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ASSESSMENT OF GENETIC DIVERSITY IN TWENTY-FIVE GENOTYPES OF EARLY MATURING PIGEONPEA (*CAJANUS CAJAN* L. MILLSP)

Preeti Kumari[1], Niraj Kumar[1]*, Manigopa Chakraborty[1], C. S. Mahto[1], H. C. Lal[2], Binay Kumar[3], Laxmi Kunkal[1] and Sanita Laguri[1]
[1]Department of Genetics and Plant Breeding, Birsa Agricultural University, Kanke, Ranchi-834 006, Jharkhand, India
[2]Department of Plant Pathology, Birsa Agricultural University, Kanke, Ranchi-834 006, Jharkhand, India
[3]Department of Entomology, Birsa Agricultural University, Kanke, Ranchi-834 006, Jharkhand, India
*Corresponding author E-mail: nirajsri224@rediffmail.com

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ABSTRACT

Genetic diversity is a crucial prerequisite for the success of crop improvement programmes. The present investigation was undertaken to assess genetic divergence among twenty-five pigeonpea genotypes using Mahalanobis D^2 statistics based on eleven yield and yield-contributing traits at BAU, Kanke during *kharif* 2024-25 in an Alpha Lattice Design with three replications. The genotypes were grouped into four distinct clusters, indicating the presence of substantial genetic variability. Cluster III contained the maximum number of genotypes, followed by Cluster II, Cluster I and Cluster IV. The maximum inter-cluster distance was observed between Cluster I and Cluster II, whereas Cluster I exhibited the highest intra-cluster distance. Among the characters studied, plant height contributed the highest proportion to total genetic divergence, followed by final plant stand, days to 50% flowering and days to maturity. The results suggest that hybridization between genotypes belonging to genetically divergent clusters may be exploited for the development of high-yielding pigeonpea varieties.

***Keywords*: Pigeonpea, genetic divergence, Mahalanobis D^2, cluster analysis, yield traits.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] ranks as the world's fifth most important legume crop, following soybean, groundnut, dry beans and peas. Worldwide, this crop is identified by several names including red gram and congo bean (English), arhar and tur (Hindi), gandul (Spanish), poid de congo and poid de Angole (French), guand (Portuguese) and ervilba de Congo in Angola. It belongs to the order Fabales, family Fabaceae (known as the legume family) and subfamily Faboideae. The pigeonpea has a diploid chromosome number of 2n = 22. It is predominantly self-pollinated crop and often-cross pollinated by bees (*Megachile spp*.). Cross-pollination ranges from 40-70% depending on genotype and insect pollinator populations (Van der Maesen, 1985). It is grown on 6.03 million hectares globally, with 5.32 million-ton production and average productivity is 882 kg/ha (Anonymous, 2023-24). India is the leading producer of pigeonpea and about 76% of the total pulse production is alone being produced in India. In India, pigeonpea ranks second among the pulse crops and accounts for nearly 20% of overall pulse production. In India, pigeonpea is grown on about 4.04 million hectares, producing 3.34 million tons with an average productivity of 826 kg/ha (Anonymous, 2023-24). In India, pigeonpea is grown primarily in Maharashtra, Karnataka, Uttar Pradesh, Gujarat, Jharkhand, Madhya Pradesh and Rajasthan. In Jharkhand, it is grown on about 0.184 million hectares, producing 0.210 million tons with an average productivity of 1,144 kg/ ha (Anonymous, 2023-24).

Pigeonpea is an important kharif pulse crop in Jharkhand and is generally cultivated as a rainfed crop on marginal lands under low input conditions. Its yield remains low due to various production constraints despite its potential for food and nutritional security. Pigeonpea yields in India remain low due to ecological challenges, insufficient modern technologies, weak post-harvest practices, limited availability of quality seeds and socio-economic barriers. Earlier Alternaria blight used to be a minor issue in Jharkhand but at present pigeonpea fields in certain localities are heavily affected. Despite positive growth in area, pigeonpea-based cropping systems face challenges. Long-duration pigeonpea genotypes yield higher, but their extended maturity period does not allow the sowing of subsequent crops like wheat and medium-duration genotype can delay the sowing of next crop. Conversely, these genotypes are more prone to lack of moisture at the flowering and pod formation. In contrast, early maturing varieties mature quickly, avoiding such stresses making them advantageous for cropping systems.

For any crop improvement programme, the effective utilization of germplasm relies on the availability of adequate genetic diversity within the lines. The evaluation and selection of high-yielding genotypes with diverse genetic makeup are fundamental steps toward increasing crop productivity at both local and global scales. Understanding the genetic differences in plant resources provides valuable insight to breeders for making appropriate parent selections in hybridization programmes. Therefore, this study focuses on evaluating genetic diversity within selected germplasm lines.

Materials and Methods

Experimental site and materials

The experimental study was undertaken at research farm of Birsa Agricultural University located in Kanke, Ranchi during the *kharif* season of 2024-25. The experiment was laid out in an Alpha Lattice Design with three replications. The plant-to-plant distance was maintained at 20 cm and the row-to-row distance at 60 cm. Each row measured 4 m in length, with six rows per plot, resulting in a plot size of 14.4 m^2. The experimental material comprised twenty-five pigeonpea genotypes evaluated for eleven yield and yield-related traits, namely initial plant stand, final plant stand, days to 50% flowering, plant height, number of primary branches per plant, number of secondary branches per plant, pods per plant, days to maturity, 100-seed weight, number of seeds per pod and yield per plant. Table-1 represents the list of twenty-five early duration pigeonpea germplasm.

Statistical analysis

Genetic divergence among genotypes was assessed using Mahalanobis D^2 statistics as suggested by Rao (1952). Based on D^2 values, genotypes were grouped into different clusters following cluster analysis. A dendrogram was constructed to illustrate the genetic relationships among genotypes. Cluster mean values were calculated for all characters. Average intra- and inter-cluster distances were estimated to assess the magnitude of genetic divergence. The relative contribution of each character towards total genetic divergence was also computed.

Result and Discussion

Cluster Formation

D^2 cluster analysis based on Mahalanobis distance was conducted to assess genetic diversity within twenty-five pigeonpea entries for yield and contributing traits. The twenty-five pigeonpea genotypes were divided into four unique, nonoverlapping groups. Table-2 indicates that twenty-five pigeonpea accessions were distributed into four clusters. Cluster III contained the greatest no. of genotypes (9 genotypes), Cluster II contains 8 genotypes, Cluster I contains 5 genotypes and Cluster IV contains 3 genotypes. The observed distribution of genotypes among various clusters indicates substantial genetic diversity in the evaluated material. Consequently, crossing genotypes from genetically distant clusters is expected to produce highly heterotic combinations and more productive recombinants. Similar clustering patterns and diversity levels in pigeonpea have also been documented by Pandey *et al.* (2013) and Rupika and Bapu (2014). For determining the proper genotypic variability between all the clusters, a dendrogram of twenty-five pigeonpea genotypes was constructed using Mahalanobis D^2 statistics (Fig. 1).

Cluster Mean Performance

The mean of eleven characters for different clusters are presented in the Table 3. Considerable variation was observed among clusters for all the traits studied. The highest mean value for initial plant stand was recorded in Cluster IV (150.22), whereas Cluster III showed the lowest (145.59). Final plant stand was highest in Cluster I (126.40) and lowest in Cluster IV (110.33). Cluster II exhibited the earliest flowering (96.38), while Cluster III showed the late flowering (107.56). Plant height was lowest in Cluster I (105.07) to the highest in Cluster IV (128.08). Cluster III recorded the highest number of primary branches per plant (7.56) and seeds per pod (3.59), whereas Cluster I showed the maximum number of secondary branches per plant (4.33) and the highest 100-seed weight (8.83). Pods per plant were highest in Cluster II (38.42) and lowest in Cluster IV (35.33). Days to maturity were minimum in Cluster II (137.63) and maximum in Cluster III (148.41). Yield per plant was highest in

Cluster III (11.47), indicating its superiority for productivity, while Cluster IV recorded the lowest yield (9.71). The observed variation in cluster means suggests the presence of exploitable genetic variability for yield improvement. Earlier studies also reported different clusters showing the highest mean values for different traits. (Sreelakshmi *et al.*, 2010, Satapathy and Panigrahi, 2014 and Verma *et al.*, 2018).

Average inter and intra cluster distances

The maximum inter-cluster distance was seen between Cluster I and Cluster II (24.52), followed by the distances between Cluster I and Cluster IV (24.38), Cluster II and Cluster IV (23.58) and Cluster I and Cluster III (23.35) indicating that these cluster pairs possess the maximum genetic divergence (Table-4). Moderate distances were observed between Cluster II and Cluster III (21.86) and between Cluster III and Cluster IV (21.68). The greatest intra-cluster distance was noted in Cluster I (11.18) while the least was seen in Cluster IV (6.48), suggesting the presence of considerable variability within Cluster I genotypes. The results imply that crosses involving genotypes from clusters with maximum inter-cluster distances particularly Cluster I × Cluster II or Cluster I × Cluster IV may produce desirable transgressive segregants. Similar observations regarding the usefulness of selecting parents from highly different clusters were made by Satapathy and Panigrahi (2014), Verma *et al.* (2018) and Bhatt *et al.* (2024).

Percentage contribution of yield attributing traits to cluster formation

Contribution of different yield attributing characters towards total genetic diversity is displayed in table-5 and figure-2. Assessment of the proportional impact of individual characters to genetic variation showed that plant height (32.88%) had the highest influence followed by final plant stand (28.54), days to 50 % flowering (17.78%) and days to maturity (17.17%). These traits collectively account for over 96% of total divergence observed in the pigeonpea genotypes. Other agronomic traits including initial plant stand (1.93%), pods per plant (0.72%), yield per plant (0.49%), primary branches per plant (0.20%), secondary branches per plant (0.19%), seeds per pod (0.06%) and 100-seed weight (0.04%) accounted for only a minor fraction of the divergence. These findings indicate that phenological traits and plant stature played a major role in discriminating the genotypes. Similar dominance of plant height, flowering behaviour and maturity duration in determining genetic diversity in pigeonpea has been reported by Pandey *et al.* (2013), Shruthi *et al.* (2020) and Bhatt *et al.* (2024).

Overall, the genetic divergence identified in this study indicates considerable variability among the twenty-five pigeonpea genotypes. Consequently, crossing genotypes chosen from clusters exhibiting the greatest divergence is likely to produce heterotic hybrids and broader segregation, thereby improving the efficacy of selection for its attributing traits and yield. These outcomes match the result of Gupta *et al.* (2008), Verma *et al.* (2018) and Bhatt *et al.* (2024), who also highlighted the importance of utilizing highly divergent parents for the genetic enhancement of pigeonpea.

Table 1: List of twenty-five early duration pigeonpea germplasm

S. No.	Genotypes	Sources
1.	PA 754	GBPUAT, Pantnagar
2.	PA 748	GBPUAT, Pantnagar
3.	AL 2463	PAU, Ludhiana
4.	AL 2492	PAU, Ludhiana
5.	Pusa Arhar 24-1	IARI, New Delhi
6.	Pusa Arhar 24-2	IARI, New Delhi
7.	VMRG 17-001	ARS, Virinjipuram
8.	NUPPC- 7B	SAS, Nagaland
9.	NUPPC- 7C	SAS, Nagaland
10.	ICPV 21333	NCRS, Behrampur, Odisha
11.	BRG 22-407	UAS, Bangalore
12.	ICPL 22408 (LRG 588)	ARS, Lam
13.	ICPL 22414 (LRG 589)	ARS, Lam
14.	IPAE 23-1	IIPR, Kanpur
15.	IPAE 23-2	IIPR, Kanpur
16.	WRGE-266(ICPL-19070)	RARS, Warangal
17.	WRGE-267(ICPL-22462)	RARS, Warangal

18.	ICPL 19060	Agriculture University, Kota
19.	ICPL 19018	Agriculture University, Kota
20.	ICPL 22393	CCSHAU, Hisar
21.	ICPL 22383	CCSHAU, Hisar
22.	ICPL 23293	IGKVV, Raipur
	Checks	
1.	UPAS 120 (Ch)	GBPUAT, Pantnagar
2.	IPA 15-6 (Ch)	IIPR, Kanpur
3.	Pusa 2018-4 (Ch)	IARI, New Delhi

Table 2: Clustering pattern of twenty-five pigeonpea genotypes for yield and its attributing traits

	No. of genotypes	**List of genotypes**
Cluster I	5	Pusa Arhar 24-2, ICPL 22408, ICPL 22393, PA 748, ICPL 22383
Cluster II	8	WRGE-267 (ICPL-22462), IPAE 23-2, ICPL 19018, Pusa Arhar 24-1, ICPL 19060, ICPV 21333, AL 2492, UPAS 120 (Ch)
Cluster III	9	BRG 22-407, AL 2463, WRGE-266 (ICPL-19070), Pusa 2018-4 (Ch), NUPPC-7C, VMRG 17-001, IPAE 23-1, NUPPC-7B, ICPL 22414 (LRG 589)
Cluster IV	3	IPA 15-6 (Ch), ICPL 23293, PA 754

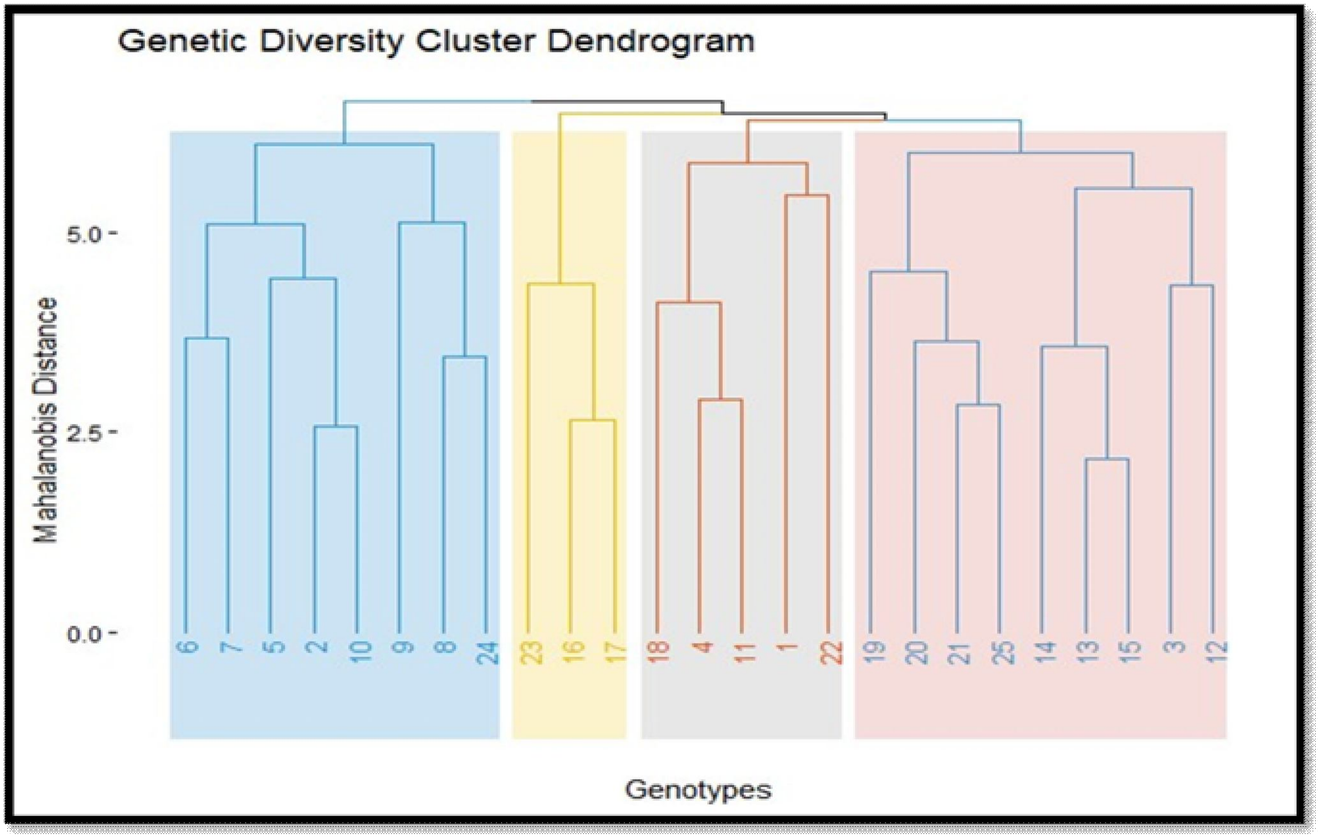

Table 3: Cluster mean performance of different clusters

Cluster	**Initial plant stand**	**Final plant stand**	**Days to 50% flowering**	**Plant height (cm)**	**Primary branches per plant**	**Secondary branches per plant**	**Pods per plant**	**Days to maturity**	**100 Seed weight (g)**	**Seeds per pod**	**Yield per plant (g)**
1	148.60	126.40	105.67	105.07	7.00	4.33	36.87	147.07	8.83	3.27	11.08
2	146.67	110.92	96.38	109.42	6.33	3.50	38.42	137.63	8.22	2.92	9.76
3	145.59	119.44	107.56	111.65	7.56	3.26	37.00	148.41	8.40	3.59	11.47
4	150.22	110.33	102.00	128.08	6.67	2.67	35.33	142.22	8.51	3.11	9.71

Table 4: Average inter and intra cluster distances

	Cluster 1	Cluster 2	Cluster 3	Cluster 4
Cluster 1	**11.18**	24.52	23.35	24.38
Cluster 2		**10.08**	21.86	23.58
Cluster 3			**9.03**	21.68
Cluster 4				**6.48**

Table 5 : Percentage contribution towards genetic diversity

Sl. No.	Characters	Contribution (%)
1	Plant height	32.88
2	Final plant stand	28.54
3	Days to 50 % flowering	17.78
4	Days to maturity	17.17
5	Initial plant stand	1.93
6	Pods per plant	0.72
7	Yield per plant	0.49
8	Primary branches per plant	0.20
9	Secondary branches per plant	0.19
10	Seeds per pod	0.06
11	100 seed weight	0.04

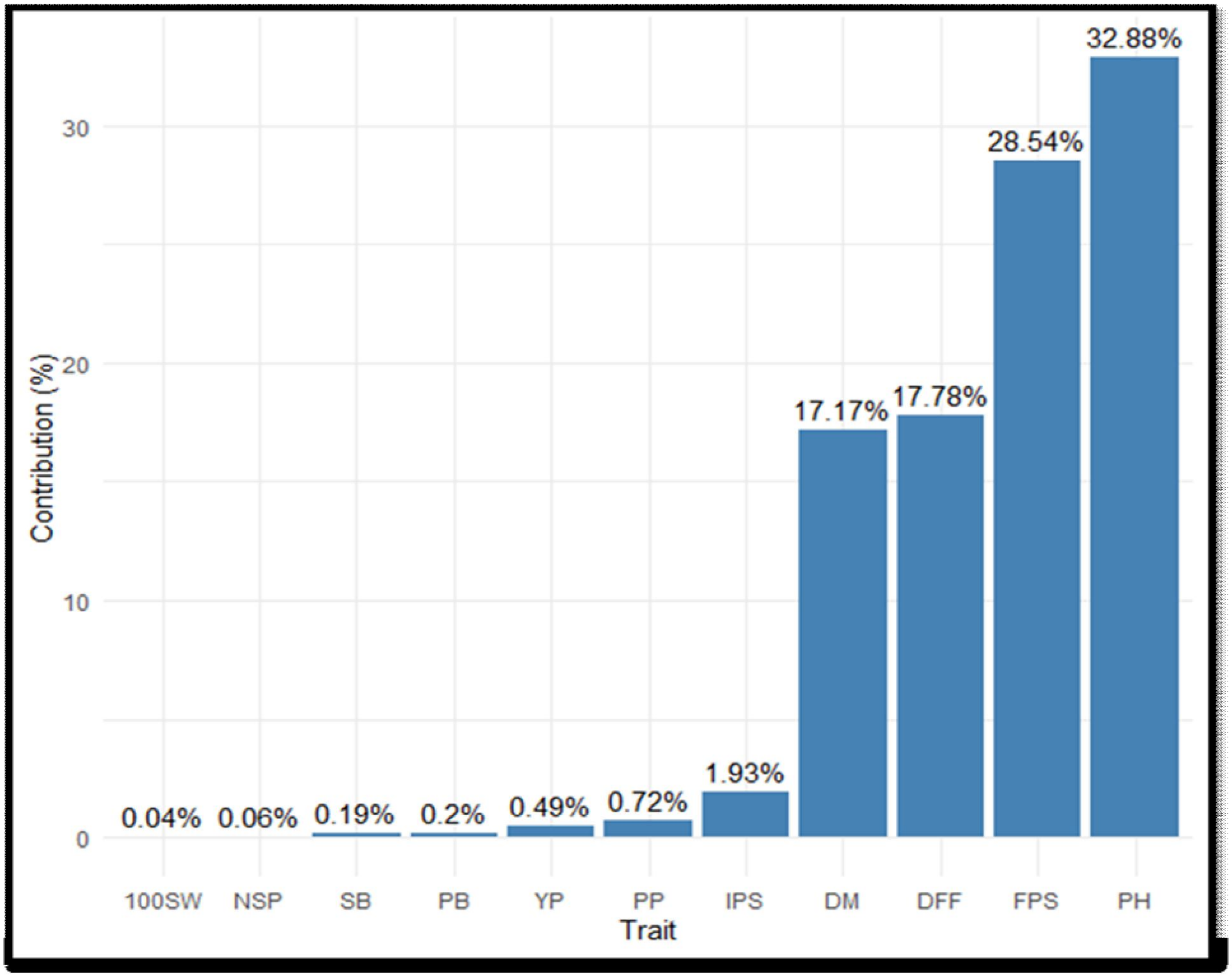

Fig. 2: Graphical representation of percentage contribution towards genetic diversity

Where, IPS = initial plant stand; **FPS** = final plant stand; **DFF** = days to 50% flowering; **PH** = plant height; **PB** = primary branches per plant; **SB** = secondary branches per plant; **PP** = pods per plant; **DM** = days to maturity; **100 SW** = 100 seed weight; **YP** = yield per plant; **NSP** = number of seeds per pod.

Conclusion

The genetic divergence analysis using Mahalanobis D² statistics revealed wide genetic variability among the twenty-five pigeonpea genotypes. The formation of four distinct clusters, high inter-cluster distances and differential contribution of traits highlight the potential for exploiting genetic diversity in pigeonpea improvement. Hybridization between genotypes belonging to highly divergent clusters, especially Cluster I with Cluster II or Cluster IV, is likely to produce superior heterotic combinations and transgressive segregants. The study underscores the importance of multivariate analysis in identifying promising parental lines for enhancing yield and adaptability in pigeonpea.

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