

Original Research Article

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Study on the Genetic Variability, Heritability and Genetic Advance in Pigeon Pea (*Cajanus cajan* (L.) under Chitrakoot Climate Condition

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ABSTRACT

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Pigeon pea or red gram [*Cajanus cajan* (L.) Millsp] is one of the important pulse crop .The Experiment was conducted at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna to evaluate the Thirty genotypes/varieties under normal soil and rain fed condition. The experiment was laid out following Randomized Block Design (RBD) with three replications during *Kharif* 2018; The place of experiment in Chitrakoot is situated at 25⁰10' North latitude and 80⁰85' East longitude. The altitude is about 200m above mean sea level The experiment was sown on 29th, July, 2018 and harvested on 18th,February,2019 . Each treatment was grown in 4 m long 6 rows per plot spaced 90 cm apart. The plant to plant distance was maintained 25cm by thinning. Recommended agronomic cultural practices and plant protection measures were adopted to raise a best crop. Observation were recorded Days to 50% flowering, Number of primary branches per plant, Number of secondary branches per plant:, Number of pods per plant, Plant height (cm), Days to Maturity (DM),100-Seed weight (g) and Seed yield (kg/ha). On the basis of above per se varieties- ICPL 87119, LRG 134 and BDN 2013-1 and BRGL 18-1 are found suitable and best performer in terms of yield and yield contributing characters in agro- climatic condition of Chitrakoot.

Introduction

Pigeon pea or red gram [*Cajanus cajan* (L.) Millsp] is one of the important *kharif* pulse crop of subsistence agriculture. Globally, pigeon pea is cultivated worldwide in developing countries under tropical and subtropical climatic conditions with variety of cropping systems. Generally, split seeds of pigeon pea is used as dhal (dry, defueled, split

seed used for cooking) which fulfills requirement of dietary protein. Besides its main use as dhal, tender green seeds are used as a vegetable, while crushed dry seeds serve as animal feed, green leaves as fodder, and stems as fuel wood and to make huts, baskets, etc. Among various grain legumes grown, pigeon pea [*Cajanus cajan* (L.) millsp.] is the second most important crop of India, belonging to tribe-Phaseoleae subtribe -

cajaninae, family – leguminosae, genus – cajanus and species – cajan with chromosome number $2n = 22$. Pigeon pea has versatile use as food, feed, fuel and fodder. It is called by an array of names viz., Arhar, Cango Pea, Angole, Rahar, Red Gram and Tur. The name pigeon pea was first reported for plants used in Barbados, where seeds were considered as most useful feed for pigeon (Plukent, 1692). According to Vander Maesen (1986) pigeon pea originated in India and spread to other countries quite early endowed with several unique characteristics.

Pigeon pea like most other grain legume crops has lost genetic variability during the process of its domestication. Most present day plant breeding efforts in developing high yielding varieties aim at defect elimination i.e., developing resistant varieties to biotic (wilt, SMD, Phytophthora, and pod borer) and abiotic (moisture, high or cold temperature) stresses. Systematic studies to rebuild the plant type to improve the genetic yield potential of pigeonpea are very limited. In view of above, the following strategies are needed for genetic enhancement in the crop. Therefore, it is necessary to increase the production of pigeon pea, which could be done opting suitable, breeding methods. To overcome such situation, genetically stable genotypes having high yield potential are urgently needed. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genetic coefficient of variability (GCV), heritability estimates (H) and genetic advance (GA). Pulse crop plays an important role in Indian economy. They are often referred to as “poor man’s meat”, since they are cheaper source of high quality protein. Grain legumes or pulses occupy an important place in man’s food and nutritional requirements. They are important constituents in the diets of a very large number of people, especially in the

developing countries and are good source of protein which helps to supplement cereal diets, improving their nutritive values.

Now a days, prices of pulses have increased significantly as compared to other food crops pushing pulses out of the reach of poor masses. Declining per capita availability of pulses indicates that pace of technological development could not commensurate with the demand of pulses. Wide fluctuation in pulses production particularly in developing countries including India remains a big challenge and needs critical analysis of the factors contributing toward instability in productivity. A holistic approach to develop improved varieties and production technology for different agro-ecological regions and cropping systems is imperative. This requires efforts in consortium mode to foster the necessary framework of knowledge and materials that will result in major scientific breakthroughs. Genetic variability is the key of any crop improvement programme. This provides an opportunity for breeders to combine desired genes into novel genotypes for enhancing the yield and stability of economically important crop plants. Germplasm serve as the most valuable natural resource for providing useful characters for developing high yielding input responsive genotypes resistant to various biotic and abiotic stresses. Therefore, evaluation of germplasm under the prevailing environments is essential for selecting the donor parents for the traits to be improved in breeding programme.

Materials and Methods

The Experiment was conducted at Agriculture Farm, Nana Ji Deshmukh New Agriculture Campus, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidyalaya, Chitrakoot, Satna to evaluate the Thirty genotypes/varieties under normal soil and rain

fed condition. The experiment was laid out following Randomized Block Design (RBD) with three replications during *Kharif* 2018, The place of experiment in Chitrakoot is situated at 25°10' North latitude and 80°85' East longitude. The altitude is about 200m above mean sea level The experiment was sown on 29th, July, 2018 and harvested on 18th, February, 2019. Each treatment was grown in 4 m long 6 rows per plot spaced 90 cm apart. The plant to plant distance was maintained 25cm by thinning. Recommended agronomic cultural practices and plant protection measures were adopted to raise a best crop. Observation were recorded Days to 50% flowering, Number of primary branches per plant, Number of secondary branches per plant:, Number of pods per plant, Plant height(Cm), Days to Maturity (DM), 100-Seed weight (g) and Seed yield (kg/ha).

Results and Discussion

The present investigation was carried out with 30 diverse genotypes/varieties of pigeon pea (*Cajanus cajan* L. Millsp.). These varieties were grown during *kharif* season 2018-19.

Genetic variability studies

The results on range and coefficient of variation are presented character wise in Table 1. In general, phenotypic coefficients of variation were higher than genotypic coefficient of variation for all the characters.

Days to 50% flowering

The data presented in the table revealed that, days to 50% flowering ranged from 89.67 days (PT 0704-1-2) to 108.33 days (LRG 134) and the grand mean was 96.48 days. The phenotypic and genotypic coefficients of variation were 5.65 and 4.92, respectively was found low values for this character.

Number of primary branches per plant

The data portrayed in table in respect of the number of primary branches per plant varied from 12.00 (SKNP 1413) to 20.00 (ICPL 15048) and the grand mean was 15.53. The phenotypic (16.21) and genotypic (12.81) coefficient of variation was found moderate values for this character indicating that environment has played significant role in the expression of this character.

Number of secondary branches per plant

The data depicted in table in respect of the number of secondary branches per plant varied from 10.33 (BRGL 18-1) to 37.67 (ICPL 87119) and the grand mean was 21.28. The phenotypic (34.93) and genotypic (33.23) coefficient of variation was found high values for this character indicating that environment has played significant role in the expression of this character.

Number of Pods per plant

The data depicted in table in respect of the number of pods per plant ranged from 276.00 (GJP 1715) to 443.33 (ICPL87119) and the grand mean was 325.59. The phenotypic (19.71) and genotypic (18.91) coefficient of variation was found very high for this character indicating that environment has played significant role in the expression of this character.

Plant height (cm)

The result portrayed in table exhibited that the plant height ranged from 91.33 (BRGL 18-1) to 152.00 (BDN 2013-1) and the grand mean was 123.62. The phenotypic (14.27) and genotypic (13.69) coefficient of variation was found moderate for this character indicating that environment has played significant role in the expression of this character.

Table.1 Mean, range, genotypic, phenotypic and coefficient of variation for Eight quantitative characters in Pigeon pea

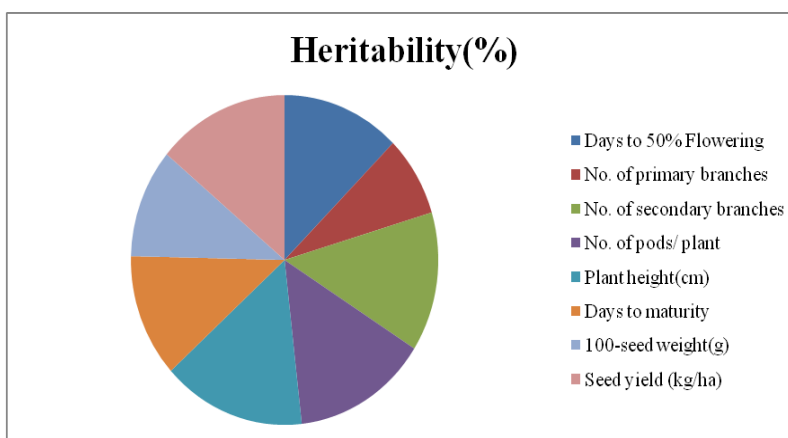
S. No.	Characters	Grand mean (\bar{X}) + SE (m)	Range		Coefficient of Variation		C.V. (%)
			Min.	Max.	GCV	PCV	
2	No. of primary branches	15.53±1.20	12.00	20.00	12.81	16.21	13.40
3	No. of secondary branches	21.28±1.61	10.33	37.67	33.23	34.93	13.12
4	No. of pods/ plant	325.59±23.44	276.00	443.33	18.91	19.71	12.47
5	Plant height(cm)	123.62±8.52	91.33	152.00	13.69	14.27	11.94
6	Days to maturity	180.11±2.90	171.00	199.33	4.19	4.95	2.80
7	100-seed weight(g)	11.64±0.52	10.07	13.57	7.70	8.89	7.70
8	Seed yield (kg/ha)	1483.22±233.60	1093.13	2473.68	27.64	30.42	17.27

* Significant at 5% probability level; ** Significant at 1% probability

Table.2 Heritability (%) in broad sense, genetic advance and genetic advance in percent of mean Tentative characters in Pigeon pea

S. N.	Parameters	Standard Deviation	Heritability (%) (in broad sense)	Genetic Advance	Genetic Advance value % means
1	Days to 50% Flowering	2.16	76.05	8.48	8.85
2	No. of primary branches	1.26	62.50	3.24	20.87
3	No. of secondary branches	1.87	90.52	13.87	65.13
4	No. of pods/ plant	14.89	92.02	122.37	37.36
5	Plant height(cm)	4.10	92.04	33.71	27.06
6	Days to maturity	3.85	71.65	13.07	7.30
7	100-seed weight(g)	0.41	75.05	1.57	13.74
8	Seed yield (kg/ha)	150.73	82.54	751.12	51.72

* Significant at 5% probability level; ** Significant at 1% probability level



Days to maturity

The data exhibited in the table revealed that days to maturity ranged from 171.00 days (RKVP 911) to 199.33 days (BRGL 18-1) and the grand mean was 180.11 days. The phenotypic (4.95) genotypic (4.19) coefficient of variation was found very low for this character.

100-seed weight (g)

The boldest seed size was found in ICPL 87119 (13.57 g) and smallest seed size was in BDN 2013-1 (10.07 g) and the grand mean was 11.64 g. The phenotypic (8.89) and genotypic (7.70) coefficient of variation was found moderate for this character indicating that environment has played significant role in the expression of this character.

Seed yield (kg/ha)

A large amount of variability was found for seed yield (kg/ha) ranged from 1093.13 kg/ha (BDN2013-1) to 2473.68 kg/ha (ICPL 87119) and the grand mean was 1483.22 kg/ha. The phenotypic (30.42) and genotypic (27.64) coefficient of variation was found high values for this character indicating that environment has played significant role in the expression of this character.

Heritability and Genetic advance characters studies

Heritability in broad sense was computed for all the characters and has been presented in Table 2. In general, high estimates of broad sense heritability were observed for all the characters. The estimate of heritability values were ranged from 46.43 per cent for No. of primary branches/ plant to 88.61 per cent for plant height. The estimate of high heritability was found for plant height (88.61%), pods / plant (83.59%), seed yield (kg/ha)(81.93%)

and no. of secondary branches(80.50%) while moderate estimate of heritability was found for days to 50% flowering (73.28%), days to maturity (71.26%) and 100-seed weight (63.00%) whereas low was found in no. of primary branches (46.43%).

The expected genetic advance in per cent of mean ranged from 7.96 per cent for days to maturity to 55.79 per cent for no. of secondary branches. High heritability was found for no. of secondary branches (55.79%) followed by seed yield kg/ha (50.07), no. of pods / plant (34.58) and plant height (26.24) while moderate expected genetic advance in per cent of mean was found for no. of primary branches (14.61%), 100-seed weight (11.14%) whereas lowest expected genetic advance in per cent of mean was recorded for days to 50% flowering (8.49%) and days to 80% maturity(7.96).

The high heritability coupled with genetic advance was found high with seed yield kg/ha, pods per plant, plant height, days to maturity and no. of secondary branches while low heritability coupled with low genetic advance and days to 50% flowering where as other characters showed low values.

On the basis of above per se varieties- ICPL 87119, LRG 134 and BDN 2013-1 and BRGL 18-1 are found suitable and best performer in terms of yield and yield contributing characters in agro- climatic condition of Chitrakoot.

References

- Anil Sirohi and Lokendra Kumar (2006). Studies on genetic variability, heritability and genetic advance in mungbean (*Vigna radiata* L. Wilczek). *International Journal of Agricultural Sciences*, 2: (1): 174-176.
- Baskaran, K., and Muthiah, A. R. (2006).

- Interpretation of hybrid vigour in different cross combinations of pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Research on Crops*, 7(1), 243.
- Byregowda, M., Chandrapratap, J. and Jagadeesh Babu, C.S. (1997). Genetic variability and inter-relationship among yield and yield components in green gram [*Vigna radiata* (L.) Wilczek]. *Crop Res.*, 13 (2): 361-368.
- Gill, J.S., Gumber, R.K., Verma, M.M., Rathore, Pankaj and Rathore, P. (2000). Genetic estimates of advanced mungbean lines derived through different selection methods. *Crop Impro.*, 27 (1): 88-98.
- Johnson, H.W., Robinson, H.F. and Comstock, R.E. (1955). Estimates of genetic and environmental variability in soybeans. *Agron. J.* 47:314-318.
- Patel, K. N. and Patel, D. R. (1998). Studies on genetic variability in pigeonpea. *International Chickpea and Pigeonpea News letter*. 5: 28- 30.
- Pundir, S.R., Singh, V.P., and Gupta, K.R. (1992). Genetic variability for some quantitative traits in mungbean [*Vigna radiata* (L.) Wilczek]. *Haryana Agric. Univ. J. Res.*, 22 (2): 109-112.
- Ranjani, M.S., Vanniarajan, C., Kumar, C V Sameer, Saxena, R. K., Sudhagar, R. And Hingane Anupama J. (2018). Genetic variability and association studies for yield and its attributes in super-early pigeon pea (*Cajanus cajan* (L.) Millsp.) Genotypes. *Electronic Journal of Plant Breeding*, 9(2): 682-691.
- Reddy, D.M., Rao, Y.K., Murthy, S.N.S. and Reddy, M.V. (2004). Genetic variability and divergence in mungbean. *Indian J. Pulses Res.*, 17(1): 77-79.
- Singh, M., Singh, T.P., Sharma, S.K. and Thakur, H.L. (2010). Influence of cropping system on combining ability and gene action for grain yield and its components in black gram (*Vigna mungo*). *Indian J. Agri. Sci.* 73: 356-35.

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