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Early Maturing Pigeon Pea (*Cajanus cajan* L.) Genotypes' Genetic Progress, Heritability, and Variability Estimation

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ABSTRACT: The experiment was conducted to examine the twenty-one genotypes' morphological variability for yield and earliness. The genotypes comprised nineteen from ICRISAT, Hyderabad, and two from Biswanath Chariali College of Agriculture, Assam Agricultural University. A randomized block design (RBD) was used with three replications, conducted at ICR Farm, Assam Agricultural University, during the 2018-19 Kharif season. Fourteen quantitative attributes or characteristics were monitored and recorded. Significant heterogeneity was seen in each attribute within the evaluation. High PCV values of the studied traits suggest the role of the environment. The hundred seed weight was found to have the highest phenotypic and genotypic coefficients of variation (PCV and GCV), followed by pods per plant, clusters per plant, harvest index, branches per plant, and seed yield per plant. Days to 50% flowering exhibited strong heritability with moderate genetic advance, indicating preponderance additive gene effects. Whilst seeds per pod and branches per plant recorded the lowest heritability coupled with a low genetic advance which suggests the presence of non-additive gene effects. ICP 15011, ICP 14927, ICP 15312, ICP 11610, ICP 11599, ICP 10920, and ICP 11639 are a few early maturing genotypes that demonstrated good performance for most of the significant quantitative attributes, as per the mean genotype performance for yield-related attributing traits. In Assam, most of the varieties are long duration and, therefore winter crops cannot be cultivated as late sowing as it results in poor yield. There is a need to breed for lines with reduced vegetative growth and higher per-day productivity. Hence in the present study, an effort has been made to study morphological variability for earliness and yield in twenty-one pigeon pea genotypes to identify diverse parents for a future breeding program suitable for the agroclimatic conditions of Assam.

Keywords: *Cajanus cajan* L., Variability, Early maturity, Heritability, Genetic advance, coefficients of variation, Quantitative traits.

INTRODUCTION

The pigeon pea is a tropical and subtropical crop adapted to the rainfed ecosystem in semi-arid areas and has a deep taproot, heat tolerance, and fast-growing habit (Mallikarjuna *et al.*, 2011). Its demand in India is significant because it can provide high-quality protein in the diet, especially to the vegetarian population (Bhattacharjee and Sharma 2013).

India is the largest producer of pigeon peas contributing 75–80 percent of world production. It is grown on a 4.80 MHA area in India, with a total production of 4.28 MT and 892 kg/ha productivity (Directorate of Economics & Statistics, 2022-23). In Assam, the area is 6 thousand ha, with a production of 4.9 thousand tons and a productivity of 833 kg/ha (Agricultural Statistics, 2018).

Both a food crop (dried peas, flour, or green vegetable peas), pigeon pea, often referred to as arhar, tur, or red grams, are also fodder or cover crop. It contains 20-21% protein (Sodavadiya *et al.*, 2009). The per capita availability of protein in the country is 48 g/day, while WHO suggests it should be 80 g/day, consequently the most serious problem of malnutrition exists among

people, where most people have a vegetarian diet and avoid animal protein (Prasad *et al.*, 2013). It is also a rich source of crude fiber, iron, sulfur, potassium, manganese, and water-soluble vitamins like thiamine, riboflavin, and niacin (Saxena *et al.*, 2010).

Traditional varieties of pigeon peas are long-duration types that take more than ten months to mature and cannot be fitted into multiple crop systems. Earlyduration pigeon pea is photo-insensitive with compact plant stature suitable for intercropping (Ranjani *et al.*, 2021). In Assam, intercropping can be done with green gram/black gram and sesame either in single or double rows or broadcasting between rows of pigeon peas to optimize yield (Boruah *et al.*, 2023). Pigeon pea as an intercrop with broom grass has been proven to be suitable for degraded areas under Jhum cultivation in the Karbi Anglong district where the farmers can earn a higher benefit-cost ratio than sole cropping (Bora, 2014).

Developing high-yielding, early maturing, and generally short-statured types that can adapt to better management and are effectively designed for newly established multiple and intercropping systems is

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crucial to increasing the economics of pigeon peas in rainfed and hilly areas. Due to their slow initial growth, most conventional varieties with medium to longer duration have prolonged vegetative growth phases (120-160 days) (Saxena, 2008). The development of early maturing varieties is inevitable, for which identification of suitable parents is necessary. The selection of parents for varietal improvement programs depends on the knowledge of available diversity. It is necessary to develop lines that have a slower vegetative growth rate and a higher day production. Pigeon peas must be bred into high-yielding, early maturing, and reasonably statured varieties consistent with the agroclimatic conditions of Assam to become a more lucrative crop. Hence, this study has made an effort to study morphological variability for earliness and yield in twenty-one pigeon pea genotypes to identify diverse parents for a future breeding program.

MATERIALS AND METHODS

The research experiment was conducted at ICR Farm, Assam Agricultural University, Jorhat, during Kharif 2018–19. Twenty-one genotypes constituted the material for the current research, of which two genotypes were obtained from BNCA, AAU, and nineteen genotypes were received from ICRISAT, Hyderabad. Three replications of the experiment were undertaken using the Randomized Block Design (RBD) method. The plot measured 16 m 11 m with a 60 cm \times 15 cm spacing. Five plants from each genotype from each of the three replications were randomly chosen to make thorough observations. The statistical significance and analysis of variance assessments were made by Panse and Sukhatme (1985). The coefficients of variation for genotypic and phenotypic traits were calculated using Singh and Chaudhary (1985). The formulas proposed by Hanson et al. (1956) were employed to measure heritability in a broad sense for several characteristics. Genetic progress was converted into a percentage using the formula given by Johnson et al. (1955). All statistical analyses were accomplished using the software Windostat v.9.2. Fourteen quantitative characters were recorded.

RESULTS AND DISCUSSION

A. Analysis of variance

Analyses of variance (Table 1) revealed that the genotypes differed significantly for the seed yield per plant and all other yield-attributing attributes, as also reported by Saroj et al. (2013); Mallesh et al. (2017); Pushpavalli et al. (2018); Satyanarayana et al. (2018). Additionally, a high magnitude of variations in the number of primary branches per plant, days to maturity, plant height, days to flowering, number of seeds per pod, and100-seeds weight in the pigeon pea genotypes (Supplementary Table 1) was in tune with Chattopadhyay & Dhiman (2006). The number of clusters per plant, 100-seed weight, and seed yield per plant had high coefficients of variation. According to (Vange and Moses 2009), these traits' coefficients of variation were also considerably high. In the pigeon pea, plant height is a critical trait. The cultivars grown Borah et al.. Biological Forum – An International Journal 15(5): 749-754(2023)

in Assam are typically very tall and late-maturing. Tall types are not suitable for intercropping and hybridization schemes, so dwarf varieties are desirable. The genotypes' variations in plant height were sufficient. ICP 15312 (61.1 cm) registered the minimum height, followed by Bahar (68.23 cm), ICP 14930 (76.47 cm), and ICP 11612 (79.3 cm). Significant genetic variation in plant height was in tune with Dahat et al. (2006); Chattopadhyay and Dhiman (2006); Techale et al. (2013). The current investigation aimed at evaluating the genotypes for earliness suitable for the agro-climatic conditions of Assam. Therefore, days to first and 50% flowering are important characteristics. ICP 14927 (79 days) was the earliest to first flowering, while ICP 14927 with 122 days took the maximum number of days to the first flowering. The character days to 50% flowering ranged from 90 days in ICP 14927 to 129 days in ICP 6973. Also, the character days to maturity ranged from 90 days in ICP 14927 to 134 days in ICP 6973.

Following the standards prescribed by Manyasa *et al.* (2009), the genotypes were categorized into three maturity durations: extra-early, early, and medium maturing (Table 3). Each category comprised seven genotypes. ICP 14927 (90 days) was the earliest maturing genotype, followed by ICP 15312 (103 days). ICP 6973 (134 days) was a late maturing genotype, followed by ICP 7645 (128 days).

Numerous variations in the traits linked to flowering and maturity have been documented by Dahat et al. (2006); Techale et al. (2013); Anuradha et al. (2013); Sharma et al. (2014); Ranjani et al. (2021); Simion et al. (2022). Another important aspect was to yield and yield-related characters. Crucial yield-related parameters include the number of branches per plant, pods per plant, clusters per plant, seeds per pod, pod length, and seed weight per hundred. While genotype ICP 11610 (13.00) produced the most pods per plant, genotype ICP 10920 (3) had the most branches per plant. The genotype ICP 6973 had the maximum hundred seed weight (40.42 g), implying that the seed was bold, and the genotype ICP 10920 had the lowest hundred seed weight (0.2 g) (5.53 g). Consumers prefer seeds in both small and large sizes. The maximum number of characteristic clusters per plant was found in ICP 10920 (five), while the seed count per pod ranged from a minimum of two in ICP 6973 to four in ICP 10920 and Local 1. For the harvest index, a notable level of variation is noted. The maximum harvest index was recorded in ICP 11639 (36.59%) whereas the minimum was in Local 1 (12.14). All the genotypes showed considerable genetic variation for desirable improvement which can be achieved through the selection of various component attributes. The findings are in agreement with those of Chattopadhyay and Dhiman (2006); Anuradha et al. (2013); Sharma et al. (2014); Rao and Rao (2021); Verma et al. (2018); Simion et al. (2022). Additionally, the largest variability in the number of pods per plant was noted by Saxena (2008); Verma et al. (2018). The genetic diversity of the sophisticated trait, such as seed yield per plant, which relies on various plant traits, aids 750

breeders in extending the genetic variability through breeding and selection. The highest and lowest seed yields per plant were evident in ICP 15011 (10.95) and ICP 6973 (4.00), respectively. Mallesh *et al.* (2017); Shedge *et al.* (2019); Simion *et al.* (2022) found considerable variations in the number of seed yields per plant.

Among the three maturity groups, the mean performances of the early maturing group were significantly superior to the other groups for all the fourteen quantitative traits (Table 2). High yield, short-statured plants along with early maturity of around 117 days and with considerable desirable traits were observed in this group comprising the genotypes namely ICP 7632 (113), ICP 11613 (116), ICP 14664 (116), ICP 14930 (118), ICP 11495 (118), ICP 15011 (118), ICP 8025 (119).

B. Estimation of genetic parameters

Estimations of phenotypic variances were discovered to be significantly higher than genotypic variance estimates (Table 4). For most traits considered, the overall phenotypic variation range was substantial, emphasizing the impact of the environment on the manifestation of these traits. Gautam et al. (2021); Ranjani et al. (2018) also observed high PCV values than GCV values. Plant height, days to the first flowering, 50% flowering, days to 90% flowering, days to pod initiation, days to maturity, one-hundred seeds weight, and harvest index showed high phenotypic variation, whilst pod length, seeds per pod, branches per plant, clusters per plant, and seed yield per plant showed a narrow range of variability. Anuradha et al. (2013); Sharma et al. (2014) both reported similar findings. High values of GCV were observed in the current study for one-hundred seeds weight, clusters per plant, pods per plant, harvest index, branches per plant, and seed yield per plant, however, a moderate GCV value was found for plant height. Saroj et al. (2013); Pushpavalli et al. (2018); Satyanarayana et al. (2018) also noted high GCV values for grain yield and pods per plant. This allows a broad range of options for selecting these attributes. High PCV values for onehundred seeds weight, pods per plant, clusters per plant, harvest index, branches per plant, and seed yield per plant suggested that there is ample heterogeneity to allow selection to enhance this attribute. A moderate estimate of PCV was apparent for plant height, seeds per pod, days to the first flowering, pod length, days to initial pod set, days to maturity, days to 50% flowering, and days to 90% flowering. For One-hundred seeds weight, pods per plant, clusters per plant, harvest index, branches per plant, and seed yield per plant, the phenotypic and genotypic coefficient of variation were high, implying that these parameters are crucial for pigeon pea improvement. High genotypic and phenotypic coefficients of variation for mung beans for pods per plant and seed yield per plot have been observed by (Rahim et al., 2010), while Anuradha et al. (2019); Techale et al. (2013) reported low values.

The GCV provides knowledge for assessing genetic variability and suggests if traits should be considered for selection. However, until the heritable proportion of variation is known, it is unable to provide a reliable sense of the magnitude of genetic gain to be attained by selection, (Burton, 1953), illustrating the the importance of heritability estimation. The selection is more effective when GCV and heritability are combined (Burton, 1953). When evaluating the impact of phenotypic selection, GCV, which quantifies the degree of genetic variability in a trait, is considered with heritability and genetic advancement. Genetic advancement is crucial. In the conducted study, high heritability with moderate genetic progress was noted for days to 50% flowering, implying the preponderance of additive gene effects for this trait, and thus, selection for this trait will be effective to some level. Plant height, days to the first flowering, days to 90% flowering, days to first pod maturity, days to pod initiation, clusters per plant, and pod length all showed heritability moderate and moderate genetic advancement, implying that environmental and genetic factors contributed equally to cumulative variability. Clusters per plant, harvest index, and seed yield per plant showed moderate heritability with strong genetic progress. Ranjani et al. (2018) reported high heritability coupled with high genetic advance as a percentage of the mean for the number of primary branches per plant, pod length, and seed yield. For one-hundred seeds weight, low heritability and strong genetic progress indicated that pedigree selection might be able to significantly enhance the trait while selection based on phenotypic assessment would be of little effect. Seeds per pod showed low heritability and minimal genetic advance, whereas branches per plant showed low heritability and moderate genetic advance. These findings suggest that non-additive gene action (dominance and epistasis) might be responsible for these attributes. The environment profoundly affects how such traits with low inheritance are expressed. Therefore, there is a limited likelihood of improving this attribute through conventional selection. The concept of population improvement might be relevant to the enhancement of such traits. High heritability coupled with high GA (% mean) was observed for characters viz., number of primary branches/plants, number of secondary branches/plants, first pod height, pods per plant, seeds per pod, 100-seed weight, biological yield, and yield were observed by Gautam et al. (2021) in chickpea. High GAM values of the harvest index, pods per plant, and seed yield per plant were observed by Venkateswarlu (2001). Additionally, high genetic gains in the pigeon pea harvest index, number of pods per plant, and seed yield per plant have also been documented Shedge et al. (2019). The number of branches per plant and seeds per pod registered a low estimate of heritability Saleem et al. (2002a); Techale et al. (2013).

Table 1: Analyses of variance	(mean squares) for the	quantitative traits.
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True 14 a	Mean Squares (Degrees of Freedom)							
Traits	Replications (2)	Genotypes (20)	Error (40)	CV (%)				
Plant height (cm)	295.40	601.77*	175.90	11.72				
Days to first flowering	310.82*	346.39**	76.16	4.95				
Days to 50% flowering	322.60**	351.66**	54.96	3.80				
Days to 90% flowering	164.10	374.56**	73.10	7.00				
Days to first pod initiation	278.56*	351.30**	67.01	7.41				
Days to first pod maturity	1068.51**	349.77**	68.88	7.21				
Number of branches/Plant	2.87**	1.02*	0.29	18.96				
Number of clusters/Plant	8.05*	4.36**	1.79	24.17				
Number of pods/Plant	57.22*	26.70*	13.74	10.10				
Pod length (cm)	0.21	0.47**	0.13	8.78				
Number of seeds/Pod	0.50	0.40*	0.19	14.47				
100-seeds weight (g)	171.30	261.91*	118.83	41.27				
Harvest index (%)	64.49*	172.00**	4.50	6.46				
Seed yield/Plant (g)	7.90	7.36**	3.01	31.53				

*, **Significant at 5 and 1% levels, respectively.

Table 2: Mean performances of the three maturity groups for the various traits.

	Maturity group						
Traits	Extra early (80-110 days)	Early (110-120 days)	Medium (120-150 days)	CD 5%			
Plant height (cm)	87.72	95.63	93.79	22.31			
Days to first flowering	90.11	103.35	112.18	10.38			
Days to 50% flowering	101.07	115.34	121.88	8.82			
Days to 90% flowering	109.60	124.65	131.90	14.11			
Days to first pod initiation	97.78	113.24	120.50	13.51			
Days to first pod maturity	102.47	116.77	126.15	13.70			
Number of branches/Plant	2.33	2.33	2.28	0.90			
Number of clusters/Plant	3.53	2.72	3.33	1.59			
Number of pods/Plant	8.13	7.71	6.11	6.12			
Pod length (cm)	3.95	4.11	4.19	0.59			
Number of seeds/Pod	3.01	3.11	2.88	0.72			
100-seeds weight (g)	13.25	13.84	18.28	17.99			
Harvest index (%)	27.71	26.50	20.23	3.57			
Seed yield/Plant (g)	5.02	5.87	5.62	2.86			

Table 3: Classification of the genotypes into maturity groups (Manyasa et al., 2009).

Extra-early (80–110)	Early (110–120)	Medium (120–150)
ICP 14927 (90)	ICP 7632 (113)	Bahar (122)
ICP 15312 (103)	ICP 11613 (116)	Local 1 (123)
ICP 11599 (103)	ICP 14664 (116)	ICP 12931 (125)
ICP 10920 (104)	ICP 14930 (118)	ICP 14665 (126)
ICP 11612 (104)	ICP 11495 (118)	ICP 11595 (126
ICP 11610 (105)	ICP 15011 (118)	ICP 7645 (128)
ICP 11639 (109)	ICP 8025 (119)	ICP 6973 (134)

 Table 4: Estimation of genetic parameters.

Traits	Range	Mean ± SE	PCV (%)	GCV (%)	h ² bs (%)	GA, % of mean
Plant height (cm)	61.10 - 109.40	92.38 ± 10.83	19.30	12.90	44.66	17.75
Days to first flowering	79.00 - 122.00	101.88 ± 5.04	12.66	9.32	54.18	14.13
Days to 50% flowering	90.00 -129.00	112.76 ± 4.28	11.00	8.82	64.28	14.56
Days to 90% flowering	99.00 - 142.00	122.05 ± 4.94	10.79	10.79 8.21		12.87
Days to pod initiation	85.00 - 132.00	110.51 ± 4.73	11.51	8.81	53.58	13.90
Days to maturity	89.00 - 134.00	115.13 ± 4.79	11.07	8.40	57.62	13.14
Number of branches/Plant	1.00-3.00	2.32 ± 0.44	49.30	21.23	18.54	18.83
Number of clusters/Plant	1.00-5.00	3.05 ± 0.77	50.93	29.00	32.41	34.01
Number of pods/Plant	4.00-13.00	7.32 ± 2.14	58.06	28.40	23.92	28.61
Pod length (cm)	3.52 - 5.16	4.08 ± 0.21	12.10	8.33	47.35	11.80
Number of seeds/Pod	2.00-4.00	3.00 ± 0.25	16.99	8.90	27.46	9.61
100-seeds weight (g)	5.53 - 40.42	15.12 ± 6.29	85.32	45.66	28.64	50.34
Harvest index (%)	12.14 - 36.59	24.81 ± 1.73	49.54	27.86	31.63	34.89
Seed yield/Plant (g)	3.93 - 10.95	5.50 ± 1.00	38.36	21.86	32.47	25.66

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	Supplementary Table I: Mean performances of the pigeon pea genotypes for the various traits.													
Genotypes	Plant height (cm)	Days to first flowering	Days to 50% flowering	Days to 90% flowering	Days to pod initiation	Days to first pod maturity	Number of branches/Plant	Number of clusters/Plant	Number of pods/Plant	Pod length (cm)	Number of seeds/Pod	100- seeds weight (g)	Harvest index (%)	Seed yield/Plant (g)
ICP 14927	81.40	79	90	99	85	89	1.67	4.33	12.47	3.64	2.67	13.00	26.74	5.65
ICP 11599	97.97	87	93	107	98	103	2.00	3.33	6.33	4.46	2.87	8.30	15.24	4.85
ICP 10920	87.80	93	101	112	100	104	3.33	4.67	10.60	4.08	3.53	5.53	26.20	4.15
ICP 15312	61.10	91	103	116	99	103	2.00	2.00	6.30	3.66	3.00	10.74	26.19	3.93
ICP 11612	79.30	90	103	103	98	104	2.33	3.80	4.40	4.13	2.80	7.55	27.16	5.67
ICP 11610	89.73	94	106	113	101	105	3.00	4.60	13.00	3.57	3.13	13.66	35.82	5.33
ICP 14930	76.47	102	107	115	108	117	2.33	2.00	6.20	4.01	3.27	26.60	32.33	5.55
ICP 14664	83.40	103	108	128	114	116	1.33	1.33	6.80	4.27	3.00	20.53	35.16	5.02
Extra early	82.15	92	101	111	100	105	2.25	3.26	8.26	3.98	3.03	13.24	28.11	5.02
ICP 11495	103.80	106	111	125	116	118	1.67	2.50	7.60	4.20	3.10	11.25	25.56	4.98
ICP 11639	116.77	97	112	118	103	109	2.00	2.00	3.80	4.10	3.10	33.95	36.59	5.45
ICP 7632	105.27	91	114	123	108	113	2.33	2.50	6.50	4.32	2.90	11.92	19.74	5.83
ICP 11595	93.48	108	117	126	119	126	2.00	2.00	5.80	3.76	2.60	7.20	30.63	4.90
Bahar	68.23	104	118	130	116	122	2.33	4.33	4.40	3.72	2.47	23.60	22.91	10.95
ICP 11613	98.20	108	119	124	114	116	3.00	5.20	8.50	3.85	3.20	7.80	30.99	4.65
ICP 12931	105.73	115	119	127	118	125	2.67	2.33	7.87	4.33	3.13	11.58	27.27	4.35
Local 1	102.73	111	120	127	117	123	3.00	5.00	11.00	5.16	3.80	8.00	12.14	4.35
Early	99.28	105	116	125	114	119	2.38	3.23	6.93	4.18	3.04	14.41	25.73	5.87
ICP 15011	112.07	106	124	128	116	118	3.33	2.00	12.70	4.36	3.20	8.30	26.43	4.70

2.33

2.33

2.33

1.33

0.90

4.00

3.67

2.00

3.03

1.59

6.00

5.70

3.73

4.00

6.43

6.12

CONCLUSIONS

113

107

113

122

112

10

124

125

125

129

125

88.73

90.20

104.53

93.10

97.73

22.31

ICP 7645

ICP 8025

ICP 14665

ICP 6973

Medium

CD 5%

The genotypes ICP 15011, ICP 14927, ICP 15312, ICP 11610, ICP 11599, ICP 10920, and ICP 11639 performed well for different quantitative characteristics and were also early maturing genotypes. Among them, ICP 15011 showed the highest seed yield and regarding early maturity, ICP 14927 was the earliest maturing genotype.

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FUTURE SCOPE

Further research can be conducted by subjecting these genotypes to a hybridization program and screening them to test their adaptability to different environments. Also, screening the genotypes for abiotic stress tolerance (waterlogging, low temperature) and biotic stress tolerance (pod fly, pod borer, sterility mosaic disease, fusarium wilt, phytophthora blight) can be done. Moreover, biochemical work can be done to assess the protein content as well as other nutritional quality of the genotypes.

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4.29

3.74

4.54

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0.72

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17 99

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3 57

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