

## RESEARCH ARTICLE

# Studies on genetic diversity, correlation and path co-efficient analysis for yield and yield contributing characters in pigeonpea [*Cajanus cajan* (L). Millipis]

■ A. A. Madke, S. B. Sarode, S. V. Pawar, P. L. Sontakke and N. M. Manchalwad

### SUMMARY

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 nine clusters which indicated diversity. Cluster I had the 25 maximum number of genotypes, Cluster II had 10, while, Cluster III, IV, V, VI, VII, VIII, IX had 01 genotype each, respectively. Correlation between yield and yield attribute component traits in forty two genotypes of pigeonpea revealed that seed yield per plant had positive and highly significant association with number of pods per plant, number of primary branches per plant, plant height, number of secondary branches per plant, days to maturity and 100 seed weight. Selection criterion can be done based on these characters for seed yield will give successful results for yield improvement in pigeonpea. Path co-efficient analysis of different traits on seed yield per plant recorded that traits *viz.*, 100 seed weight, number of primary branches per plant, days to maturity, plant height and number of seeds per pod showed highest positive direct effect.

Key Words : Pigeonpea, Genetic diversity, Correlation, Path analysis, Clusters, D<sup>2</sup> Analysis

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### MEMBERS OF THE RESEARCH FORUM

Author to be contacted :

S. B. Sarode, College of Agriculture (V.N.M.K.V.), Badnapur (M.S.) India

Email : [shrisarode24@gmail.com](mailto:shrisarode24@gmail.com)

Address of the Co-authors:

A. Madke, S. V. Pawar, P. L. and N. M. Manchalwad, College of Agriculture (V.N.M.K.V.), Badnapur (M.S.) India

A. Sontakke, Agricultural Research Station, Badnapur (M.S.) India

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is always grown as an annual crop despite being a short-lived perennial member of the fabaceae family. The chromosome number of pigeonpea is ( $2n=2x=22$ ). Total 20–70% of pigeonpea plants undergo cross pollination. The majority of vegetarians in India depends on red grams as a source of protein supplements. According to estimates, the country's per capita protein

availability is just 28 grams per day, compared to the WHO's recommended of 80 grams per day (Prasad *et al.*, 2013). In area and production of pigeonpea, India is the first in world. The important pigeonpea growing states are *viz.*, Maharashtra, Karnataka, Madhyapradesh and Uttar Pradesh.

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

## MATERIAL 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 thirty genotypes were received from Agricultural Research Station, Badnapur including 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. Phenotypic co-efficient correlations were computed using the formula suggested by Falconer (1964). The path co-efficient analysis was conducted as described by Dewey and Lu (1959). The genetic diversity analysis will be carried out by  $D^2$  statistical method as per by Mahalanobis (1936).

## RESULTS AND DISCUSSION

All the forty two genotypes of pigeonpea were grouped into nine clusters using the Toucher's method (Singh and Chaudhary, 1977). The result indicated that Cluster I had the maximum number of 25 germplasms, Cluster II had 10, Cluster III, IV, V, VI, VII, VIII and XI had 01 germplasm each, respectively showed in Table 2. According to research genetic divergence in pigeonpea 42 genotypes were divided into 9 cluster, similarly result were was founded by Sreelaksmi *et al.* (2011), Kumara *et al.* (2013) and Patel *et al.* (2018).

The least distance was recorded between cluster VII and IV (11.22) increases with cluster V and I (15.53), cluster VII and V (15.88) cluster V and VI (16.51) and indicating least genetic divergence among genotypes. Whereas The greatest distance between two clusters was existed between cluster VIII and VII (37.77) indicating greatest divergence, followed by cluster VIII and IV (35.70), cluster IX and VI (32.35), cluster VII and III (32.16) and cluster IV and III (31.67). Intra and inter cluster distance showed in Table 3 and Fig 1. The intra cluster values varied from 0.00 to 14.49. The maximum intra-cluster distance of 14.49 was noticed in cluster II followed by 12.65 in cluster I. Cluster mean showed in Table 4. Highest cluster mean for plant height was found in cluster VIII (221.80) followed by cluster IV (216.40) while, lowest mean for plant height recorded in cluster IX (111.10). According to research genetic divergence in pigeonpea 42 genotypes intra-cluster distance found in cluster II and cluster I, similarly result were was founded by Sreelaksmi *et al.* (2011), Kumara *et al.* (2013), Patel *et al.* (2018). Kumara *et al.* (2013) stated 19 genotypes divided into nine cluster, in cluster I maximum number of genotypes present (35 genotypes).

The phenotypic and genotypic correlations for yield and its components characters studied are presented in

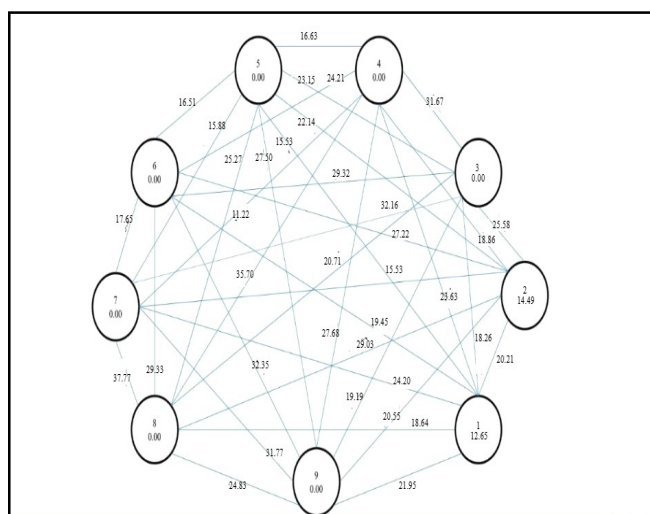
Sr. No	Name of genotype	Sr. No	Name of genotype
1.	ICP- 10331	21.	ICP- 6536
2.	ICP- 13258	22.	ICP- 6924
3.	ICP- 13011	23.	ICP- 2223
4.	ICP- 13191	24.	ICP- 1083
5.	ICP- 13564	25.	ICP- 1355
6.	ICP- 12796	26.	ICP- 2641
7.	ICP- 13579	27.	ICP- 2630
8.	ICP- 13270	28.	ICP- 19720
9.	ICP- 13732	29.	ICP- 14113
10.	ICP- 12816	30.	ICP- 14337
11.	ICP- 13082	31.	BDN- 2018-37
12.	ICP- 6666	32.	BDN- 2013-45
13.	ICP- 6681	33.	BDN- 2019-08
14.	ICP- 6992	34.	BDN- 2019-34
15.	ICP- 3945	35.	BDN- 2019-05
16.	ICP- 7057	36.	PT- 2017-2
17.	ICP- 4476	37.	PT- 12-5-5
18.	ICP- 6427	38.	PT-12-19
19.	ICP- 6519	39.	PT- 2017-1
20.	ICP- 6906	40.	PT- 12-8-2
41.	BDN-716 (Ch)	42.	Godawari (Ch)

**Table 2 : Composition of forty two pigeonpea genotypes into different clusters by Toucher's Method**

Cluster number	No. of strains	Genotype included in the cluster
I	25	ICP-13564, ICP-14113, ICP-2630, ICP-12816, ICP-10331, ICP-13258, ICP-13732, BDN-2019-5, ICP-13579, ICP-12796, BDN-2018-37, Godavari, ICP-13270, PT-12-8-2, PT-2017-2, ICP-6519, ICP-6666, ICP-6427, PT-12-19, BDN-2019-34, PT-12-5-5, BDN-716, BDN-2013-45, ICP-6992, PT-2017-1.
II	10	ICP-2223, ICP-2641, ICP-4476, ICP-6536, ICP-6906, ICP-1355, ICP-1083, ICP-19720, ICP-6681, ICP-13082.
III	1	BDN-2019-8
IV	1	ICP-13011
V	1	ICP-14337
VI	1	ICP-6924
VII	1	ICP-3945
VIII	1	ICP-7057
IX	1	ICP-13191

**Table 3 : Average cluster D<sup>2</sup> values of pigeonpea**

Cluster number	I	II	III	IV	V	VI	VII	VIII	IX
I	12.65	20.21	18.26	23.63	15.53	19.45	24.20	18.64	21.95
II		14.49	25.58	18.86	22.14	27.22	23.36	29.03	20.55
III			0	31.67	23.15	29.32	32.16	20.71	19.19
IV				0	16.63	24.21	11.22	35.70	27.68
V					0	16.51	15.88	25.26	27.50
VI						0	17.65	29.33	32.35
VII							0	37.77	31.37
VIII								0	24.83
IX									0



**Fig. 1 : Diagram showing the cluster distance**

Table 5 and Table 6. Seed yield per plant had significant positive associations with number of pods per plant ( $p=0.7597$ ;  $g=0.7566$ ), Primary branches ( $p=0.3546$ ;  $g=0.3363$ ), plant height ( $p=0.3108$ ;  $g=0.2935$ ) number of

secondary branches per plant ( $p=0.3081$ ;  $g=0.2819$ ), Days to maturity ( $p=0.1168$ ;  $g=0.1136$ ), 100 seed weight ( $p=0.0977$ ;  $g=0.0945$ ) both at phenotypic and genotypic levels, respectively. Earlier studies too have indicated such positive significant correlation for 100 seed weight, number of secondary branches per plant with seed yield by Salunkhe *et al.* (1995), Patel and Acharya (2011), Sharma *et al.* (2012) and Yerimani *et al.*(2013).

Path co-efficient analysis was done to determine direct and indirect contribution of different traits towards seed yield per plant with phenotypic and genotypic level. The result were presented in Table 7 and Table 8. Among all the components Genotypic number of pods per plant exhibited the highest direct effect ( $G=0.9588$ ) on seed yield followed by 100 seed weight ( $G=0.5482$ ). At phenotypic level number of pod per plant exhibited the highest positive direct effect ( $P=0.9729$ ) on seed yield followed by 100 seed weight ( $P =0.5458$ ). Number of pods per plant showed highest positive direct effect on seed yield studied by Patel and Patel (1998), Musaana and Nadhy (1998) and Saroj *et al.*

**Table 4 : Cluster means for seed yield and its components in pigeonpea**

Cluster	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches/plant	Number of secondary branches /plant	Number of pods /plant	Number of seeds /pod	100 seed weight	Seed yield /plant
I	118.40	168.54	198.90	7.80	19.59	198.94	4.25	10.75	78.37
II	119.80	169.95	211.39	9.71	22.44	359.44	3.90	7.92	92.65
III	113.00	170.50	165.10	8.80	16.10	219.30	4.45	13.20	110.60
IV	113.00	166.50	216.40	11.20	23.05	188.70	3.75	7.15	49.61
V	131.00	177.00	206.50	9.20	18.80	81.40	3.70	11.05	32.60
VI	117.00	171.50	143.50	7.70	26.95	118.50	4.10	10.70	36.75
VII	124.00	170.50	158.15	11.55	27.75	167.60	3.50	8.50	47.00
VIII	123.00	171.50	221.80	3.80	7.30	52.40	5.45	11.80	31.85
IX	90.00	139.50	111.10	5.70	7.70	70.60	4.55	7.75	15.61

**Table 5: Estimation of phenotypic correlation co-efficient in pigeonpea**

Character	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches /plant	Number of secondary branches /plant	Number of pods /plant	Number of seeds /pod	100 seed weight (gm)	Seed yield /plant
Days to 50% flowering	1.0000	0.8075 ***	0.4295 ***	0.2104	0.2601 *	0.041	-0.2490 *	-0.0641	-0.0784
Days to maturity		1.0000	0.4863 ***	0.2587 *	0.3004 **	0.0924	-0.0546	0.0658	0.1168
Plant height (cm)			1.0000	0.1500	0.2089	0.3498 **	0.0301	-0.1881	0.3108 ***
Number of primary branches/plant				1.0000	0.7132 ***	0.5043 ***	-0.4537 ***	-0.3746 ***	0.3546 ***
Number of secondary branches/plant					1.0000	0.4775 ***	-0.4364 ***	-0.2737 *	0.3081 ***
Number pods/plant						1.0000	-0.3521 **	-0.4607 ***	0.7597 ***
Number of seeds/ pod							1.0000	0.3794 ***	0.0065
100 seed weight (gm)								1.0000	0.0977

**Table 6 : Estimation of genotypic correlation co-efficient in pigeonpea**

Character	Daysto 50% flowering	Days to maturity	Plant height	Number of primary branches /plant	Number of secondary branches /plant	Number of pods /plant	Number of seeds /pod	100 seed weight (gm)	Seed yield /plant
Days to 50% flowering	1.0000	0.8806***	0.5015***	0.2047	0.3016**	0.0315	-0.3146 ***	-0.0798	-0.1191
Days to maturity		1.0000	0.5378***	0.2683**	0.3402**	0.0944	-0.0965	0.0616	0.1136
Plant height (cm)			1.0000	0.1373	0.2013	0.3395**	0.0092	-0.2059	0.2935**
Number of primary branches/plant				1.0000	0.7141***	0.498	-0.4826 ***	-0.3878 ***	0.3363 ***
Number of secondary branches/plant					1.0000	0.4628	-0.4597 ***	-0.2865 **	0.2819 **
Number pods/ plant						1.0000	-0.3753 ***	-0.4801 ***	0.7566 ***
Number of seeds/ pod							1.0000	0.3953***	0.0000
100 seed weight (g)								1.0000	0.0945

**Table 7: Direct and indirect effect of yield and its components characters on grain yield and at phenotypic level**

Character	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches /plant	Number of secondary branches /plant	Number of pods /plant	Number of seeds /pod	100 seed weight	Seed yield /plant
Days to 50% flowering	-0.1260	-0.1017	-0.0541	-0.0265	-0.0328	-0.0052	0.0314	0.0081	-0.0784
Days to maturity	0.0204	0.0253	0.0123	0.0065	0.0076	0.0023	-0.0014	0.0017	0.1168
Plant height (cm)	0.0406	0.046	0.0945	0.0142	0.0197	0.0331	0.0028	-0.0178	0.3108
Number of primary branches/plant	0.0426	0.0524	0.0304	0.2026	0.1445	0.1022	-0.0919	-0.0759	0.3546
Number of secondary branches/plant	-0.0187	-0.0216	-0.0150	-0.0514	-0.0721	-0.0344	0.0314	0.0197	0.3081
Number pods/plant	0.0399	0.0899	0.3403	0.4906	0.4645	0.9729	-0.3425	-0.4482	0.7597
Number of seeds/ pod	-0.0422	-0.0093	0.0051	-0.0769	-0.074	-0.0597	0.1696	0.0643	0.0065
100 seed weight (g)	-0.035	0.0359	-0.1027	-0.2045	-0.1494	-0.2514	0.2071	0.5458	0.0977

Residual effect=0.3018 under lined figures indicates direct effect

**Table 8: Direct and indirect effect of yield and its components characters on grain yield and at genotypic level**

Character	Days to 50% flowering	Days to maturity	Plant height	Number of primary branches /plant	Number of secondary branches /plant	Number of pods /plant	Number of seeds /pod	100 seed weight	Seed yield /plant
Days to 50% flowering	-0.299	-0.2630	-0.1500	-0.0612	-0.0902	-0.0094	0.0941	0.0239	-0.1191
Days to maturity	0.1518	0.1724	0.0927	0.0462	0.0586	0.0163	-0.0166	0.0106	0.1136
Plant height (cm)	0.0638	0.0684	0.1271	0.0175	0.0256	0.0432	0.0012	-0.0262	0.2935
Number of primary branches/plant	0.0360	0.0472	0.0241	0.1758	0.1255	0.0875	-0.0848	-0.0682	0.3363
Number of secondary branches/plant	-0.0213	-0.024	-0.0142	-0.0504	-0.0706	-0.0327	0.0325	0.0202	0.2819
Number pods/plant	0.0302	0.0905	0.3255	0.4775	0.4438	0.9588	-0.3599	-0.4603	0.7566
Number of seeds/ pod	-0.0368	-0.0110	0.0011	-0.0564	-0.0538	-0.0439	0.1169	0.0462	0.0000
100 seed weight (g)	-0.0437	0.0338	-0.1129	-0.2126	-0.1571	-0.2632	0.2167	0.5482	0.0945

(2013), Chauhan *et al.* (2021), Rajmani *et al.* (2022). Basavarajaiah *et al.* (2000) recorded days to maturity as well as number of primary branches per plants effected on seed yield.

#### Future scope of the study :

High yielding diverse genotypes *viz.*, PT-12-8-2, BDN-716, ICP-6992 of cluster I, ICP-4476, ICP-2641 of cluster II, ICP-7057 of VIII and BDN-2019-8 of cluster III may be used for future hybridization program for further yield improvement in pigeonpea.

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#### Conclusion :

Genotypes “BDN-2019-8, ICP-13011, ICP-14337, ICP-6924, ICP-3945, ICP7057, ICP-13191” formed into different solitary clusters. The genotypes that falls into solitary cluster more often have some unique characters which make them divergent. So this genotypes can be utilized in future breeding programmes. Based on correlation studies number of pods per plant and number of secondary branches per plant showed highly positive association with seed yield per plant. Hence this trait could be used for breeding programme.

#### REFERENCES

Basavarajaiah, D., Gowda, M. B., Lohithaswa, H. C. and Kulkarni, R. S. (2000). Assessment of pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm and isolation of elite genotypes for Karnataka. *Crop Res.*, **20** (3) : 444-448.

- Chauhan, C., Verma, S. K., Panwar, R. K., Gaur, A., Gautam, A. and Yadav, H. (2021). Co-efficient analysis for yield and its contributing traits in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Biological Forum-An International Journal*, **13** (3a): 184-188.
- Dewey, D. R. and Lu, K. H. (1959). A correlation and path co-efficient analysis of component of wheatgrass seed production. *Agron. J.*, **51** : 515-518.
- Falconer, D. S. (1960). *Correlated character, introduction to quantitative genetics*, 312, published by Longman Group Ltd., London.
- Kumara, N., Santosh, G. B., Nishanth, G. K. and Dharmaraj, P. S. (2013) Genetic diversity, variability and correlation studies in advanced genotypes of pigeonpea [*Cajanus cajan* (L.) Millsp.] *Research Article, Acta Biologica Indica.*, **2**(2):406-411.
- Mahalanobis, P.C. (1936). On generalized distance in statistics. *Proc. Nat. Ins. Sci. India*. **2** : 49-55.
- Musaana, M.S. and Nadhy, M.S. (1998). Path co-efficient analysis of yield and its components in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *African J. Agri. Sci.*, **6**(2): 143-14.
- Patel, H., Patel, A., Patel, J. and Patel, N. (2018). Genetic divergence study through D2 analysis in pigeonpea (*Cajanus cajan* L. Millspaugh). *International Journal of Chemical Studies.*, **6** (5) : 1947-1950.
- Patel, J. B. and Acharya, S. (2011). Genetic divergence and character association in Indo-African derivatives of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *J. Food Legu.*, **24** (3) : 198-201.
- Patel, K.N. and Patel, D. R. (1998). Studies on genetic variability in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *International Chickpea and Pigeonpea Newsletter*, **5** : 28-30.
- Prasad, Y., Kumar, K. and Mishra, S.B. (2013). Studies on genetic parameters and inter-relationships among yield and yield contributing traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *The Bioscan*, **8** (1) : 207-211.
- Rajamani, S., Sreekanth, M. and Ramana, M. P. (2022). Path coefficient analysis in pigeonpea (*Cajanus cajan* L. Millsp.). *The Pharma Innovation Journal.*, **11**(5) : 483-485.
- Salunke, J. S., Aher, R. P., Shinde, G. C. and Kute, N. S. (1995). Correlation and path analysis in early pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Res.*, **18**(4) : 162-166.
- Saroj, S. K., Singh, M. N., Kumar, R., Singh, T. and Singh, M. K. (2013). Genetic variability, correlation and path analysis for yield attributes in pigeonpea. *Int. J. of life science.*, **8**(3): 941-944.
- Sharma, R., Gangwar, R. K. and Yadav, V. (2012). A study on genetic variability and correlation in pigeonpea. *Internat.J.Agril.Sci.*, **3** (9) : 214-218.
- Sreelakshmi, C. H., Sameer Kumar, S. V. and Shivani, D. (2010). Genetic divergence and stability analysis in pigeonpea (*Cajanus cajan* L.). *Electronic Journal of Plant Breeding.*, **1** (4) : 530-535.
- Yerimani, A. S., Mehetre, S. and Kharde, M. N. (2013). Genetic variability for yield and yield component traits in advanced F3 and F4 generations of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Molecular Plant Breeding*, 136- 140pp.

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