

To Study the Cluster Analysis in Pigeonpea Germplasm Accessions

Yogesh Kumar Nag¹, Dr. R. N. Sharma²

Department of Genetics and Plant Breeding, Indira Gandhi Krishi Viswavidyalaya, Raipur (C.G.), India

Abstract: Cluster analysis result showed existence of considerable diversity in pigeonpea germplasm accessions. The maximum inter cluster distance was observed in between cluster I and VI. Hence, genotypes belonging to cluster IV may be utilized as parent in future breeding programmes with the genotypes belonging to cluster I to obtain better/heterotic segregants.

1. Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp] is the major pulse crop of India after chickpea which contributes significantly to nourishment of a sizeable population. It belongs to the family of 'Fabaceae' and is also known as 'Arhar' or 'Tur', generally used in preparing *dal* which is rich in protein and minerals and eaten by majority of Indian population. Apart from the many direct uses pigeonpea is a good crop to improve soil fertility through biological nitrogen fixation into soil. Pigeonpea forms nodules on its roots which contain special bacteria which are naturally present in the soil.

In Chhattisgarh, pigeonpea is grown mainly in cropping systems such as monocropping and mixed cropping with soybean and early duration upland rice and on rice bunds which leads better economic returns. The poor and stagnate yield levels is another major constraint, which may be due to unavailability of superior high yielding area specific desirable varieties.

2. Materials and Methods

Experimental Detail

The experimental material was comprised of 45 pigeonpea germplasm accessions. The experiment was laid out in Randomized Complete Block Design (RBD) in two replications during *kharij*-2010-11. Experimental site has heavy (vertisol) soil. A fertilizer dose of 20N: 50P: 20K kg / ha was applied. Each entry was sown in two rows of four meter length keeping 60 cm between rows and 15 cm between plants spacings. All the recommended package of practices were adopted to raise a good crop.

Table 3.1: List of germplasm accessions

S.No.	Germplasm Accessions	Source of material
1.	ICPL-87119	IIPR, Kanpur
2.	BDN-2	IIPR, Kanpur
3.	UPAS-120	IIPR, Kanpur
4.	ICPL-6992	CRISAT, Patancheru
5.	ICPL-6994	ICRISAT, Patancheru
6.	ICPL-6995	ICRISAT, Patancheru
7.	ICPL-6996	ICRISAT, Patancheru
8.	ICPL-6997	ICRISAT, Patancheru
9.	ICPL-6999	ICRISAT, Patancheru
10.	ICPL-7000	ICRISAT, Patancheru
11.	ICPL-7001	ICRISAT, Patancheru
12.	ICPL-7002	ICRISAT, Patancheru
13.	ICPL-7003	ICRISAT, Patancheru

14.	ICPL-7004	ICRISAT, Patancheru
15.	ICPL-7005	ICRISAT, Patancheru
16.	ICPL-7349	ICRISAT, Patancheru
17.	ICPL-7358	ICRISAT, Patancheru
18.	ICPL-7359	ICRISAT, Patancheru
19.	ICPL-7362	ICRISAT, Patancheru
20.	ICPL-7363	ICRISAT, Patancheru
21.	ICPL-7364	ICRISAT, Patancheru
22.	ICPL-7366	ICRISAT, Patancheru
23.	ICPL-7367	ICRISAT, Patancheru
24.	ICPL-7373	ICRISAT, Patancheru
25.	ICPL-7374	ICRISAT, Patancheru
26.	ICPL-7376	ICRISAT, Patancheru
27.	ICPL-7379	ICRISAT, Patancheru
28.	ICPL-7382	ICRISAT, Patancheru
29.	ICPL-7384	ICRISAT, Patancheru
30.	ICPL-7385	ICRISAT, Patancheru
31.	ICPL-7387	ICRISAT, Patancheru
32.	ICPL-7388	ICRISAT, Patancheru
33.	ICPL-7389	ICRISAT, Patancheru
34.	ICPL-7391	ICRISAT, Patancheru
35.	ICPL-7392	ICRISAT, Patancheru
36.	ICPL-7393	ICRISAT, Patancheru
37.	ICPL-7397	ICRISAT, Patancheru
38.	ICPL-7398	ICRISAT, Patancheru
39.	ICPL-7404	ICRISAT, Patancheru
40.	ICPL-7405	ICRISAT, Patancheru
41.	ICPL-7406	ICRISAT, Patancheru
42.	ICPL-7409	ICRISAT, Patancheru
43.	ICPL-7420	ICRISAT, Patancheru
44.	ICPL-7429	ICRISAT, Patancheru
45.	ICPL-7430	ICRISAT, Patancheru

3. Observations Recorded

Observations on metric traits were recorded on single plant basis from five randomly selected competitive plants from each genotype separately. Observations on flowering and maturity were recorded on plot basis as per the descriptors developed by IBPGR and ICRISAT for pigeonpea.

Days to flower initiation

This was noted in terms of days from the date of sowing to the opening of first flower.

Days to 50% flowering

It was noted in days from the date of sowing to the opening of first flower on approximately 50 % plants in each plot.

Days to maturity

It was noted in terms of days from the date of sowing to the stage when over 90 % pods have matured.

Plant height (cm)

The height of plant was measured in cm from ground level to the tip of main axis of physiologically matured plants.

Number of primary branches per plant

Total numbers of primary branches were counted at physiological maturity.

Number of pods per plant

All the effective pods were counted from each selected plant at physiological maturity.

No of pods per cluster

Total number of pods were counted from each selected plant at physiological maturity.

No of pod clusters per plant

Total numbers of clusters were counted from each selected plant at physiological maturity.

Number of seeds per pod

Total numbers of seeds from the effective pods each selected plant were counted at physiological maturity.

100 seed weight (g)

Test weight of dried 100 healthy seeds in grams at 10 per cent (air dry) moisture content was recorded.

Seed yield per plant (g)

The selected plants were harvested, threshed and winnowed separately. Finally the seeds were weighed in grams after drying them to appropriate moisture level.

3.1 Statistical Analysis

3.1.1 Analysis of variance

The data obtained from the individual plant observations from randomized block design experiment were analyzed statistically as per the procedure given by Cochran and Cox (1957).

Table 3.2: The skeleton of analysis of variance for Randomized Complete Block Design (RBD)

Source	D.F.	SS	MSS	F value
Replications	(r-1)	SSR	MSR	MSR / MSE
Genotypes	(t-1)	SST	MST	MST / MSE
Error	(r-1)(t-1)	SSE	MSE	
Total	rt-1	TSS		

Where, r = Number of replications. t = number of genotypes.

To test the significance of treatment, the calculated value of 'F' was compared with tabular value of 'F' at 5 and 1 per cent levels of probability against error degree of freedom, i.e. (r-1) (t-1).

3.1.2 Estimation of genetic parameters of variation

1) Mean

Mean of the character was estimated by summing up of all the observation and dividing the sum by the number of observations.

$$\bar{X} = \frac{\sum X_i}{N}$$

Where, $\sum X_i$ = Summation of all the observations

N = Number of observations

2) Range

Range is the difference between the least and the greatest terms of a series of observation and thus provides the information about the variability present in the genotypes.

3) Estimation of coefficients of variation

The coefficient of variation for different characters was estimated by formula as suggested by Burton (1952).

$$GCV (\%) = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

$$PCV (\%) = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

\bar{X} = Mean of character

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$ = Phenotypic variance

The estimates of genotypic and phenotypic coefficient of variance were classified as low, moderate and high as suggested by Sivasubramaniam and Madhavamenon (1973)

< 10% = Low

10% to 20% = Moderate

< 20% = High

4) Genetic advance

Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. The expected genetic advance was calculated by the formula given by Johnson *et al.* (1955) as described below.

$$GA = K.h^2.\sigma_p$$

Where,

GA = Genetic advance

K = Constant (Standardized selection differential) having the value of 2.06 at 5 per cent level of selection intensity.

h^2 = Heritability

σ_p = Phenotypic standard deviation

The genetic advance as percentage of mean was estimated as per the below formula

$$\text{Genetic advance as percentage of mean} = \frac{GA}{\bar{X}} \times 100$$

Where,

\bar{X} = Grand mean

GA = Genetic advance

The magnitude of genetic advance as percentage of mean was categorized as high (> 30%), moderate (30% - 10%) and low (< 10%).

5) Estimation of Heritability

Heritability in broad sense (h^2_{bs}) defined as the proportion of the genotypic variance to the total variance (phenotypic) was calculated as per the formula suggested by Burton (1956).

$$h^2 (bs) \% = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

$h^2 (bs)$ = Heritability in broad sense,

σ^2_g = Genotypic variance,

σ^2_p = Phenotypic variance

The broad sense heritability estimates were classified as low (<50%), moderate (50-70%) and high (>70%) as suggested by Robinson (1966).

4. Results and Discussion

Cluster analysis

In plant breeding, genetic diversity plays an important role because hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related parents. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability.

The choice of genetically diverse parents for hybridization is an important feature of any crop improvement programme for getting desirable segregants. The multivariate analysis based on Mahalanobis D^2 or non-hierarchical Euclidean cluster analysis is used for divergence analysis. Multivariate analysis by means of Mahalanobis D^2 statistic is a powerful tool in quantifying the degree of divergence between biological population at genotypic level to assess the relative contribution of different components to the total divergence. The D^2 analysis classifies the genotypes into relatively homogeneous groups in such a way that within cluster diversity is minimized and between clusters diversity is maximized. The respective genotypes from diverse clusters can be utilized in breeding programme depending upon the breeding objectives.

A set of 45 genotypes of pigeonpea were subjected to D^2 analysis for twelve characters. Based on D^2 values four clusters were formed (Table 4.5). This indicated that substantial diversity exists in the available gene pool of pigeonpea. Results of cluster analysis revealed that the cluster II was the largest which consisted of (16 accessions) followed by cluster III (12 accessions), I (9 accessions) and IV (8 accessions). From the clustering pattern, it was found that the pigeonpea germplasm accessions received from ICRISAT of Bastar origin were genetically diverse to each other. Hence, the genotypes studied are reliable enough for hybridization and selection.

The maximum inter cluster distance was observed in between cluster I and VI (4.904) followed by between cluster II and IV (4.048) and cluster III and IV (3.599). This suggested that the hybridization programme involving

parents from these clusters is expected to give higher frequency of better segregates or desirable combination for development of useful genetic stocks or varieties. The minimum inter cluster distance was observed in between II and III (2.125) followed by cluster I and II (2.518) and cluster I and III (3.178) indicating minimal diversity (differences) for the genes under study.

The maximum intra cluster distances was observed in cluster IV (3.674) followed by cluster I (2.818), cluster III (2.634) and cluster II (2.364). The mean values for different characters were compared across the cluster and are presented in Table. 4.7. Results of the analysis revealed that cluster I was found to be better for earliest days to flower initiation (100.50 days), earliest days to 50% flowering (122.72 days), earliest days to maturity (169.33 days) and number of seeds per pod (4.83) whereas, cluster III exhibited the highest 100 seed weight (10.17 g). Similarly, cluster IV has better genotypes for more number of primary branches (16.38), number of pods per plant (375.75), number pods per cluster (3.12), number of pod clusters per plant (102.56), pod length (5.58 cm) and high seed yield per plant (45.06 g).

The pattern of distribution of pigeonpea genotypes in various clusters revealed existence of considerable diversity present in the material (Table 4.8). The highest intra cluster distance was observed for the cluster IV. Hence, genotypes belonging to this cluster *viz.*, ICPL-7373, ICPL-7384, ICPL-7430 and ICPL-7405 may be utilized as parent in future breeding programmes with the genotypes belonging to cluster I *i.e.*, UPAS-120, ICPL-6994, ICPL-6996 and ICPL-7409 as the maximum inter cluster distance was noted between the cluster I and Cluster IV. The experimental findings of cluster analysis are in general agreement with the findings of Sarma and Roy (1994), Nandan *et al.* (1996), Basawarajiah *et al.* (2000), Gohil (2006), Mahamad *et al.* (2006).

Table 4.5: Genotypes of pigeonpea included in different clusters

Cluster number	Number of genotypes included	Names of genotypes
I	9	UPAS-120, ICPL-6994, ICPL-6996, ICPL-6999, ICPL-7000, ICPL-7359, ICPL-7364, ICPL-7409, ICPL-7429
II	16	ICPL-6992, ICPL-7001, ICPL-7003, ICPL-7004, ICPL-7005, ICPL-7358, ICPL-7362, ICPL-7363, ICPL-7366, ICPL-7367, ICPL-7374, ICPL-7389, ICPL-7391, ICPL-7397, ICPL-7404, ICPL-7420
III	12	ICPL-87119, BDN-2, ICPL-6992, ICPL-6997, ICPL-7002, ICPL-7349, ICPL-7376, ICPL-7379, ICPL-7382, ICPL-7392, ICPL-7393, ICPL-7406
IV	8	ICPL-7373, ICPL-7384, ICPL-7385, ICPL-7388, ICPL-7398, ICPL-7405, ICPL-7430

Table 4.6: Inter and Intra cluster distance of genotypes in pigeonpea

Cluster	I	II	III	IV
I	2.818	2.518	3.178	4.904
II		2.364	2.125	4.048
III			2.624	3.599
IV				3.674

Table 4.7: Mean performance of genotypes in individual cluster for different yield traits

Clusters	Characters												
	Entries	Days to flower initiation	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches /plant	No. of pods/plant	No. of pods/ cluster	No. of pod clusters/ plant	Pod length (cm)	No. of seeds/pod	100 seed weight (g)	Seed yield per plant (g)
I	9	100.50	122.72	169.33	184.85	13.28	251.00	2.67	60.39	5.30	4.83	8.58	28.13
II	16	102.31	127.72	175.56	193.70	15.06	242.31	2.75	55.31	5.27	4.00	7.76	30.74
III	12	106.29	132.83	182.00	179.34	14.83	260.67	2.79	55.25	5.30	4.00	10.17	35.40
IV	8	112.12	134.88	196.19	203.16	16.38	375.75	3.12	102.56	5.58	4.25	8.70	45.06

Table 4.8: Desirable genotypes based on cluster performance

Characters	Clusters			
	I	II	III	IV
Days to flower initiation	UPAS-120	ICPL-6992	ICPL-6995	ICPL-7373
Days to 50% flowering	UPAS-120	ICPL-6994	ICPL-6997	ICPL-7373
Days to maturity	UPAS-120	ICPL-6992	ICPL-7392	ICPL-7373
Plant height (cm)	ICPL-6994	ICPL-7005	ICPL-ICPL	ICPL-7384
No. of primary branches/plant	ICPL-6999	ICPL-7366	ICPL-87119	ICPL-7384
No. of pods/plant	ICPL-7409	ICPL-6992	ICPL-7392	ICPL-7430
Number of pods/cluster	UPAS-120	ICPL-7389	ICPL-87119	ICPL-7385
No. of pod clusters/plant	UPAS-120	ICPL-7366	ICPL-7392	ICPL-7405
Pod length (cm)	UPAS-120	ICPL-7003	ICPL-6997	ICPL-7373
No. of seeds/pod	ICPL-6996	ICPL-6992	ICPL-87119	ICPL-7373
100 seed weight (g)	ICPL-7000	ICPL-7389	ICPL-7382	ICPL-7385
Seed yield/plant	UPAS-120	ICPL-7363	ICPL-7392	ICPL-7373

5. Summary, Conclusions

Cluster analysis result showed existence of considerable diversity in pigeonpea germplasm accessions. The highest intra cluster distance was observed for the cluster IV. Hence, genotypes belonging to this cluster viz., ICPL-7373, ICPL-7384, ICPL-7430 and ICPL-7405 may be utilized as parent in future breeding programmes with the genotypes belonging to cluster I i.e., UPAS-120, ICPL-6994, ICPL-6996 and ICPL-7409 as the maximum inter cluster distance was noted between the cluster I and Cluster IV. This suggested that the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates or desirable combination for development of useful genetic stocks or varieties.

Considerable amount of genetic divergence was present among 45 genotypes. Intercrossing of genotypes from different clusters showing superior mean performance may help in obtaining heterotic segregants. The highest intra cluster distance was observed for the cluster IV. Hence, genotypes belonging to this cluster viz., ICPL-7373, ICPL-7384, ICPL-7430 and ICPL-7405 may be utilized as parent in future breeding programmes with the genotypes belonging to cluster I i.e., UPAS-120, ICPL-6994, ICPL-

6996 and ICPL-7409 as the maximum inter cluster distance was noted between the cluster I and Cluster IV. This suggested that the hybridization programme involving parents from these clusters is expected to give higher frequency of better segregates or desirable combination for development of useful genetic stocks or varieties.

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