



## Genetic Variability for Yield, Physiological and Quality Traits in Novel Super-Early Pigeonpea (*Cajanus cajan* (L.) Millsp.)

H.B. Shruthi<sup>1,2</sup>, A.J. Hingane<sup>1\*</sup>, M. Reddi Sekhar<sup>2</sup>, C.V. Sameer Kumar<sup>3</sup>, J. Srivarsha<sup>1</sup>, T.M. Bhosle<sup>1</sup>, L. Prashanthi<sup>2</sup>, B.V. Bhaskar Reddy<sup>2</sup>, P. Sudhakar<sup>2</sup>, Rathore A.<sup>1</sup> and Anil Kumar, V.<sup>1</sup>

<sup>1</sup>Pigeonpea Breeding, International Crops Research Institute for Semi-arid Tropics Patancheru, Telangana, 502324, India

<sup>2</sup>Department of Genetics and Plant Breeding, S.V. Agricultural College, ANGRAU, Tirupati, Andhra Pradesh, 517501, India

<sup>3</sup>Pulses Breeding Division, Regional Agricultural Research Station, Palem, PJTSAU, Hyderabad, Telangana

\*Corresponding Author E-mail: [h.anupama@cgiar.org](mailto:h.anupama@cgiar.org)

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### ABSTRACT

*Super-early pigeonpea are novel genotypes that are reported to be photoperiod insensitive making it possible to grow it in non-traditional regions. Estimation of genetic parameters would be useful in developing appropriate selection and breeding strategies. A study was conducted to evaluate 37 super-early pigeonpea genotypes to access the magnitude of variability and to study heritable component of variation present in the yield, physiological and quality traits. The results revealed that traits leaf area duration between 60 DAS & maturity followed by leaf area & leaf area index at maturity, net assimilation between 60 DAS & maturity, leaf area index & leaf area at 60 DAS, leaf area duration between 60 DAS & maturity and plant height had high had higher PCV and GCV values. In general, phenotypic coefficients of variation (PCV) estimates were higher than genotypic coefficients of variation (GCV) estimates for all the characters under study, but the difference was relatively small indicating that these characters were less influenced by the environment and selection to improve those traits might be effective. High heritability combined with high genetic advance as a percent of mean was noted for all the traits except protein content conveying the governance of additive gene on trait expression. Anticipating these traits as selection index reaps competent improvement in yield, physiological and quality traits in early maturing pigeonpea.*

**Keywords:** Super-early pigeonpea, Variability, Heritability, Genetic advance

### INTRODUCTION

Pigeonpea is an age-old legume crop playing a pivotal role in the sustainable rain-fed farming system of tropical and sub-tropical regions of

Asia, Africa, and the Caribbean islands. Globally cultivated in 7 mha with production and productivity of 6.8 mt and 969 Kg/ha respectively (FAOSTAT, 2019).

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The crop has many uses; grain is cooked and eaten as a dhal (dry split cotyledons) which accosts for 20-24% protein, 2.76mg of zinc and 5.23mg of iron (per 100g of seed) undoubtedly making an energy-rich food (Janila et al., 2016). Apart from grain, high protein in leaf (16-18%) and grain husk (28%-30%) make pigeonpea a quality fodder and feed too. The deep root system of pigeonpea vouches for drought tolerance. Effective use of dry stem as fuelwood, fencing and thatched roofs affirms every part goes unwaste in the crop (Mula & Saxena, 2010).

Pro-farmer long and medium-duration pigeonpea ruled successfully for 4decades in Indian rainfed farms. But the domination of the latter broke, with the realization of climate change and increased incidence of the terminal drought of late. The long-standing crop added to the drudgery by scarce resources, tough maintenance strategies, and stagnant productivity, ultimately making earliness as a necessitous trait in pigeonpea breeding. Hence efforts were made at ICRISAT to develop a novel 'super-early' maturity group of pigeonpea.

Super-early pigeonpea with the lifespan of lesser than 100 days, proves to be the foundation of future breeding. Its earliness, mechanization pro stature, photo-insensitivity, impressive per day productivity, adaptability across the varying range of altitudes, stress escape mechanism, niche to fit in wheat-pulse cropping patterns, rice fallows as well as high-density cropping system is much appreciated (Srivastava et al., 2012). Faster generation turns over, is a boon to the breeders for faster introgression of traits, emphasizing the genetics of biotic and abiotic stress by developing mapping population. With the plethora of advantages, an attempt to study the genetic variability in 37 genotypes of super-early pigeonpea for yield, yield attributes, physiological and quality traits were done to foresee the future breeding scope in the latter.

## MATERIALS AND METHODS

The experimental material comprised of 37 super-early pigeonpea genotypes laid at

pigeonpea breeding fields at ICRISAT, Patancheru during rainy 2016. The study material consisted of 13 determinate types(DT) and 21 non-determinate types (NDT) with two DT checks MN1, MN5, and one NDT check ICPL 20325. Each genotype was sown in 4 rows of 4 m length with a spacing of 30×10 cm in Randomized Complete Block Design (RCBD) with 2 replications. The experiment plot was located at 17.51°N latitude, 78.27° E longitude, an altitude of 545 meters above MSL, with an annual rainfall of 877.82 mm and alfisol being soil type. Field observations for traits *viz.*, plant height (cm), number of primary branches, pods per plant, seeds per pod, grain weight per plant (g), 100 seed weight (g), harvest index (%) were recorded, on five randomly selected plants whereas days to 50% flowering, days to maturity and yield per hectare (Kg) was calculated on plot yield basis. Dry matter content (g) at 30 DAS, 60 DAS and maturity, leaf area (cm<sup>2</sup>) at 30 DAS, 60 DAS, and maturity were recorded, on five randomly uprooted plants at each interval (0 days interval) whereas canopy volume (cm<sup>3</sup>) (Rodríguez, et al., 2008), leaf area index (LAI) Watson (1952) at 30 DAS, 60 DAS & maturity, crop growth rate (CGR) (g/m<sup>2</sup>/d) Radford (1967), net assimilation rate (NAR) (g/m<sup>2</sup>/d) Williams (1946), leaf area duration (LAD) (m<sup>2</sup> days) between 30-60 DAS & 60 DAS-maturity (Hunt (1978), protein content (%) Sahrawat et al., (2002) , phenol content (mg GAE/100g) Singleton and Rossi (1965), dal cooking time (min) Sethi et al. (2014): Singh et al. (1984); Akinoso and Oladeji (2017) and dal recovery (%) (Sawargaonkar, 2010) were calculated methodically. Standard cultural practices were followed to maintain good crop stand. Data collected were subjected to analysis of variance using SAS v. 9.4 program (SAS, 2017). The phenotypic and genotypic coefficient of variation was calculated as per Burton's (1952) formulae. Whereas, heritability (broad sense) and genetic advance as percent of mean was computed based on Lush (1940) and Johnson et al. (1955).

## RESULT AND DISCUSSION

Analysis of variance revealed significant differences for all the 30 traits under study (Table 1), suggesting existence of considerable genetic variation for yield, physiological and quality traits in studies super-early pigeonpea lines. These findings were in conformity with Ranjani et al. (2018) and pushavalli et al. (2018). Variability split into phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) sum up the magnitude of variability. Higher PCV and GCV were found for trait leaf area duration between 60 DAS & maturity (41.47 & 41.9) followed by leaf area & leaf area index at maturity and net assimilation between 60<sup>th</sup> DAS & maturity. Interestingly all the physiological traits topped the higher PCV, GCV list underlining the importance in breeding parallelly with yield attributing traits (Table 2). Lower PCV and GCV were revealed by protein content (4.12 & 1.89) followed by seeds per pod, days to maturity and days to 50% flowering. Higher PCV and GCV corresponding a trait enables successful selection whereas lower PCV and GCV traits if selected has no uniqueness profiting the breeding programme. The majority of traits in the study showed higher PCV over GCV. However, the difference between the magnitudes of PCV and GCV was very low conveying the governance of genes over trait expression with negligible environmental influence. Similar results are in agreement with the findings of Rajamani et al. (2015), Kesh et al. (2017), Mallesh et al. (2017), Deepak et al. (2018), Ranjani et al. (2018), pushavalli et al. (2018) and Baldaniya et al. (2018).

The proportion of total variability due to genetic control is computed in terms of heritability (Nadarajan et al., 2016). Heritability is a measure of trait transmission from parents to offsprings. It ranged from 20.99% to 99.98% in the present study (Table 2). High heritability (>60%) was found in all the traits except for protein content. Protein content depicted the lowest heritability (20.99%) whereas leaf area at 60 DAS

(99.98%), leaf area at maturity (99.98%) and leaf area index at 60 DAS (99.98%), topped the list. Heritability plays a key role in the selection process in plant breeding as it is estimated from fixable genetic variance. High heritability was also reported by Saroj et al. (2015) (number of primary branches per plant), Verma et al. (2018) (number of pods per plant), Mallesh et al. (2017) (number of seeds per pod), Pandey et al. (2015) (yield per plant; harvest index), Ranjani et al. (2018) (plant height; number of branches). Whereas Saroj et al. (2015) noted moderate (days to 50% flowering) and Vanisree et al. (2013) documented low heritability (number of branches per plant).

The measure of genetic gain under selection is genetic advance and expressed as a percentage of the mean (GAM). It is completely reliant on genetic variability, heritability and selection intensity from a base population (Nadarajan et al., 2016). Genetic advance as a percent of mean ranged from 1.28% to 85.11%. Higher GAM was noted for traits, leaf area duration (85.11%) and leaf area at maturity (82.99%) followed by leaf area index at maturity (82.98), net assimilation rate between 60 DAS and maturity (72.69%). Moderate GAM was found for number of branches per plant (18.03%), dal recovery (16.62%), 100 seed weight (14.26%) and days to 50% flowering (12.93%) whereas days to maturity (8.79%), seeds per pod (7.96%) and protein content (1.78%) reported low GAM (Table 2). Higher GAM was reported by Ranjani et al. (2018) (plant height; number of pods per plant; seed yield per plant; number of branches per plant), pushavalli et al. (2017) (days to 50% flowering; plant height) and Verma et al. (2018) (number of primary branches). Moderate GAM was testified by Pandey et al. (2015) (number of primary branches; seeds per pod), Kesh et al. (2017) (number of pods per plant) and Vanishree et al. (2013) (seed yield per plant) and low GAM was documented for 100 seed weight by Sharma et al. (2012) and Mallesh et al. (2017).

High heritability combined with high GAM was noted for traits leaf area duration

between 60 DAS and maturity followed by leaf area and leaf area index at maturity, net assimilation rate between 60 DAS & maturity, leaf area index and leaf area at 60 DAS, leaf area duration between 60DAS and maturity, plant height (pushpavalli et al., 2017), conveying the governance of additive gene on trait expression (Table 2). The selection of these traits in further breeding would be effective. High heritability and moderate GAM was reported for traits number of primary branches per plant, dal recovery, 100 seed

weight and days to 50% flowering (Rao et al., 2013). Selection in these traits is possible, however, the end being partially effective. High heritability and low GAM was seen in traits days to maturity and seeds per pod elucidating the non-additive gene action, resulting in non-rewarding selection. Low heritability and low GAM were seen for protein content indicating that the trait is highly influenced by environment and selection would be ineffective.

**Table 1: Analysis of Variance for 30 yield, yield attributes and quality traits under study for 37 super-early pigeonpea**

Sl. No	Traits	Mean sum of squares		
		Replication (1)	Genotypes (36)	Error (36)
1	Days to 50% flowering	2.61	10.44**	0.83
2	Days to maturity	1.68	13.69**	3.05
3	Plant height (cm)	0.01	857.62**	4.63
4	Number of primary branches plant <sup>-1</sup>	2.30	0.83**	0.45
5	Pods plant <sup>-1</sup>	0.41	86.67**	8.00
6	Seeds pod <sup>-1</sup>	0.16	0.02**	0.00
7	100 seed weight (g)	0.47	0.28**	0.01
8	Canopy volume (cm <sup>3</sup> )	0.04	211510**	954.27
9	Seed yield plant <sup>-1</sup> (g)	2.29	4.45**	0.53
10	Yield ha <sup>-1</sup> (kg)	2.37	140687**	46302.00
11	Harvest Index (%)	0.04	50.76**	4.30
12	Dry matter content (g) at 30 DAS	0.81	13.9**	0.39
13	Dry matter content (g) at 60 DAS	1.19	50.31**	1.40
14	Dry matter content (g) at maturity	2.27	200.06**	4.08
15	Leaf area (cm <sup>2</sup> ) at 30 DAS	1.77	4458.05**	6.90
16	Leaf area (cm <sup>2</sup> ) at 60 DAS	1.40	43076**	18.64
17	Leaf area (cm <sup>2</sup> ) at maturity	0.55	42761**	21.07
18	Leaf area index at 30 DAS	0.78	0.04**	0.00
19	Leaf area index at 60 DAS	1.36	0.46**	0.00
20	Leaf area index at maturity	0.47	0.46**	0.00
21	Crop growth rate (gm <sup>-2</sup> d <sup>-1</sup> ) - 30 DAS & 60 DAS	0.51	15.85**	1.09
22	Crop growth rate (gm <sup>-2</sup> d <sup>-1</sup> ) -60 DAS & maturity	3.50	26.799**	1.96
23	Net assimilation rate (gm <sup>-2</sup> d <sup>-1</sup> ) -30 DAS & 60 DAS	0.74	0.0001581**	0.00
24	Net assimilation rate (gm <sup>-2</sup> d <sup>-1</sup> ) -60 DAS & maturity	1.21	0.000268**	0.00
25	Leaf area duration -30 DAS & 60 DAS	1.80	184.14**	0.10
26	Leaf area duration -60 DAS & maturity	2.86	1135.11**	8.21
27	Protein content (%)	16.98	0.15*	1.13
28	Phenol content (mg GAE 100g <sup>-1</sup> )	2.08	2580.88**	783.63
29	Dal cooking time (min)	70.09	527.69**	0.29
30	Dal recovery (%)	2.91	40.22**	1.50

Note: \*, \*\*, \*\*\* Significant at 0.05, 0.01, < 0.001 levels of probability, respectively

**Table 2: Genetic parameters for 30 yield, yield attributes and quality traits in super-early pigeonpea**

Sl.No	Traits	Mean	Range		h <sup>2</sup>	GCV %	PCV %	GAM %
			Min	Max				
1	Days to 50% flowering	50.49	44	58	96.17	6.40	6.53	12.93
2	Days to maturity	82.25	76	91	89.96	4.50	4.74	8.79
3	Plant height (cm)	91.16	49.3	132.3	99.73	32.13	32.17	66.09
4	Number of primary branches plant <sup>-1</sup>	9.27	7.8	10.7	78.74	9.87	11.12	18.03
5	Pods plant <sup>-1</sup>	44.29	26.6	59.8	95.59	21.02	21.50	42.33
6	Seeds pod <sup>-1</sup>	3.76	3.4	4.1	93.22	4.00	4.15	7.96
7	100 seed weight (g)	7.66	6.7	8.6	98.95	6.96	7.00	14.26
8	Canopy volume (cm <sup>3</sup> )	1452.49	737.0	2123.0	99.77	31.66	31.70	65.15
9	Seed yield plant <sup>-1</sup> (g)	14.04	10.7	18.0	94.31	15.03	15.48	30.07
10	Yield ha <sup>-1</sup> (kg)	1645.19	1015.7	2363.4	85.87	22.80	24.60	43.52
11	Harvest Index (%)	26.53	15.1	46.5	95.86	26.86	27.43	54.17
12	Dry matter content (g) at 30 DAS	12.14	6.8	21.4	98.59	30.71	30.93	62.81
13	Dry matter content (g) at 60 DAS	25.80	15.8	43.7	98.62	27.49	27.68	56.24
14	Dry matter content (g) at maturity	55.87	33.1	91.6	98.99	25.32	25.44	51.89
15	Leaf area (cm <sup>2</sup> ) at 30 DAS	209.08	120.5	365.3	99.92	31.93	31.95	65.76
16	Leaf area (cm <sup>2</sup> ) at 60 DAS	633.32	361.3	1096.2	99.98	32.77	32.78	67.50
17	Leaf area (cm <sup>2</sup> ) at maturity	513.22	243.3	980.7	99.98	40.29	40.30	82.99
18	Leaf area index at 30 DAS	0.69	0.4	1.2	99.92	31.98	32.00	65.86
19	Leaf area index at 60 DAS	2.09	1.2	3.6	99.98	32.78	32.78	67.51
20	Leaf area index at maturity	1.69	0.8	3.2	99.97	40.29	40.29	82.98
21	Crop growth rate (gm <sup>-2</sup> d <sup>-1</sup> ) - 30 DAS & 60 DAS	15.02	8.4	24.4	96.66	26.51	26.97	53.70
22	Crop growth rate (gm <sup>-2</sup> d <sup>-1</sup> ) -60 DAS & maturity	23.54	14.5	37.2	96.47	21.99	22.39	44.49
23	Net assimilation rate (gm <sup>-2</sup> d <sup>-1</sup> ) -30 DAS & 60 DAS	0.04	0.02	0.08	96.76	30.29	30.79	61.37
24	Net assimilation rate (gm <sup>-2</sup> d <sup>-1</sup> ) -60 DAS & maturity	0.05	0.02	0.08	96.93	35.84	36.41	72.69
25	Leaf area duration -30 DAS & 60 DAS	41.70	23.8	72.3	99.97	32.54	32.55	67.03
26	Leaf area duration -60 DAS & maturity	81.40	38.6	151.1	99.64	41.39	41.47	85.11
27	Protein content (%)	20.59	20.0	21.0	20.99	1.89	4.12	1.78
28	Phenol content (mg GAE 100g <sup>-1</sup> )	233.26	147.1	361.3	86.82	21.78	23.37	41.80
29	Dal cooking time (min)	220.40	180.4	270.8	99.97	10.42	10.42	21.47
30	Dal recovery (%)	77.85	62.3	85.4	98.06	8.15	8.23	16.62

**CONCLUSION**

Genetic variability studies in super-early genotypes of pigeonpea, embark on the potentials of selectional breeding to beat extended crop-stand drudgery. The present study revealed that the leaf area duration between 60DAS and maturity, leaf area and leaf area index at maturity, net assimilation rate between 60 DAS & maturity, leaf area index and leaf area at 60 DAS, leaf area duration between 60 DAS and maturity, plant height, leaf area index and leaf area at 30 DAS, canopy volume, dry matter at 30 DAS, net assimilation rate between 30 DAS & 60 DAS, dry matter yield at 60 DAS, harvest index, crop growth rate between 30 DAS & 60 DAS, dry matter content at maturity, crop growth rate between 60 DAS & maturity, yield per hectare, pods per plant, phenol content, seed yield per plant and cooking time vary enormously with high heritability and GAM. Thus, the selection of the above traits directed by fixed genes secures competent crop improvement in pigeonpea. However, consideration of physiological traits laterally with yield and quality traits as a selection index is the utmost requirement in current breeding.

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