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Genetic characterization and trait association studies in pigeon pea (*Cajanus cajan* L. Millsp.) germplasm

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Abstract

The present investigation was conducted to examine the 20 Pigeon pea genotypes along with 2 checks to study the genetic parameters, correlation and genetic diversity. The experiment was carried out in main experimental station of Agricultural Research Farm, Rama University (U.P), Mandhana, Kanpur during Kharif Season, 2023-24 in Randomized Block Design (RBD) with three replications. Analysis of variance showed highly significant differences among 20 Pigeon pea genotypes for 12 characters studied. On the basis of mean performance, Analysis of variance showed highly significant differences among 20 Pigeon pea genotypes for 12 characters studied. The results showed that, phenotypic coefficient of variation (PCV) was greater in magnitude than the respective genotypic coefficient of variation (GCV). The characters viz., seed yield per plant (28.33), biological yield per plant (23.77), showed highest phenotypic coefficient of variation. Moderate phenotypic coefficient of variation was observed for total pods per plant (19.12), test weight (13.36%), number of branches per plant (13.35%), harvest index (10.11%). The lowest magnitude of phenotypic coefficient of variation was reported in days to 75% maturity (4.26%) followed by secondary branches per plant (4.92%), pod length (6.19%), days to 50% flowering (6.29) total seeds per pod (6.74%) and plant height (6.90%). The amount of genetic variation present in the 20 genotypes was worked out in terms of genotypic coefficient of variation (GCV). The highest genotypic coefficient of variation was recorded in percent by seed yield per plant (25.27%) followed by biological yield per plant (21.93%).The moderate GCV was observed in traits, viz., number of pods per plant(17.26%), seed index (12.51%), primary branches per plant (11.53%), whereas lowest GCV was seen in harvest index(9.74),days to 50% flowering (5.88),plant height (5.23%), number of seeds per pod (4.38%), days to maturity (3.84%), pod length (2.35%), secondary branches per plant (1.27%).

Keywords: PCV, GCV, seed yield, correlation. genetic variability

Introduction

Pulses play a significant role in our daily diets and are an essential source of protein for the majority of vegetarians in our nation. Pulses are also known to increase the soil fertility and productivity of succeeding crop. Pigeonpea or *Cajanus cajan* (L.) Millsp. is a frequently cross pollinated crop, is a diploid species (2n = 2x = 22) and has a genome sequence of 833.1 Mb. 11 connections. group. It belongs to the Fabaceae family, Pigeonpea genus, Pigeon pea species, Phaseolus vulgaris family, Caenaceae family, Fabaceae order. It is one of the most important food crops in the world and is grown in tropical and subtropical regions and plays an important role in the Indian economy (Varshney *et al*., 2017). 2012) [1]. It comes from India, but it comes from Africa. Both are hotspots for pigeon pea. It is true that these plants have been cultivated for a long time and were introduced by traders thousands of years ago. Pigeon pea is now grown in tropical regions and has become endemic in many regions, including the U.S. Virgin Islands, Florida, and Puerto Rico. Pigeon pea is the second most important legume crop in India after chickpea and provides mostly high protein food for vegetarians in India. Despite its production India is the largest consumer of pigeonpea also. In India from last 3 decades production of pigeonpea has increased but still there is huge gap in the demand and supply due to its consumption. In India productivity of pigeonpea is very low as compared to African countries like Mozambik and Zinbabwe. So, its serious need to breed high yielding pigeonpea varirty with resistant to biotic and abiotic stress tolerance. Before starting any judicious plant breeding activity presence of variability among the genotypes is prerequisite. Present investigation is aimed to screen the genetically more variable and high yield potential lines from the diverse genotypes which could be used as parent in the future breeding program.

Methods and Materials

The investigation was conducted with 20 diverse genotypes (Table 1) of pigeonpea in RBD field experimental design with 3 replications during kharif 2023-24 at the research farm of FADAI, Rama University Mandhana Kanpur. Each plot consists of paired rows of 5.0 m length. Recommended Plant to Plant (20 cm) and Row to Row (60 cm) distance were maintained. All essential agronomic practices were followed to raise the good crop. Data from each replication were recorded by selecting 5 competitive plants randomly and their mean value were used in further analysis. Observation on twelve heritable traits viz., Days to 50% flowering (DFF), Days to 75% maturity (DM), plant height (PHT cm), Pods per plant (PPP), Primary branches per plant (PB), Secondary branches per plant (SBP), Seeds per pod (SPP), PL (cm), Biological yield per plant (BYPP g.), Seed Index (SI g.), Harvest index (HI%) and Seed yield per plant (SYPP g.) have been recorded and subjected to various statistical analysis.

Table 1: List of pigeon pea genotypes and their source are given below;

S. No.	Name of genotypes	Source	S. No.		Source
1	ICPL-84031	ICAR_IIPR, Kanpur	11	PA-291	ICAR_IIPR, Kanpur
2	AL-15		12	AL-1992	
3	ICPL-151		13	AL-201	
4	ICPL-87		14	Manak	
5	Pusa Arhar-16		15	CORG-9701	
6	Pusa-33		16	UPAS-120 (Ch)	
7	Pusa-991		17	PAU-881	
8	Pusa-992(Ch)		18	GT-100	
9	Pusa-84		19	GT-101	
10	Paras		20	VLA-1	

Results and Discussion

Analysis of variance varied significantly for almost all the traits under study (Table 2). Variation due to replication as well as treatment is also recorded significant except for the traits Seed per pods and seed index. Highest MSS value have been recorded for the Pods per plant (147.63). Error due to biological yield per plant exhibited high value (108.99). It means very high fluctuation have been seed in this trait.

Table 2: Analysis of variance for 12 quantitative characters in pigeon pea

S. No	Characters	MSS Replication	MSS Treatments	MSS Error
1.	Days to 50% flowering (DTF)	24.258**	93.498**	6.357
2.	Days to & 75% maturity (DM)	95.947**	101.850**	10.613
3.	Plant height (PHT) cm	17.609**	138.764**	37.393
4.	Primary branches per plant (PBP)	0.158*	1.626*	0.236
5.	Secondary branches per plant (SBP)	16.67**	1.189*	1.040
6.	Total pods per plant (PPP)	54.580**	147.63**	15.043
7.	Pod length (cm) (PL)	0.531*	0.064*	0.085
8.	Seeds per pod (SPP)	0.149	0.016*	0.025
9.	Biological yield per plant(g) (BYPP)	780.5**	1354.17**	108.997
10.	Harvest Index (HI%)	0.844*	24.398**	0.916
11.	Seed Index(g)	0.144	0.013	0.091
12.	Seed yield per plant	29.519	68.749**	7.823

Mean performance and range of variability

Study reveals that considerable number of variations among the genotypes is present. The minimum days to 50% flowering were observed in genotypes ICPL-84301, ICPL-151, and PAU-881, while the maximum days to 50% flowering were in genotype PARAS, P-219, and AL-15. The minimum days to 75% maturity were in genotypes Pusa-84, Pusa-33, and Pusa-991, while the maximum days to maturity were in genotypes Pusa-992 (CH), PARAS, and P-219. The plant height varied among genotypes, with CORG-9701 reporting the minimum plant height. The number of primary branches per plant ranged from 4.60 to 9.10, with an average of 7.23 branches per plant. Secondary branches per plant were also significant, with the lowest observed in UPAS-120(CH) (18.76), PARAS (19.8), and VLA 1 (20.95). The seed yield per plot varied from 380.0g (ICPL-87) to 485.0g (UPAS-120(CH), with the highest yield in genotype UPAS-120. The harvest index ranged from 28.75% (PUSA ARHAR-16) to 43.60% (UPAS-120(CH), with the lowest weight observed in PUSA ARAHR-16 (7.40 g) (Table 3).

Component of genetic variability analysis

Seed yield per plant (28.33) and biological yield per plant (23.77) displayed the greatest phenotypic coefficient of variation, as observed by Mourya *et al.* (2022) [3], Pashwan *et al.* (2021) [4]. Phenotypic coefficient of variation (PCV) tended to exceed genotypic coefficient of variation (GCV) in magnitude. Traits like total pods per plant (19.12%), test weight (13.36%), number of branches per plant (13.35%), and harvest index (10.11%) exhibited moderate levels of PCV, while days to 75% maturity (4.26%), secondary branches per plant (4.92%), pod length (6.19%), days to 50% flowering (6.29%), total seeds per pod (6.74%), and plant height (6.90%) showed the lowest PCV. Kumar *et al.* (2014) [6] also reported high PCV for seed yield per plant, whereas Pashwan *et al.* (2021) [4] found similar results for the lowest PCV in plant height and seed index.

Regarding genotypic coefficient of variation, it was highest for seed yield per plant (25.27%) and biological yield per plant (21.93%), with moderate GCV observed in traits such as number of pods per plant (17.26%), seed index (12.51%), and primary branches per plant (11.53%). Traits like harvest index (9.74%), days to 50% flowering (5.88%), plant height (5.23%), number of seeds per pod (4.38%), days to maturity (3.84%), pod length (2.35%), and secondary branches per plant (1.27%) exhibited the lowest GCV. High heritability was noted for traits such as harvest index (92.80%), seed index (87.70%), days to 50% flowering (87.30%), biological yield per plant (85.10%), and others, while pod length (14.40%) and secondary branches per plant (6.70%) showed the lowest heritability. The genetic advance varied across traits, with the lowest observed for total pods per plant (15.14%), days to 50% flowering (12.70%), and others. These findings align with previous studies by Mourya *et al.* (2022) [3], Pashwan *et al.* (2021) [4], highlighting the influence of genetic factors on specific traits in chickpea varieties. This classification of traits was based on the standard scale provided by Johnson *et al.* (1955) [7], providing valuable insights for breeding programs aimed at improving chickpea varieties

Table 3: Mean Performance of the genotypes evaluated during Kharif 2023-24

GENOTYPE	DFF	PHT (cm)	DF (75%)	PB	SB	BYPP (gm)	PL (cm)	PPP	SI (gm)	SYPP (g)	HI%
ICPL-84031	95.2	129.2	122	9.1	25.3	386	4.85	146.3	7.83	15	38.1
ICPL-151	99	125.7	122.9	7.2	22.6	405	4.4	145.7	11	19.35	41
ICPL-87	103.7	132.5	128	8.5	23.5	380	4.2	128	7.6	15.2	31.0
AL-15	122.2	129.9	132	6.1	20.97	407	4.6	143.18	10.48	21.17	35
PUSA ARHAR -16	118.2	146.7	123	8.6	26.25	385	4.15	127.7	7.4	13.5	28.75
PUSA-33	109	141.3	121	8.1	26.45	398	4.5	149.11	9.05	17.27	40.8
PUSA-991	111.5	145	121.5	5.9	24.9	388	4.63	130.89	8.11	21.09	37
PUSA-992 (CH)	104.9	144.6	140.4	7.3	21.2	411.5	5.4	129.2	7.75	15.1	31.10
PUSA-84	109	140.8	120.3	6.9	25.1	403.87	4.52	136.8	11.01	23.7	39
PARAS	117	137.6	139.35	5.5	23	477	4.61	142.1	9.75	18.39	41.9
P-219	124.6	135	138.97	6.3	21.4	402	4.16	156.88	7.8	17.2	34.6
AL-1992	102	142.6	122.5	7.7	23.9	409	4.66	149.26	9.6	21.36	40.6
AL-201	116	137	135	6.2	21.77	387	4.8	160.99	8.27	26.2	32.17
MANAK	108	128	124.8	6.8	25.4	410	4.7	163	11.75	35.8	42.90
CORG-9701	111	116.2	131	5.6	20.6	399	4.25	148.5	11.21	18.5	33.5
UPAS-120 (CH)	102	134	126	4.5	18.76	485	4.1	160.7	12.3	37	43.60
PAU-881	115	121.5	137	8.05	22.7	384	4.05	164.6	12.22	36	43.20
GT-100	113.7	120.3	130	7.11	23.1	386	4.39	155.2	9.6	17	36.3
GT-101	117	120.5	136.9	6.98	21.8	411	4.56	141.09	8.1	19.52	35.0
VLA-1	104	143.4	122.99	4.7	20.95	476	4.2	153.6	9.01	23.6	41.3
Range Lowest	95.2	116.2	120.3	4.5	18.76	380	4.05	127.7	7.4	15	28.8
Range Highest	124.6	146.7	140.4	9.1	26.5	485	5.4	164.6	12.3	37	43.6
Mean	112.29	136.02	132.05	7.23	23.49	412.5	4.43	147.18	9.32	21.84	35.19
C.V.	2.25	4.5	1.85	6.73	4.75	9.17	6.62	8.22	4.69	12.8	2.27
S.E	1.78	4.32	2.3	0.34	0.72	7.38	0.21	2.74	0.31	1.98	0.68

Table 4: Estimates of Genetic parameters of variability among the 12 quantitative traits

Sr. No.	Character	σ^2p	σ^2p	σ^2p	PCV%	GCV%	ECV%	H^2b%	GA	GAM%
1	Days to 50% Flowering	9.93	43.57	6.36	6.29	5.88	2.25	87.3	12.7	11.31
2	Days to 75% Maturity	56.23	45.62	10.61	4.26	3.84	1.85	81.1	12.53	7.12
3	Plant Height	88.08	50.69	37.39	6.9	5.23	4.5	57.5	11.13	8.18
4	Primary Branch	0.93	0.7	0.24	13.35	11.53	6.73	74.6	1.48	20.52
5	Secondary Branch	1.12	0.07	1.04	4.92	1.27	4.75	6.7	0.15	0.68
6	Biological yield/Plant (g)	731.59	622.59	109	23.77	21.93	9.18	85.1	47.42	41.67
7	Pod length	0.08	0.01	0.09	6.19	2.35	6.62	14.4	0.08	1.84
8	Seeds per pod	0.04	0.02	0.03	6.74	4.38	5.13	42.1	0.18	5.85
9	Total pods per plant	81.34	66.3	15.05	19.12	17.26	8.22	81.5	15.14	32.1
10	Seed Index	1.55	1.36	0.19	13.36	12.51	4.69	87.7	2.25	24.14
11	Seed yield per plant	38.29	30.46	7.82	28.33	25.27	12.8	79.6	10.14	46.43
12	Harvest Index	12.66	11.74	0.92	10.11	9.74	2.72	92.8	6.8	19.32

Correlation analysis

Therefore, correlation coefficients were calculated for all combinations of the characters under study at the phenotypic and genotypic levels.

The study reveals that seed yield per plant is significantly correlated with various traits such as days to maturity (0.360), pods per plant (0.595**), harvest index (0.702**), biological yield per plant (0.876), primary branches per plant (0.419**), and secondary branches per plant (0.315). These correlations are consistent with previous studies by Kandarkar *et al.* (2020) [9] and Saroj *et al.* (2013) [5]. Plant height also shows significant positive correlations with total pods per plant (0.588**) and secondary branches per plant (0.440**), while non-significant positive correlations with other traits. The number of primary branches per plant also shows significant positive correlations with Pods per plant

(0.4114**), Secondary branch per plant (0.567**) seeds per plant (0.727**). Secondary branches per plant show significant positive correlations with harvest index, biological yield per plant, and seed yield per plant, but a non-significant negative correlation with pod length. Biological yield per plant has a highly significant positive correlation with seed yield per plant, indicating its importance in breeding programs aimed at improving yield and other desirable characteristics. our finding is in close agreement with the result of Chisa *et al*. (2021) [16]. These correlations provide valuable insights into the interrelationships among various traits in chickpea varieties, aiding in breeding programs aimed at improving yield and other desirable characteristics.

Genetic coefficient of variation for all major direct yield contributing traits shown positive and significant correlation. Primary branch per plants is positively correlated with plant height (0.478**), and Days to maturity (0.334*). Pods per plant is also positively correlated with plant height (cm) (0.560**), and Primary branch (0.673**). Secondary branch per plant is significantly correlated with Days to 50% flowering (0.917**), days to maturity (0.562**), Plant height (0.351*), Primary branch per plant (0.783**) and Pods per plant (0.877**). Our result is in close agreement with the finding of Saroj *et al*. (2013) [5]. thus selection of genotypes based on this traits will be rewarding because these traits are directly correlated with major yield attributing traits.

Characters	DFF	DTM	PH	PBPP	PPP	SPP	SI	SBPP	HI	PL	SYPP	BYPP
DFF	1.00	0.514**	0.143	-0.237	-0.174	0.077	0.455**	0.252*	0.0331	-0.105	0.519**	0.1479
DTM	0.075	1.00	0.0725	-0.1422	-0.1136	0.0905**	0.1618	0.376*	0.261*	0.0084	0.418**	0.361*
PH	0.173	0.116	1.00	0.440**	0.1967	0.588**	0.022	0.283	0.1444	0.0668	0.1853	0.1677
PBPP	0.035	0.334*	0.478**	1.00	0.539**	0.414**	-0.259	0.567**	0.2057	0.0263	0.727**	0.519**
PPP	0.0021	0.121	0.560**	0.673**	1.00	0.236	-0.1227	0.091	0.1127	0.1722	0.223	0.266*
SPP	0.123	0.003	0.003	0.043	0.021	1.00	-0.075	0.357*	0.557**	0.097	0.595**	0.595**
SI	0.511*	-0.325	0.024	0.166	0.009	0.103	1.00	0.321*	0.252	-0.0055	0.337**	0.315*
SBPP	0.917**	-0.562**	0.351*	0.783**	0.877**	0.052	0.133	1.00	0.219	0.005	0.255*	0.349*
HI	0.672**	-0.455	0.435	0.555**	0.589**	0.376*	0.231	0.466**	1.00	0.1642	0.688**	0.702**
PL	0.421**	0.023	0.008	0.169	0.003	0.033	0.008	0.256*	0.091	1.00	0.1646	0.1486
SYPP	0.011	0.042	0.004	0.056	0.053	0.699**	0.210	0.045	0.642**	0.583**	1.00	0.876**
BYPP	0.461**	0.0117	0.563	0.492**	0.004	0.214	0.006	0.671	0.111	0.219	0.031	1.00

*Significant at 5% level; **Significant at 1% level

Conclusion

It is to be confessed that, broad range of variability was present between the genotypes studied for the different quantitative characters. High heritability coupled with high genetic advance percent mean was observed for biological yield per plant (g) and seed yield per plant (g). The higher estimates of heritability coupled with high genetic advance as percent of mean shows additive gene action and make in suitable for direct selection. On the basis of correlation and path analysis, seed yield per plant could be improved through simultaneously selection of seeds per pod, harvest index, primary branches per plant, plant height, pod length, total pods per plant, seed index, secondary branches per plant and days to 75% maturity. It is desirable to give more magnitude of weightage to these characters during selection programme. The genotypes UPAS 120 (CH) followed by MANAK and PAU 881 were observed as best performers in the genotypes studied. These had the highest seed yield per plant and also maximum yield attributing characters. The genotype PAU 881 had maximum seed index, MANAK had highest plant height with maximum total pods per plant and seed yield. All above genotypes are applicable to be used as promising genetic material in future breeding programmes.

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