AU DOI: 10.15740/HAS/AU/13.4/429-434 **Agriculture Update**
Volume 13 | Issue 4 | November, 2018 | 429-434
Visit us : *www.researchjournal.co.in*
ISSN-0973-1520

RESEARCH ARTICLE :

Evaluation of phenotypic and yield attributing traits in mid late pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes

M. R. Kondawar and K. P. Ingle

ARTICLE CHRONICLE :
Received : *14.05.2018;*
Revised : *26.09.2018;*
Accepted : *11.10.2018*

SUMMARY : The present investigation was undertaken with a view of identification of superior mid late genotypes of pigeonpea [*Cajanus cajan* (L.). Millsp.] based on the evaluation of phenotypic and yield attributing traits. The various morphological characters *viz*., plant height, number of primary and secondary branches and number of leaves per plant were evaluated and mid late genotypes, AKTHR-2001-18 and AKTHR-2001-01 were found superior over the checks, Asha and PKV-Tara. Similarly, AKTHR-2001-18 and AKTHR-2001-01 mid late genotypes contributed significant increase in yield attributing traits compared to checks which were further used in the crop improvement programme to enhance the productivity of pigeonpea.

How to cite this article : Kondawar, M.R. and Ingle, K.P. (2018). Evaluation of phenotypic and yield attributing traits in mid late pigeonpea [*Cajanus cajan* (L.) Millsp.] genotypes. *Agric. Update*, **13**(4): 429-434; **DOI : 10.15740/HAS/AU/13.4/429-434.**

KEY WORDS :
Pigeonpea, Morphological traits, Yield attributing traits

Author for correspondence :
M. R. Kondawar
Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (M.S.) India
Email:manoj.kondawar@gmail.com
See end of the article for authors' affiliations

BACKGROUND AND OBJECTIVES

Pigeonpea (*Cajanus cajan* L.) commonly known as 'tur' is the fifth most important food legume crop in the world after soybean, groundnut, dry beans and peas (Kaur, 2016). This crop occupies an essential place in our daily diet as very high-quality source of protein. It is mainly cultivated for its dry seeds and green vegetables in dry areas of the tropics and subtropics.The major pigeonpea producing areas in the world are India, Eastern Africa, Central and South America, the Caribbean and West Indies. India with a total area of 3.90 million hectares with production 3.17 million ton and an average productivity is 813 kg/ha (Anonymous, 2014) produces nearly 90 per cent of the world's entire pigeonpea crop. To increase its yield potential several morphological and physiological characters are responsible to seed yield. Seed yield also governed by many physiological changes within the plant and influenced by many environmental factors when cultivated, hence, it is not an efficient character for selection. Inter-relationship among direct and indirect effect of morphological and physiological characters of yield is important in predicting the correlated response to direct selection and in the detection of traits with much effect. The present study was undertaken to elucidate the association between yield and its attributes in mid late pigeonpea genotype.

RESOURCES AND METHODS

Experimental site:

The experiment was carried out during *Kharif* season of 2009-10 at the experimental field of Department of Agricultural Botany, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, Maharashtra state, India located at 307.4 meters above mean sea level. The geographical situation is 20.42°N latitude and 77.02°E longitude. The soil was medium black with clay, fairly levelled and uniform in topography with appropriate drainage system.

Plant material:

The experimental material comprised of nine different promising mid late genotypes of pigeonpea AKT-221030, AKT-9928, AKTHR-2001-18, AKTHR-2001-01, AKT-08-02, AKT-222529, AKT-222527 and two checks, Asha (Ch) and PKV Tara (Ch.) were sown with three replications.

Experimental design and setting the experiment:

The experiment was laid out in a Randomized Complete Block Design with three replicates. The plot was ploughed one month before sowing and followed by three harrowing to bring the land to a fine tilth. Each genotype was grown in two rows of 3 m length in each replication. The spacing of row to row and plant to plant was of 60× 30 cm. Seeds were sown using dibbling method during *Kharif*- 2010. The fertilizers were applied at the rate of 25 kg N, 50 kg P_2O_5 and 0 kg K_2O per hectare at the time of sowing. As flowering initiated, 2-3 irrigations were provided. Harvesting was done as per maturity of the genotypes.

Data collection:

Five plants from each replicate were randomly selected for various traits *viz.*, plant height, number of primary branches per plant, number of leaves per plant. The mean value of five plants for each character was recorded and calculated the mean for statistical analysis. The periodical observations were taken at 30, 60, 90, 120 DAS (days after sowing). Yield attributing characters *viz*., plant population, number of pods per cluster, number of pods per plant, pod length (cm), number of seed per pod, seed yield per plant (g), seed yield per net plot (g), biological yield (g), harvest index per cent were evaluated at harvest.

Statistical analysis:

Statistical analysis of phenotypic characters and yield attributing traits was done during the course of investigation using analysis of variance as described by Panse and Sukhatme (1985). The standard error of mean (S.E.) was worked out and the critical difference at 5 per cent level of significance was calculated and the results were recorded.

OBSERVATIONS AND ANALYSIS

In the present investigation, amongst various pigeonpea genotypes, AKTHR-2001-18 was found superior as compared other genotypes, whereas the genotype Asha and PKV-Tara revealed the poorest performance. The observations on different phenotypic characters were recorded periodically and the results are presented (Table 1).

Phenotypic assessment of pigeonpea genotypes for plant height (cm):

Plant height is basically a genetically controlled character; it is being influenced by environmental condition and genotypes. The present study revealed significant differences in plant height among the genotypes at different growth stages. Plant height constitutes a morphological parameter as a major component of yield and recorded at various growth stages (Table 1). The height of the plant was found significant at all growth stages in different mid late pigeonpea genotypes. Mid late genotype AKTHR-2001-18 and AKTHR-2001-01 recorded statistically more plant height over the both checks at 30, 60, 90 and 120 DAS. The present investigation results resembles with those of Kataria and Mishra (1993) and Singh and Prasad (1987).

Phenotypic assessment of pigeonpea genotypes for number of branches per plant:

The data on mean number of primary and secondary branches per plant revealed that there was continuous increase in mean number of primary and secondary branches per plant upto harvest. There were significant differences among the genotypes for mean number of primary and secondary branches (Table 1). These results are in agreement with the findings of Kataria and Mishra (1993) who reported that pigeonpea cultivars differed significantly for mean number of branches per plant. Significant increase in branches was recorded in genotype AKTHR-2001-18 and AKTHR-2001-01 over the checks, Asha and PKV-Tara at 30, 60, 90 and 120 DAS. However, AKT-222529 produced less branches/plant at all the stages over both the checks. Similar results were reported by Wakankar and Yadav (1975); Upadhyaya and Saharia (1980); Reddy and Rao (1980); Dumbre and Deshmukh (1983); Patel *et al*. (1988); More (1989) and Lal and Raina (2002).

Phenotypic assessment of pigeonpea genotypes for number of leaves per plant:

The leaf of a plant is the main organ of photosynthesis and the data on number of leaves per plant is presented in Table 1. The genotypes AKT- 221030, AKTHR-2001-18, AKTHR-2001-01 produced significantly more number of leaves over control, Asha and PKV-Tara at 30, 60, 90 and 120 DAS showing continuous source of assimilation through leaves by these mid late genotypes even upto at harvest, whereas, mid late genotype AKT-222529 has statistically produced less number of leaves at all the growth stages over both the checks. Mid late genotypes AKTHR-2001-18 and AKTHR-2001-01 produced significantly more number of leaves over the both checks.

Evaluation of yield attributing traits:

Yield attributing characters *viz*., plant population, number of pods per cluster, number of pods per plant, number of seed per pod, seed yield per plant (g), seed yield per net plot (g), biological yield (g), harvest index per cent were evaluated as these characters plays an crucial role in the yield enhancement and enlisted in Table 2.

Number of pods/clusters:

Number of pods showing significant difference in all the genotypes at harvest (Table 2 and Fig.1). Mid late genotype AKTHR-2001-18 (5.59) and AKTHR-2001-01 (5.53) and AKT-221030 (5.60) were significant for number of pod/clusters over both the checks, Asha (5.36) and PKV Tara (5.39), whereas the mid late genotype AKT-222529 statistically found inferior respective to yield attributing trait number of pod/cluster (3.55) compared to checks, Asha and PKV Tara. Similar results were reported by Senger and Sharma (2000).

Number of pods/plants:

The number of pod contributes to the production efficiency. The difference in the number of pods per plant at harvest was found to be significant (Table 2 and Fig.1). Among the mid late genotypes, AKTHR-2001-18 (239.18), AKTHR-2001-01(234.32) and AKT-221030 (197.56) recorded significantly more number of pods/ plant over both the control Asha (185.57) and PKV Tara

Table 1: Phenotypic parameters observations of mid late pigeonpea genotypes

Genotypes	Plant height (CM)				No. of branches/plant				No. of leaves/plant			
	Days				Days				Days			
	30	60	90	120	30	60	90	120	30	60	90	120
AKT-221030	37.47	106.13	145.11	163.39	11.54	31.27	56.63	64.89	24.30	174.82	412.22	485.77
AKT-9928	33.80	97.71	122.58	142.78	10.57	29.30	36.55	49.87	20.56	152.42	346.67	312.00
AKTHR-2001-18	39.00	114.60	146.06	169.16	13.36	38.07	45.74	65.70	24.77	187.21	436.66	799.88
AKTHR-2001-01	38.93	108.85	141.70	165.79	12.52	36.99	50.82	63.72	29.22	181.80	415.33	702.55
AKT-08-02	38.17	100.37	123.16	146.13	10.12	28.05	36.49	55.65	20.78	121.04	405.51	481.35
AKT-222529	31.60	88.61	108.31	126.34	8.37	25.55	30.82	51.82	19.78	103.84	301.42	273.81
AKT-222527	33.93	106.73	132.52	164.60	11.53	32.97	39.78	56.78	22.56	168.70	384.51	465.63
ASHA (CH)	36.90	110.27	134.64	166.01	11.04	33.49	42.65	60.62	23.73	167.98	397.89	474.83
PKV-TARA (CH)	38.90	114.50	137.52	167.85	12.50	33.92	43.79	62.71	24.60	171.24	401.72	487.89
F Test	Sig.	Sig.	Sig.	Sig.	NS	Sig.	Sig.	Sig.	Sig.	Sig.	Sig.	Sig.
S.E.±	1.4	1.18	0.82	0.78	0.28	0.30	0.49	0.37	0.09	0.23	0.19	0.14
C.D. (P=0.05)	3.34	3.54	2.46	2.33	-	0.90	1,48	1.39	0.27	0.68	0.61	0.45

NS= Non-significant

(196.33). About 49 to 83 per cent increase in pod number per plant was found in AKTHR-2001-18, AKTHR-2001-01 and AKT-221030 over control Asha and PKV Tara.

Number of seed/pod:

The mid late genotypes differed significantly in number of seeds per pod among all the genotypes (Table 2 and Fig.1). Mid late genotypes AKTHR-2001-18 (4.23) and AKTHR-2001-01 (4.25) recorded more seeds/pod over the both checks Asha (4.18) and PKV Tara (4.21). The genotype AKT-221030 and observed more over the control Asha, respectively. The genotypes AKT-08-02 (3.43) recorded significantly lowest number of seed/pod over the control, Asha and PKV Tara. Singh *et al.* (2009) reported the similar findings and suggested that seed yield showed positive and significant association with yield attributing traits.

Seed yield/plant (g):

The statistical difference in seed yield/plant (g) found significant. The mid late genotype AKTHR-2001-18 and AKT-2001-01 showed significant difference in seed yield

Table 2: Yield and yield attributing traits of mid late pigeonpea genotypes at harvest

Genotype	Plant population	No. of pods/cluster	No. of pods/plant	No. of seed/pod (g)	Seed yield/plant (g)	Biological yield (g)	Seed yield /net plot (g)	Harvest index (%)
AKT-221030	30	5.60	197.56	4.11	83.60	180.87	476	46.25
AKT-9928	29	3.70	172.04	3.63	73.00	163.16	347	44.74
AKTHR-2001-18	28	5.59	239.18	4.23	111.53	236.91	569	48.07
AKTHR-2001-01	30	5.53	234.32	4.25	103.46	217.21	503	47.63
AKT-08-02	28	4.18	129.29	3.43	75.45	153.56	341	49.13
AKT-222529	29	3.55	127.36	3.12	64.97	220.96	264	29.40
AKT-222527	31	4.22	187.90	4.19	82.50	179.70	430	45.90
Asha (Ch)	31	5.36	185.57	4.18	88.29	204.61	406	46.26
PKV Tara (Ch.)	30	5.39	196.33	4.21	89.21	213.51	495	47.03
'F' test	NS	Sig.	Sig.	Sig.	Sig.	Sig.	Sig.	Sig.
S.E.±	0.27	0.07	0.82	0.05	0.58	0.74	0.09	0.47
C.D. (P=0.05)	-	0.21	2.45	0.15	1.75	2.23	0.27	1.39

NS= Non-significant

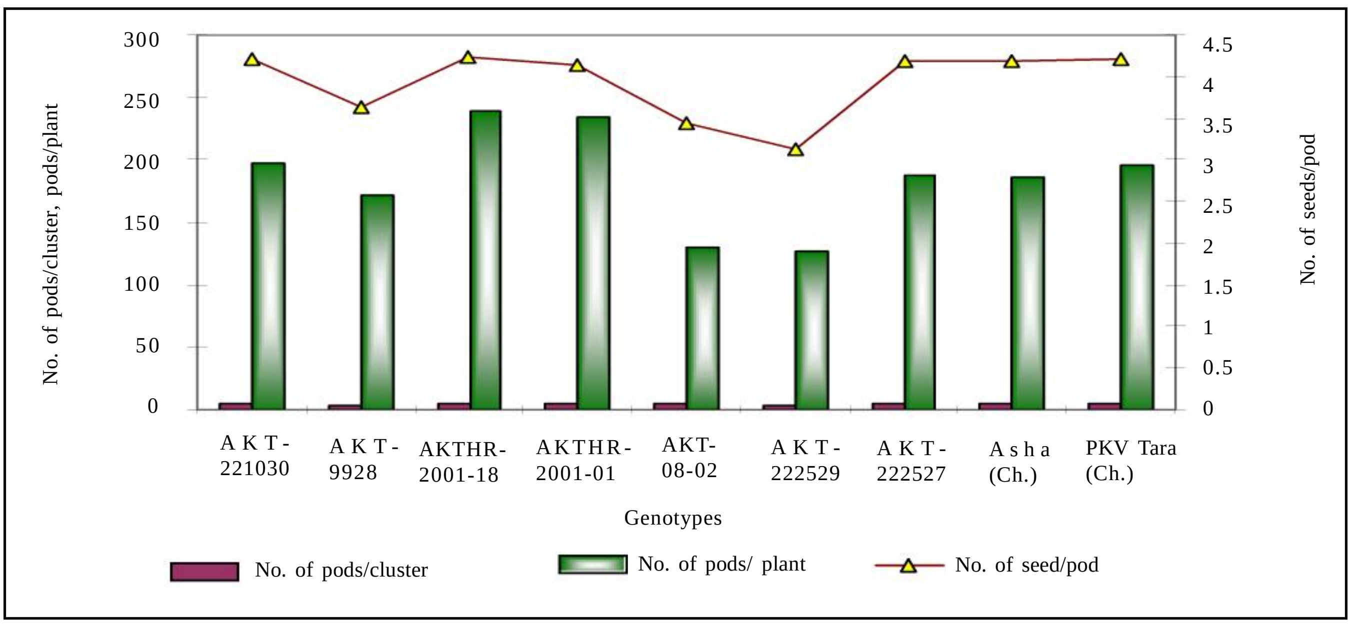

Fig. 1 : Number of pods/cluster, number of pods/plants and number of seed/pod of mid late pigeonpea genotypes

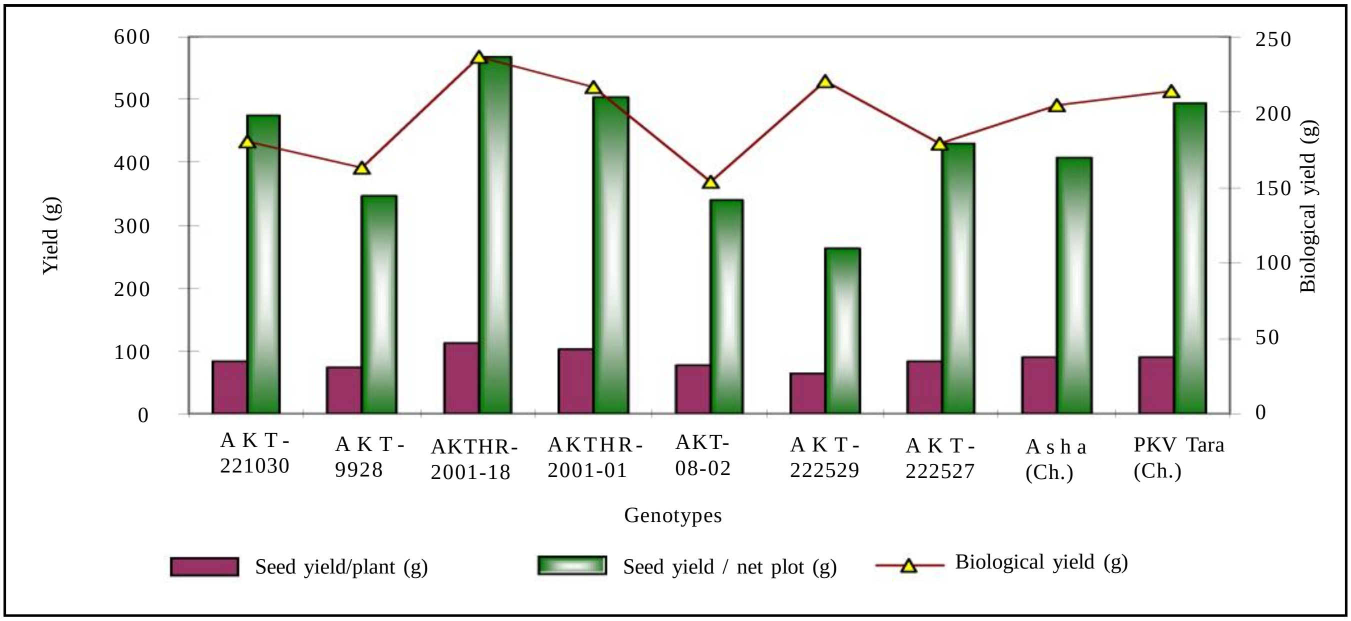

Fig. 2 : Seed yield/plant (g), seed yield/net plot (g) and biological yield/plant (g) of mid late pigeonpea genotypes

over check (Table 2 and Fig. 2). Mid late genotype AKTHR-2001-18 produced significantly highest (111.53 g/plant *i.e.* 22 to 23 per cent increase) over control (*i.e.* 88.29 g and 89.21 g/plant) Asha and PKV Tara, respectively. The genotypes AKT-222529 *i.e.* 64.97 g/ plant produced significantly lowest seed yield/plant over the both control as compared to other genotypes several results were reported by Mukewar and Muley (1974).

Seed yield/net plot (g):

The mid late genotype *i.e.* AKTHR-2001-18 and AKTHR-2001-01 shown significant highest seed yield/ net plot (569 g) and (503g), respectively over the checks, Asha (406.00 g) and PKV Tara (495g). The genotypes AKT-222529 produced statistically lowest seed yield/net plot *i.e.* (264 g) among all the genotypes and both the control Asha and PKV Tara, respectively (Table 2 and Fig. 2).

Biological yield /plant (g):

Potential yield is after controlled by the efficiency to utilize solar energy in the farm of dry matter. The mid late genotypes showed significant differences in the biological yield per plant (Table 2 and Fig.2). The genotypes AKTHR-2001-18 had produced higher biological yield 236.91 g/plant; whereas, the mid late genotypes AKT-221030, AKTHR-2000-01, AKT-08-02, AKT-222527 showed significant improvement in biological yield over control *i.e.* Asha. The lowest biological yield was observed in mid late genotype AKT-08-02 (153.56 g/plant). Similar findings reported by Singh *et al.* (2009).

In general, it is imperative to state that, for improvement in seed yield one has to consider biological yield and harvest index in respect of indeterminate field crops.

Conclusion:

The phenotypic characters *viz*., plant height, number of primary branches per plant, number of leaves per plant had maximum contribution in determining grain yield in pigeonpea. AKTHR-2001-18 and AKTHR-2001-01 were found superior in all morphological traits. The yield contributing characters *i.e.* number of pods per plant and number of seed per pod was positively and significantly correlated with seed yield. The significant increase in seed yield noted in genotypes AKTHR-2001-18 and AKTHR-2001-01 was due to the combination of most of the above characters. A wide range of variation was observed in number of branches and pods per plant. Thus, it is concluded that the mid late genotypes showed wide variation in many characters. Such variation could be exploited in breeding programme for increasing the productivity of pigeonpea.

Authors' affiliations :

K.P. Ingle, Department of Agricultural Botany, Biotechnology Centre, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (M.S.) India

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