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Morphological Characterization and Genetic Variability Study on Early Maturing Pigeonpea [*Cajanus cajan* (L.) Millsp.] Lines

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ABSTRACT

Background: Pigeonpea [*Cajanus cajan* (L.) Millsp. (2n=22)] is the second most important pulse crop in India after chickpea. In the present study, two-hundred early maturing (less than 140 days) pigeonpea germplasm accessions were evaluated for their genetic parameters based on morphological characters and were subsequently characterized as per the DUS descriptors for pigeonpea. Genetic variability of the population was assessed through genetic parameters and character association analysis.

Methods: The plant material comprised of 193 pigeonpea genotypes along with seven checks and the experiment was conducted during *kharif* 2020-21 and 2021-22 in augmented design.

Result: The twenty-one DUS characters were recorded at different crop growth stages. Out of those, the characters for plant height, branching pattern, plant growth habit, time to 50% flowering, colour of base of petal, pattern of streaks on petal, pod colour, pod number of seeds, seed colour, seed colour pattern, seed shape and seed size exhibited variation across the accessions. The analysis of variance was executed for the eight different biometrical characters. The highest GCV and PCV value was obtained for the character seed yield per plant (19.91 and 21.4 respectively). Almost all the yield attributing characters except plant height showed high heritability indicating that selection for the characters for crop improvement would be highly effective. Highest genetic advance was observed for the trait pods per plant (42.34) and highest genetic advance as percent of mean was obtained for seed yield per plant (38.24). Correlation analysis among the characters for yield revealed that high positive correlation existed between seed yield per plant with pods per plant (0.580).

Key words: DUS characters, Early maturing, Genetic variability, Pigeonpea.

INTRODUCTION

Cajanus cajan (L.) Millsp., also known as pigeonpea, *Arhar*, redgram or *Tur* is an often cross pollinated crop belonging to the family fabaceae. The crop is significantly propagated through seeds and is cultivated majorly in the tropical semi-arid regions of the world. In India the crop stands second to chickpea in terms of importance. It is mostly cultivated in the states of Karnataka, Maharashtra andhra Pradesh, Madhya Pradesh, Punjab, Rajasthan and Haryana. Being rich in seed protein (21-24%) it is consumed as a *dhal* or split peas (Chaudhary *et al*., 2021). As of 2020-21 pigeonpea is cultivated in 35.21 mha area with a production of 1005 kg/ha and productivity of 35.87 mt (INDIASTAT, 2022). Despite being drought tolerant and having high seed protein content the cultivation of pigeonpea is fraught with various biotic and abiotic stresses (Khalekar *et al*., 2014). India being the primary centre of origin of pigeonpea there is a potential scope of variation existing among the Indian germplasm lines. Such prospective variability of the population is lucrative to the plant breeders for targeted crop improvement, improving quality traits and achieving productive sustainability. To achieve such utility of the germplasms proper cataloguing and characterization of the accessions is necessary. To this aspect clear guidelines for distinctness (D), uniformity (U) and stability (S) laid down by plant variety protection under general agreement on trade and tariff (GATT) have been very useful (Sahu *et al*., 2018). Hence considering the current production statistics of pigeonpea and with the ultimate objective of sustainable crop production by the farmers, such categorization and characterization of germplasm accessions would enable accurate identification of a particular line based on the clearly defined stable phenotypic characters needed for successful variety development programmes. The inherent genetic diversity of the population is further clarified from such evaluations. Genetic diversity is fundamental to crop improvement. Study of genetic parameters and their relative correlation illuminates superior traits and henceforth effective selections as well. Hence with the objective of characterizing new pigeonpea accession lines and understanding their genetic variability the present investigation classifies 200 hundred pigeonpea germplasm lines as per the DUS descriptors and

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also estimates the genetic parameters along with correlation among the yield and yield attributing characters.

MATERIALS AND METHODS

The trial was conducted during *Kharif* 2020-21 and 2021-22 at the dryland crop research field of Pulses Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. The experimental materials consisted of 193 germplasm lines along with seven check varieties sown in augmented block design (ABD) (Suppl. Table 1). The genotypes were sown in a single row of 3 m length with a spacing of 45 × 15 cm (Fig 1). The observations recorded were days to flowering, days to maturity, number of branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight, plant height and seed yield per plant. Eventually the accessions were then subsequently characterized as per the DUS descriptors for pigeonpea. For each character observations were recorded from five randomly selected plants for each genotype. The mean data obtained for the yield and yield attributing traits was then subjected to analysis of variance as laid down by Mahalanobis (1936). Estimation of genetic parameters,

Supplementary Table 1: List of the genotypes under study.

Sr. no.	Accessions	Sr. no.	Accessions	Sr. no.	Accessions	Sr. no.	Accessions	Sr. no.	Accessions
1	H 88-41	41	AH 09-04	81	AL 1600	121	IPA 15-03	161	AL 2256
2	H 90-04	42	AH 09-06	82	AL 1604	122	IPA 15-07	162	AL 2250
3	H 90-13	43	AH 09-31	83	AL 1614	123	AH 16-36	163	AL 1465
4	H 91-10	44	AH 09-35	84	AL 1685	124	AH 17-28	164	AL 2025
5	H 91-12-01	45	AH 09-36	85	AL 2028	125	RKPV 704	165	AL 2048
6	H 91-23	46	AH 09-38	86	KAE-17	126	AH 17-27	166	AL 2205
7	H 93-08	47	AH 09-44	87	ICPL-87	127	AL 292	167	AL 1922
8	H 93-13	48	AH 09-45	88	ICPL-8500	128	AL 1765	168	AL 2088
9	H 93-43	49	AH 09-46	89	ICPL-9102	129	AL 4554	169	AL 2019
10	H 93-24	50	AH 10-08	90	ICPL-20388	130	AL 1380	170	AL 2101
11	H 99-1	51	AH 10-13	91	ICPL-28323	131	AL 1758	171	AL 2096
12	H 00-8	52	AH 10-30	92	ICPL-85012	132	AL 1449	172	P-935
13	H 00-15	53	AH 10-39	93	ICPL-88039	133	AL 1594	173	P-2679
14	H 00-28	54	AH 14-01	94	ICPL-91007	134	AL 2102	174	P-3123
15	H 00-38	55	AL-13	95	ICPL-91008	135	AL 1786	175	Pant A-1
16	H 93-22	56	AL 265	96	PUSA 204-1	136	AL 1800	176	P-74
17	H 01-3	57	AL 283	97	PUSA 855-2	137	AL 1403	177	TT-15-15
18	H 01-8	58	AL 311-6	98	PUSA 945	138	AL 1490	178	P 4836
19	H 01-33	59	AL 345-22	99	PUSA 2008-2	139	AL 1856	179	UC 14-63
20	H 01-37	60	AL 360-5	100	PUSA 2015-2	140	AL 307	180	Pant A-2
21	H 02-20	61	AL 442	101	PUSA 7601	141	AL 1853	181	P 376-1
22	H 02-65	62	AL 601	102	D-3	142	AL 1761	182	P-3497
23	H 03-29	63	AL 1313	103	CRG 1407	143	D-5	183	ICPL 11255
24	H 03-41	64	AL 1313-2-2	104	PA 414	144	AL 2207	184	AL 882
25	H 04-20	65	AL 1322-6-5-2	105	PA 421	145	AL 1476	185	AH 17-13
26	H 04-24	66	AL 1323-1-2	106	SJP 102	146	AL 1392	186	AH 16-38
27	PA-477	67	AL 1356-04	107	CRG 2012-20	147	AL 1599	187	AH 16-40
28	H 05-10	68	AL 1366-1	108	VRG 13-001	148	AL 1736	188	AH 16-42
29	H 05-11	69	AL 1389	109	PADT-16 (C)	149	AL 1491	189	AH 16-43
30	H 05-37	70	AL 1401	110	PARAS (C)	150	AL 2170	190	AH 16-44
31	H 05-70	71	AL 1404	111	MANAK (C)	151	AL 1459	191	ICPL 92034
32	H 08-148	72	AL 1416	112	PAU 881 (C)	152	AL 2087	192	ICPL 90036
33	H 09-47	73	AL 1417	113	PUSA 992 (C)	153	AL 1747	193	AL 344-1
34	AH 05-67	74	AL 1419	114	UPAS 120 (C)	154	AL 1508	194	H 04-26
35	AH 06-01	75	AL 1425	115	VLA-1 (C)	155	AL 1781	195	AL 345
36	AH 06-03	76	AL 1444	116	PA 536	156	AL 1736	196	HDM 04-01
37	AH 06-07	77	AL 1452	117	RKPV 705	157	AL 1466	197	AH 17-28
38	AH 16-02	78	AL 1484	118	AH 09-08	158	AL 2095	198	H 00-37
39	AH 06-10	79	AL 1502	119	PA 554	159	AL 2255	199	H 01-11
40	AH 07-07	80	AL 1590	120	IPA 15-06	160	AL 2184	200	AH 10-29

genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance at 5% selection intensity and correlation coefficients were done as per Singh and Chaudhary (1979). Data analysis were carried out in R studio software v. 4.2.2.

RESULTS AND DISCUSSION

DUS characterization

The two hundred pigeonpea germplasm lines were characterized as per twenty-one different morphological DUS descriptors (Table 1). The twenty-one different DUS characters were catalogued at different crop growth stages. Across the accessions twelve out of twenty-one descriptors exhibited variations *viz*., the characters for time to 50% flowering, plant height, branching pattern, plant growth habit, colour of base of petal, pattern of streaks on petal, pod colour, pod number of seeds, pod size, seed colour, seed colour pattern, seed shape and seed size. The trait time of 50% flowering exhibited two states early flowering (61-90 days) and medium flowering (91-130 days) having 194 and 6 genotypes respectively. Similarly, the trait plant branching pattern showed 197 genotypes having semi-spreading (30°-60°) branching and three genotypes having erect (<30°) branching pattern (Fig 2). Two different states for plant height were observed 199 genotypes were tall (>150 cm) and one genotype was medium (100-150 cm) in plant height (Fig 3). The trait plant growth habit exhibited two different states, 194 genotypes displayed indeterminate growth habit whereas 6 genotypes showed determinate growth habit (Fig 4). Flower: Colour of base of petal (Standard) displayed three types of variations, 96 genotypes showed light yellow flowering, 102 showed yellow and only two genotypes showed orange yellow flower petal colour (Fig 5). Maximum variation was observed for the trait flower: pattern of streaks on petal (standard) wherein 7 genotypes showed absence of streaks, 171 genotypes displayed sparse streaks, 21 genotypes displayed medium streak patterns and only one genotype showed dense streak patterns (Fig 6). Among the pod characters, the trait for pod colour had two states one genotype with green pods and rest 199 genotypes displaying green with purple streaks (Fig 7). Pod size exhibited two kinds of variations, 176 genotypes had pod length of 4-5 cm and 24 genotypes showed more than 5cm pod length (Fig 8). Pod; number of seeds showed two states of variation out of three, 194 genotypes had 4 seeds and 6 genotypes had 3 seeds (Fig 9). Among the seed characters two genotypes displayed cream seed colour, 191 displayed brown and seven genotypes showed dark brown coloration (Fig 10). 195 genotypes exhibited uniform colour pattern whereas five genotypes showed mottled seed colour pattern (Fig 11). Similarly, 188 genotypes showed oval seed shape whereas five and seven genotypes were showing globular and elongate seed shape (Fig 12). With respect to seed size: 100 seed weight: 31 genotypes were small (<7 g), 159 were medium (7-9 g) and 10 genotypes were large (>9-11 g). Chaudhary *et al*. (2021) reported DUS descriptor studies on 200 germplasm lines wherein variations in pattern of streaks on standard petal, time of flowering, pod size and seed size were reported. Ranjani and Jayamani (2021) conducted DUS characterization studies on 60 genotypes and variations were reported in plant height, pattern of streaks on standard petal, seed shape, seed colour and seed size. Padma priya *et al*. (2022) also reported DUS evaluation of 55 early maturing pigeonpea genotypes and variations were observed in flower colour, pattern of streaks on petals, pod colour, seed colour, seed shape and seed size.

Fig 1: Augmented block design of the experiment.

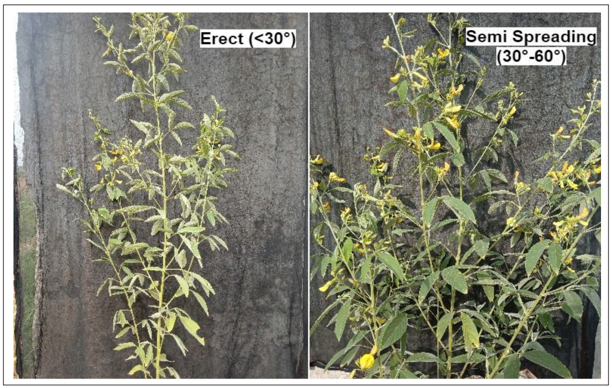

Fig 2: DUS trait representing variation in plant branching pattern.

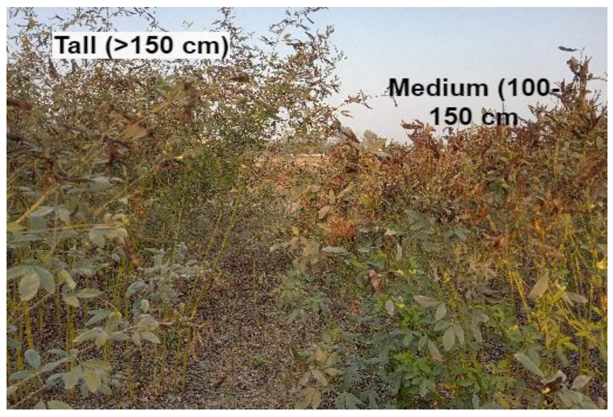

Fig 3: DUS trait representing variation in plant height.

Fig 4: DUS trait representing plant: growth habit.

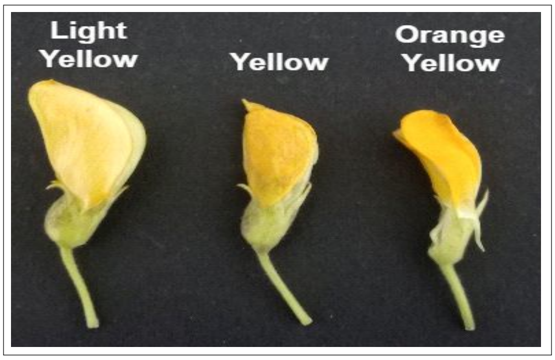

Fig 5: DUS trait representing variation in flower colour of base of petal.

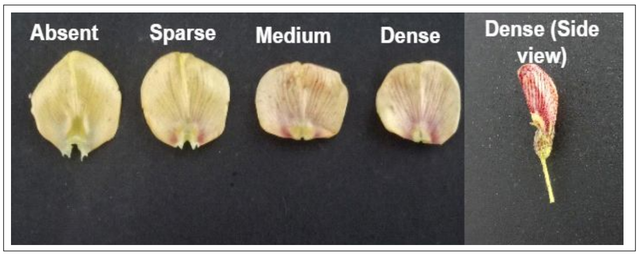

Fig 6: DUS trait representing variation in flower pattern of streaks on petal.

Fig 7: DUS trait representing variation in pod colour.

Fig 8: DUS trait representing variation in pod size.

Fig 9: DUS trait representing pod: Number of seeds.

Fig 10: DUS trait representing seed colour.

Fig 11: DUS trait representing seed colour pattern.

Table 1: Characterization of 200 pigeonpea genotypes based on DUS characters.

Morphological characters	States	Code	No. of genotypes	Relative frequency	Stage of observation
Plant: Anthocyanin colouration of hypocotyl	Absent	1	0	0	Seedling
	Present	9	200	100	
Plant: Branching pattern	Erect (<30°)Semi-	3	3	1.07	First flowering
	spreading (30°-60°)	5	197	98.93	
	Spreading (>60°)	7	0	0	
Time of flowering (50% of the plants with at least one open flower)	Very early (<60 days)	1	0	0	
	Early (61-90 days)	3	194	97	First flowering
	Medium (91-130 days)	5	6	3	
	Late (131-160 days)	7	0	0	
	Very late (>160 days)	9	0	0	
Plant: Growth habit	Determinate	1	6	3	50% flowering
	Indeterminate	3	194	97	
Stem: Colour	Green	1	200	100	50% flowering
	Purple	2	0	0	
Leaf: Shape	Oblong	1	200	100	50% flowering
	Obovate	3	0	0	
	Narrowly	5	0	0	
Leaf: Pubescence on lower surface of leaf	Absent	1	200	100	50% flowering
	Present	9	0	0	
Flower: Colour of base of petal (Standard)	Light yellow	1	96	48	50% flowering
	Yellow	2	102	51	
	Orange yellow	3	2	1	
	Purple	4	0	0	
	Red	5	0	0	
Flower: Pattern of streaks on petal (standard)	Absent	1	7	3.5	50% flowering
	Sparse	3	171	85.5	
	Medium	5	21	10.5	
	Dense	7	1	0.5	
	Mosaic	9	0	0	
Pod: Colour	Green	1	1	0.36	Premature pod dough stage
	Green with brown streaks	2	0	0	
	Green with purple streaks	3	199	99.64	
	Purple	4	0	0	
	Dark purple	5	0	0	
Pod: Pubescence	Absent	1	0	0	Fully developed green pods
	Present	9	200	100	
Pod: Waxiness	Absent	1	200	100	Premature pods dough stage
	Present	9	0	0	
Pod: Surface stickiness	Absent	1	200	100	
	Present	9	0	0	Premature pods
Pod: Constriction	Slight	3	0	0	Mature pods
	Prominent	7	200	100	Mature pods
Pod: Size (cm)	<4 cm	3	0	0	
	4-5 cm	5	176	88	
	>5 cm	7	24	12	
Pod: No. of seeds	2	3	0	0	Mature pods
	3	5	6	3	
	4	7	194	97	

Table 1: Continue...

Table 1: Continue...

Plant: Height	Short (<100 cm)	3	0	0	Harvest maturity
	Medium (100-150 cm)	5	1	0.5	
	Tall (>150 cm)	7	199	99.5	
Seed: Colour	Cream	1	2	0.72	Ripe seeds
	Brown	2	191	96.79	
	Dark brown	3	7	2.49	
	Grey	4	0	0	
	Purple	5	0	0	
Seed: Colour pattern	Uniform	1	195	97.5	Dry seeds
	Mottled	2	5	2.5	
Seed: Shape	Oval	1	188	94	Dry seeds
	Globular	2	5	2.5	
	Elongate	3	7	3.5	
Seed: Size (100 seed weight)	Small (<7 g)	3	31	15.5	Dry seeds
	Medium (7-9 g)	5	159	79.5	
	Large (>9-11 g)	7	10	5	
	Very large(>11 g)	9	0	0	

Table 2: Mean performance and analysis of variance (ANOVA) for eight quantitative characters of pigeonpea.

		Mean sum of squares							
Source of variation	DF	Days to flowering	Days to maturity	Branches per plant	Plant height	Pods/ plant	Seeds/ pod	100 seed weight	Seed yield/ plant
Block (Ignoring genotypes)	10	258.4**	72.26**	3.63**	908.83**	1444.25**	0.04**	1.18**	49.71**
Genotypes (Eliminating blocks)	199	101.46**	58.24**	2.06**	397.06**	974.24**	0.03**	0.98**	27.72**
Check	6	286.81**	177.11**	4.66**	5493.21**	12090.02**	0.01	10.09**	117.34**
Checks + genotypes vs. genotypes	193	95.7**	54.55**	1.98**	238.63	628.67**	0.03**	0.7**	24.93**
Error	60	4.23	10.37	0.34	168.24	139.92	0.01	0.08	3.51
Contrast analysis									
Among control	6	286.81**	177.11**	4.66**	5493.21**	12090.02**	0.01	10.09**	17.34**
Among genotypes	193	99.49**	45.14**	1.81**	282.72*	671.85**	0.03**	0.74**	26.27**
Control vs genotype	1	1863.25**	2393.21**	56.5**	584.61	5224.71**	0.02	4.26**	34.09**

**Significant at 1% level of probability.

Fig 12: DUS trait representing seed shape.

ANOVA, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance

The analysis of variance was executed for the eight different biometrical characters. Significant variability was apparent across the accessions under study for all the eight biometrical phenological and morphological traits except among the checks for the character seeds per pod (SPP) as justified from the p values (<0.01) (Table 2). From the ANOVA table, it is clear that the environmental variance for all the characters is comparatively less. Such results justify that the characters are completely under genetic control with least environmental influence. Hence the uniformity and stability of the traits based on the DUS descriptor defined characterization is justified. Reports of low environmental variances were also found in the investigations of Saroj *et al*. (2013), Bishnoi *et al*. (2019). For the estimation of role and extent of genetic variation existing in the test material the study of genotypic (GCV) and phenotypic coefficient of variations (PCV) are important (Sharma *et al*. 2022). As per the findings of Deshmukh *et al*. (1986), PCV and GCV values less than 10% are considered as low, values between 10 and 20% to be medium and the values greater than 20% are regarded as high. Hence from the Table 3 it could be inferred that the highest GCV and PCV value was obtained for seed yield per plant (19.91 and 21.31 respectively) and the characters days to flowering (10.86 and 11.11), branches per plant (BPP) (16.67 and 18.39), Pods per plant (PPP) (16.09 and 18.08) and 100 seed weight (HSW) (10.49 and 11.07) had medium GCV and PCV values which connotative of fruitful genetic improvement through selection for these traits. On the contrary the characters days to maturity (DM) (4.33 and 4.93), plant height (PH) (4.68 and 7.35) and seeds per pod (SPP) (3.31 and 4.38) exhibited low GCV and PCV values. Shukla *et al*. (2022) also mentioned low GCV and PCV values for DM (3.71 and 3.82% respectively). All the yield attributing characters showed high to medium heritability indicating that selection for the characters for crop improvement would be highly effective. The character DF exhibited highest broad sense heritability (h^2_{BS}) (95.74%). Similarly, the characters HSW (89.76), SYPP (86.63), PPP (79.17) and DM (77.02) also showed high heritability. High heritability coupled with high genetic advance is a requisite for effective crop improvement. Highest genetic advance (GA) was observed for the trait PPP (42.34) followed by DF (19.7) and PH (14.05). This justifies the early flowering character of the population which could be selected for breeding for earliness in pigeonpea. Similarly, high heritability values for HSW, SYPP and PPP are suggestive that effective selections could be exercised for bold seeded character along with high yield. Highest genetic advance as percent of mean (GAM) was seen for SYPP (38.24). The characters DF, BPP, PPP and HSW also displayed high GAM (Table 3). This is implicative of underlying additive gene action and hence direct selection for these traits would be highly beneficial for pigeonpea improvement. Congruently, high h^2_{BS} coupled with high GA for DF, DM, PPP and SYPP were found in the reports of Mourya *et al*. (2022). Synonymous outcomes were mentioned in the published reports of Sharma *et al*. (2021), Bhagat *et al*. (2022). It was noted that the characters PH and SPP have low GAM (6.14 and 5.16 respectively) which implies that despite having high heritability the mean improvement of traits through selection would be less and hence careful trait selection has to be done for breeding objectives.

Correlation analysis

Correlation between characters is a consequence of underlying gene actions which manifest itself in form of phenotypic alterations in the plants. The direction and the extent of character association with yield are explained in the correlation studies. Useful correlation between economic characters could be exploited and such correlation of different characters henceforth enables plant breeders in selection of superior genotypes (Sharma *et al*. 2022). The present investigation reveals high positive correlation between SYPP with PPP (0.580) which implies that higher seed yield could be obtained through direct selection for plants having high pod numbers (Table 4). Congruent results

Table 3: Genetic variation in pigeonpea for the different quantitative traits.

Traits	Heritability (Broad sense) h^2_{BS}	GCV (%)	PCV (%)	Genetic advance 5%	Genetic advance per cent of mean
DF	95.74	10.86	11.1	19.7	21.92
DM	77.02	4.33	4.93	10.68	7.83
BPP	81.22	16.67	18.5	2.25	31
PH	40.49	4.68	7.35	14.05	6.14
PPP	79.17	16.09	18.08	42.34	29.53
SPP	57.11	3.31	4.38	0.21	5.16
HSW	89.76	10.49	11.07	1.59	20.5
SYPP	86.63	19.91	21.4	9.16	38.24

BPP: Branches per plant; DF: Days to flowering; DM: Days to maturity; GCV: Genotypic coefficient of variance; PCV: Phenotypic coefficient of variance; PH: Plant height; PPP: Pods per plant; HSW: 100 seed weight; SPP: Seeds per pod; SYPP: Seed yield per plant.

Table 4: Estimates for correlation coefficients for different yield contributing characters in genotypes.

Traits	DF	DM	BPP	PH	PPP	SPP	HSW
DM	0.600**						
BPP	-0.011^{NS}	0.044^{NS}					
PH	0.082^{NS}	0.133^{NS}	0.157*				
PPP	0.031^{NS}	-0.014^{NS}	0.143*	0.092^{NS}			
SPP	-0.139*	-0.103^{NS}	0.034^{NS}	0.018^{NS}	-0.096^{NS}		
HSW	-0.236**	-0.122^{NS}	0.106^{NS}	0.018^{NS}	-0.240**	0.204**	
SYPP	-0.105^{NS}	-0.101^{NS}	0.149*	0.185**	0.580**	0.138^{NS}	0.044^{NS}

**Significant at 1% level of Probability, *Significant at 5% level of Probability.

BPP: Branches per plant; DF: Days to flowering; DM: Days to maturity; NS: Non significant; PH: Plant heigh; PPP: Pods per plant; HSW: 100 seed weight; SPP: Seeds per pod; SYPP: Seed yield per plant.

were reported by Singh *et al*. (2019), Sharma *et al*. (2021), Chaudhary *et al*. (2022). Similarly, fair positive association was found for BPP (0.149). In concurrence to the reports of Chauhan *et al*. (2021) in the current study the character for PH also showed high correlation with seed yield (0.185) which is indicative that tall plant character contributes significantly towards yield enhancement. The character DF was also found to be positively correlated with DM (0.600) justifying the early maturing character of the population. Significantly negative correlations were found between HSW with DF and PPP which are however contrary to the findings of Vanniarajan *et al*. (2021) wherein positive associations between HSW with PH and DF were reported. Probable reason for such could be that small seeded trait contributes towards early flowering and higher photosynthate partioning towards pods so as to compensate for plant biomass output. Hence for future crop improvement investigations this point should be kept in mind.

CONCLUSION

Identification and selection of suitable germplasms is an important activity in plant breeding for crop improvement. The current investigation characterizes 200 pigeonpea accessions as per DUS descriptors and further evaluates the genetic variability of the population through genetic parameters along with correlation among yield and yield attributing traits. Twelve out of twenty-one DUS descriptors exhibited variation. In terms of genetic variability, significant but stable variation exists in the population as evident from the analysis of variance and other genetic parameters. High to medium heritability for all the traits was observed indicating the stability of traits and henceforth effective trait selection benefits. The highest GCV and PCV value was obtained for pods per plant whereas the characters days to flowering, branches per plant, pods per plant and 100 seed weight displayed medium GCV and PCV values. Highest genetic advance was observed for the trait pods per plant and highest genetic advance as percent of mean was obtained for seed yield per plant. Thus an underlying additive gene action is evident and fruitful crop improvement through trait selections could be sustained. Correlation analysis among the characters for yield revealed significant positive correlation between seed yield per plant with pods per plant and plant height. Hence it could be concluded that the present germplasm comprising of extra early and high yielding accessions is stable, uniform and has sufficient genetic variability which could be utilized in future breeding programmes for pigeonpea improvement.

Conflict of interest: None.

REFERENCES

Bhagat, P., Giri, S.K., Kumar, K., Tiwari, J.K. and Sinha, S.K. (2022). Genetic variability and association studies for seed yield and related trait in pigeonpea [*Cajanus cajan* (L.) Millsp.]. The Pharma Innovation Journal. 11: 2963-2966.

Bishnoi, S.K., Rathi, R.S., Choudhary, S.B., Malav, P.K. and Ahlawat, S.P. (2019). Phenotypic Characterization of Pigeonpea (*Cajanus cajan*) Germplasm Collected from Jharkhand, India. Indian Journal of Plant Genetic Resources. 32: 354-359.

Chaudhary, L., Sharma, R., Kumar, M. and Kumar, S. (2021). Morphological characterization and assessment of genetic diversity in pigeonpea [*Cajanus cajan* (L.) Millsp.] germplasm. Electronic Journal of Plant Breeding. 12: 707-711.

Chaudhary, L., Yadav, R., Kumar, S. and Devi, U. (2022). Studies on correlation and path analysis for yield and yield attributing traits in extra early genotypes of Pigeonpea [*Cajanus Cajan* (L.) Millsp.]. The Pharma Innovation Journal. 11: 4618-4621.

Chauhan, C., Verma, S.K., Panwar, R.K., Gaur, A., Gautam, A., Aparna, Harsh Deep, Yadav, H., Karn, A., Bisht, C. and Gupta, A. (2021). Character association and path coefficient analysis for yield and its contributing traits in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. Biological Forum-An International Journal. 13: 184-188.

Deshmukh, S.N., Basu, M.S. and Reddy, P.S. (1986). Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. Indian Journal of Agricultural Sciences. 56: 816-821.

INDIASTAT. (2022) https://www.indiastat.com/haryana (accessed on 16 June 2023).

Khalekar, G.D., Akhare, A.A., Gahukar, S.J., Singh, N.K. and Kumar, M. (2014) Identification of simple sequence repeat markers associated with wilt resistance in pigeonpea. Journal of Environmental Biology. 35: 955-960.

Mahalanobis, P.C. (1936). On the generalised distance in statistics. Proceedings of the National Institute of Science of India. 12: 49-56.

Mourya, A.K., Srivastava, A.K., Srivastava, A., Nikhil, Jaisawal, M., Kumar, A., Tiwari, U. and Saini, E. (2022). 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. International Journal of Plant and Soil Science. 34: 949-956.

Padma Priya, M., Gnanamalar, R.P., Karthiba, L. and Hemavathy, A.T. (2022). Morphological characterization of early duration pigeonpea genotypes. Electronic Journal of Plant Breeding. 13: 679-689.

Ranjani, M.S. and Jayamani, P. (2021). Characterization of pigeonpea genotypes based on DUS traits. International Journal of Plant and Soil Science. 33: 289-297.

Sahu, J.K., Sinha, S.K., Ekka, R.E. and Tiwari, J.K. (2018). Morphological characterization of germplasm of pigeonpea [*Cajanus cajan* (L.) millsp.]. Multilogic in Science. 8: 181-183.

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. The Bioscan. 8: 941-944.

Sharma, P., Singh, I., Khosla, G., Singh, G., Singh, S., Dhaliwal, S. K. and Singh, S. (2021). Variability and association studies for yield and yield related traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. Legume Research-An International Journal. 1: 6. DOI: 10.18805/LR-4374.

Sharma, R., Chaudhary, L., Kumar, M. and Panwar, N. (2022). Analysis of genetic parameters and trait relationship for seed yield and its attributing components in lentil (*Lens culinaris* Medik.). Legume Research-An International Journal. 45: 1344-1350. DOI: 10.18805/LR-4969.

Shukla, S., Mishra, S.P. and Mehandi, S. (2022). Exploiting the natural variation and inter-relationship among medium maturity pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes. Electronic Journal of Plant Breeding. 13: 717-723.

Singh, G., Singh, I., Sharma, P., Gupta, M. and Singh, S. (2019). Devising selection criteria based on variability and association studies in segregating populations derived from an interspecific cross between *Cajanus scarabaeoides* × *C. cajan*. Legume Research. 6: 615-620. DOI: 10.18805/LR-4137.

Singh, R.K. and Chaudhary, B.D. (1979). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, Ludhiana, New Delhi, India. 318.

Vanniarajan, C., Magudeeswari, P., Gowthami, R., Indhu, S.M., Ramya, K.R. and Monisha, K. (2021). Assessment of genetic variability and traits association in pigeonpea [*Cajanus cajan* (L.) Millsp.] Germplasm. Legume Research-An International Journal. 1: 8. DOI: 10.18805/LR-4442.