



Assessment of Genetic Variability to Contribute Yield and its Components Characters in Pigeonpea [*Cajanus cajan* (L.) Millsp.] Genotypes in Central Plain Agro-Climatic Region of Uttar Pradesh, India

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation entitled “assessment of genetic variability to contribute yield and its components Characters in Pigeon pea [*Cajanus cajan* (L.) Millsp.]” genotypes in central plain agro-climatic region of uttar pradesh” was conducted at Oilseed Research Farm, Kalyanpur, C. S. Azad University of Agriculture and Technology, Kanpur- 208002 (U.P.) during *kharif* season 2021-22. Genetic variability studies were carried out for 34 pigeon pea genotypes during the years 2021-2022. The analysis of variance revealed that there was significant amount of variation for all the characters during these years. Days to maturity, plant height, number of secondary branches, days of 50% flowering, 100 seed weight, number of primary branches, biological yield, seed yield per plant, harvest index, number of pods per plant and number of seeds per pod was shown to have identified as high heritability value. High estimate of (phenotypic coefficient of variance and genotypic coefficient of variance) PCV and GCV were observed for the number of secondary branches, number of primary branches and days to maturity while moderate estimate of PCV and GCV were observed for plant height, 100 seed weight, days to 50% flowering, seed yield per plant, number of pods per plant and harvest index. The character association studies revealed that at genotypic and phenotypic level, seed yield per plant had positive and high significant correlation to harvest index, days to maturity, biological yield, 100 seed weight and number of pods per plant.

Keywords: Genetic advance; genetic variability; heritability; correlation; pigeon-pea; quantitative traits.

1. INTRODUCTION

“Pigeonpea has significant contribution to Indian agriculture economy but despite research efforts the productivity of pigeonpea is very low. Pigeonpea [*Cajanus cajan* (L.) Millsp.], also called redgram, tur or arhar is predominantly an annual food legume, which is grown in different cropping systems as *kharif* crop in the Indian sub-continent. Pigeonpeas the second most important pulse crop in India” [1]. “As an integral part of the human diet pigeonpea serves as an affordable and rich source of proteins and essential micronutrients, particularly in India. Other diverse usages of pigeonpea include fodder and feed for animals, fuel wood for rural households, soil binder to protect soil erosion and as border crop to protect the main crop. Several edible legumes such as Lablab, Dolichos, Phaseolus, Vigna and *Cajanus* belong to the tribe Phaseoleae, but in the genus *Cajaninae* only one species, *Cajanus cajan*, has been domesticated and cultivated. India is considered to be the origin of the pigeon pea” [2]. The alternative hypothesis that Africa is the center of origin does not appear to be true because there is only one wild relative, *C. kerstingii*, in West Africa. In addition, *C. scarabaeoides* has also been found in Africa, but its spread is limited to coastal areas. Therefore, Van der Maesen, (1980) proposed Africa as a secondary center of origin. Pigeon pea seeds provide essential amino acids such as lysine, tyrosine and arginine, while being low in cystine and methionine [3]. “Pigeon peas are also rich in

iron (5.23 mg), zinc (2.76 mg), calcium (130 mg), manganese (1.791 mg), niacin (2.965 mg), thiamin (0.643 mg), riboflavin (0.187 mg), pyridoxine (0.283 mg), folate (456 µg) and pantothenic acid (1.266 mg)” [4].

“Globally, it is grown in about 5.52 mha area with an annual production of 4.32 m tons with an average productivity around 790 kg/ha. The distribution of pigeon pea is asymmetrical across the globe. It is grown in different parts of the world spanning over 23 countries including India, Myanmar, Tanzania, Malawi, Kenya and the United Republic of Tanzania” [5]. In Southeast Asia, pigeon pea is mainly grown in India, Philippines, Myanmar, Nepal and Bangladesh. It is widely grown in India, where it plays an important role in legume-based crop systems and occupies the second largest area among legumes. Recently, this crop has also been introduced to China, where it is grown on hillsides mainly to control soil erosion (Saxena, 2008). It is an important legume of Asia (especially the Indian subcontinent), Latin America, and eastern and southern Africa. Pigeon pea occupies a unique place in Indian agriculture and India accounts for about 77.60% of world production [6,7]. It is mainly intercropped with beans, moong beans, castor beans, sorghum, soybeans, cotton and chili peppers, etc [8,9].

India ranked first in area and production in the world with 82.20% and 77.60% of world's acreage and production respectively [5]. India's

total area, coverage and production of pigeon pea was 4.54 Mha and 3.83 MT respectively in the year..... More than 80% of Pigeon pea production comes from 6 states of, Karnataka, Maharastra, Uttar Pradesh, Telangana, Madhya Pradesh and Andhra Pradesh. The state-wise trend showed that Karnataka ranked 1st both in area and production (34% and 28.59%). Maharastrallnd for area and production (26.32 and 27.50%).Uttar Pradesh ranks 3rd in production (7.30%). The highest productivity has been recorded by Gujrat (1132 kg/ha) followed by Odisha (1124kg/ha), Jharkhand (1049 kg/ha) and Uttar Pradesh (980 kg/ha) [10].

2. MATERIALS AND METHODS

The experimental material used in present investigation consisted of 34 advance lines of pigeonpea developed at C.S. Azad University of Agriculture and Technology, Kanpur.

The experiment was laid out in Randomized Block Design (RBD). All the recommended agronomic practices were followed to raise a good crop of pigeon pea with keeping row to row distance of 75cm and plant to plant distance of 25cm respectively. Observations were recorded on yield and yield attributing characters. All the observations were taken from each plot,

on randomly five selected plants from each genotype. The data were recorded for the following characters viz.plant height (X_1), Days to 50% flowering (X_2), days to maturity (X_3), Number of primary branches per plant (X_4), Number of secondary branches per plant (X_5), Number of pods per pod(X_6), Number of seeds per plant (X_7), biological yield (X_8), Harvest index (X_9),100 Seed Weight (X_{10}), Seed yield per plant (X_{11}).The mean values of genotypes in each replication were used for statistical analysis. The steps involved in the analysis of the variance were as described by [11]. The genotypic and phenotypic coefficients of variation were calculated as per the formula suggested by [12]. GCV and PCV values were categorized as low (0-10%), moderate (11-20%) and high (> 20%) as indicated by Sivasubramaniam and Madhavamenon [13]. Heritability (broad sense) was calculated as per Allard (1956). The heritability percentage was categorized as low (0-30%), moderate (30 -60 %) and high (>60%) as given by Johnson et al. [14] and genetic advance as per Johnson et al. [14] were also worked out. Genetic advance as per cent of mean was categorized as low (0-10%), moderate (11 – 20%) and high (>20%) as suggested by Johnson et al. [14]. Genotypic and phenotypic correlation coefficient was calculated by the formulae suggested by Robinson et al. [15].

Chart 1. List of genotypes

Sr. No.	Name of genotype	Place of origin	Sr. no.	Name of genotype	Place of origin
1	KA-16-1	C. S. A. U.A.&T, Kanpur	18	MANAK	C.C.S, Haryana
2	KA-16-5	C. S. A. U.A.&T, Kanpur	19	UPAS-120	G.B.P.U.A.&T, Pantnagar
3	KA-17-1	C. S. A. U.A.&T, Kanpur	20	DA-11	RPCAU, Dholi
4	KA-17-2	C. S. A. U.A.&T, Kanpur	21	BAHAR	RPCAU, Dholi
5	KA-17-3	C. S. A. U.A.&T, Kanpur	22	MAL-6	B.H.U,Varansi
6	KA-18-1	C. S. A. U.A.&T, Kanpur	23	IPA-7-F	I.I.P.R. Kanpur
7	KA-18-2	C. S. A. U.A.&T, Kanpur	24	IPA-8-F	I.I.P.R. Kanpur
8	KA-12-01	C. S. A. U.A.&T, Kanpur	25	IPA-9-F	I.I.P.R. Kanpur
9	KA-12-03	C. S. A. U.A.&T, Kanpur	26	IPA-203	I.I.P.R. Kanpur
10	KA-12-05	C. S. A. U.A.&T, Kanpur	27	ASHA(ICPL-87119)	ICRISAT,Hyderabad
11	T-7	C. S. A. U.A.&T, Kanpur	28	MARUTHI(ICPL-8863)	ICRISAT,Hyderabad
12	TYPE-17		29	PUSA-9	I.A.R.I, New Delhi
13	TYPE-21	C. S. A. U.A.&T, Kanpur	30	AL-201	P.A.U,Ludhiana
14	AMAR	C. S. A. U.A.&T ,Kanpur	31	PUSA ARHAR-16(PADT16)	I.A.R.I, New Delhi
15	AZAD	C. S. A. U.A.&T, Kanpur	32	AL-15	P.A.U,Ludhiana
16	NDA-1	A.N.D.U.A.&T, Kumarganj	33	VIPULA	MPKV, Rahuri
17	NDA-2	A.N.D.U.A.&T, Kumarganj	34	PUSA 33	I.A.R.I, New Delhi

Table 1. Analysis of variance for 11 quantitative characters in 34 genotypes of pigeon pea

Source of variation	DF	Plant height	Days to 50% flowering	Days to maturity	No of primary branches	No of secondary branches	No of pods/plant	No of seeds/pod	Biological Yield (g)	Harvest Index (%)	100 Seed Weight (g)	Seed Yield/plant (g)
Replication	2	0.16	3.08	1.14	0.50	0.14	88.87	0.00	1.49	0.64	0.01	2.05
Treatment	33	2817.56**	1102.57**	5434.53**	87.62**	599.55**	3327.62**	0.32**	534.05**	11.55**	10.08**	93.07**
Error	66	0.61	1.35	0.53	0.55	0.50	100.88	0.05	3.89	0.33	0.01	1.42
Total	10	920.99	361.19	1776.01	29.00	196.22	1154.92	0.14	177.07	4.00	3.30	31.38

*Significant at 5% level, ** Significant at 1% level

Table 2. Genotypic, phenotypic coefficient of variance, heritability, genetic advance and genetic advance percent over mean for 11 characters in pigeon pea

Character	PCV	GCV	Heritability h^2 (bs) (%)	Genetic advance	GA% of mean
Plant height (cm)	18.03	18.03	99.93	63.10	37.13
Days to 50% flowering	17.00	16.97	99.63	39.40	34.90
Days to maturity	20.74	20.74	99.97	87.66	42.72
No. of primary branches	31.76	31.46	98.14	10.99	64.20
No. of secondary branches	38.54	38.49	99.75	29.07	79.20
No. of pods per plant	12.83	12.26	91.42	64.60	24.15
No. of seeds per pod	9.05	7.24	63.95	0.49	11.93
Biological Yield (g)	6.10	6.04	97.84	27.09	12.30
Harvest Index (%)	10.11	9.69	91.92	3.82	19.15
100 Seed Weight(g)	17.12	17.08	99.61	3.77	35.12
Seed Yield per plant(g)	13.04	12.74	95.56	11.13	25.66

*Significant at 5% level, ** Significant at 1% level

Table 3. Genotypic correlation coefficient in 34 genotypes of pigeon pea

Characters	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches	No. of secondary branches	No. of pods/plant	No. of seeds/pod	Biological yield (g)	Harvest Index (%)	100 Seed weight (g)	Seed yield/plant (g)
Plant height	1.000	0.630**	0.578**	0.523**	0.587**	0.688**	0.244*	0.294**	-0.065	0.574**	0.202*
Days to 50% flowering		1.000	0.724**	0.384**	0.592**	0.661**	0.110	0.059	0.089	0.719**	0.222*
Days to maturity			1.000	0.340**	0.542**	0.714**	0.253*	0.227*	0.361**	0.785**	0.504**
No of primary branches				1.000	0.719**	0.597**	0.687**	0.038	-0.125	0.321**	-0.009
No of secondary branches					1.000	0.626**	0.478**	0.198*	-0.074	0.488**	0.114
No of pods/plant						1.000	0.357**	0.162	0.296**	0.706**	0.418**
No of seeds/pod							1.000	0.018	-0.078	0.056	-0.011
Biological Yield(g)								1.000	-0.023	0.137	0.489**
Harvest Index									1.000	0.384**	0.831**
100 Seed Weight(g)										1.000	0.437**
Seed Yield/plant(g)											1.000

*Significant at 5% level, ** Significant at 1% level

Table 4. Phenotypic correlation coefficient in 34 genotypes of pigeon pea

Characters	Plant height (cm)	Days to 50% flowering	Days to maturity	No. of primary branches	No. of secondary branches	No. of pods/plant	No. of seeds/pod	Biological yield (g)	Harvest index (%)	100 Seed weight (g)	Seed yield/plant (g)
Plant height	1.000	0.629**	0.578**	0.518**	0.586**	0.659**	0.197*	0.291**	-0.062	0.573**	0.198*
Days to 50% flowering		1.000	0.723**	0.380**	0.589**	0.629**	0.087	0.058	0.086	0.716**	0.218*
Days to maturity			1.000	0.337**	0.542**	0.683**	0.203*	0.225*	0.346**	0.783**	0.492**
No of primary branches				1.000	0.711**	0.561**	0.548**	0.037	-0.114	0.317**	-0.006
No of secondary branches					1.000	0.599**	0.382**	0.195*	-0.074	0.487**	0.109
No of pods/plant						1.000	0.244*	0.159	0.264**	0.674**	0.388**
No of seeds/pod							1.000	0.012	-0.060	0.049	-0.002
Biological Yield(g)								1.000	-0.017	0.135	0.485**
Harvest Index									1.000	0.361**	0.828**
100 Seed Weight(g)										1.000	0.425**
Seed Yield/plant(g)											1.000

*Significant at 5% level, ** Significant at 1% level

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance

The analysis of variance revealed significant differences for all the 11 characters studied in 34 pigeon pea genotypes Table 1 and it revealed that mean sum of squares due to genotypes were highly significant for all the characters under study viz., plant height, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, biological yield, harvest index, 100 seed weight, seed yield per plant. The results of the present study are in accordance with the Pandey et al. [16] and Gaur et al. [17] who had also reported the high variability in pigeon pea for different traits.

3.2 Heritability Analysis

The high estimates of heritability were reported for days to maturity (99.97%), plant height (99.93%), number of secondary branches (99.75%), days of 50% flowering (99.63%), 100 seed weight (99.61%), number of primary branches (98.14%), biological yield (97.84%), seed yield per plant (95.56%), harvest index (91.92%), number of pods per plant (91.42%) and number of seeds per pod (63.95%). The finding of heritability was in consonance with the finding of [18,19,20,21,22,23].

3.3 Genetic Advance Analysis

The high estimate of genetic advance as percent of mean were observed for number of secondary branches (79.20), number of primary branches (64.20), days to maturity (42.72), plant height (37.13), 100 seed weight (35.12), days to 50% flowering (34.90), seed yield per plant (25.66) and number of pod per plant (24.15). The moderate value of genetic advance over mean was recorded for harvest index (19.15), biological yield (12.30) and number of seeds per pod (11.93). The finding was in agreement with the finding of [24,25,26,27]. The present investigation revealed high heritability coupled with high genetic advance as percent mean for most of the characters indicating the presence of considerable genetic variation and additive gene effects. Moreover, it is always desirable to compute broad sense heritability in conjunction with genetic advance because the information of heritability coupled with genetic advance help to explain the role of phenotypic variance.

3.4 Correlation Coefficient Analysis

The present investigation of the relationship between seed yield and associated traits helps to reveal their significance in pigeonpea breeding programs. The estimates of Pearson's correlations among eleven studied characters are present tables showing that at genotypic and phenotypic level seed yield per plant had positive and high significant correlation to harvest index (G0.831 P0.828), days to maturity (G0.504 P0.492), biological yield (G0.489 P0.485), 100 seed weight (G0.437 P0.425), number of pods per plant (G0.418 P0.388), positive significant genotypic correlation with days to 50% flowering (G0.222 P0.218), plant height (G0.202 P0.198) and positive genotypic correlation with number of secondary branches (G0.114 P0.109) The above results aligned with the earlier reports of [28,29,30], while negative genotypic correlation with number of seeds per pod (G-0.011 P-0.002) and number of primary branches (G-0.009 P-0.006) were in consonance with the earlier reports of Lakhote et al. [31,32].

4. CONCLUSION

The accomplishment of any breeding program objective depends upon the extent of genetic variability in base population and it is essential to subject a population for selection to achieve improvement in a particular trait. In the present study the analysis of variation shows highly significant differences among the genotypes for characters studied viz. number of secondary branches, number of primary branches, days to maturity, plant height, 100 seed weight, days to 50% flowering, seed yield per plant, number of pods per plant and harvest index would be important for bringing on crop improvement. High estimate of PCV and GCV were observed for the number of secondary branches, number of primary branches and days to maturity, while moderate estimate of PCV and GCV were observed for plant height, 100 seed weight, days to 50% flowering, seed yield per plant, number of pods per plant and harvest index. The PCV and GCV for seed yield per plant showed more differences between these two mean and showed more interaction of environment for expression of characters. The magnitude of phenotypic coefficients of variation in selected pigeon pea genotypes was higher than that of the genotypic coefficients of variation, indicating that environmental factors are influencing studied characters. Studies on heritability and genetic

advance revealed days to maturity, plant height, number of secondary branches, days of 50% flowering, 100 seed weight, number of primary branches, biological yield, seed yield per plant, harvest index, number of pods per plant and number of seeds per pod may be improved through simple selection procedures. The character association studies revealed that at genotypic level seed yield per plant had positive and high significant correlation to harvest index, days to maturity, biological yield, 100 seed weight, number of pods per plant, positive significant genotypic correlation with days to 50% flowering, plant height and positive genotypic correlation with number of secondary branches while negative genotypic correlation with number of seeds per pod and number of primary branches.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Bohra A, Saxena KB, Varshney RK, Saxena RK. Genomics assisted breeding for pigeonpea improvement. *Theor. Appl. Genet*; 2020. DOI: 10.1007/s00122-020-03563-7
2. Vavilov NI. The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica*. 1951;13:1-366.
3. Saxena KB, Kumar RV, Sultana R (). Quality nutrition through pigeonpea—A review. *Health*. 2010a; 11:1335-1344.
4. Mazur WM, Duke JA, Kristiina W, Rasku S, Adlercreutz H. Isoflavonoids and lignans in legumes: Nutritional and health aspects in humans. *Nutritional Biochem*. 1998;9:193-200.
5. FAO-STAT. FAO statistical databases (FAO stat), food and agriculture organization of the United Nations (FAO); 2021-22. Available:<http://faostat.fao.org>
6. Allard RW. Principles of plant breeding (1st Edn.), John Wiley and Sons. Inc., New York; 1960.
7. Vanniarajan C, Magudeeswari P, Gowthami R, Indhu SM, Monisha K. Assessment of genetic variability and traits association in pigeon pea [*Cajanus cajan* (L.) Millsp.] Germplasm Legume Research-An Int. J. 2021;1:8.
8. Massen LJGVD. India is the native home of the pigeon pea. 1980;257-262.
9. Saxena KB, Mallikarjuna N. A new cytoplasmic male sterility system derived from cultivated pigeon pea cytoplasm. *Euphytica*. 2005;142:143–148.
10. DES. Agricultural statistics at a glance, Department of Agriculture and cooperation, Ministry of Agriculture, Government of India; 2021-22. Available:<http://agricoop.nic.in>
11. Fisher RA. Statistical methods and scientific Induction. J. of the Royal Statistical Society. Series B (Methodological). 1955;17(1):69-78.
12. Burton GW, Devane EH. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material, *Agronomy J*. 1952;45:478-481.
13. Sivasubramanian S, Madhavamenon P. Genotypic and phenotypic variability in rice. *Madras Agricul. J*. 1973;60:1093–1096.
14. Johnson HW, Robinson HF, Comstock RE. Genotypic and phenotypic correlations in soybeans and their implications in selection. *Agronomy J*. 1955;47(10):477-483.
15. Robinson HF, Comstock RE, Harvey PH. Genotypic and phenotypic correlation's in wheat and their implications in selection. *Agronm. J*. 1951;43:282-287.
16. Pandey P, Kumar R, Pandey VR. Genetic association studies for yield and yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Legume Research*. 2016; 39(2): 189-193.
17. Gaur A K, Singh I, Singh S, Sharma S. Genetic analysis of M₄ mutant lines of pigeonpea (*Cajanus cajan* (L.) Millspaugh) developed through gamma irradiation. *Journal of Food Legumes*; 2018.
18. Saroj SK, Singh MN, Kumar R, Singh T, Singh MK. Genetic variability, correlation and path analysis for yield attributes in pigeon pea. *The bioscan*. 2013;8(3):941-944.
19. Rangare NR, Reddy GE, Kumar SR. Study of heritability, genetic advance and variability for yield contributing characters in pigeon pea [*Cajanus cajan* (L.) Millspaugh]. *Trends in Biosciences*. 2013; 6(5):660-662.
20. Mula MG, Galian JL, Mula RP. Variability, heritability and genetic advance of medium to long duration pigeon pea [*Cajanus cajan* (L.) Millsp.]lines. *Green Farming*. 2019; 10(2):127-130.

21. Sharma SC, Kumar R, Aarif M. Association studies in pigeon pea [*Cajanus cajan* (L.) Millsp.]. J. of Pharmacognosy and Phytochem. 2020;9(3):1176-1178.
22. Ranjani MS, Jayamani P, Manonmani S, Latha KR, Sethuraman K. Genetic analysis and diversity in early duration pigeon pea [*Cajanus cajan* (L.) MillSp.] genotype. Elet.J. of Plant Breeding. 2021;12(2):540-548.
23. Aswini MS, Ramasamy SP, Hemavathy AT. Genetic studies for quantitative traits in pigeon pea (*Cajanus cajan*). Crop Res. 2021;56:0970-4884.
24. Yadav SK, Kumar N, Prasad K, Mahto CS, Lal HC, Sen S. Estimation of variance and its component for different quantitative characters in pigeon pea [*Cajanus cajan* (L.) Millsp.] Germplasm. Int. J. Curr. Microbiol. App. Sci. 2019;9: 427-436.
25. Sahu JK, Ekka RE. Genetic variability studies in germplasm accession of pigeon pea [*Cajanus cajan* (L.) Millsp.].J. of Pharmacognosy and Phytochem. 2020; 377-379.
26. Rao VT, Rao PJM. Studies on genetic variability and character association in Pigeon pea [*Cajanus cajan* (L.) Mill sp.].I.J.C.S. 2020;8(4):1051-1053.
27. Patel PR, Sharma M, Patel MP. Study of heritability, genetic advancement, variability and character association for yield contributing characters in pigeon pea [*Cajanus cajan* (L.) Millspaugh]. Emer Life Sci Res. 2021;7(2):1-4.
28. Kandarkar KG, Kute NS, Shinde GC, Al. Genetic divergence studies in Pigeon pea [*Cajanus cajan* L. Millsp.]. I.J.C.S. 2020; 8(4):2067-2070.
29. Chauhan C, Verma SK, Panwar RK, Gaur A, Gautam A. et al. Character association and path coefficient analysis for yield and its contributing traits in pigeonpea [*Cajanus cajan* (L.) Millspaugh].Bio. Forum-An Int. J. 2021;13(3a):184-188.
30. Ramasamy SP, Aswini MS, Hemavathy AT. Correlation and path analysis in pigeon pea [*Cajanus cajan* (L.) Millsp.]. Ind. J. Pure App. Biosci. 2021;9(6):1-7.
31. Lakhote SJ, Patil HE, Mali RA, Ingle P. Genetic analysis for yield and yield contributing traits in vegetable type genotypes in Pigeon pea [*Cajanus cajan* (L.) Millsp.]. Int. J. of Trp. Agri. 2015;33(2):161-167.
32. Pushpavalli, SNCL, Yamini KN, Saxena R, Rajeev, Kumar S. Genetic variability and correlation in pigeonpea genotypes. Electronic J. of Plant Breeding. 2018;9: 343-349.

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