.103	ICP-7001	3.225	ICP-7391	2.134
4	RP-144	3.486	RP-131	3.067	RP-181	2.962	RP-167	2.114
5	RP-124	3.366	RP-195	3.057	RP-157	2.804	RP-164	2.039
6	RP-175	3.356	RP-160	2.887	RP-159	2.435	RP-142	2.030
7	RP-129	3.322	RP-126	2.693	ICP-7003	2.153	RP-191	1.857
8	RP-162	3.234	RP-139	2.671	RP-178	2.019	RP-129	1.786
9	RP-138	3.190	ICP-6996	2.550	RP-146	1.881	RP-174	1.587
10	RP-170	2.812	ICP-7392	2.424	ICP-7005	1.865	RP-140	1.522

Thus, it is cleared that the principal component analysis highlights the characters with supreme variability. So, through selection measures can be deliberate to bring about rapid improvement of yield and quality traits. PCA also help in ranking of genotypes on the basis of PC scores in corresponding component. So, genotypes showing top scores in their respective components (Table 2.1) can be selected for breeding programmes in association with the traits showing high factor loading in their respective components.

Cluster analysis
Genetic divergence analysis was established to be a useful tool to measure the comparative involvement of divergent traits to the total divergence both inter and intra group intensities. Analysis was performed by Un-weighted variable Pair Group Method of the Average Linkage Cluster Analysis (UPGMA) using Euclidean distance as dissimilarity measure divided the 104 entries of Pigeonpea into 8 clusters. The entries were not uniformly distributed between the clusters. The cluster I constituted of 90 accessions, forming the largest cluster followed by cluster IV (5 accessions), cluster II, V and VII (2 accessions respectively), cluster III, VI and cluster VIII have only (1 accessions respectively). The pattern of group arrangement proved the reality of substantial aggregate of variability. These results are support with the verdicts of previous workers (Tharageshwari and Hemavathy, 2017) [4].
Calculated intra and inter cluster distances between 8 clusters

and were having been given in Table 4.17 and Fig. 25. The cluster distance ranged from 0.00 intra (cluster III, cluster VI and VIII) to 35.285 (cluster IV). The cluster distance was extreme between inter cluster III and VIII (75.207) and inter cluster distance was least detected between cluster I and cluster IV (18.454). To recognize much variability and high heterotic effect, parents should be particular from two clusters taking broader inter cluster distance. These outcomes are confirmation with the findings of earlier workers (Shruthi *et al.* 2020) [9].
The cluster mean values showed a wide range of variations for all the characters undertaken in the study (Table 4.18 and Fig. 26). Cluster III exhibited highest mean value for the days to 50% flowering (136.755), number of pods per plant (77.2), number of seed per pods (4.79), seed yield (g) per plant (39.02) while cluster II contained genotypes with highest mean value for plant height (cm) (210.008), biological yield (g) per plant (105.98), while highest mean value for pod length (cm) (5.785), pod width (cm) (0.815) and 100 seed weight (g) (13.54) was recorded by cluster VI. While highest mean value for number of primary branches per plant (13.215) and number of secondary branches per plant (18.65) was recorded by cluster VII. Cluster IV exhibited highest mean value for the days to maturity (201.565) and highest mean value for harvest index (%) (83.045) was recorded by cluster V.

Table 3: Distribution of 104 Pigeonpea genotypes among 8 clusters

Cluster number	Number of genotypes	Genotypes
I	90	CGA2, CGA1, RJLN, ASHA, RP-124. RP-126, RP-127, RP-128, RP-129, RP-130, RP-131, RP-132, RP-133, RP-134, RP-135, RP-136, RP-137, RP-139, RP140, RP-141, RP-142, RP-143, RP-146, RP-149, RP-150, RP-152, RP-155, RP-156, RP-158, RP-159, RP-160, RP-161, RP-162, RP-163, RP-164, RP-165, RP-166, RP-167, RP-169, RP-170, RP-171, RP-172, RP-173, RP-174, RP-175, RP-176, RP-178, RP-179, RP-180, RP-182, RP-183, RP-184, RP-185, RP-186, RP-187, RP-189, RP-190, RP-191, RP-192, RP-193, RP-195, RP-196, RP-199, RP-200, ICP-6993, ICP-6993, ICP-6993 ICP-6994, ICP-6995, ICP-6996, ICP-6997, ICP-69938, ICP-7000 ICP-7001, ICP-7002, ICP-7003, ICP-7004, ICP-7005, ICP-7349, ICP-7358, ICP-7359, ICP-7363, ICP-7364, ICP-7366, ICP-7367, ICP-7373, ICP-7376, ICP-7379, ICP-7382, ICP-7384, ICP-7389, ICP-7391, ICP-7397,
II	2	RP-126, RP-196
III	1	RP-138
IV	5	RP-144, RP-145, RP-157, RP-177, RP-197
V	2	RP-181, RP-188
VI	1	RP-198
VII	2	ICP-7362, ICP-7392
VIII	1	ICP-7393

Table 4: Estimates of intra (diagonal and bold) and inter cluster distances among ten clusters.

Class	I	II	III	IV	V	VI	VII	VIII
I	32.078	39.446	49.804	18.454	42.296	20.438	23.805	31.095
II		27.283	69.585	41.825	65.570	51.351	44.485	40.020
III			0.000	48.863	44.304	61.729	47.900	75.207
IV				35.285	50.859	25.043	22.399	42.888
V					27.604	53.268	57.295	52.802
VI						0.000	36.179	39.812
VII							24.408	46.779
VIII								0.000

These results are validation within the findings of earlier workers (Shreelaskmi and Shivani, 2015) [6]

The assortment and choice of parents predominantly be contingent upon involvement of traits to divergence. It recognized that crosses among divergent parents generally benefit countless heterotic outcomes than amid closely interconnected ones. Since the significance of genetic detachment and relation involvement of traits to entire divergence, it's showed that parents designated from cluster II (RP-126 and RP-196) plant height (cm) and biological yield (g) per plant and from cluster III (RP-138) days to 50% flowering, number of pods per plant, number of seeds per pod, seed yield (g) per plant and cluster IV (RP-145) for days to maturity and cluster V (RP-181 and RP-188) harvest index (%) whereas cluster VI (RP-198) pod length (cm), pod width (cm) and 100 seed weight (g) whereas cluster VII (ICP-7362) number of primary branches per plant and number of secondary branches per plant might be useful in breeding programs to achieve desired plant type.

Table 5: Cluster mean values of ten clusters for different characters in varying genotypes of Pigeonpea (bold valves are highest mean of traits)

Characters	I	II	II	IV	V	VI	VII	VIII
125.012	136.1	136.755	123.089	120.195	123.195	126.68	112.055	
184.386	186.173	201.245	201.564	176.35	185	196.465	168.69	
187.899	210.008	197.915	185.854	188.75	169.75	197.81	196.61	
11.503	9.77	13.15	11.042	11.533	12.22	13.215	7.735	
15.221	14.24	14.895	18.035	13.9	12.865	18.65	15.565	
55.16	38.745	77.2	55.633	49.38	53.96	70.785	37.19	
5.036	5.403	5.755	5.188	4.75	5.785	5.298	4.82	
0.598	0.69	0.58	0.633	0.545	0.815	0.605	0.545	
4.074	4.788	4.79	4.246	3.723	3.18	3.95	3.6	
12.056	13.015	10.395	12.432	11.323	13.54	11.663	8.245	
24.102	21.588	39.02	26.415	26.55	27.145	19.83	15.785	
BY	82.943	105.98	83.695	87.292	80.49	82.26	82.588	84.665
HI	42.409	31.066	77.606	40.276	**83.**045	34.464	35.932	35.17

Days to 50% Flowering = DTF, Days to Maturity = DTM, Plant Height (cm) = PH, No of Primary Branches = NPB, No of Secondary Branches = NSB, No of Pods/plant = NPP, No of Seeds/Pod = NSP, Pods Length (cm) = PL, Pod Width (cm) = PW, 1000 Seed Weight (gm) = TSW, Seed Yield (gm/plant) Seed yield per plant = SYPP, Biological Yield (gm/plant) = BY, Harvest Index = HI
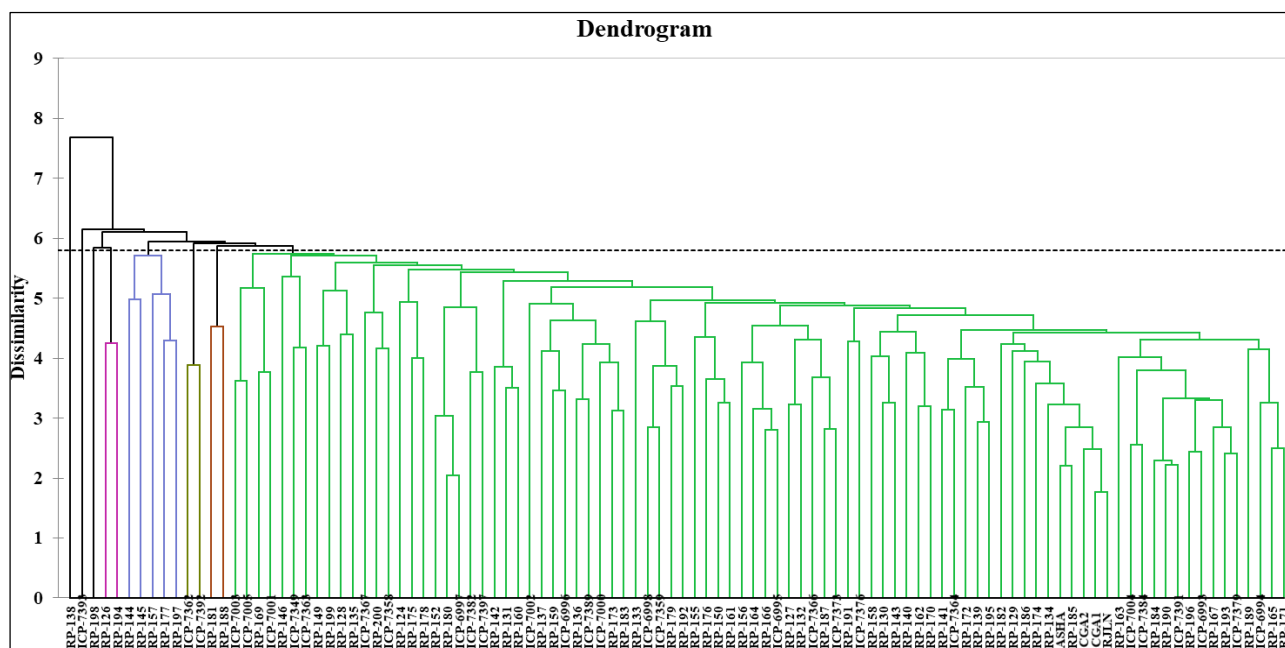
Fig 2: Dendrogram showing the distribution of genotypes

Conclusions
Component table revealed that the PC1 was ordinarily related with yield-related traits although PC2, PC3 and PC4 were ordinarily associated by plant physiological growth and quality traits respectively. So, a good breeding programmed can be started by choosing the genotypes from PC1 for yield aspect and plant physiological growth and quality traits genotypes from PC2 and PC3 can be nominated. Cluster analysis divided the 104 entries of pigeonpea into eight clusters. The cluster I constituted of 90 accessions, forming the largest cluster followed by cluster IV (5 accessions), cluster II, V and VII (2 respectively), cluster III, VI and VIII (1 accessions respectively). It is fine recognized that crosses among divergent parents generally benefit countless heterotic outcome than amid closely interconnected ones.

Acknowledgement

Conflict of interest
None

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