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Research Article

PERFORMANCE OF PIGEON PEA (*Cajanus cajan*) GENOTYPES UNDER MID ALTITUDE CONDITIONS OF NAGALAND

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ABSTRACT

Eleven genotypes along with one check variety of Pigeon pea (*Cajanus cajan*) were evaluated under the research field of Genetics and Plant Breeding Medziphema, Nagaland during kharif season 2017-2018. Data were recorded on nine quantitative characters and the analysis of variance revealed significant differences among genotypes for all characters, indicating high degree of variability present in the material. The maximum genotypic variance was observed for secondary branches per plant followed by number of pods per plant. High phenotypic variance was also observed for secondary branches per plant followed by number of pods per plant. The high estimates of genotypic and phenotypic coefficient of variation were obtained for number of pods per plant highlighting the presence of wider genetic variability for this character. Secondary branches per plant revealed maximum heritability estimates followed by number of pods per plant, days to 50% flowering and days to maturity. Genetic advance as percentage of mean was recorded highest for number of pods per plant followed by secondary branches per plant and primary branches per plant. High heritability along with high genetic advance were observed for primary branches per plant, secondary branches per plant and number of pods per plant suggesting additive gene action for these characters.

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INTRODUCTION

Pigeon pea is an important multi-use shrub legume of the tropics, sub-tropics and warmer regions of the world between 30°N and 35°S latitude. Unlike other grain legumes, Pigeon pea production is concentrated in developing countries, particularly in South and South East Asia and eastern and southern African countries. Its main use is as Daal in the vast majority of the vegetarian diet, and also serves as a back bone of nutritional security as its grain is of high nutritional value with high protein content that ranges from 21% to over 25%. Besides its rich nutritional value, it also helps in sustaining the soil productivity through symbiotic fixation of atmospheric nitrogen into the soil as well as the leaf fall helps in recycling of nutrients in the soil.

Seeds of arhar are also rich in iron and iodine. They are rich in essential amino acids like lycine, tyrosine, cystine and arginine. According to FAO statistics 2013-14, the world production of pigeon pea was 4.68 million tons in an area of 4.23 million hectares. India is the largest producer of pigeon pea accounting up to 66 % of total production. It occupies an area of 5.32 million hectares with a production of 4.78 million tons respectively during 2016-2017. In Nagaland, pigeon pea

occupies an area of 3,010 hectare with production of 2,701 metric tonnes according to statistic from National Conference on Agriculture from Kharif Crop, Govt of Nagaland, 2015. In this crop, breeding of early maturing pigeon pea parents is an important tool to develop varieties that can avoid frost and widen the genetic base of hybrids and also adoption of varieties in new potential areas is to be studied so as to widen total area under this crop. Therefore study of amount of variability present in crop species is a pre-requisite as it provides basis for effective selection and also for selecting desirable genotypes needed for further crop improvement programs. Considering the importance of above mentioned points, studies to assess genetic variability and performance of genotypes was conducted.

MATERIALS AND METHODS

The investigation was carried out in the experimental field of Genetics and Plant Breeding Department, NU; SASRD, Medziphema campus during Kharif season of 2017 with 11 early varieties of Pigeon pea along with one check variety. The genotypes were evaluated under randomized block design with three replications with spacing of 60X30 cms between rows and plants respectively.

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Table 1 Details of the genotypes

CODE	GENOTYPE	CODE	GENOTYPE
G1	AL-1849	G7	AL-1758
G2	AL-1756	G8	PA-440
G3	AL-2025	G9	PA-421
G4	AL-1871	G10	PA-441
G5	AL-2021	G11	PA-291
G6	AL-1760	G12	UPAS-120 (check)

significance, indicating the presence of considerable amount of variability among the genotypes.

High genotypic coefficient variation (GCV) was observed for number of pods per plant (21.03%) (Table III). Joshi *et al.* (2003) and Bhadru (2010) also observed high GCV in number of pods per plant. Moderate GCV was observed for secondary branches per plant (18.64%) followed by primary branches per plant (11.57%).

Table 2 Analysis of variance for nine characters in 12 genotypes of pigeon pea.

Source of variation	Degree of freedom	Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	Primary branches per plant	Secondary branches per plant	Number of pods per plant	Number of seeds per pod	Test weight (g)	Yield per plant
Replication	2	65.44	342.19	2589.36	81.19	130.52	540.77	0.01	0.24	3.65
Genotypes	11	280.39**	29.32**	781.44*	43.56**	4639.66**	3613.89**	0.54**	4.98**	19.05*
Error	22	35.41	3.98	251.42	7.01	56.31	431.80	0.11	1.29	7.67

** , *:- Significant at 1% and 5% levels of probability respectively

Table 3 Mean performance in respect of nine characters for 12 genotypes of Pigeon pea.

Characters Sl no.	Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	Primary branches per plant	Secondary branches per plant	No. of pods per plant	No. of seeds per pod	Test weight (g)	Yield per plant (g)
1	114.33	193.67	176.00	26.33	205.33	129.00	3.46	17.46	31.13
2	122.67	193.00	182.00	29.33	193.33	106.67	3.52	17.11	32.40
3	108.00	192.33	172.00	23.33	132.33	121.00	4.16	17.65	27.37
4	98.33	191.00	181.00	28.00	187.00	159.00	5.04	19.36	30.06
5	107.00	192.00	200.00	34.00	253.33	120.00	4.09	18.66	33.49
6	116.33	193.00	204.67	30.33	207.67	187.67	4.18	16.85	32.59
7	108.67	193.00	219.67	33.33	235.67	155.00	4.53	19.58	29.73
8	123.67	193.67	194.00	30.33	177.67	120.00	4.45	16.53	29.31
9	120.67	194.00	170.67	33.00	251.00	187.67	4.52	20.30	34.47
10	115.67	193.33	195.33	32.00	173.67	204.67	4.28	19.17	33.47
11	113.00	196.33	183.67	35.67	264.67	197.67	4.33	20.04	36.35
12	91.33	183.33	164.33	25.00	234.00	169.00	4.30	18.29	33.27
G. Mean	111.64	192.39	186.94	30.06	209.64	154.78	4.24	18.42	31.97
SEM±	1.98	0.66	5.28	0.88	2.50	6.92	0.11	0.37	0.92
C.D-5%	10.01	3.35	26.78	4.47	12.66	35.10	0.53	1.90	4.67
C.D-1%	13.67	4.56	36.49	6.09	17.25	47.82	0.73	2.59	6.37

Table 4 Genetic parameters for nine quantitative characters of pigeon pea.

Characters	Components of Variance		Coefficient of variation (%)		Heritability (%)	GA at percent of Mean		
	Mean	Range	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)			GCV	PCV
Days to 50% flowering	111.64	91.33-123.67	81.66	117.07	8.08	9.67	83.53	16.55
Days to maturity	192.39	183.3-196.3	8.44	12.42	1.50	1.82	83.38	3.08
Plant Height (cm)	186.94	164.3-219.6	176.67	428.09	7.10	11.06	64.23	14.58
Primary branches per plant	30.06	23.33-35.67	12.18	19.19	11.57	14.57	79.45	23.68
Secondary branches per plant	209.64	132.3-264.6	1527.78	1584.09	18.64	18.38	98.19	38.32
Number of pods per plant	154.78	106.6-204.6	1060.69	1492.49	21.03	24.95	84.28	43.18
Number of seeds per pod	4.24	3.46-5.04	0.14	0.25	8.72	11.79	74	17.92
Test weight (g)	18.42	16.53-20.30	1.23	2.52	5.97	8.57	69.62	12.16
Yield per plant (g)	31.97	27.37-36.35	3.79	11.46	6.06	10.57	57.39	12.38

Observations were recorded on nine quantitative characters viz, days to 50% flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, number of pods per plant, number of seeds per pod, test weight and seed yield per plant. The details of the genotypes are given in Table I

RESULTS AND DISCUSSION

The analysis of variance for yield and its component character are presented in Table II. All the genotypes differed significantly for all the quantitative characters, All the genotypes were found to be significant at 1% and 5% level of

Low GCV was observed for number of seeds per pod (8.72%), days to 50 % flowering (8.08%), plant height (7.10%), test weight (5.97%), yield per plant (6.06%) and days to maturity (1.50%).

High phenotypic coefficient of variation (PCV) was exhibited by number of pods per plant (24.95%). Rangare *et al.* (2013) and Bhadru (2010) also observed high PCV for number of pods per plant. Moderate PCV was observed in secondary branches per plant (18.38%), followed by primary branches per plant (14.57%). number of seeds per pod (11.79%), plant height (11.06%) and yield per plant (10.57%). Singh *et al.* (2013) also observed moderate PCV in the same character. The lowest PCV was observed in days to maturity (1.82%) followed by

test weight (8.57%) and days to 50 % flowering (9.67%). In the present investigation, the comparisons among the characters revealed that, high estimates of GCV and PCV was observed for number of pods per plant, highlighting the presence of wider variability for this character as compared to other characters.

Similar findings were also reported by Bhadru (2010), Singh *et al.* (2013), Rangare *et al.* (2013), Rao and Rao (2015). This signifies that there is sufficient scope for the improvement of this character through selection. The analysis of genotypic and phenotypic coefficient of variation showed that GCV estimates were closer to the PCV estimates for days to maturity and secondary branches per plant, indicating lesser influence of environment in the expression of the characters.

This seems to be valid as the heritability estimates of these characters are high. On the other hand, the characters days to 50% flowering, plant height, primary branches per plant, no. of seeds per pod, test weight and yield per plant, PCV was of much higher magnitude than the GCV, indicating the characters are much prone to environmental fluctuation. Meena *et al.* (2017) also reported that magnitude of PCV was higher than GCV for the same characters. Thus, from the present study, it can be suggested that a magnitude of variability is present in these genotypes, which can be exploited in genetic improvement.

A high estimates of heritability coupled with high genetic advance indicates that such characters are under predominant control of additive gene action, but if the high heritability is due to non-additive gene effects, the genetic advance will be low. High heritability along with high genetic advance were observed for primary branches per plant, secondary branches per plant and number of pods per plant suggesting additive gene action for these characters leading to further improvement for their performance and these traits can be used as selection criteria in breeding programmes. Gowda *et al.* (2003), Kumara *et al.* (2013) and Sharma *et al.* (2014) also reported high heritability coupled with high genetic advance for number of pods per plant while Saroj *et al.* (2015) reported for primary and secondary branches per plant.

However, high heritability associated with moderate to low genetic advance was observed in yield per plant, days to 50% flowering, plant height, number of seeds per pod, test weight and days to maturity which indicates that these characters were under control of complex nature of inheritance. Similar findings were reported by Gowda *et al.* (2003), Arshad *et al.* (2003).

The findings suggest that, PA-291 can be used as a promising genotype since it exhibited high primary and secondary branches, high number of pods per plant, high test weight and exhibited higher yield over the check variety UPAS 120. The genotypes *viz.* UPAS-120 which takes the least days to flower and shortest height, PA-421 which has the maximum test weight and PA-441 which have the maximum pods per plant may be considered as potential genotypes for incorporation in pigeon pea breeding programme.

References

1. Arshad M, Bakhsh A, Zubiar M and Abudul Ghafoor. 2003. Genetic variability and correlation studies in chickpea. *Pakistan Journal of Botany*. 35 (4): 605-611.
2. Bhadru D. 2010. Studies on genetic parameters and interrelationships among yield and yield contributing traits in pigeon pea [*Cajanus cajan* (L.) Millsp.].
3. Gowda C L L, Gaur P M and Saxena K B. 2003. International Research and Development Activities on Chickpea and Pigeon Pea. In: Souvenir of National symposium on pulses for crop diversification and natural resources management, Kanpur, 20-22 December 2003. Indian Institute of pulse Research, Kanpur. ppl 17-25.
4. Joshi V C, Patel, Parmar L D, Solanki S D and Chauhan R M. 2003. Variability and association analysis in pigeon pea [*Cajanus cajan* (L.) Millsp.]. In: Abstract of the National Symposium on Pulse for crop diversification and National resource management. 76.
5. Kumara B N, Santoshagowda G B, Nishanth G K and Dharmaraj P S. 2013. Genetic diversity, variability and correlation studies in advanced genotypes of pigeon pea [*Cajanus cajan* (L.) Millsp.]. *Research Article, Acta Biological Indica*. 2 (2): 406-411.
6. Meena B L, Das S P, Meena S K, Kumari R, Devi A G and Devi H L. 2017. Assessment of GCV, PCV, heritability and genetic advance for yield and its components in field pea (*Pisum sativum* L.). *International Journal of Current Microbiology and Applied Sciences*. 6 (5): 1025-1033.
7. Rangare N R, Reddy G E and Kumar S R. 2013. Study of heritability, genetic advance and variability for yield contributing characters in pigeon pea (*Cajanus cajan* (L.) Millsp). *Trends in Biosciences*. 6 (5):660-662.
8. Rao Jagan Mohan and Rao Thirumalala. 2015. Genetic analysis for yield and its components in pigeon pea. *International Journal of Applied Biology and Pharmaceutical Technology*. 6 (2): 189-190.
9. Saroj S K, Singh R S, Singh M and Pathak N. 2015. Studies on genetic variability of parents, F₁'S and F₂'S populations in pigeon pea. *Agriculture for sustainable Development*. 3 (1): 32-36.
10. Sharma Ritesh, Gangwar Raveesh Kumar, Yadav Vivek 2014. A study on genetic variability and correlation in pigeon pea. *International Journal of Science and Research*. 3 (9): 826-828.
11. Singh J, Fiyaz R A, Sudhir Kumar M A, Anasari and Sanjay Gupta. 2013. Genetic variability, correlation and path coefficient analysis for yield and its attributing traits in pigeon pea grown under rainfed conditions of Manipur. *Indian Journal of Agricultural Sciences*. 83 (8):858.
