# The Pharma Innovation

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# Genetic diversity analysis in pigeonpea [*Cajanus cajan* (L.) Millspaugh] germplasm under rainfed agro-ecological condition

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### Abstract
The existence of genetic diversity among the 85 genotypes of pigeonpea was examined by employing Mahalanobis $D^2$-statistics. The genotypes were a grouped into seven clusters. The highest number of genotypes appeared in cluster I which possessed 50 genotypes namely RP-67, RP-70, RP-110, RP-64, RP-20, RP-66, RP-55, RP-19, RP-116, RP-109, RP-124, RP-102, RP-44, RP-54, RP-60, RP-56, RP-43, RP-32, RP-74, RP-127, RP-118, RP-122, RP-167, RP-48, RP-115, RP-152, RP-24, RP-164, RP-45, RP-85, RP-72, RP-16, RP-140, RP-141, RP-62, RP-131, RP-101, RP-91, RP-145, RP-73, RP-106, RP-79, RP-144, RP-92, RP-163, RP-27, RP-105, RP-146, RP-84, RP-100 and RP-150. The second highest number of genotypes found in cluster II which was comprised of 15 genotypes namely, RP-35, RP-46, RP-53, RP-38, RP-107, RP-36, RP-137, RP-37, RP-111, RP-149, RP-89, RP-80, RP-4, RP-158 and RP-63. Cluster III comprised of 11 genotypes *viz*; RP-112, RP-166, RP-165, RP-108, RP-126, RP-15, RP-76, RP-78, RP-75, RP-143 and RP-42. The lowest genotypes were found in cluster V (Asha), VI (RP-159), and VII (Rajeevlochan). They all possessed only one genotype. Genetics divergence analysis revealed existence of considerable diversity in pigeonpea germplasm accessions. The genotypes belonging to cluster V, VI and VIII. On the basis of cluster wise mean yield performance it was noted that accessions *viz*., Rajeevlochan, RP-159 and Asha may be taken in to be consideration in future breeding programme in pigeonpea genotypes.

**Keywords:** Pigeonpea, genetic diversity, *Cajanus cajan*

## Introduction
Pigeonpea [*Cajanus cajan* (L.) Millspaugh] 2n =2x = 22 chromosome number belongs to the family Leguminosae. Pigeonpea is the second most important pulse crop of India after chickpea. Peninsular India is considered as the native of pigeonpea (Maesan, 1980) [12], because of its availability in large natural diversity, genetic variability in the available local germplasm and presence of numbers of wild relatives in the country. It can grow in any warm climate, because of its deep rooting and drought-tolerant nature. It is a leguminous food crop and cultivated throughout tropical and sub-tropical region. It is known by different names in different regions of India *viz*., arhar, red gram, tur, cango pea, angole, and rahar. Pigeonpea has been recognized as a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low-priced vegetarian foods. Pigeonpea have high proteinaceous values and seed can be used for preparation of various meals. Its seed contain 62.78 g. carbohydrate, 1.49 g fats and 21.7 g proteins per 100 g. Generally, the protein content ranges from 18-29% which is about 3 times value found in cereals.

Information on genetic divergence among the plant materials is vital to a plant breeder for efficient choice of parents are likely to contribute desirable segregants and or to produce high heterotic crosses. The multivariate analysis based on Mahalanobis $D^2$ or non-hierarchical Euclidean cluster analysis is used for divergence analysis. 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.

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## Materials and Methods

The experimental materials for present investigation was consisted of 85 genotypes of pigeonpea. The genotypes were sown in Randomized Complete Block Design (RBD) with two replications at IGKV, RMD CARS, research and instructional farm Ambikapur during *Kharif* 2020. The every genotypes was sown in double row of 4.0 m length with 60 cm × 20 cm spacing. Observations were recorded for eleven quantitative traits. They are days to 50% flowering, days to maturity, plant height(cm), number of primary branches per plant, number of pods per plant, number of pods per cluster, number of pod cluster per plant, pod length (cm), number of seeds per pod, 100 seed weight and seed yield per plant (g). The multivariate analysis based on Mahalanobis $D^2$ or non-hierarchical Euclidean cluster analysis is used for divergence analysis.

## Results and Discussion

Using Mahalanobis $D^2$ statistics, the existence of genetic divergence among the 85 genotypes of pigeonpea was investigated. Table 1 shows the clustering pattern of 85 genotypes based on $D^2$-statistics analysis. The genotypes were divided into seven different groups. Cluster I presented highest 50 genotypes namely. RP-67, RP-70, RP-110, RP-64, RP-20, RP-66, RP-55, RP-19, RP-116, RP-109, RP-124, RP-102, RP-44, RP-54, RP-60, RP-56, RP-43, RP-32, RP-74, RP-127, RP-118, RP-122, RP-167, RP-48, RP-115, RP-152, RP-24, RP-164, RP-45, RP-85, RP-72, RP-16, RP-140, RP-141, RP-62, RP-131, RP-101, RP-91, RP-145, RP-73, RP-106, RP-79, RP-144, RP-92, RP-163, RP-27, RP-105, RP-146, RP-84, RP-100 and RP-150. The 2nd highest number of genotypes was found in cluster II which was comprised of 15 genotypes namely, RP-35, RP-46, RP-53, RP-38, RP-107, RP-36, RP-137, RP-37, RP-111, RP-149, RP-89, RP-80, RP-4, RP-158 and RP-63. Cluster III comprised of 11 genotypes *viz*; RP-112, RP-166, RP-165, RP-108, RP-126, RP-15, RP-76, RP-78, RP-75, RP-143 and RP-42. The lowest genotypes were found in cluster V (Asha), VI (RP-159), and VII (Rajeevlochan). They all possessed only one genotype.

Table 2 shows the estimated intra and inter cluster distances represented by $D^2$ values. Cluster IV (41.89) had the greatest intra-cluster distance, followed by cluster III (29.42), and cluster II (26.86) and Cluster I (26.35). The cluster V, VI and VII had the lowest intra cluster $D^2$ value (0.00), the all have only one genotypes. Cluster V and VII had the lowest inter cluster $D^2$ values (39.81), followed by cluster V and VII (39.81), cluster II and V (45.82), cluster I and III (51.76), and cluster I and II (55.35). Cluster III and VII had the greatest inter-cluster $D^2$ value (296.66), followed by Cluster III and VI (219.72) and cluster IV and VII (219.24).

Table 3 shows the estimated Inter cluster mean values. Cluster III (137.82) had the highest cluster mean for days to 50% flowering, followed by cluster I (130.23), and cluster II (129.63). Cluster V had the lowest cluster mean (122.5). Cluster III had the highest cluster mean for days to maturity (225.34), followed by Cluster I (212.92) and Cluster VI (210.56). Cluster IV had the lowest cluster mean (198.4). The greatest cluster mean for plant height was found in Cluster I (258.56), followed by Cluster II (257.93) and Cluster IV (255.9). Cluster VII had the lowest cluster mean (207.8). Cluster VII (14.1) had the highest cluster mean for primary branch number/plant, followed by Cluster V (12.5) and Cluster II (10.19). Cluster III had the lowest cluster mean (6.18). Cluster VII (211.6) had the highest cluster mean for total number of pods/plant, followed by Cluster VI (189.63), and Cluster V (176.5). Cluster III had the lowest cluster mean (79.19). Cluster VII (4.1) had the largest mean number of pods/cluster, followed by Cluster V (3.7) and Cluster II (3.01). Cluster VI had the lowest cluster mean (2.64). Cluster VI (53.85) had the greatest cluster mean for the number of pod clusters/plant, followed by Cluster V (47.15) and Cluster VII (45.89). Cluster II had the lowest cluster mean (42.34). The highest cluster mean for pod length was found in Cluster VI (5.96), followed by Cluster III (5.86) and Cluster IV (5.82). Cluster VII had the lowest cluster mean (5.5). Cluster III (4.44) had the largest number of seeds/pod cluster mean, followed by Cluster II (4.37) and Cluster I (4.34). Cluster V had the lowest cluster mean (3.8). Cluster VI (11.18) had the highest cluster mean for 100 seed weight, followed by Cluster II (10.62), and Cluster I (10.47). Cluster V had the lowest cluster mean (9.43). Seed yield was highest in Cluster VII (38.82), followed by Cluster VI (38.75), and Cluster II (33.52). Cluster III had the lowest cluster mean (20.12). The results of cluster analysis ex/iments coincide with those of Viramgama and Goyal (1994) [11], Basavarajaiah *et al.,* (2000) [1], Samal *et al.,* (2001) [5], Nag and Sharma (2012) [3], Gendley *et al.,* (2015) [2].

**Table 1:** Genotypes of pigeonpea included in different cluster

| Clusters | Number of accessions | Name of the genotypes |
|---|---|---|
| I | 50 | RP-67, RP-70, RP-110, RP-64, , RP-20, RP-66, RP-55, RP-19, RP-116, RP-109, RP-124, RP-102, RP-44, RP-54, RP60, RP-56, RP-43, RP-32, RP-74, RP-127, RP-118, RP-122, RP-167, RP-48, RP-115, RP-152, RP-24, RP-164, RP-45, RP-85, RP-72, RP-16, RP-140, RP-141, RP-62, RP-131, RP-101, RP-91, RP-145, RP-73, RP-106, RP-79, RP-144, RP-92, RP-163, RP-27, RP-105, RP-146, RP-84, RP-100, RP-150 |
| II | 15 | RP-35, RP-46, RP-53, RP-38, RP-107, RP-36, RP-137, RP-37, RP-111, RP-149, RP-89, RP-80, RP-4, RP-158, RP-63 |
| III | 11 | RP-112, RP-166, RP-165, RP-108, RP-126, RP-15, RP-76, RP-78, RP-75, RP-143, RP-42 |
| IV | 6 | RP-25, RP-26, RP-17, RP-161, RP-61 |
| V | 1 | Asha |
| VI | 1 | RP-159 |
| VII | 1 | Rajeevlochan |

**Table 2:** Intra and Inter cluster distance of genotypes in pigeonpea

|  | Cluster 1 | Cluster 2 | Cluster 3 | Cluster 4 | Cluster 5 | Cluster 6 | Cluster 7 |
|---|---|---|---|---|---|---|---|
| Cluster 1 | 26.35 |  |  |  |  |  |  |
| Cluster 2 | 55.35 | 26.86 |  |  |  |  |  |
| Cluster 3 | 51.76 | 116.53 | 29.42 |  |  |  |  |
| Cluster 4 | 39.85 | 78.16 | 83.37 | 41.89 |  |  |  |
| Cluster 5 | 99.86 | 45.29 | 203.14 | 101.45 | 0 |  |  |
| Cluster 6 | 120.02 | 56.93 | 219.72 | 135.32 | 45.82 | 0 |  |
| Cluster 7 | 188.41 | 80.9 | 296.66 | 219.24 | 39.81 | 63.92 | 0 |

**Table 3:** Mean performance of genotypes in individual cluster for different yield traits

| Cluster no. | Days to 50% Flowering | Days to Maturity | Plant Height (cm) | No. of primary branches/plant | Number of pods/plant | Number of pods/cluster | Number of pod cluster per plant | Pod length (cm) | Number of seeds/pod | 100 seed weight (g) | Seed yield per plant (g) |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Cluster 1 | 130.23 | 212.92 | 258.56 | 7.81 | 106.35 | 2.88 | 29.27 | 5.71 | 4.34 | 10.47 | 25.15 |
| Cluster 2 | 129.63 | 206.01 | 257.53 | 10.19 | 153.41 | 3.01 | 42.34 | 5.51 | 4.37 | 10.62 | 33.52 |
| Cluster 3 | 137.82 | 225.34 | 251.75 | 6.18 | 79.19 | 2.88 | 19.95 | 5.86 | 4.44 | 10.12 | 20.12 |
| Cluster 4 | 124.50 | 198.40 | 255.90 | 7.84 | 100.52 | 2.87 | 30.31 | 5.82 | 4.33 | 10.18 | 23.68 |
| Cluster 5 | 122.50 | 205.50 | 221.10 | 12.50 | 176.50 | 3.70 | 47.15 | 5.25 | 3.80 | 9.43 | 31.98 |
| Cluster 6 | 123.50 | 210.56 | 230.60 | 6.34 | 189.63 | 2.64 | 53.85 | 5.96 | 4.10 | 11.18 | 38.75 |
| Cluster 7 | 127.00 | 210.00 | 207.80 | 14.10 | 211.60 | 4.10 | 45.89 | 5.50 | 4.10 | 9.73 | 38.82 |
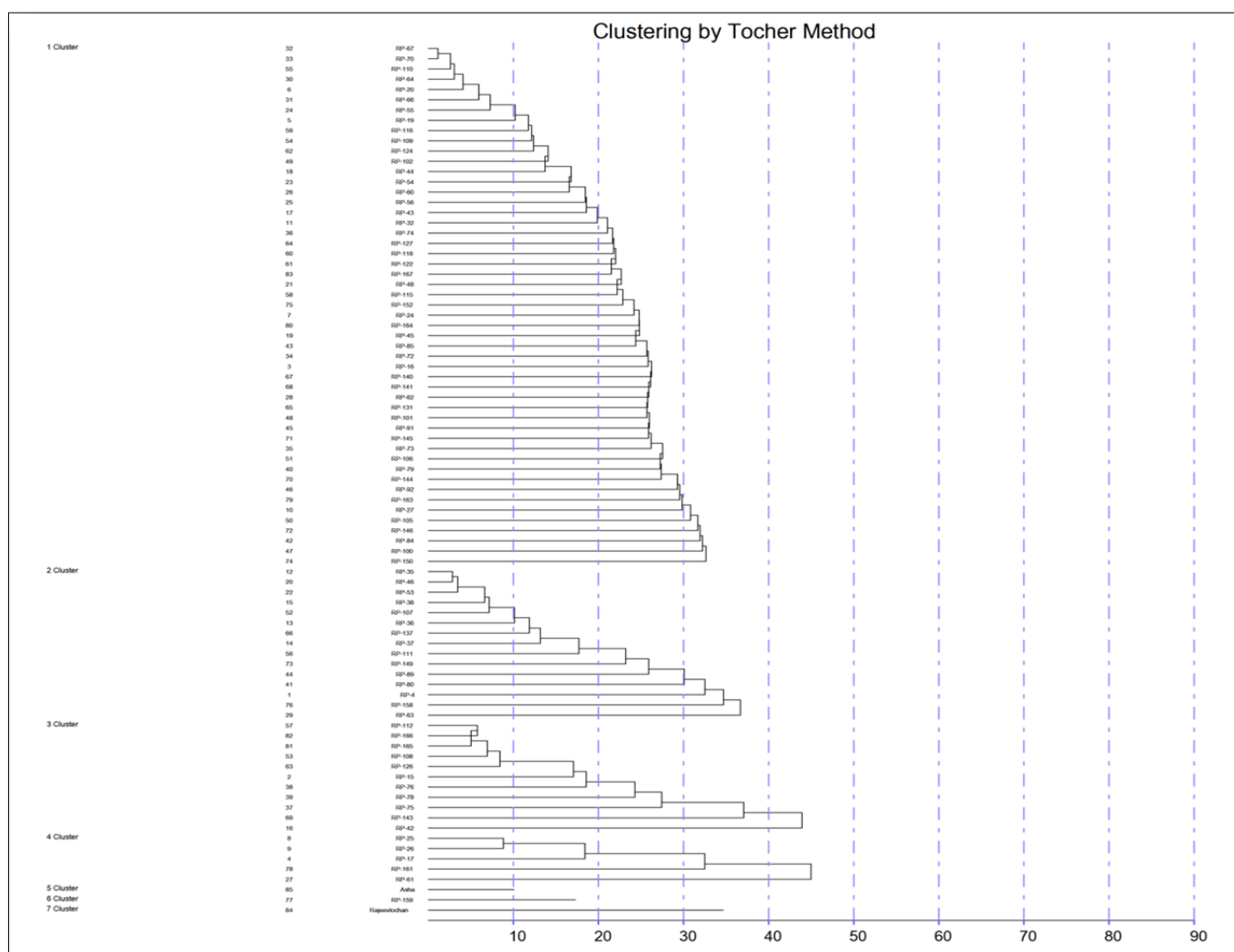


Clustering by Tocher Method

## Conclusion
In conclusion the genetic divergence analysis revealed existence of considerable diversity in pigeonpea germplasm accessions. The genotypes belonging to cluster I can be used utilized as percent in future breeding programme with the desirable genotypes belonging to cluster V, VI and VIII. On the basis of Cluster wise mean yield performance, it was noted that accessions *viz*., Rajeevlochan, RP -159 and Asha may be taken in to be consideration in future breeding programme in pigeonpea genotypes.

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