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Estimation of heritability in pigeonpea [*Cajanus cajan* (L.) millsp.]

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Abstract

Six generations (P₁, P₂, F₁, F₂, BC₁ and BC₂) derived from three crosses (BDN 708 X BSMR 571, BDN 708 X BDN 2010-1 and BDN 711 X SKNP 0632) between different parents (BDN 708, BSMR 571, BDN 2010-1, BDN 711 and SKNP 0632) along with check BDN 716. The material was evaluated during Kharif 2018 in randomized block design with randomization of generation replicated twice at Agricultural research station, Badnapur. Narrow sense heritability was higher due to higher value of additive gene action for all the crosses. High estimates of heritability were observed in the cross BDN 708 X BSMR 571 for days to 50% flowering, days to maturity, number of primary branches per plant, pod length and seed yield per plant. The cross BDN 708 X BDN 2010-1 showed high heritability for plant height, number of seeds per pod and pod length. The cross BDN 711 X SKNP 0632 showed high heritability for number of primary branches per plant, number of pods per plant and pod length. Some crosses showed negligible heritability. Narrow sense heritability play an important role for selection of traits in plant breeding for crop improvement.

Keywords: Heritability, narrow sense heritability, high estimates, pigeonpea

Introduction

Pigeonpea (*Cajanus cajan* (L.) Millsp.) is the sixth most important grain legumes of tropics and subtropics. Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an often cross pollinated crop (20 – 70%) with diploid (2n = 2x) chromosome number of 22. It is commonly known as tur, red gram or arhar. It belongs to family leguminosae, sub family papilionaceae. It is a short-lived perennial shrub in which plants may grow for about five years and turn into small trees. It is a hardy, widely adapted and drought tolerant crop with a large temporal variation (90–300 days) for maturity. These traits allow its cultivation in a range of environments and cropping systems. It is the most versatile food legume with diversified uses as food, feed, fodder and fuel. It is one of the important pulse crop of India and ranks second to chickpea in area and production. Invariably, the traditional pigeonpea cultivars and landraces are of long duration and grown as intercrop with other earlier maturing cereals and legumes. It is an important pulse mostly grown in Asia, Africa, Latin America and the Caribbean islands. Considering the vast natural genetic variability in local germplasm and presence of various wild relatives, India is considered as the primary centre of origin of pigeonpea. Pulses are also important for sustainable agriculture, enriching the soil through biological nitrogen fixation. They enrich the soil with nitrogen up to 20-40 kg N/ha and organic matter through leaf fall and profuse underground root growth. Its roots help in releasing soil-bound phosphorus to make it available for plant growth with so many benefits at low cost, pigeonpea has become an ideal crop for sustainable agriculture systems in rain-dependent areas. In India pigeonpea is grown on an area of 4.45 M. ha with average total production of 4.18 M. tones and productivity about 937 kg/ha during 2018-19. In Maharashtra during 2018-19 pigeonpea cover the area about 12.20 lakh ha with production about 10.56 lakh tones and productivity about 866 kg/ha (Anonymous, 2019). Major pigeonpea producing states are Maharashtra (27.56%, 25.33%), Karnataka (19.85%, 17.44%), Madhya Pradesh (14.51%, 20.07%), Andhra Pradesh (6.23%, 2.82%), Uttar Pradesh (6.32%, 7.25%) and Gujarat (6.08%, 7.68%) with area and production respectively. In pigeonpea Maharashtra is first in area (27.56%) and production (25.33%). The choice of an appropriate selection/breeding method and its success for improvement of quantitative traits largely depends on the extent of genetic variability present in segregating material and gene action. Knowledge on genetic architecture of yield and related traits plays an important role in deciding breeding strategies and methodologies for crop improvement. In

Comparison to other economically important crops, relatively less effort has been made to understand the genetics of important quantitative traits in pigeonpea. Pleiotropic effects of gene, physiological changes and highly sensitive nature of pigeonpea towards the environmental changes make it difficult to interpret the inheritance of yield and associated traits. There are different analysis methods to estimate genetic basis of quantitative variability of the selected plant characters. One of the best methods for the estimation of genetic parameters is the generation mean analysis, in which epistatic effects could also be estimated. Information about nature and magnitude of gene action can be useful for breeding program. Yield and its component characters that are quantitative in nature exhibit all the three types of gene action.

Materials and Methods

Six basic generations viz., P₁, P₂, F₁, F₂, B₁ and B₂ derived from two crosses viz., BDN 708 × BSMR 571, BDN 708 × BDN 2010-1 and BDN 711 × SKNP 0632 were produced and evaluated in a Compact Family Block Design with two replications during *Kharif* 2018 season at Agricultural Research Station, Badnapur. Each plot consisted of a two rows of parents, F_{1s}, BC₁ and BC₂ each and four rows of F₂ generation. Recommended package of practices were followed throughout the crop season. Data were recorded on

five randomly selected plants from each generations excluding border plants. Each row was consisted of 3m length and row to row and plant to plant distance being 90 and 20 cm, respectively. All the agronomic practices were followed to raise a good crop. For each family the plot means values in each generation were averaged over replication to obtained generation means. These generations mean formed the basis of calculation of various genetic parameters. The means, variance, variances of mean and standard errors of each of the six generations were estimated. Analysis of data was performed following six parameter model.

Result and Discussion

Heritability estimates for days to 50% flowering (Table 1) revealed low level of narrow sense heritability for the crosses viz., BDN 708 X BDN 2010-1 (1.75%) and BDN 711 X SKNP 0632 (8.35%), whereas high estimates of narrow sense of heritability were observed in the cross BDN 708 X BSMR 571 (41.33%).

Heritability estimates for days to maturity (Table 1) revealed low level of narrow sense heritability for the crosses viz., BDN 708 X BDN 2010-1 (17.7%) and BDN 711 X SKNP 0632 (14.5%), whereas high estimates of narrow sense of heritability was observed in the cross BDN 708 X BSMR 571 (29.41%).

Table 1: Narrow sense heritability percentage in three crosses of pigeonpea (*Cajanus cajan* (L.) Millsp.)

Sr. No. Crosses	Heritability	BDN 708 X BSMR 571	BDN 708 X BDN 2010-1	BDN 711 X SKNP 0632
Character days to 50% flowering				
1.	h ² (Narrow sense Heritability)	41.33	1.75	8.35
Character days to maturity				
2.	h ² (Narrow sense Heritability)	29.41	17.7	14.5
Characters plant height				
3.	h ² (Narrow sense Heritability)	29.8	75.8	18.4
Character No. of primary branches				
4.	h ² (Narrow sense Heritability)	50.2	38.6	91.4
Character No. of secondary branches				
5.	h ² (Narrow sense Heritability)	13.66	8.20	22
Character No. of pods per plant				
6.	h ² (Narrow sense Heritability)	32.1	17.9	64
Character No. of seeds per pod				
7.	h ² (Narrow sense Heritability)	10.01	49.4	37.04
Character pod length				
8.	h ² (Narrow sense Heritability)	51.7	80.2	56.3
Character 100-seeds weight				
9.	h ² (Narrow sense Heritability)	20.5	10.2	5.15
Character Seed yield per plant				
10.	h ² (Narrow sense Heritability)	52.9	23.7	20.7

The high level of narrow sense heritability for plant height were observed (Table 1) for the crosses viz., BDN 708 X BDN 2010-1 (75.8%) and BDN 708 X BSMR 571 (29.8%), whereas low estimates of narrow sense of heritability were observed in the cross BDN 711 X SKNP 0632 (18.4%).

The high level of narrow sense heritability for number of primary branches per plant were observed (Table 1) for the crosses viz., BDN 708 X BSMR 571 (50.2%), BDN 708 X BDN 2010-1 (38.6%) and BDN 711 X SKNP 0632 (91.4%), whereas low estimates of narrow sense of heritability were not observed.

The low level of narrow sense heritability for number of secondary branches per plant were observed (Table 1) for the crosses viz., BDN 708 X BSMR 571 (13.66%), BDN 708 X BDN 2010-1 (8.20%) and BDN 711 X SKNP 0632 (22%),

whereas high estimates of narrow sense heritability were not observed in the crosses.

Heritability estimates for number of pods per plant (Table 1) revealed low level of narrow sense heritability for the crosses viz., BDN 708 X BSMR 571 (32.10%) and BDN 708 X BDN 2010-1 (17.90%), whereas high estimates of narrow sense of heritability were observed in the cross BDN 711 X SKNP 0632 (64%).

Heritability estimates for number of seeds per pod (Table 1) revealed low level of narrow sense heritability for the crosses viz., BDN 708 X BSMR 571 (10.10%), BDN 708 X BDN 2010-1 (49.4%) and BDN 711 X SKNP 0632 (37.04%), whereas high estimates of narrow sense of heritability were not observed.

Heritability estimates for pod length (Table 1) revealed high level of narrow sense heritability for the crosses viz., BDN 708 X BSMR 571 (51.70%), BDN 708 X BDN 2010-1 (80.20%) and BDN 711 X SKNP 0632 (56.30%), whereas low estimates of narrow sense of heritability were not observed.

Heritability estimates for 100-seeds weight (Table 1) revealed low level of narrow sense heritability for the crosses viz., BDN 708 X BSMR 571 (20.50%), BDN 708 X BDN 2010-1 (10.20%) and BDN 711 X SKNP 0632 (5.15%), whereas high estimates of narrow sense of heritability were not observed.

Heritability estimates for seed yield per plant (Table 1) revealed low level of narrow sense heritability for the crosses viz., BDN 708 X BSMR 571 (52.90%), BDN 708 X BDN 2010-1 (23.70%) and BDN 711 X SKNP 0632 (20.70%), whereas high estimates of narrow sense of heritability were not observed.

Conclusion

Narrow sense heritability was higher due to higher value of additive gene action for all the crosses. High estimates of heritability were observed in the cross BDN 708 X BSMR 571 for days to 50% flowering, days to maturity, number of primary branches per plant, pod length and seed yield per plant. The cross BDN 708 X BDN 2010-1 showed high heritability for plant height, number of seeds per pod and pod length. The cross BDN 711 X SKNP 0632 showed high heritability for number of primary branches per plant, number of pods per plant and pod length. Some crosses showed negligible heritability. Narrow sense heritability play an important role for selection of traits in plant breeding for crop improvement.

References

1. Aher RP, Thombare BB, Dahat DV. Genetic variability and character association in pigeonpea (*Cajanus cajan* (L.) Millsp.). Legumes Res. 1998; 21(1):41-44.
2. Basavarajaiah D, Gowda MB, Lohithaswa HC, Kulkarni RS. Assessment of pigeonpea (*Cajanus cajan* (L.) Millsp.) germplasm and isolation of elite genotypes and isolation of elite genotypes for Karnataka. Crop Res. 2000; 20(3):444-448.
3. Chetkuri I Anuradha, Vijaylakshmi P, Bhargavi V, Pavankumar. D, Sreelaxmi Am, Siddiq EA. Correlation, Variability and Heritability in pigeonpea, Advance in Bioresearch. 2013; 4(2):129-134.
4. Kalaimagal T, Balu PA, Sumathi P. Genetic studies in segregating populations of pigeonpea (*Cajanus cajan* (L.) Millsp.). J. Crop Importance. 2008; 35(1):31-34.
5. Lokhote SJ, Patil HE, Mali RA, Ingle P. Genetic analysis for yield and yield contributing traits in vegetable types in pigeonpea (*Cajanus cajan* (L.) Millsp.). 2015; 33(2).
6. Mallesh P, Nanda CH, Durgaraju CV, Sameer Kumar, Nidhi Mohan, Lee J. Variability, Heritability and Genetic Advance for Quantitative traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. International Journal of Pure and applied Bioscience. 2017; 5(5):25-28.
7. Naik SJ, Satheesh Gowda B, Dinesh M, Miyan HB, Asif, Pushpa HD. Genetic analysis in advanced breeding lines (F5) of pigeonpea (*Cajanus cajan* (L.) Millsp.). A Quarterly J Life Sci. 2013; 10(1):196-200.
8. Niranjana kumara B, Dharamraj PS, Vijaya B, Wali. Genetic diversity and variability studies of advanced breeding lines of pigeonpea (*Cajanus cajan* (L.) Millsp.) IJAPBC. 2014; 3(2):2277-4688.
9. Pandey P, Pandey VR, Tiwari DK, Yadav SK. Studies on direct selection parameters and its component traits in pigeonpea (*Cajanus cajan* (L.) Millsp.) African. J Agril. Research. 2013; 10(6):485-490.
10. Pansuriya G, Pandya HM, Kathria KB. Genetic Variability and Correlations in early maturing genotypes of pigeonpea (*Cajanus cajan* (L.) Millsp.). Gujarat Agril. Univ. Res. J. 1998; 23(2):23-27.
11. Ram R. Estimation of gene effects and heterosis for yield traits in pigeonpea [*Cajanus cajan* (L.) Millsp.]. M.Sc. (Ag.) Thesis submitted to Banaras Hindu University, Varanasi (Unpublished). 1997; 1-104.
12. Sreelakshmi CH, Sameer Kumar CV, Shivani D. Genetic analysis for yield and its components in hybrid pigeonpea Electronic J. of Plant Breeding. 2011; 2(3):413-416.
13. Venkateswarlu O. Genetic variability studies in pigeonpea (*Cajanus cajan* (L.) Millsp.). Legume Res. 2001; 24(3):205-206.