



## Genetic Divergence Analysis in Pigeonpea [*Cajanus cajan* (L.) Millsp.] at Multiple Environments

Gautam Kumar Jatav\* and Suryakant Sahu

Department of Genetics and Plant Breeding,  
Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh), India.

(Corresponding author: Gautam Kumar Jatav\*)

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**ABSTRACT:** In the kharif of 2022–2023, genetic divergence analysis of the 20 pigeonpea genotypes was obtained for eight characters in a randomised complete block design (RCBD) with two replications at three locations: Shaheed Gundadthur College of Agriculture and Research station, Jagdalpur; Sant Kabir College of Agriculture and Research Station, Kabirdham; and Research Cum Instructional Farm College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur. The  $D^2$  statistic of Mahalanobis (1936) was used to analyse divergence, while Rao (1952) described Tocher's approach for cluster formation. Five clusters were formed from twenty genotypes. Cluster I (9) had the most genotypes, followed by Cluster II (8), Cluster III (1), Cluster IV (1), and Cluster V (1). Cluster II had the largest average intra-cluster distance (0.73), followed by Cluster I (0.64). Cluster I and Cluster III had the greatest inter-cluster distance (2.00), followed by Cluster III and V (1.78). The intra-cluster distance was greatest in Cluster II. The genotypes RP-7, RP-7373, RPS2014-19, RPS2014-03, RPS2014-32, RPS2014-34, and ICP 7005 may therefore be used as parents in upcoming breeding initiatives.

**Keywords:** Genetic divergence, genotype, pigeonpea.

### INTRODUCTION

India is expected to have 168 billion inhabitants by 2030, according to the Indian Institute of Pulses Research. Sarkar *et al.* (2018) estimate that the demand for pulses would reach 332 million metric tonnes by 2030, growing at a pace of 4.2% per year. In the Caribbean, Africa, India, Malaysia, Indonesia, and other tropical and subtropical areas, the pigeon pea [*Cajanus cajan* (L.) Millsp.] is a major legume crop. Particularly in developing countries like India, it is well-known for being a good source of vegetarian protein. The great majority of individuals eat cheap vegetarian food (Gupta *et al.*, 2024). All the pulses, pigeonpeas are the second most important kharif grain legume in India. Between 1949 and 2004, India's production grew at an annual rate of 0.8% due to several pressures (Sarkar *et al.*, 2018). The diversity that is available determines which parents should be used for varietal development programs. The early-duration pigeon pea is photo-insensitive and has a compact plant stature that makes it perfect for intercropping (Ranjani *et al.*, 2021).

Due to a mismatch between supply and demand throughout time, pigeon pea output is stalling as a result

of a lack of diversity and photosensitivity (Sameerkumar *et al.*, 2016). Different heterotic groups in germplasm that can be useful for breeding in the manifestation of genotypes' breeding potential can be categorised and identified through the assessment of genetic diversity. It is possible to identify genetic parents for different heterosis breeding programs through genetic variety, and progenies from varied crosses are expected to be highly variable, which will help isolate transgressive segregates in subsequent generations (Mahalanobis, 1936). It is possible to evaluate genetic diversity among many genotypes using  $D^2$  analysis. When assessing the genetic diversity of various crops, this method is most commonly employed (Teli *et al.*, 2019).

### MATERIAL AND METHODS

The experimental material for this study consisted of 20 pigeonpea genotypes, including two checks (BDN-716 & Chhattisgarh Arhar-1). The study's materials were from the Department of Genetics and Plant Breeding College of Agriculture, Raipur's AICRP pigeonpea division. At each site, two replications were set up using a Randomised Block Design. The current study was

conducted in three different locations: Shaheed Gundadhur College of Agriculture and Research Station, Jagdalpur; Sant Kabir College of Agriculture and Research Station, Kabirdham; and College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur. Each genotype was planted in a single plot that had six rows, each measuring  $4 \times 3.6$  meters, with an interrow spacing of 60 cm and an intrarow spacing of 20 cm. To improve the uniform crop stand, suggested agronomic techniques and plant protection measures were implemented. Five competitive plants were randomly chosen from each genotype and replication at each site, and observations were made on eight distinct morphological characteristics: days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of pods/plant, number of seeds/pod, 100 seed weight (g), and seed yield/plant (g). Mean values from pooled data were used to study variability. Homogeneity of variance was tested using Bartlett's test. To ascertain stability regression coefficients and regression deviations, stability analysis was performed. Using the proper test recommended by Eberhart and Russell (1966), the mean square for regression deviations was compared to the residual mean square. Using Mahalanobis (1936)  $D^2$  statistics, the genetic diversity of the types was ascertained, and they were categorised into various groups.

## RESULTS AND DISCUSSION

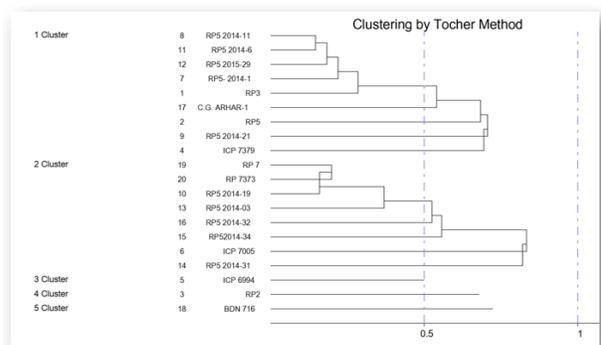
The current study's findings are being examined in relation to the genotypes' variability.

Table 1 displays the results of the cluster analysis. The calculation of the number of branches, number of pods per plant, plant height (cm), days to 50% flowering, and days to maturity number of seeds per pod, 100 seed weight (g), seed yield per plant (g) Twenty genotypes' traits were used to calculate the  $D^2$  value, which was then used to arrange the genotypes into five clusters. The  $D^2$  value was calculated so that the genotypes inside a cluster had a higher  $D^2$  value than the genotypes between the clusters. Nine genotypes were found in cluster I, whereas eight, one, one, and one were found in clusters II, III, IV, and V, respectively. According to the clustering pattern, genotypes gathered from the same geographic area were found to be dispersed throughout multiple clusters, while genotypes gathered from different locations were also accommodated within the same cluster. Therefore, there was no correlation between the genotypes' geographic origin and their distribution into distinct clusters. The highest cluster mean for days to 50% flowering was obtained in cluster IV (124.67) and lowest in cluster III (123.67). Cluster IV had the longest days to maturity mean (179.67), while cluster III had the lowest mean (177.33). Cluster IV had the greatest cluster mean value (192.67) for plant height, whereas cluster II had the lowest (182.46). For the

number of branches, cluster I had the greatest cluster mean value (11.45), while cluster IV had the lowest mean value (9.07). In terms of the number of pods per plant, Cluster II had the highest cluster mean (161.35). However, cluster V had the lowest mean value (126.20). Cluster III had the greatest cluster mean (3.80) for the number of seeds per pod, whereas cluster I had the lowest (3.54). Cluster V had the highest cluster mean values for 100 seed weight (10.49), while cluster III had the lowest (9.51). Cluster V had the greatest cluster mean value (26.74) for seed yield per plant, while cluster I had the lowest (23.93) Table 2. The cluster with high average mean values for yield and yield-contributing traits can be used for crop development to achieve high productivity, according to previous findings. Significant differences in the cluster mean values of the attributes indicated that the genotypes under study were not all the same. The range of the intra-cluster distance was 0 to 0.73. In terms of genetic distance ( $D^2$ ), it showed a broad spectrum of variability. The presence of wide genetic diversity among the genotypes in cluster II (0.73), which had eight genotypes (RP 7, RP 7373, RPS 2014-03, RPS 2014-32, RPS 2014-34, and ICP 7005), was indicated by the high intra-cluster distance. Cluster I (0.64), which had nine genotypes (RP 2014-11, RPS 2014-6, RPS 2015-29, RPS 2014-1, RP 3, C.G. Arhar-1, and RP-5), came next. ICP 6994, RP 2, and BDN 716 are the only genotypes found in Clusters III, IV, and V. Significant genetic variety was found in the sample, according to the  $D^2$  study. The inter cluster varied from 0.64 to 2.0 it clearly demonstrated considerable amount of genetic divergence present in material study. The intra cluster distance varied from 0 to 0.73. It is indicated wide range of diversity in term of genetic distance ( $D^2$ ). The highest inter cluster distance between obtain cluster III and cluster I (2.00) followed by cluster V and III (1.78), cluster IV and II (1.64), cluster V and IV (1.63) has been reflected in the relatively higher mean value for traits *viz.*, days to 50% flowering, days to maturity, plant height, number of branches Table 3. The results were consistent with the findings of other researchers, including Sreelakshmi *et al.* (2013); Yohane *et al.* (2020); Chauhan *et al.* (2021); Patel *et al.*, (2022); Dhanushasree and Hemavathy (2022). From a diversity perspective, the most significant factors are plant height, number of pods, days to maturity, 100 seed weight, and seed yield per plant. The percentage that each character contributed According to Table 4, the major factor contributing to genetic divergence was seed yield per plant (24.74%), which was followed by the number of seeds per pod (20.00%), plant height (12.63%), number of branches (11.05%), number of pods per plant (11.05%), 100 seed weight (8.42%), days to maturity, and days to 50% flowering.

**Table 1: Genotypes in different clusters.**

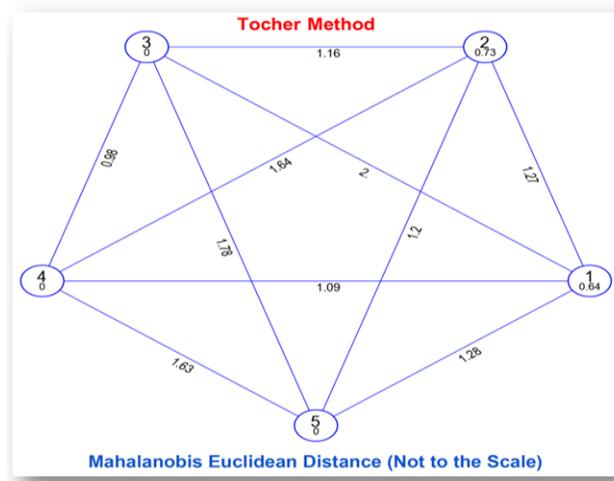
Cluster Group	No. of Genotypes	List of Genotypes
I	9	RP5 2014-11, RP5 2014-6, RP5 2015-29, RP5-2014-1, RP3, C.G. Arhar-1, RP5, RP5 2014-21 & ICP 7379
II	8	RP 7, RP 7373, RP5 2014-19, RP5 2014-03, RP5 2014-32, RP52014-34, ICP 7005 & RP5 2014-31
III	1	ICP 6994
IV	1	RP2
V	1	BDN 716



**Fig. 1.** Dendrogram showing genotypes falling under different clusters.

**Table 2: Cluster mean for different characters.**

Cluster	I	II	III	IV	V
I	<b>0.64</b>	1.27	2.00	1.09	1.28
II		<b>0.73</b>	1.16	1.64	1.20
III			<b>0.00</b>	0.98	1.78
IV				<b>0.00</b>	1.63
V					<b>0.00</b>



**Fig. 2.** Cluster diagram showing Inter and Intra cluster distance.

**Table 3: Distance between cluster centroids (intra and inter-cluster D<sup>2</sup> values).**

Cluster	Days to 50% flowering	Days to Maturity	Plant height (cm)	Number of Branches	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)
I	124.48	179.44	189.36	11.45	146.61	3.54	10.14	23.93
II	124.50	179.38	182.46	11.20	161.35	3.69	9.78	26.57
III	123.67	177.33	184.80	9.30	150.87	3.80	9.51	26.45
IV	124.67	179.67	192.67	9.07	134.03	3.60	9.73	24.22
V	124.17	179.33	175.53	10.67	126.20	3.60	10.49	26.74

**Table 4: Relative contribution (%) of individual trait to the genetic divergence in pigeonpea.**

Sr. No.	Source	Contribution %	Times ranked 1st
1.	Days to 50% flowering	4.74	9
2.	Days to Maturity	7.37	14
3.	Plant height (cm)	12.63	24
4.	Number of Branches	11.05	21
5.	Number of pods per plant	11.05	21
6.	Number of seeds per pod	20	38
7.	100 seed weight (g)	8.42	16
8.	Seed yield per plant (g)	24.74	47

**CONCLUSIONS**

Pigeonpea diversity research shows a great deal of genetic variation between accessions, which is important for breeding and agricultural improvement initiatives 20 genotypes were split into 5 clusters using cluster analysis using the mean; cluster I had the most genotypes, followed by cluster II, while cluster III, IV, and V had

the fewest. Clusters III and I had the greatest inter-cluster distance, suggesting that there was enough genetic variation across the genotypes, while clusters II and V had the most intra-cluster distance, suggesting that genetic diversity was present.

## FUTURE SCOPE

Research on pigeonpea genetic diversity analysis should focus on studying key agronomic traits like plant height, pod count, branch number, and seed yield per plant in various settings. Tests across multiple locations can help identify stable genotypes that do well in different climates. Scientists can use statistical methods such as cluster analysis to examine their physical features. By looking at how genotypes interact with their environment, researchers can better pick varieties that suit specific regions. This approach will support breeding programs to develop pigeonpea varieties that can handle stress and produce high yields.

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