

GENETIC DIVERSITY, CORRELATION COEFFICIENT AND PATH ANALYSIS FOR YIELD AND ITS ATTRIBUTING CHARACTERS IN PIGEONPEA [*Cajanus cajan* L. Millsp].**N. M. Manchalwad¹, S. B. Sarode¹, S. T. Rathod² and P.L.Sontakke³****1. Department of Agricultural Botany, College of Agriculture, Badnapur, VNMKV Parbhani****2. Department of Agricultural Botany, College of Agriculture, Ambajogai VNMKV Parbhani,****3. Agricultural Research Station, Badnapur, VNMKV Parbhani, Maharashtra, India.***MS Received: 27.06.2025; MS Revised: 28.07.2025; MS Accepted: 29.07.2025)***MS 3433****(RESEARCH PAPER IN AGRICULTURAL BOTANY)****Abstract**

The nature and magnitude of genetic diversity was assessed among 45 genotypes of pigeonpea in randomized block design. The analysis revealed a wide genetic diversity among the traits studied, as indicated by the formation of seven distinct clusters. The analysis demonstrated that the greatest genetic divergence observed between Cluster VI and Cluster VII (417.47), indicating the highest degree of divergence. This was followed by the distances between Cluster IV and Cluster VI (390.57), Cluster I and Cluster VII (291.86), Cluster IV and Cluster VII (231.71), Cluster III and Cluster VII (224.85), Cluster IV and Cluster V (223.35), Cluster III and Cluster VI (202.63), Cluster I and Cluster III (199.44), Cluster III and Cluster VII (175.17) and Cluster V and Cluster VII (173.57). Correlation between yield and yield contributing component characters in forty five genotypes of pigeonpea revealed that seed yield per plant had positive and highly significant association with number of pods per plant, primary branches, number of seeds per pod, number of secondary branches per plant. Selection criterion can be done based on these characters for seed yield will give successful results for yield improvement in pigeonpea. Path coefficient analysis of different traits on seed yield per plant recorded that traits viz., number of pods per plant, number of secondary branches per plant, number of seeds per pod, number of primary branches per plant, days to 50% flowering showed positive direct effect.

Keywords - genetic diversity, Cluster, pigeonpea.. lowering.**Introduction**

Pigeonpea (*Cajanus cajan* L.) considered the second most important pulse crop in India after chickpea, plays a crucial role in the country's predominantly vegetarian diet by providing a key source of plant-based protein. As noted by Van der Maesen (1980), this species is diploid with 22 chromosomes and has an estimated genome size of 858 megabase pairs (Mbp). Due to its extensive root system, as described by Varshney et al. (2012), pigeonpea is highly drought-tolerant and capable of growing in areas receiving as little as 650 mm of rainfall annually. Its resilience makes it especially valuable in tropical and subtropical climates where water scarcity and erratic rainfall are frequent issues. In addition to its nutritional benefits, pigeonpea supports sustainable farming methods. Pigeonpea is widely grown in Indian subcontinent which consist of almost 90 percent of the world's crop. Pigeonpea main used as *dal*, its green seeds are used as vegetables, crushed dry seeds as animal feed, green leaves as fodder, stem as fuel wood and to make huts, baskets etc. and plants are also used to culture Lac producing insects. The high protein genotypes also contain higher (about 25 %) sulphur containing amino acids, namely methionine and cysteine (Singh et al. 1990). Seed contains about 57.3 to 58.7 per cent carbohydrate, 1.2 to 8.1 per cent crude fibre and 0.6 to 3.8 per cent lipids (Sinha, 1977). According to Saxena (2008), the crop engages in symbiotic nitrogen fixation, enriching soil fertility by converting atmospheric nitrogen into a form that plants can absorb. This process reduces dependence on chemical fertilizers and enhances soil health, positioning pigeonpea as a key component in environmentally friendly agriculture. From a nutritional perspective, pigeonpea helps combat protein deficiency, a widespread issue in India, particularly among vegetarians. Saxena et al. (2010) stress that such advancements will not only boost crop productivity but also enhance adaptability to various environmental conditions, strengthening food security and improving national protein intake. Access to genetically diverse germplasm remains a critical factor in driving progress in pigeonpea breeding efforts. Selecting appropriate parent lines is a fundamental step in hybridization aimed at creating new genetic diversity. Among various biometrical techniques, D² (Mahalanobis' D-squared) analysis stands out as one of the most effective and commonly used

methods for grouping parental lines based on genetic divergence. A thorough understanding of the genetic variability in yield and yield-associated traits is essential for the successful development of high-yielding pigeonpea varieties. This variability is influenced by both genetic makeup and environmental conditions. Evaluating the genetic divergence, correlation and path coefficient analysis among genotypes helps identify promising candidates for cross-breeding, particularly those with the potential to produce transgressive segregants—offspring that outperform both parents. While systematic breeding programs for the improvement of high-yielding pigeonpea genotypes are still relatively limited, initial efforts have been made to address this need.

Materials and Methods

The experiment was laid out in a randomized block design with two replications at Department of Agricultural Botany field, College of Agriculture, Badnapur in *kharif* 2024. This study was performed with forty five genotypes of pigeonpea received from Agricultural Research Station, Badnapur to assess the genetic diversity, correlation and path analysis among this genotypes. Rows were spaced 90 cm apart and plant to plant distance was maintained at 20 cm. Data were recorded on individual plant basis from 5 randomly selected plants of each genotype in each replication. Among the characters studied as *i.e.* days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, pod length, number of seeds per pod, 100 seed weight(g) and seed yield per plant(g) were recorded in the field.

Results and Discussion

The Mahalanobis D² cluster analysis grouped all the forty five pigeonpea genotypes of the present investigation into seven distinct non-overlapping clusters (Table-1). This study reflecting considerable genetic variability among the experimental material across most traits. The squared euclidean distance method was utilized to calculate inter-genotypic distances and clustering was carried out using Tocher's method. Cluster mean values were calculated for nine yield-contributing traits in pigeonpea, demonstrating a broad spectrum of variation (Table 2). The lowest mean value for days to 50% flowering was recorded in Cluster VI (87.00), indicating the presence of early-flowering genotypes, whereas the highest mean was found in Cluster VII (119.00), consisting

of late-flowering genotypes. Regarding days to maturity, the shortest duration was noted in Cluster VI (137.50), comprising early-maturing genotypes, while the longest was observed in Cluster VII (179.00), which included late-maturing types. For plant height, the highest cluster mean was observed in Cluster IV (208.70) while Cluster VI shows lowest cluster mean for plant height i.e. (163.75). The mean number of primary branches per plant ranged from 4.50 in Cluster VI to 16.20 in Cluster IV. In terms of secondary branches per plant, Cluster IV exhibited the highest mean (23.70), while Cluster VI had the lowest (9.10). The number of pods per plant showed maximum cluster mean in Cluster IV (268.50) and the minimum in Cluster VI (68.70). The mean number of seeds per pod peaked in Cluster IV at 4.45, while Clusters II and cluster VI had a lower mean of 3.70. The cluster mean for 100-seed weight was highest in Cluster IV (12.21 grams) and lowest in Cluster VII (7.74 grams). Lastly, the cluster mean for seed yield per plant varied from 21.65 grams in Cluster VI to 88.50 grams in Cluster IV. The clustering pattern of the genotypes further validated the presence of substantial genetic diversity. Among the seven clusters, Cluster III included the largest number of genotypes, comprising 22 entries. Cluster I consisted of 18 genotypes. In contrast, Clusters II, IV, V, VI, and VII each contained only a single genotype. The variation observed within clusters suggests the existence of genetic variability among genotypes grouped together, while divergence between clusters reflects the genetic distance separating different groups. Both intra- and inter-cluster D^2 values were derived from the divergence analysis. A thorough evaluation of the clusters revealed significant heterogeneity both within and among clusters, based on key agronomic traits. The composition of each cluster, along with the values of inter- and intra-cluster distances, is detailed in [Table 3](#). A cluster diagram illustrating the relationships among different populations was constructed. The greatest distance between two clusters was observed between Cluster VI and Cluster VII (417.47), indicating the highest degree of divergence. This was followed by the distances between Cluster IV and Cluster VI (390.57), Cluster I and Cluster VII (291.86), Cluster IV and Cluster VII (231.71), Cluster III and Cluster VII (224.85), Cluster IV and Cluster V (223.35), Cluster III and Cluster VI (202.63), Cluster I and Cluster III (199.44), Cluster III and Cluster VII (175.17), and finally, Cluster V and Cluster VII (173.57). The average intra-cluster D^2 values for various clusters are presented in [Table 3](#). Intra-cluster distances ranged from 0.00 to 79.77, with the highest intra-cluster distance of 79.77 observed in Cluster III followed by 64.19 in Cluster I. Genotypes belonging to these clusters, which show substantial genetic divergence, serve as promising candidates for hybridization programs. They are likely to produce superior breeding material and contribute to genetic improvement for targeted traits. This indicates that genotypes from these diverse clusters can be effectively utilized as parents in crossing programs, as hybridization between genetically distant parents often results in transgressive segregants. Therefore, traits that contribute most significantly to genetic divergence should be prioritized when selecting parental lines within clusters for hybridization. The frequency of each yield component character appearing in the first rank and its respective contribution percentage towards genetic divergence is presented in Table 4. The days to 50% flowering contributed the most to genetic divergence, accounting for 31.11%. This was followed by days to maturity at 21.01%, 100 seed weight (g) at 19.39%, number of pods per plant at 11.72%, and number of primary branches per plant at 6.57%. Contributions from number of secondary branches per plant were 5.45%, while the plant height and the seed yield per plant contributed 3.43% and 0.81% respectively. Number of seeds per pod had the lowest contribution at 0.51%. From the above study, it can be concluded that the diversity in pigeonpea genotypes for yield and yield-attributing characters may be due to 100-seed weight, days to 50% flowering, number of pods per plant, and seed yield per plant. The findings align with those reported by Patel *et al.* (2018) who identified days to flowering as the primary

contributor to genetic divergence, followed by the number of pods per plant, plant height, days to maturity. Likewise, Prasad *et al.* (2013) emphasized that seed yield, 100-seed weight, number of seeds per pod, days to maturity, and plant height were the most significant contributors to genetic diversity.

Correlation and path analysis were employed to estimate the nature and magnitude of associations among various traits influencing yield. These analyses facilitate the understanding of the underlying causes of associations, which can then be leveraged in the development of selection criteria for yield enhancement. At both phenotypic and genotypic level seed yield per plant showed significantly and positive correlation with primary branches per plant, plant height, days to maturity, secondary branches and number of pods per plant. Among yield components, at phenotypic and genotypic level the trait days to 50 percent flowering was recorded to have significant and positive correlation with days to maturity, primary branches per plant, plant height and yield per plant. The results are in agreement with, Kumara *et al.* (2013) and Ojwang *et al.* (2016). Interrelationship of yield components among traits is followed as Days to 50% flowering demonstrated a strong and significant positive correlation with days to maturity and with plant height, Days to maturity exhibited a non-significant yet positive association with primary branches, number of seeds per pod, plant height, 100 seed weight, number of pods per plant and number of secondary branches, Plant height exhibited a significant and positive association with number of pods per plant, The number of primary branches per plant demonstrated a robust and significant positive correlation with the number of seeds per pod, Number of secondary branches per plant exhibited a non-significant yet positive association with the number of pods per plant, The number of pods per plant exhibited a non-significant positive correlation with both the number of seeds per pod, and the 100 seed weight, The number of seeds per pod exhibited a significant positive correlation with 100 seed weight, The 100-seed weight displayed a negative correlation with seed yield, with correlation coefficients of.

To better understand the direct and indirect contributions of individual traits to seed yield per plant, a path coefficient analysis was performed. This method involves partitioning the significant genotypic and phenotypic correlation coefficients into their respective direct and indirect effects. Among all the traits evaluated, the number of pods per plant exhibited the most pronounced direct genotypic effect on seed yield, with a coefficient of ($g = 0.8070$). This was followed by number of pods per plant ($g = 0.8002$), the number of secondary branches per plant ($g = 0.1698$), number of seeds per pod ($g = 0.1125$), number of primary branches per plant ($g = 0.0665$), days to 50% flowering ($g = 0.0349$). Conversely, 100 seed weight ($g = -0.2728$), days to maturity ($g = -0.1088$) and plant height ($g = -0.0716$) displayed negative direct effects at the genotypic level (Table 5). While at phenotypic level also, number of pods per plant exhibited the highest positive direct effect ($p = 0.7225$) followed by number of secondary branches per plant ($p = 0.1533$), the number of seeds per pod ($p = 0.1437$), the number of primary branches per plant ($p = 0.0987$). Conversely, 100 seed weight ($p = -0.2834$), days to maturity ($p = -0.0713$), plant height ($p = -0.0088$) and days to 50% flowering ($p = -0.0051$) displayed negative direct effects at the phenotypic level (Table 6).

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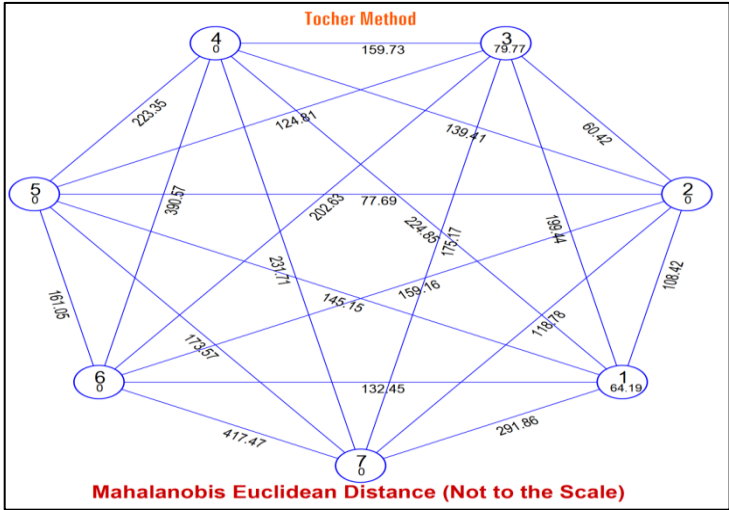


Fig1: Distances among cluster by Tocher's method

Table1 : Composition of forty five pigeonpea genotypes into different clusters by Tocher’s method.

Cluster Number	No. of genotypes	Germplasm included in the cluster
I	18	BP 16-184, IPAAE 19-22, WRGE 178, NAAM 88, GJP 2209, JKM 189, NUPPC7A, RKPV1147, AL 2481, LRG 504, RPS 2014-19, AKTM 2123, SKNP2127, AKTE2101, ICPL22242, IPAM 22-2, AKTM 1918, AKTM 1917
II	1	NAM 329
III	22	BDN 2, RKPV 1156, ICPL18119, BWR 23, Phule Trupti, Phule Rajeshwari, BSMR 243, Vipula, PT 13-3, PT 12-8, VMRG 14-002, BSMR 853, PA 739, PDKV Ashlesha, BDN 2019-29, BDN716, BAUPP 19-11, VMRG 16-006, CRG 18004, RKPV 1152, IPAM 22-1, BSMR 74
IV	1	Renuka
V	1	IPAB 5
VI	1	IPAE 22-2
VII	1	PKV Tara

Table 2 : Cluster means for seed yield and its components in pigeonpea.

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches/plants	Number of secondary branches/plants	Number of pods/plants	Number of seeds/pods	100 Seed weight(g)	Seed yield /plant (g)
Cluster 1	93.53	140.39	181.45	8.01	14.06	192.20	3.83	9.76	63.00
Cluster 2	111.50	159.00	172.90	7.90	13.10	188.40	3.70	10.32	57.85
Cluster 3	115.34	166.41	187.06	8.27	15.38	180.41	3.85	11.56	54.76
Cluster 4	115.00	169.00	208.70	16.20	23.70	268.50	4.45	12.21	88.50
Cluster 5	115.50	150.50	188.20	8.10	17.55	118.80	3.80	10.72	48.13
Cluster 6	87.00	137.50	166.20	4.50	9.10	68.70	3.70	11.55	21.65
Cluster 7	119.00	179.00	186.70	8.10	22.50	195.25	3.80	7.74	69.70

Table 3 : Average intra and inter cluster distance (D^2) values in pigeonpea.

Cluster Number	I	II	III	IV	V	VI	VII
I	64.19	108.42	199.44	224.85	145.15	132.45	291.86
II		0.00	60.42	139.41	77.69	159.16	118.78
III			79.77	159.73	124.81	202.63	175.17
IV				0.00	223.35	390.57	231.71
V					0.00	161.05	173.57
VI						0.00	417.47
VII							0.00

Table 4 : Percent contribution of different characters of pigeonpea to genetic diversity.

Sr.No	Characters	No. of times appearing I in ranking	% contribution
1	Days to 50% Flowering.	308	31.11 %
2	Days to Maturity.	208	21.01 %
3	Plant Height (cm).	34	3.43 %
4	Number of primary branches/plant.	65	6.57 %
5	Number of secondary branches/plant.	54	5.45 %
6	Number of pods/plant.	116	11.72 %
7	Number of seeds/pod.	5	0.51 %
8	100 seed Weight(g).	192	19.39 %
9	Seed yield/Plant.	8	0.81 %
10	Total	990	100%

Table 5 : Direct and indirect effect of yield and its components characters on seed yield and at Phenotypic level.

Characters	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)	Correlation with Seed yield/plant
Days to 50% Flowering.	-0.0051	-0.0047	-0.0018	-0.0008	-0.0018	-0.0000	-0.0002	-0.0026	-0.1521
Days to Maturity.	-0.0660	-0.0713	-0.0284	-0.0130	-0.0294	-0.0041	-0.0048	-0.0333	-0.0792
Plant Height (cm).	-0.0032	-0.0035	-0.0088	-0.0048	-0.0062	-0.0048	-0.0001	-0.0040	0.3856
Number of primary branches/plant.	0.0154	0.0180	0.0533	0.0987	0.0620	0.0590	0.0229	0.0285	0.5596
Number of secondary branches/plant	0.0534	0.0631	0.1072	0.0964	0.1533	0.0904	0.0105	0.0353	0.5489
Number of pods/plant	-0.0071	0.0420	0.3928	0.4317	0.4263	0.7225	0.0108	0.1183	0.8188
Number of seeds/pod.	0.0052	0.0096	0.0012	0.0333	0.0099	0.0021	0.1437	0.0190	0.1454
100 seed Weight (g).	-0.1446	-0.1324	-0.1299	-0.819	-0.0653	-0.0464	-0.0375	-0.2834	-0.1222

Table 6 : Direct and indirect effect of yield and its components characters on seed yield and at genotypic level.

Characters	Days to 50% Flowering	Days to Maturity	Plant Height (cm)	No. of Primary Branches/Plant	No. of Secondary Branches/Plant	No. of Pods/Plant	No. of Seeds/Pod	100 Seed Weight (g)	Correlation with Seed Yield/Plant
Days to 50% Flowering	0.0349	0.0327	0.0131	0.0057	0.0126	-0.0009	0.0024	0.0184	-0.1777
Days to Maturity	-0.1019	-0.1088	-0.0453	-0.0206	-0.0452	-0.0056	-0.0108	-0.0529	-0.1035
Plant Height (cm)	-0.0269	-0.0298	-0.0716	-0.0432	-0.0528	-0.0412	0.0019	-0.0371	0.3783
No. of Primary Branches/Plant	0.0109	0.0126	0.0401	0.0665	0.0443	0.0452	0.0231	0.0199	0.6225
No. of Secondary Branches/Plant	0.0614	0.0706	0.1252	0.1130	0.1698	0.1045	0.0133	0.0414	0.5633
Number of Pods/Plant	-0.0201	0.0408	0.4609	0.5435	0.4924	0.8002	0.0648	0.1477	0.8610
Number of Seeds/Pod	0.0078	0.0112	-0.003	0.0392	0.0088	0.0091	0.1125	0.0104	0.1820
100 Seed Weight (g)	-0.1438	-0.1327	-0.1412	-0.0815	-0.0665	-0.0503	-0.0252	-0.2728	-0.1250