

## Genetic Divergence Studies in Pigeonpea [*Cajanus cajan* (L). Millipis] Genotypes

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**ABSTRACT:** The experiment was conducted during *Kharif-2023* for study of genetic diversity of 42 genotypes of pigeonpea using D<sup>2</sup> statistics method of Mahalanobis. Genetic diversity of the forty two genotypes of pigeonpea was accessed for nine characters in a randomized block design with two replications at Agriculture Research Station, Badnapur. Forty two genotypes of pigeonpea were grouped into six clusters which indicated diversity. Cluster I had the maximum number of 24 germplasms, Cluster III had 9, Cluster II had 6, Cluster IV, V and VI had 01 germplasm each respectively. The highest distance between two clusters was existed between Cluster II and V (31.48) indicating greatest divergence. The maximum intra-cluster distance of 9.96 was noticed in cluster III. High yielding diverse genotypes *viz.*, BDN-2013-02, AKTM-2117, BDN-2019-05 and BDN-2013-05 of cluster I and ICP-7952, ICP-7939, ICP-16553 of cluster II and BDN-2019-33 of cluster III may be used for future hybridization programme for further yield improvement in pigeonpea.

**Keywords:** Pigeonpea, Genetic diversity, Clusters and D<sup>2</sup> Analysis.

### INTRODUCTION

Natural diversity of pigeonpea genes found in the local germplasm and the existence of its wild relatives there, India is regarded as the origin of the pigeonpea (Vander Maesen, 1980). Red gram, commonly known as pigeonpea, is used for a variety of things, including food, fuel, firewood, material for fences and soil enhancement through N fixation. In India pigeonpea is grown in an area 47.17 lakh hectares with production 41.37 lakh tonnes. Pigeonpea contribute 17 percent in total pulses production in India. Pigeonpea is used to make dal, the dish that Indian vegetarians love the most and is high in protein (24–25%) and minerals (Sodavadiya *et al.*, 2009).

In a hybridization programme, genetic diversity is a prerequisite and a significant element. High yield improvement programs' success is mostly influenced by the kind and level of genetic variety and variability found in germplasm.

### MATERIALS AND METHODS

The research experiment was conducted at College of Agriculture, Badnapur during *kharif -2023* were evaluated in Randomized Block Design with two replications for nine quantitative characters *viz.*, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number seeds per pod, 100 seed weight and seed yield per

plant. Total forty two germplasm material constituted for research, of which twenty nine genotypes were received from NBPGR, New Delhi, six genotypes were received from PDKV, Akola and five genotypes were received from ARS, Badnapur along with two checks. Each genotype sown in single row of 4 m length with row to row distance 90 cm and plant to plant distance 20 cm. Data were recorded for five selective plants from each genotype. The genetic diversity analysis will be carried out by D<sup>2</sup> statistical method as per by Mahalanobis (1936).

### RESULT AND DISCUSSION

All the forty two genotypes of pigeonpea were grouped into six clusters using the Toucher's method (Singh and Chaudhary 1977). The result indicated that Cluster I had the maximum number of 24 germplasms, Cluster III had 9, Cluster II had 6, Cluster IV, V and VI had 01 germplasm each respectively. Previous result of Rupika *et al.* (2014) showed six cluster formed by genotypes. In cluster I had large number of genotypes and five cluster had single genotypes.

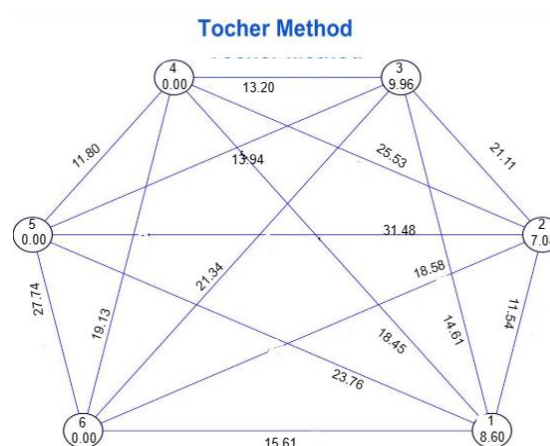
The intra and inter cluster distances between all pairs of six cluster indicated in Table 2 and Fig. 1. Clustering pattern shows that genotypes of different source were clubbed into single cluster and genotypes of same source clubbed into different clusters. The intra cluster values varied from 0.00 to 9.96. The maximum intra-cluster distance of 9.96 was noticed in cluster III.

Showed lowest intra cluster distance of cluster II that similar result earlier evaluated by Teli *et al.* (2019). The greatest distance between two clusters was existed between Cluster II and V (31.48) indicating highest divergence, followed by Cluster V and VI (27.74), Cluster II and IV (25.53), Cluster I and V (23.76) and Cluster III and VI (21.34). Whereas the latest distance was recorded between cluster I and II (11.54) followed by cluster IV and V (11.80), cluster III and IV (13.20), cluster I and III (14.61) and cluster I and VI (15.61) indicating least genetic divergence among germplasm. Less distance between two clusters, Greatest distance between cluster VI and VII was 22.18 this similar result showed by Ranjani *et al.* (2021).

The utility of D2 analysis is enhanced by its application to estimates the relative contribution of various characters to genetic diversity. The contribution of each character towards genetic diversity is presented in Table 3. 100 seed weight (59.00%) has the major contribution to total genetic diversity, Days to maturity (9.99%), number of pods per plant (9.41%), number of seeds per pod (8.71%), Seed yield per plant (8.13%), number of secondary branches per plant (2.44%), plant height (1.86%), days to 50% flowering (0.23%) and number of primary branches per plant (0.23%). Relative contribution towards diversity showed lowest contribution of number of primary branches per plant estimation were earlier reported by Rupika *et al.* (2014). Relative contribution towards diversity showed highest contribution of 100 seed weight followed by days to maturity and number of pods per plant according to Quatadah *et al.* (2019).

The mean performance of cluster value of all characters is presented in Table 4. The cluster means for days to 50 per cent flowering ranged from 98.50 (cluster VI) to 121.92 (cluster II), from 154.30 (cluster VI) to 255.70 (cluster IV) for plant height, number of primary branches per plant ranged from 5.50 (cluster V) to

10.88 (cluster II), from 10.60 (cluster V) to 28.62 (cluster II) for number of secondary branches per plant, the cluster mean for number of pods per plant from 73.50 (cluster V) to 312.25 (cluster II), from 3.85 (cluster II) to 4.44 (cluster III) for number of seeds per pod, for days to maturity from 146.00 (cluster VI) to 178.58 (cluster II), from 7.71 (cluster II) to 15.95 (cluster V) for 100 seed weight. The seed yield ranged from 27.15 (cluster VI) to 96.49 (cluster II). Shunyu *et al.* (2013) reported similar result that was cluster mean for number of pods per plant showed highest range in cluster II. Days to 50% flowering, days to maturity and number of pods per plant showed highest cluster means of cluster II that earlier result finding by Teli *et al.* (2019). According to Ranjani *et al.* (2021) cluster for days to maturity showed highest of cluster II and cluster mean of seed yield per plant highest for cluster II.



**Mahalanobis Euclidean Distance (Not to the Scale)**

**Fig. 1.** Diagram Showing the Cluster Distance.

**Table 1: Composition of forty two pigeonpea genotypes into different clusters by Tocher's method.**

| Cluster Number | No. of genotypes | Germplasm included in the cluster                                                                                                                                                                                                                                              |
|----------------|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| I              | 24               | ICP-15600, AKTM-1637, ICP-10325, ICP-13872, ICP-10384, ICP-7242, ICP-13947, ICP-7265, ICP-810, BDN-2019-05, AKTM-1914, BDN-2013-02, AKTM-1914, AKTM-2117, ICP-2925, AKTM-1917, AKTM-1644, ICP-15068, AKTM-1604, ICP-11667, ICP-1878, ICP-811, Godawari, BDN-2013-05, ICP-9922. |
| II             | 6                | ICP-7939, ICP-752, ICP-7947, ICP-7952, ICP-16553, ICP-7949                                                                                                                                                                                                                     |
| III            | 9                | ICP-1861, ICP-238, ICP-14147, ICP-709, ICP-9905, ICP-14056, BDN-716, BDN-2019-33, BDN-2019-09.                                                                                                                                                                                 |
| IV             | 1                | ICP-15153.                                                                                                                                                                                                                                                                     |
| V              | 1                | ICP-7999.                                                                                                                                                                                                                                                                      |
| VI             | 1                | ICP-7172.                                                                                                                                                                                                                                                                      |

**Table 2: Average cluster D<sup>2</sup> values of pigeonpea.**

| Cluster Number | I    | II    | III   | IV    | V     | VI    |
|----------------|------|-------|-------|-------|-------|-------|
| I              | 8.60 | 11.54 | 14.61 | 18.45 | 23.76 | 15.61 |
| II             |      | 7.04  | 21.11 | 25.53 | 31.48 | 18.58 |
| III            |      |       | 9.96  | 13.20 | 13.94 | 21.34 |
| IV             |      |       |       | 0.00  | 11.80 | 19.13 |
| V              |      |       |       |       | 0.00  | 27.74 |
| VI             |      |       |       |       |       | 0.00  |

**Table 3: Percent contribution of different characters to genetic diversity.**

| Sr. No. | Characters                         | No. of times appearing I in ranking | % contribution |
|---------|------------------------------------|-------------------------------------|----------------|
| 1.      | Days to 50% Flowering              | 2                                   | 0.23           |
| 2.      | Days to Maturity                   | 86                                  | 9.99           |
| 3.      | Plant Height(cm)                   | 16                                  | 1.86           |
| 4.      | Number of primary branches/Plant   | 2                                   | 0.23           |
| 5.      | Number of secondary branches/Plant | 21                                  | 2.44           |
| 6.      | Number of pods/Plant               | 81                                  | 9.41           |
| 7.      | Number of seeds/Pod                | 75                                  | 8.71           |
| 8.      | 100 seed weight(g)                 | 508                                 | 59.00          |
| 9.      | Seed yield/Plant                   | 70                                  | 8.13           |
| 10.     | Total                              | 861                                 | 100            |

**Table 4: Cluster means for Seed yield and its components in Pigeonpea.**

|           | Days to 50 % Flowering | Days to Maturity | Plant Height (cm) | Number of primary branches/Plant | Number of secondary branches/Plant | Number of pods/Plant | Number of seeds/Pod | 100 seed weight(g) | Seed yield /Plant |
|-----------|------------------------|------------------|-------------------|----------------------------------|------------------------------------|----------------------|---------------------|--------------------|-------------------|
| 1 Cluster | 117.88                 | 175.38           | 227.91            | 9.19                             | 18.43                              | 225.23               | 4.16                | 9.55               | 73.27             |
| 2 Cluster | 121.92                 | 178.58           | 220.06            | 10.88                            | 28.62                              | 312.25               | 3.85                | 7.71               | 96.49             |
| 3 Cluster | 121.44                 | 178.28           | 220.78            | 7.57                             | 15.16                              | 192.33               | 4.44                | 12.85              | 61.06             |
| 4 Cluster | 104.00                 | 152.50           | 255.70            | 9.40                             | 19.40                              | 192.50               | 3.95                | 13.65              | 35.75             |
| 5 Cluster | 120.00                 | 171.00           | 228.00            | 5.50                             | 10.60                              | 73.50                | 4.30                | 15.95              | 47.65             |
| 6 Cluster | 98.50                  | 146.00           | 154.30            | 8.50                             | 17.50                              | 103.00               | 4.30                | 7.85               | 27.15             |

## CONCLUSIONS

Out of the nine characters that were examined, the number of secondary branches was found to have the greatest contribution to genetic divergence followed by plant height, 100 seed weight, days to maturity, number of primary branches, days to 50% flowering, number of pods per plant, number of seeds per pod and seed yield per plant.

## FUTURE SCOPE

High yielding diverse genotypes viz., BDN-2013-02, AKTM-2117, BDN-2019-05 and BDN-2013-05 of cluster I and ICP-7952, ICP-7939, ICP-16553 of cluster II and BDN-2019-33 of cluster III may be used for future hybridization programme for further yield improvement in pigeonpea.

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