



P-ISSN: 2349-8528
E-ISSN: 2321-4902
IJCS 2019; SP6: 547-551

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(Special Issue -6)
3rd National Conference
On

**PROMOTING & REINVIGORATING AGRI-HORTI,
TECHNOLOGICAL INNOVATIONS
[PRAGATI-2019]
(14-15 December, 2019)**

Genetic diversity and principal component analysis for yield characters of Pigeonpea landraces of Eastern India

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Abstract

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is one of major food legume crops with its centre of origin in eastern India. Assessment of genetic diversity for yield and yield characters and its application for Pigeonpea breeding results in enhanced and sustainable nutritional security. Fourteen land races with three checks were characterized for various characters viz., total grain yield, plant height, days to 50% flowering, days to harvest, total biological yield, number of seeds per pod, shelling percentage and 100 seed weight. Cluster analysis indicated significant genetic variability among tested genotypes which provides an opportunity for crop improvement through hybridization of selected genotypes present in distant clusters. The data was further subjected to PCA (principal component analysis) and genotype by trait biplot analysis. The first three principal components accounted for 77% of total variation indicating wide genetic variability among the genotypes. All the genotypes clustered into two major clusters with nine and eight genotypes each. Promising genotypes viz., IC-611232, IC-611230 and IC-611256 can be successfully incorporated in the Pigeonpea breeding programme.

Keywords: Principal component analysis, Correlation, Biplot, Scatter plot, Clustering, Pigeonpea, land races

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is one of the major food legumes of tropics and sub tropics. Its centre of origin is in eastern India. It is the most heat and drought tolerant crop and has a wide range of adaptation across environments and cropping systems. It is a rich source of protein, vitamins and certain minerals. Pigeonpea is a multipurpose crop which is used for food, feed and fuel. It is most widely eaten in the form of split seeds or dal. India is the major producer of pigeon pea in the world with an area of 3.92 mha and 2.84MT^[1]. It exhibits great variation in size, habit, behaviour and in seed characteristics. Evolution of Pigeonpea through natural and human selection under different cropping systems has resulted in a wide variety of locally adapted landraces. Diversity analysis of released cultivars in the country indicates limited genetic diversity compared to the vast diversity available in the land races and wild relatives. It offers a very good scope for genetic improvement in the crop by utilization of the concealed diversity. Genomic resources now available in the crop are to be exploited to hasten crop improvement. Assessment of genetic diversity for yield and yield characters and its application for Pigeonpea breeding results in enhanced and sustainable nutritional security. Hence the objective of the present study was collection & evaluation of indigenous germplasm and identification of potential genotypes for cultivation in Eastern plateau and hill region.

Materials and Methods

All the experiments under this study were conducted at Experimental Farm of ICAR RCER Research Centre, Ranchi (23.35°N and 85.33° E at 629m altitude) during 2016-17. Total annual rainfall was 1430mm with 1100 mm during June to September and the average maximum and minimum temperatures 37°C and 4°C respectively. Fourteen land races of pigeon pea were obtained from National Bureau of Plant Genetic Resources, Regional Centre, Ranchi and were evaluated along with three checks viz., NDA-1, Bahar and Asha for various morphological, yield and yield related traits using augmented block design. Accessions were sown in three rows of 4m long with a spacing of 90cm between rows and 20cm between plants. The crop was fertilized and managed by recommended cultural and plant protection practices. Observations were recorded as mean of three representative plants from the middle row for plant height, number of seeds per pod, shelling percentage and 100 seed weight according to the plant descriptors of Pigeonpea (IBPGR and ICRISAT) [2]. Days to 50% flowering, days to harvest, total biological yield and total grain yield were recorded on plot basis.

Statistical analysis

Statistical method of classification is done by multivariate methods as it has extensive use in summarizing and describing the inherent variation present among crop genotypes. Multivariate statistical tools include Principal

Component Analysis (PCA), Cluster analysis and discriminant analysis (Oyelola) [3]. Principal Component Analysis (PCA) can be used to uncover similarities between variable and classify the genotypes, while cluster analysis on the other hand is concerned with classifying previously unclassified materials (Leonard and Peter) [4]. Clustering done according to Paired Group (UPGMA) method using Euclidean Similarity Index. Principal Component Analysis (PCA) was done using the Eigen values and scatter plot was computed. PAST 3.15 (PA leontological ST atistics) software (Hammer *et al.*) [5] was used to analyze data recorded for various characters.

Results and Discussion

Among the seventeen genotypes of pigeon pea evaluated for various yield characters, Bahar recorded the highest grain yield (4.05 t/ha) followed by IC 611232 (3.88 t/ha) (Table 1). Average plant height was 3.1m. IC 611232 was early (98 days to 50% flowering and 204 days to harvest). IC 611245 had highest number of seeds per pod (9.5). Shelling percentage was highest for IC 611230, IC 611232 and IC 611256 (80%). IC 611682 recorded highest biological yield (7.41 t/ha) and highest 100 seed weight (11.99g). The results obtained from the present study indicate that the collection was diverse and had superior genotypes with regards to characters related to yield.

Table 1: Mean performance of Pigeonpea land races for various yield characters

Landraces	Plant height (m)	Days to 50% flowering	Days to harvest	Total Biological yield (t/ha)	Total grain yield (t/ha)	No. of Seeds per pod	Shelling Percentage	100 seed weight (g)
IC 611205	3.0	121	204	3.5	2.71	5.6	75	10.59
IC 611212	2.95	119	204	2.5	2.46	7.0	67	10.05
IC 611215	3.5	119	249	2.0	2.76	8.0	60	7.97
IC 611230	3.1	120	204	3.5	2.73	8.8	80	9.23
IC 611232	3.0	98	204	2.75	3.88	8.2	80	9.72
IC 611242	3.5	137	242	4.5	1.46	7.0	60	7.81
IC 611243	3.4	119	242	3.0	2.58	8.0	60	7.73
IC 611244	3.2	123	244	3.0	1.97	7.8	80	7.88
IC 611245	3.5	140	244	3.5	2.35	9.5	75	7.28
IC 611256	3.4	152	244	3.0	1.88	8.0	80	6.71
SKB 1/89	3.2	140	244	4.0	1.57	5.2	67	10.1
IC 611261	2.8	109	204	2.0	2.12	5.4	63	10.39
IC 611682	2.75	109	204	8.0	1.82	6.4	57	11.99
IC 614683	2.8	119	204	3.0	1.15	5.1	67	9.49
NDA-1	2.8	154	260	2.47	3.42	6.09	70	10.38
BAHAR	3.02	119	204	2.93	4.05	8.18	68	11.25
ASHA	2.84	138	242	1.58	3.34	7.07	78	9.87
Range	2.75-3.5	98-154	204-260	1.58-7.41	1.06-4.05	5.11-9.5	57-80	6.71-11.99
Mean	3.1	125.65	226.06	3.04	2.35	7.14	69.82	9.32
SD	0.27	15.39	21.82	1.31	0.84	1.32	8.15	1.50
SE	0.07	3.73	5.29	0.32	0.20	0.32	1.98	0.36
CV	8.78	12.25	9.65	42.96	35.95	18.53	11.67	16.11

Simple correlation for the association among the characters studied for 17 genotypes is shown in Table 2. Plant height and days to 50% flowering were positively significantly correlated to days to harvest. Plant height also correlated significantly to number of seeds per pod. 100 seed weight and number of seeds per pod are negatively correlated. However total grain yield exhibited positive but not significant correlation with number of seeds per pod, shelling percentage and 100 seed weight. Non-significant negative correlation was noticed with

plant height, days to 50% flowering, days to harvest and total biological yield. Similar results were obtained by Bal *et al.*, [6] while evaluation of 34 genotypes of pigeon pea. Anuradha *et al.*, [7] reported positive correlation between days to 50% flowering and days to pod initiation, days to physical maturity, plant height, number of pods per plant, number of seeds per plant and total grain yield but negatively correlated to number of seeds per pod and 100 seed weight.

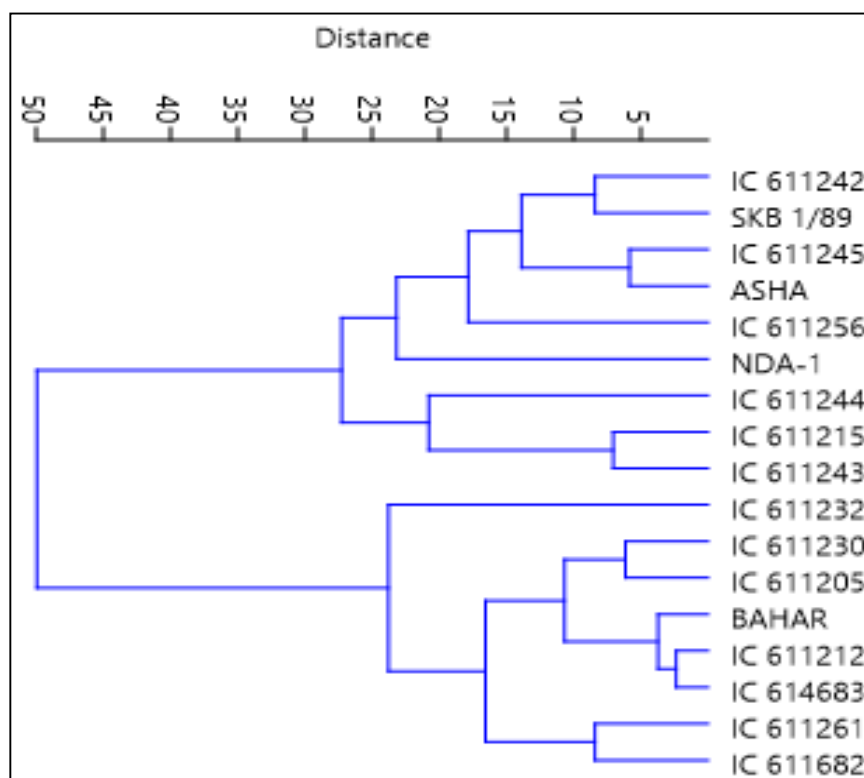
Table 2: Correlation Matrix for various yield characters in Pigeonpea landraces

	Plant height	Days to 50% flowering	Days to harvest	Total Biological yield	Total grain yield	No. of Seeds per pod	Shelling Percentage	100 seed weight
Plant height	1.000	0.306	0.553*	-0.080	-0.218	0.576*	-0.020	-0.838**
Days to 50% flowering	0.306	1.000	0.750**	-0.123	-0.102	0.002	0.206	-0.382
Days to harvest	0.553	0.750	1.000	-0.206	-0.057	0.178	0.014	-0.593*
Total Biological yield	-0.080	-0.123	-0.206	1.000	-0.373	-0.104	-0.363	0.310
Total grain yield	-0.218	-0.102	-0.057	-0.373	1.000	0.366	0.301	0.311
No. of Seeds per pod	0.576	0.002	0.178	-0.104	0.366	1.000	0.360	-0.530*
Shelling Percentage	-0.020	0.206	0.014	-0.363	0.301	0.360	1.000	-0.222
100 seed weight	-0.838	-0.382	-0.593	0.310	0.311	-0.530	-0.222	1.000

Clustering using paired group method

Dendrogram was generated to examine the relationships among different genotypes based on Euclidean distances, calculated by the Paired group method is presented in Figure 1. All the seventeen genotypes grouped into two main clusters (Fig 1). Nine genotypes formed one major cluster A and the other eight genotypes formed another major cluster B. Cluster A is again sub clustered into two sub clusters a1 and b1, of which a1 had six genotypes IC 611242, SKB1/89, IC 611245, Asha, IC 611256 and NDA-1. Sub cluster b1 had three genotypes IC 611244, IC 611215 and IC 211243. Major cluster B had two sub clusters a2 and b2. IC 611232 formed

separate sub cluster a2 and the remaining seven genotypes IC 611230, IC 611205, Bahar, IC 611212, IC 614683, IC 611261 and IC 611682 formed the sub cluster b2. Cluster analysis showed that there was significant genetic variability among Pigeonpea genotypes tested which indicated the presence of excellent opportunity to bring about improvement through hybridizing genotypes from different clusters. Choudhary *et al.*,^[8] grouped the 24 genotypes of pigeon pea into three clusters based on Jaccard's similarity coefficient using UPGMA. Sreelakshmi and Shivani^[9] grouped 66 genotypes into nine clusters using wards minimum variance method.

**Fig 1:** Dendrogram depicting genetic relationships among 17 Pigeonpea genotypes

Principal Component Analysis for Pigeonpea germplasm

PCA analysis reduces the dimensions of a multi variate data to a few principal axes, generates an Eigen vector for each axis and produces component scores for the characters (Ariyo *et al.*,)^[10]. The result of the PCA explained the genetic diversity of the Pigeonpea collection. There are no standard tests to prove significance of proper values and the coefficients. Principal component analysis has shown the genetic diversity of the germplasm lines. The cumulative variance of 77% (Table 3) by the first three axes with Eigen value of > 1.0 indicates that the identified traits (plant height, days to harvest, total grain yield, shelling % and days to 50%

flowering) within the axes exhibited great influence on the phenotype of germplasm lines. The variability on the first PC (38.77%) was accounted for by high positive loadings for plant height, days to harvest, days to 50% flowering and number of seeds per pod whereas total grain yield, shelling percentage and number of seeds per pod contributed more to the second PC with high positive loadings. Manyasa *et al.*,^[11] reported a cumulative variance of 76.9% of total variation among 12 characters as explained by the first five axes in a genetic diversity analysis conducted among 29 Uganda Pigeonpea germplasm.

Table 3: PC scores, Eigen value and Percentage Variance of Pigeonpea genotypes for various yield characters

	PC 1	PC 2	PC 3	PC 4	PC 5	PC 6	PC 7	PC 8
Plant height	0.4759	-0.1667	-0.3509	0.0439	-0.1499	0.3342	0.6804	0.1534
Days to 50% flowering	0.3538	-0.1481	0.5671	0.2340	0.3050	0.5794	-0.2156	-0.0359
Days to harvest	0.4470	-0.1699	0.3516	0.3281	-0.1286	-0.6872	0.0662	0.2167
Total Biological yield	-0.1988	-0.4213	-0.3091	0.4535	0.6026	-0.1569	0.1206	-0.2820
Total grain yield	-0.0372	0.6210	0.0753	0.5572	-0.2037	0.0427	0.2175	-0.4541
No. of Seeds per pod	0.3319	0.3290	-0.5272	0.2808	0.1451	0.0398	-0.5132	0.3725
Shelling Percentage	0.1737	0.4916	0.1310	-0.3656	0.6624	-0.1889	0.3137	0.0665
100 seed weight	-0.5170	0.0920	0.1879	0.3272	0.0582	0.1293	0.2500	0.7066
Eigenvalue	3.1015	1.8297	1.2488	0.7731	0.7330	0.1603	0.1216	0.0320
% variance	38.769	22.872	15.61	9.663	9.163	2.004	1.520	0.399

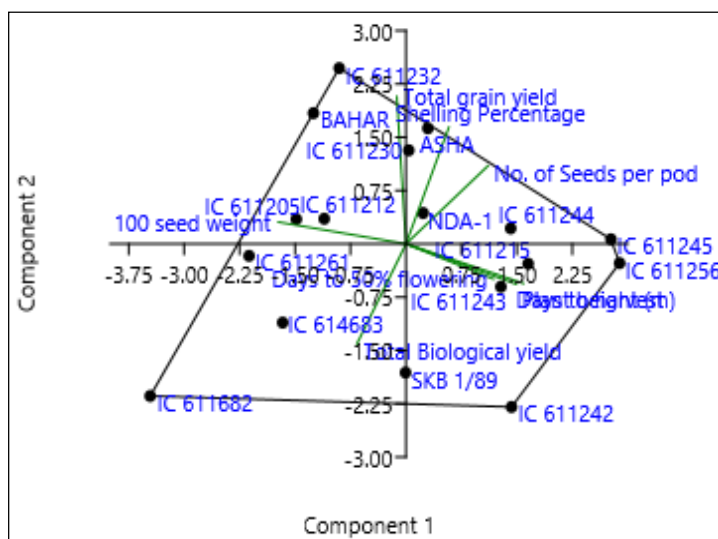
Scatter plot for Pigeonpea germplasm

A scatter plot drawn between PC1 and PC2 depicted a clear pattern of grouping genotypes in the factor plane (Fig 2). Convex of the hull showing the outliers was occupied by the genotypes namely IC 611232, Asha, IC 611245, IC 611256, IC 611242, IC 611682 and Bahar. All the genotypes were widely scattered across different quarters (Figure 2). These promising landraces can be used in crossing programme for enhancing yield characters. In this study, we chose to follow the criterion used by Clifford and Stephenson [12] and corroborated by Guei *et al.*, [13] which suggested that the first three principal components are often the most important in reflecting the variation patterns among accessions, and the characters associated with these are more useful in differentiating accessions. According to this criterion, the first three components account for more than 77 % of total variation giving a clear idea of the structure underlying the variables analysed. Similar results were obtained by Manyasa *et al.*, [11] and Hemavathy *et al.*, [14].

The phenotypic value of the each trait measures the importance and contribution of each component to total

variance, whereas each coefficient of proper vectors indicates the degree of contribution of every original variable with which each principal component is associated. The first 5 components accounted for 96.07% of the total variation. Characters with high variability are expected to provide high level of gene transfer during breeding programs (Gana [15] and Varthini [16]).

In GT biplot, a vector drawn from origin to each trait facilitates the visualization of interrelationships among traits. The vector length of the trait measures the magnitude of its effects on the dependent character. Traits are positively correlated if the angle between their vectors is an acute angle ($<90^\circ$) while they are negatively correlated if their vectors are an obtuse angle ($>90^\circ$) (Yan and Kang) [17]. Among the genotypes tested, shelling percentage and number of seeds per pod were positively correlated with total grain yield. The vector trait total biological yield made 180° angle with shelling percentage indicating traits to be opposite in genotype ranking.

**Fig 2:** Distribution of Pigeonpea genotypes across two components

Conclusions

Among fourteen genotypes screened along with three checks, IC-611232, IC-611230 and IC-611256 were found promising with respect to yield and yield parameters. Correlation analysis indicated that total grain yield exhibited positive but not significant correlation with number of seeds per pod, shelling percentage and 100 seed weight. The cluster analysis showed that there is significant genetic variability among tested genotypes which indicates the presence of excellent opportunity to bring about improvement through hybridizing

the selected genotypes present in distant clusters. PCA indicated that the first three principal components accounted for 77% of total variation indicating wide genetic variability among the genotypes. All the genotypes clustered into two major clusters with nine and eight genotypes each. In GT biplot, shelling percentage and number of seeds per pod were positively correlated with total grain yield. The vector trait total biological yield made 180° angle with shelling percentage indicating traits to be opposite in genotype ranking.

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