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MEAN PERFORMANCE OF EXTRA-EARLY GENOTYPES OF PIGEON PEA (*CAJANUS CAJAN* L.) FOR NODULATION CAPACITY ALONG WITH THEIR MORPHOLOGICAL TRAITS

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ABSTRACT

Pigeon pea (*Cajanus cajan* L.) is a vital legume crop known for its role in enhancing the sustainability of agricultural systems, particularly in semi-arid and resource-limited regions. Its ability to fix atmospheric nitrogen through symbiotic association with *Rhizobium*, by producing nodules should be explored further. The present investigation was carried out with 53 extra-early genotypes of pigeon pea during *Kharif* 2024 using completely randomized design (CRD) with three replications at ICRISAT, Patancheru. Significant variation was recorded for majority of traits. High GCV and PCV were observed for nodule dry weight followed by total number of nodules. High heritability along with high genetic advance as per cent of mean was observed for days to 50 per cent flowering, total number of nodules and nodule dry weight. The results indicated that higher plant dry weight was associated with higher nodule number and nodule weight along with better morphological traits. Among 53 genotypes studied ICPX 181018-B-SS3-SS1-1-B and ICPX 181028-B-SS22-SS1-1-B were found to have higher mean performance for all the observed characters.

Keywords: Pigeon pea, nodulation, GCV, PCV.

Introduction

Cajanus cajan L., with 11 pairs of chromosomes ($2n = 2x = 22$) is commonly known as pigeon pea, red gram, arhar, tur, togari, kandi (Sandeep *et al.*, 2013) a multipurpose drought-tolerant crop cultivated mainly for its edible seeds which are high in dietary protein. It plays a crucial role in food and nutritional security by serving as a rich source of protein, carbohydrates, vitamins, and minerals for millions of people. In India, pigeon pea is traditionally grown under rainfed conditions and often intercropped with cereals or oilseeds due to its drought tolerance and ability to fix atmospheric nitrogen, thereby improving soil fertility. Apart from human consumption, it is also used as forage, feed, and meal for animals, piggery, and fishery.

Pigeon pea is a crucial crop in the semi-arid tropics, cultivated across 24 countries on approximately 6.03 million hectares, yielding about 5.3 million tons annually. India dominates this landscape, accounting for 82.20 per cent of the cultivated area (5.01 million hectares) and 77.60 per cent of the total production (4.3 million tons). Other significant contributors to pigeon pea production include Myanmar, Malawi, Kenya and Tanzania, each contributing over 2 per cent. Within India, pigeon pea is grown in 25 states, covering an area of 5 million hectares and producing 4.3 million tons, resulting in a productivity rate of 861.2 kg per hectare FAO, (2023). The major states in terms of area and production are Karnataka (0.89 million hectares) Telangana (0.30 million hectares), Uttar Pradesh (0.29 million hectares), Gujarat (0.24 million hectares), Jharkhand

(0.23 million hectares) Andhra Pradesh (0.24 million hectares), Madhya Pradesh (0.25 million hectares) and Odisha (Indiastat, 2023).

Pigeon pea exhibits wide genetic diversity and adaptability to varied agro-climatic conditions. It is especially valued for its resilience to abiotic stresses such as drought and heat, and its ability to thrive in marginal soils. Moreover, its deep rooting system and symbiotic association with Rhizobium species make it a sustainable crop for low-input agriculture. Despite its importance, pigeon pea productivity remains relatively low due to constraints like susceptibility to pests and diseases, limited genetic improvement, and delayed adoption of high-yielding genotypes. To address important element of the pigeon pea breeding program and prevent a significant reliance on synthetic fertilizers, a well-designed study on root nodules is necessary. Therefore, choosing parents for breeding programs requires determining which genotypes of pigeon peas have the most root nodules in natural soil.

Assessing the mean performance of extra early genotypes for morphological traits along with their nodulation capacity will be one of the key components for sustainable agriculture.

Materials and Methods

The present experiment was conducted at International Crop Research Institute for the Semi-Arid Tropics, Patancheru, Hyderabad, Telangana (17.51°N latitude, 78.27°E longitude) state with 53 extra early genotypes of pigeon pea during *Kharif* 2024. Completely Randomized design was used to layout the experiment in the net house with three replications. Each genotype was sown in three plastic covers of with two plants in each cover. Homogenous mixture of red soil, sand and compost were filled in each cover in the ratio of 3:2:1. Plants were uprooted during flowering stage to observe their nodulation capacity. Observation from each plant was recorded on 11 morphological traits *viz.,* days to 50 per cent flowering (DFF), shoot length (SL) (cm) , primary branches (PB), shoot dry weight (SDW) (g) , root length (RL) (cm) , number of basal roots (NBR), number of secondary roots (NSR), root dry weight (RDW) (g) , total number of nodules (TNN), nodules dry weight (NDW) (mg) , plant dry weight (PDW) (g). The data was recorded and was subjected to the analysis of variance using CRD ANOVA (Panse and Sukhatme, 1978). Phenotypic coefficient of variation and genotypic coefficient of variation interpretation was done as per Burton and DeVane 1953. Heritability and genetic advance as percentage of mean interpretation was done as per Johnson *et al.*, 1995.

Results and Discussion

Analysis of variance revealed significant differences among the genotypes with respect to all the characters studied at five percent level of significance. It also revealed significant differences between genotypes for all the characters except for number of basal roots indicating presence of sufficient amount of variability in all the 10 characters out of 11 characters studied. The grand mean, range, standard error, critical difference at five percent level of significance, phenotypic and genotypic coefficients of variation, heritability, genetic advance and genetic advance as percentage of mean are presented in table 1.

For days to 50 per cent flowering the range observed was from 42 days to 76.33 days and the mean observed for this trait was 61.55 days. These results are in concurrence with the findings of those reported by Shruthi *et al.* (2019) and Hussain *et al.* (2021). Twenty-nine genotypes had significantly less days to 50 per cent flowering compared to mean and twenty-four genotypes had more. Earliest flowering was observed in Pusa Arhar 16 which flowered within 42 days and late flowering in ICPL 22393 which flowered in 76.33 days. Standard error (SE) observed for the trait was 0.786 with critical difference (CD) of 2.77.

For shoot length the range observed was from 63.83 cm to 118.08 cm and the mean observed for this trait was 89.65 cm. Similar results were obtained by Ranjani *et al.* (2018), Shruthi *et al.* (2019) and Hussain *et al.* (2021). Twenty-eight genotypes had significantly higher shoot length than the grand mean of 89.65 cm. Minimum length was observed in Pusa Arhar 16 (63.83 cm) and maximum length in ICPL 19337 (118.08 cm). SE for this trait was 1.041 with CD of 12.05. For number of primary branches, the range observed was from 0.89 to 3.96 and the mean observed for this trait was 2.12. Twenty-five genotypes had significantly more branches than the grand mean of 2.12. Minimum number of branches were observed in ICPL 19105 (0.89) and maximum in ICPX 181028-B-SS22-SS1-1-B (3.96). SE for this trait was 0.076 with CD of 1.26.

For root length the range observed was from 23 cm to 55.58 cm and the mean observed for this trait was 36.41 cm. Similar results were obtained by Desai *et al.*, (2009). Twenty-seven genotypes had significantly more length than the grand mean of 36.41 cm. Minimum length was observed in ICPL 19364 (23.0 cm) and maximum length in ICPX 181004-B-SS6-SS1-1-B (55.58 cm). SE for this trait was 0.518 with CD of 8.01. For number of root nodules, the range observed was from 11.74 to 97.78 and the mean observed for this trait was 43.53. Similar results were obtained by Rupela *et al.*, (1995). Twenty-five genotypes had significantly more nodules than the grand mean of 50.34. Minimum number of root nodules were observed in ICPL 22300 (10.78) and maximum in ICPX 181018-B-SS45-SS1-1-B (135.41). SE for this trait was 1.759 with CD of 19.48.

For number of basal roots, the range observed was from 2.33 to 5.31 and the mean observed for this trait was 3.80. Twenty-two genotypes had significantly more basal roots than the grand mean of 4.03. Minimum number of basal roots were observed in ICP 14178-1 (1.8) and maximum in ICPL 22388 (7.3). SE for this trait was 0.098 with CD of 1.92. For number of secondary roots, the range observed was from 8.49 to 21.66 and the mean observed for this trait was 12.91. Twenty-six genotypes had significantly more secondary roots than the grand mean of 13.79. Minimum number of secondary roots were observed in ICPL 19362 (8.4) and maximum in ICPX 181018-B-SS3-SS1-1-B (22.24). SE for this trait was 0.229 with CD of 3.34.

For Shoot dry weight, the range observed was from 2.92 g to 6.68 g (Rupela, 1995) and the mean observed for this trait was 4.68 g. Twenty-three genotypes had significantly more shoot weight than the grand mean of 4.68 g. Minimum shoot dry weight was observed in ICPL 85010 (2.59 g) and maximum in ICPL 19337 (6.68 g). SE for this trait was 0.121 with CD of 2.08. For root dry weight, the range observed was from 0.45 g to 1.79 g and the mean observed for this trait was 0.96 g. Similar results were obtained by Rupela *et al.* (1995). Twenty-three genotypes had significantly more root weight than the grand mean of 0.96 g. Minimum root dry weight was observed in ICPL 22300 (0.45 g) and maximum in ICPL 19072 (1.79 g). SE for this trait was 0.033 with CD of 0.46.

For root nodule dry weight, the range observed was from 2.81 mg to 353.26 mg and the mean observed for this trait was 97.17 mg. Similar results were obtained by Rupela *et al.* (1995). Twenty-two genotypes had significantly more nodule weight than the grand mean of 144.69. Minimum root nodule dry weight was observed in ICPL 22300 (2.81 mg) and maximum in ICPX 181018-B-SS45-SS1-1-B (353.26 mg). SE for this trait was 8.881 with CD of 80.44. For plant dry weight, the range observed was from 3.5 g to 8.03 g and the mean observed for this trait was 5.76 g. Thirty genotypes had significantly more plant weight than the grand mean of 5.76g. Minimum plant dry weight was observed in ICPL 85010 (3.5 g) and maximum in ICPX 181018-B-SS3-SS1-1-B (8.03 g). SE for this trait was 0.147 with CD of 2.49.

Mean value of all the characters for top 10 genotypes is given in Table 2. Two genotypes were found to have higher values for all the characters studied than grand mean.

ICPX 181018-B-SS3-SS1-1-B was having days to 50 per cent flowering 42 days with shoot length of 101.58 cm, primary branches 2.48, shoot dry weight 6.22 g, root length 43.92 cm, basal roots 4.46, secondary roots 21.66, root dry weight 1.60 g, total number of nodules 64.93, nodules dry weight 211.16 mg, plant dry weight 8.03 g.

ICPX 181028-B-SS22-SS1-1-B days to 50 per cent flowering of 53.67 with shoot length 102.50 cm, primary branches 3.96, shoot dry weight 6.01 g, root length 38.70 cm, basal roots 4.97, secondary roots 13.25, root dry weight 1.12 g, total number of nodules 45.21, nodules dry weight 209.66 mg, plant dry weight 7.35 g.

Table 1 : Estimation of variability parameters for different morphological traits

Traits	Range		Mean	Standard error	CD	GCV	PCV	h^2	GA	GAM
	Min	Max								
DFF	42.00	76.33	61.55	0.786	2.78	15.88	16.12	97.00	19.8	32.22
SL	63.83	118.08	89.65	1.041	12.05	12.04	14.64	67.73	18.29	20.4
NPB	0.89	3.96	2.12	0.076	1.26	24.99	44.19	31.98	0.62	29.11
RL	23.00	55.58	36.41	0.518	8.01	11.67	17.92	42.43	5.70	15.66
TNN	11.74	97.78	43.53	1.759	19.48	39.32	47.56	68.37	30.13	66.99
NBR	2.33	5.31	3.80	0.098	1.92	7.90	31.87	6.15	0.15	4.03
NSR	8.49	21.66	12.91	0.229	3.34	15.20	22.00	47.76	2.8	21.64
SDW	2.92	6.68	4.68	0.121	2.08	16.79	32.25	27.12	0.84	18.01
RDW	0.45	1.79	0.96	0.033	0.46	30.00	42.45	49.94	0.41	43.67
NDW	2.81	353.26	97.17	8.881	80.44	88.95	100.64	78.11	170.8	161.94
PDW	3.50	8.03	5.76	0.147	2.49	17.02	31.72	28.8	1.08	18.82

DFF: Days to 50 per cent flowering, SL: Shoot length (cm), NPB: Number of primary branches, RL: Root length (cm), TNN: Total number of nodules, NBR: Number of basal roots, NSR: Number of secondary roots, SDW: Shoot dry weight (g), RDW: Root dry weight (g), NDW: Nodules dry weight (mg), PDW: Plant dry weight (g).

Table 2 : Mean performance of top ten genotypes

Genotypes	DFF	SL	PB	RL	TNN	SDW	RDW	NDW	BR	SR	PDW
ICP 14178-1	48.30	92.17	3.30	38.00	80.90	5.43	0.79	168.44	2.33	11.30	6.39
ICP 7147-1	50.00	94.83	1.16	30.67	48.00	6.12	1.70	205.00	4.50	13.90	8.04
ICPL 19105	71.00	90.67	0.89	37.25	61.40	4.73	0.87	156.04	3.37	13.50	5.76
ICPL 22411	60.00	100.50	1.86	39.67	79.10	6.26	0.82	125.10	2.72	11.70	7.22
ICPL 22426	60.30	102.60	1.98	36.83	62.40	6.24	0.87	328.62	3.75	11.20	7.44
ICPL 87	49.00	73.87	2.57	38.28	65.30	4.56	0.98	199.28	5.16	17.80	5.76
ICP× 181018-B-SS3-SS1-1-B	42.00	101.50	2.48	43.92	64.90	6.22	1.60	211.16	4.46	21.60	8.03
ICPX 181018-B-SS45-SS1-1-B	59.00	88.83	1.30	41.17	97.70	4.77	1.19	353.26	4.80	13.30	6.32
ICPX 181018-B-SS66-SS1-1-B	68.30	92.17	1.47	42.00	55.80	5.59	1.30	98.01	3.64	10.90	7.00
ICPX 181028-B-SS22-SS1-1-B	53.60	102.50	3.96	38.70	45.20	6.01	1.12	209.66	4.97	13.20	7.35

DFF: Days to 50 per cent flowering, SL: Shoot length (cm), NPB: Number of primary branches, RL: Root length (cm), TNN: Total number of nodules, NBR: Number of basal roots, NSR: Number of secondary roots, SDW: Shoot dry weight (g), RDW: Root dry weight (g), NDW: Nodules dry weight (mg), PDW: Plant dry weight (g).

Coefficient of variation studied indicated that estimates of phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters. High GCV was observed for nodule dry weight (88.95) followed by total number of nodules (39.32), root dry weight (30.00) and number of primary branches (24.99). Similar results were observed by Hamid *et al.* (2011) and Saroj *et al.* (2013). Medium GCV was observed for plant dry weight (17.02), shoot dry weight (16.79), days to 50 per cent flowering (15.88), number of secondary roots (15.20) and shoot length (12.04). Low GCV was observed for number of basal roots (7.90). High PCV was observed for nodule dry weight (100.64) followed by total number of nodules (47.56), number of primary branches (44.19), root dry weight (42.45), shoot dry weight (32.25), number of basal roots (31.87), plant dry weight (31.72) and number of secondary roots (22.00). Medium PCV was observed for root length (17.92), days to 50 per cent flowering (16.12), shoot length (14.64). Similar results were obtained by SNCVL *et al.* (2018). The difference between PCV and GCV was lesser for the traits *viz.*, days to 50 per cent flowering and shoot length, indicating the lesser environmental influence for these traits suggesting simple selection will be rewarding for improving these traits. In contrast, the traits like number of primary branches, root length, total number of nodules, number of basal roots, number of secondary roots, shoot dry weight, root dry weight, nodules dry weight, plant dry weight exhibited a larger difference between PCV and GCV, suggesting a greater influence of environmental factors and hence, reduced efficiency of direct selection for these traits.

High heritability was observed for days to 50 per cent flowering (97.00) which is in accordance with the result obtained by Shruthi *et al.*, (2019) followed by nodules dry weight and least for basal roots (6.15). Genetic advance as percentage of mean was high for nodule dry weight (161.94) indicating this trait could be governed by additive gene action selection will be good based on this character. High heritability along with high genetic advance as per cent of mean was observed for days to 50 per cent flowering (97.00% and 32.22%) total number of nodules (68.37% and 66.99%) and nodule dry weight (78.11% and 161.94). Which means these traits could be governed by additive genes and selection will be very effective by considering these traits.

High heritability along with medium GAM was observed for shoot length (67.73% and 32.22). Which means the trait is genetically inherited, the expected gain through selection is modest and involvement of both additive and non-additive gene actions. Medium heritability along with high GAM was observed for number of primary branches (31.98% and 29.11%) and root dry weight (49.94% and 43.67%). Similar results were obtained by Vanniarajan *et al.* (2023). This suggests that the traits could be governed by additive gene action and could respond well to phenotypic selection. Medium heritability along with medium GAM was observed for number of secondary roots (47.76% and 21.64%). This suggests the possible involvement of additive and non-additive gene actions, and improvement through selection would be moderately effective.

Medium heritability along with low genetic advance as per cent of mean was observed for root length (42.43% and 15.66%) indicating the trait is likely influenced by non-additive gene action. Low heritability with medium GAM was observed for shoot dry weight (27.12% and 18.01%) and plant dry weight (28.80% and 18.82%). Indicating that the trait is largely influenced by environmental factors and selection may be effective under controlled conditions or over multiple environments. Low heritability and low GAM were observed for number of basal roots (6.15% and 4.03%). Which means the trait is environmentally influenced and selection should be delayed or based on multiple environments. Higher plant dry weight was observed to be associated with higher nodule number and nodule weight along with better morphological traits.

In any selection program, one of the key criteria for eliminating the unwanted types is the genotypes' average performance for each specific character. The current study's results identified notable variations in 53 pigeon pea genotypes for various morphological characters studied along with their nodulation efficiency. The mean performance of the genotypes revealed the superiority of the genotypes ICPX 181018-B-SS3-SS1-1-B and ICPX 181028-B-SS22-SS1-1-B. Hence, the two genotypes should be utilized extensively in further breeding programmes for exploitation of desirable traits. These genotypes should be further assessed for yield and related traits in field condition and can be used in breeding programmes as a donor.

Conclusion

As the root system architecture and nodulation plays a major role in defining the performance of the genotypes in the current study an attempt was made to study the root nodulation capacity in extra early pigeon pea genotypes. Significant variation was observed among the genotypes for all traits under study, except for the number of basal roots. High GCV and PCV values were recorded for nodule dry weight, followed by the total number of nodules, indicating a high degree of variability for these traits among the genotypes studied. High heritability coupled with high genetic advance as per cent of mean was observed for days to 50 per cent flowering, total number of nodules and nodule dry weight indicating the additive gene action so the selection for these traits will be effective. Among the studied genotypes ICPX 181018-B-SS3-SS1-1-B and ICPX 181028-B-SS22-SS1-1-B were found to be best performing based on *per se* performance for all the traits. The identified genotypes could serve as a potential donors for further in-depth nodulation studies in pigeon pea.

References

Burton, G. W. and E. H DeVane (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron. J.,* **45(10)**: 478-481.

Desai, S. E. (2009). Genetics of fertility restoration and variability for nodulation and yield traits in pigeon pea (*Cajanus cajan* (L.) millsp.) (Doctoral dissertation, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani).

FAO (2023). FAOSTAT. Food and Agriculture Organization of the United Nations, Rome, Italy. Available at: https://www.fao.org/faostat/

Hamid, A., Husna, A., Haque, M.M. and Islam, M.R., 2011. Genetic variability in pigeon pea (*Cajanus cajan* L. Millspaugh). *Electron. J. Plant Breed.* **2(1)**: 117-123.

Hussain, M.E., S. Sharma, A.J. Joel, R. Ravikesavan, N. Senthil, and A. Senthil (2021). Genetic variability of agronomic traits in extra-early maturing Introgression Lines (ILs) of pigeon pea [*Cajanus cajan* (L.)]. *Electron. J. Plant Breed.*, **12(2)**: 507-514.

IndiaStat (2023). IndiaStat database. Datanet India Pvt. Ltd., New Delhi, India. Available at: https://www.indiastat. com/

Johnson, H.W., H.F. Robinson, and R.E. Comstock (1955). Estimates of genetic and environmental variability in soybeans. *Agron. J.,* **47**: 314–318.

Panse, V.G. and P. V. Sukhatme, 1967. Statistical methods for agricultural workers. ICAR, New Delhi. p. 134-192.

Ranjani, M.S., C. Vanniarajan, R.K. Saxena, A.J. Hingane, R Sudhagar and C.V. Kumar, 2018. Genetic variability and association studies for yield and its attributes in super-early pigeon pea (*Cajanus cajan* (L.) Millsp.) Genotypes. *Electron. J. Plant Breed.*, 9(2): 682-691.

Rupela, O.P. and C. Johansen 1995. Identification of non-nodulating, and low and high nodulating plants in pigeon pea. *Soil Biol. Biochem.*, **27(4-5)**: 539-544.

Sameer Kumar, C.V., S.J. Satheesh Naik, N. Mohan, R.K. Saxena, and R.K. Varshney (2017). Botanical description of pigeon pea [*Cajanus cajan* (L.) Millsp.]. *The pigeon pea genome*, pp.17-29.

Sandeep, T.N., S.H. Sharanakumar Hiregoudart, V. Arunkumar, and M. Lokesh (2013). Study on physico-chemical properties of selected pigeon pea (*Cajanus cajan* L.) cultivars. *Int. J. Process. Postharvest Technol.* 4(1): 1-6.

Saroj, S.K., M.N. Singh, Kumar, R.A.V.I.N.D.R.A., Singh, T.E.J.V.E.E.R. and M.K. Singh, 2013. Genetic variability, correlation and path analysis for yield attributes in pigeon pea. The bioscan, **8(3)**: 941-944.

SNCVL, P., K.N. Yamini, R. Anuradha, G. Kumar, C.S. Rani, C. Sudhakar, R.K. Saxena, R.K. Varshney, and C.S. Kumar, 2018. Genetic variability and correlation in pigeon pea genotypes. *Electron. J. Plant Breed.*, **9(1)**: 343-349.

Shruthi, H.B., A.J. Hingane, M.R. Sekhar, C.S. Kumar, J. Srivarsha, T.M. Bhosle, L. Prashanthi, B.B. Reddy, P. Sudhakar, A. Rathore and V. Anil Kumar (2019). Genetic variability for yield, physiological and quality traits in novel super-early pigeon pea (*Cajanus cajan* (L.) Millsp.). *Indian J. Pure Appl. Biosci.,* **7(6)**: 378-385.

Sreekumar, K., 1995. Genetic analysis of biological nitrogen fixation traits and yield components in cowpea (*Vigna unguiculata* (Linn). walp) (Doctoral dissertation, Department of Plant Breeding and Genetics, College of Agriculture, Vellayani).

Vanniarajan, C., P. Magudeeswari, R. Gowthami, S.M. Indhu, K.R. Ramya, K. Monisha, M.A. Pillai, N. J.K. Verma and Yasin (2023). Assessment of genetic variability and traits association in pigeon pea [*Cajanus cajan* (L.) Millsp.] germplasm. *Legume Res.*, **46(10)**: 1280-1287.