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Research Article

Principal Component Analysis in Pigeonpea (*Cajanus cajan* (L.)Millsp.)

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Abstract
An experiment was conducted in fifty seven genotypes of pigeonpea for the Principal Component Analysis at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore during *kharif*, 2015. Twelve quantitative characters were taken under observation to estimate substantial variation and relationship among pigeonpea genotypes to identify the best performing lines. Analysis of variation for such quantitative traits in diverse line showed considerable and dissimilar level of variability. The largest variation was found for number of pods per plant, plant height, days to maturity, days to 50 per cent flowering and pod bearing length. Single plant yield was highly significant and positively correlated with number of pods per plant, number of secondary branches, number of raceme, days to 50 per flowering, days to maturity, pod bearing length, number of seeds per pod and pod size however hundred seed weight was non significantly correlated with single plant yield. Principal component analysis showed the amount of variation by the principal components assigned from component1 to component4. Clustering analysis based on various morphological traits assorted 57 pigeonpea genotypes into three main groups and seven subclusters. Dendrogram based on hierarchal clustering grouped genotypes based on their morphological traits rather than geographic origin. Grouping of genotypes based on morphological traits is not always associated with their geographical origin. The diverse genotypes will be used for future breeding programme.

Keywords: Pigeonpea, Principal component analysis, Clustering, Diversity

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millspaugh) ($2n = 22$) is the second most important pulse crop of India after chickpea. Correlation studies provide an opportunity to study the magnitude and direction of association of yield with its components and also among various components. 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. Hence selection of parents for hybridization should be based more on genetic diversity rather than geographic 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.

Materials and Methods

Genetic evaluation of 57 pigeonpea genotypes on the basis of agro-morphological traits was evaluated at Department of Pulses, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University,Coimbatore. Experiment was conducted by RBD during *Kharif*, 2015. Quantitative characters were taken into consideration for estimating substantial variation and relationship among Pigeonpea genotypes. Twelve quantitative characters *viz.*, days to 50 per cent flowering, plant height (cm), seeds per primary branches per plant, secondary branches per plant, clusters per plant, pods per cluster, pod length (cm), seeds per pod, pods per plant, 100-seed weight (g), single plant yield (g) and days to maturity were considered for estimating genetic diversity. Mean values of accessions were computed for determining analysis of variance and correlation coefficients. Principal component analysis (PCA) and cluster analysis were also performed to assess genetic diversity among pigeonpea accessions.

Results and Discussion

Twelve quantitative traits were observed for all 57 pigeonpea accessions and observations were recorded for further analysis. Analysis of variation depicted considerable level of variability among different accessions for most of the traits. Basic descriptive statistics for 12 characters was presented in Table 1**.** The largest variation was observed for number of pods per plant (479.30%), single plant yield (333.27%), plant height (265.66%) and pod bearing length (65.48%). Comparatively, low variation was noticed for number of seeds per pod, pod size, 100 seed weight and number of primary branches. Observed variability found among the Pigeonpea accessions can be probably attributed to the genetic differences and the environment, in which these accessions were grown.

Correlation coefficient for different quantitative characters was presented in Table 2. Single plant yield was highly significant and positively correlated with number of pods per plant, number of secondary branches, number of raceme, days to 50 percent flowering, days to maturity, pod bearing length, number of seeds per pod and pod size however hundred seed weight was non significantly correlated with single plant yield. Regarding inter-correlation, days to 50 per cent flowering had positive significant correlation with plant height, number of racemes, number of primary branches, number of secondary branches, number of pods per plant and days to maturity. Hence selection of these traits will be useful for future breeding programme. The results are in agreement with Singh (1999) and Bainiwal *et al*. (1981).

Principal component analysis showed that the amount of variation by principal components (PCs) 1to4*viz*.41.46,16.09, 14.08 and 8.94% respectively. PCA identified four principal components with eigen values more than one which contributed 80.57 per cent of the cumulative variance. The first Principal Component (PC1) contributed maximum towards variability (41.46%) was correlated with number of secondary branches, number of pods per plant, days to maturity, days to 50 per cent flowering, 100 seed weight and plant height (Table 3). Thus, this component was the weighted average of the characters which determined the yield level. These traits had the largest participation in the divergence and carried the largest portion of its variability. Similar findings with regard to number of secondary branches per plant, number of pods per plant and plant height was reported by Rekha *et al.*, 2013 in Pigeonpea. The second Principal Component (PC2) accounted 16.09 per cent of total variance and it reflected positive loading of pod size, number of seeds per pod and 100 seed weight. The third PC3 was characterized noticeably by high loading of single plant yield, pod bearing length, number of primary branches and plant height. The fourth PC was correlated with single plant yield, days to maturity, days to 50 per cent flowering, 100 seed weight and plant height. Hierarchical cluster analysis based on quantitative traits divided pigeonpea genotypes into three main groups and six sub-clusters (Fig. 1, Table 4).

Analysis performed by UPGMA divided the 57 genotypes into 3 clusters (Fig. 1). The distribution of genotypes into various clusters was random, indicating lack of parallelism between genetic and geographic diversities. The maximum inter cluster distance was observed between cluster III and II (212.619) followed by cluster I and III (205.441) as shown in Table.5. Cluster III and cluster II was the largest comprising of 28 genotypes (Fig. 1). Among the three clusters, cluster III recorded high mean values for all the characters *viz.*, days to 50 per cent flowering (79.67), plant height (165.83), pod bearing length (67.73), pod size (7.93), number of seeds per pod (5.67), number of racemes (25.43), number of primary branches (12.77), number of secondary branches (31.33), number of pods per plant (346.33), 100 seed weight (11.37), days to maturity (120.67) and single plant yield (134.67) respectively (Table 6). Similar results of utilization of principal component analysis combined with hierarchical cluster analysis in genetic diversity studies were reported by Vasantha Rao *et al.* (2010) and Rekha *et al.* (2013) in pigeonpea.

The present study showed considerable variability for most of the characteristics that could be exploited for crop improvement. The clustering pattern could be utilised in identifying the best cross combinations for generating variability with respect to various characters under study. The genotypes clubbed in the different clusters if inter crossed may generate wide variability. Clustering pattern indicated no association between geographical distribution of accessions and genetic divergence (Murthy and Arunachalam, 1966). Similar results were derived by Virangama and Goyal (1994) and Katiyar *et al*. (2004). Cluster analysis based on plant morphology suggested that the accessions could be grouped. Such groupings are useful to breeders in identifying possible genotypes that may be used as parents in breeding for any of the morphological traits that were studied. Above all, the information generated will reduce the overall time required by plant breeders to screen large populations for potential breeding stock.

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Table 1. Variation in quantitative traits of Pigeonpea accessions

Traits	Minimum	Maximum	Range	Mean	Std. Deviation	CV(%)	Variance (%)	PCV	GCV	Heritability (%)	Genetic advance as per cent of mean
Days to 50% flowering	58.00	79.00	21.00	70.74	3.99	5.64	15.91	5.61	5.56	98.06	11.34
Plant height (cm)	93.00	165.00	72.00	128.53	16.30	12.68	265.66	12.57	12.46	98.24	25.44
Pod bearing length (cm)	33.00	79.60	46.60	65.37	8.15	12.47	65.48	12.42	12.31	98.16	25.12
Pod size (cm)	4.16	7.82	3.66	5.04	0.56	11.11	0.14	10.85	10.56	94.66	21.17
Seeds per pod	3.60	5.80	2.20	4.29	0.37	8.62	0.14	8.73	8.61	97.25	17.50
No. of racemes	7.20	15.60	8.40	10.58	3.40	32.14	11.54	29.39	29.36	99.77	60.41
No. of primary branches	8.20	14.20	6.00	10.77	1.31	12.16	1.72	12.36	12.28	98.65	25.12
No. of secondary branches	0.00	30.00	30.00	4.68	5.21	111.32	27.13	111.80	111.73	99.87	230.00
No. of pods per plant	72.00	367.00	295.00	170.55	69.22	40.59	479.30	40.75	40.73	99.93	83.88
100 seed weight (g)	6.72	11.50	4.78	8.57	1.02	11.90	1.03	11.93	11.82	98.10	24.11
Days to maturity	100.00	120.00	20.00	112.07	3.94	3.52	15.50	3.56	3.53	98.24	7.20
Single plant yield (g)	22.80	133.00	110.20	45.97	18.26	39.72	333.27	39.70	39.48	98.90	80.89

Table 2. Correlation coefficients among 12 quantitative traits in pigeonpea accessions

	DFF	PH	PLGTH	PS	SEEDS	RACEME	PB	SB	PP	HSW	DM	SPY
DFF	1.000											
PH	0.529**	1.000										
PLGTH	0.033	0.516**	1.000									
PS	-0.102	0.064	0.009	1.000								
SEEDS	0.085	0.136	0.211	0.713**	1.000							
RACEME	0.542**	0.668**	0.218	-0.131	0.221	1.000						
PB	0.138	0.305*	0.251	0.117	0.125	0.458*	1.000					
SB	0.541**	0.583**	0.201	0.333*	0.333*	0.796**	0.369**	1.000				
PP	0.546**	0.614**	0.362**	0.086	0.179	0.776**	0.350**	0.678**	1.000			
HSW	-0.162	0.048	-0.062	0.446**	0.097	-0.058	0.089	0.254	-0.074	1.000		

DM	0. 975**	0.509**	0.060	-0.075	0.109	0.523**	0.156	0.558**	0.519**	-0.149	1.000	
SPY	0.427**	0.617**	0.378**	0.365**	0.370**	0.591**	0.343**	0.736**	0.860**	0.218	0.402**	1.000

*Significant at 0.05% level of probability ** Significance at 0.01% level of probability Traits DFF(Days to 50% flowering), PH (Plant height), PLGTH(Pod bearing length), PS(Pod size), Seeds(No. of seeds/pod), Raceme(No. of raceme), PB(No. of primary branches), SB(No. of secondary branches), PP(No. of pods per plant), HSW(100 seed weight), DM(Days to maturity), SPY(Single plant yield)

Table 3. Eigen vectors, principal components for quantitative traits in pigeonpea accessions

Traits	PCA1	PCA2	PCA3	PCA4
Days to 50% flowering	0.15	-0.18	-0.27	0.26
Plant height (cm)	0.14	-0.20	0.19	-0.01
Pod bearing length (cm)	0.08	-0.05	0.27	-0.57
Pod size (cm)	0.06	0.41	0.18	0.29
No. of seeds per pod	0.08	0.33	0.19	0.31
No. of racemes	0.19	0.02	0.05	-0.06
No. of primary branches	0.09	-0.04	0.23	-0.15
No. of secondary branches	0.17	0.02	0.05	0.15
No. of pods per plant	0.17	-0.07	0.03	-0.15
100 seed weight (g)	0.14	0.24	-0.22	-0.31
Days to maturity	0.15	-0.17	-0.24	0.28
Single plant yield (g)	-0.03	-0.27	0.42	0.35
Eigen value	4.98	1.93	1.69	1.07
Per cent variation (%)	41.46	16.09	14.08	8.94
Cumulative variance (%)	41.46	57.55	71.63	80.57

Table 4. Characteristics of pigeonpea accessions in sub-clusters

Main group	Sub-cluster	No. of lines	% of lines	Prominent lines
I	1	1	1.75	Tall in height, highest pod size, no. of seeds per pod, no. of raceme, no. of secondary branches, 100 seed weight, single plant grain yield and late in days to maturity
II	1	23	40.31	Highest in no. of pods per plant
	2	5	8.77	Highest in pod bearing length
III	1	25	43.86	Early flowering, no. of primary branches
	2	3	5.26	

Table 5. Intra cluster (diagonal) an inter cluster distances for three clusters in pigeonpea

	Cluster I	Cluster II	Cluster III
Cluster I	67.586	69.531	205.441
Cluster II		91.511	212.619
Cluster III			0.000

Table 6. Mean of quantitative traits of pigeonpea accessions

	Clusters		
Characters	**I**	**II**	**III**
Days to 50% flowering	70.61	71.00	79.67
Plant height (cm)	128.20	113.73	165.83
Pod bearing length (cm)	66.11	49.90	67.73
Pod size (cm)	5.07	5.43	7.93
No. of seeds per pod	4.23	4.27	5.67
No. of racemes	11.27	11.12	25.43
No. of primary branches	10.81	9.80	12.77
No. of secondary branches	4.35	2.75	31.33
No. of pods per plant	167.80	175.79	346.33
100 seed weight (g)	8.49	8.23	11.37
Days to maturity	111.61	112.00	120.67
Single plant yield (g)	44.80	47.15	134.67

Fig. 1. Dendrogram based on cluster analysis for various agro- morphological traits of pigeonpea accessions