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Narrow-sense heritability and genetic advance for seed yield and yield attributing traits in medium duration pigeonpea [*Cajanus cajan* (L.) Mill sp.]

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Abstract

The present study was undertaken with a view to investigate narrow-sense heritability and genetic advance of seed yield and yield attributing traits in medium duration pigeonpea. The experimental material comprised of six generations *viz*., P_1, P_2, F_1, F_2, BC_1 and BC_2 of five crosses of pigeonpea, namely of GRG 152 × GJP 1, GRG 152 × AGT 2, JSP 6 × GJP 1, JSP 6 × BDN 711 and WRG 173 × BDN 711. All five crosses were evaluated using Compact Family Block Design at two different agro-climatic zone *viz*., South Saurashtra agro-climatic zone and North Saurashtra agro-climatic zone during *Kharif* 2021-22. The observations were recorded for nine characters *viz*., days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, length of pod (cm), 100-seed weight (g) and seed yield per plant (g) on five randomly selected plants in each replication for P_1, P_2 and F_1; twenty plants for F_2 and ten plants for BC_1 and BC_2. High heritability coupled with moderate genetic advance was observed in JSP 6 × GJP 1 at both locations, whereas for GRG 152 × AGT 2 at Junagadh for number of branches per plant; for GRG 152 × GJP 1 at Kukada for number of seeds per pod and, for GRG 152 × GJP 1 at Kukada for seed yield per plant. Almost characters showed high heritability with low genetic advance.

Keywords: Pigeonpea, agro-climatic zone, narrow-sense heritability, genetic advance

1. Introduction

Pigeonpea (*Cajanus cajan* (L.) Mill sp.) is an open cross-pollinated (20-70%) crop with diploid chromosome number (2n = 2x = 22), and genome size 1C=858 Mbp. The term 'pigeonpea' was coined in Barbados, where its seeds were considered an important pigeon feed (Gowda *et al*., 2011) [4]. Pigeonpea is the fourth most important pulse crop in the world we're in, and India alone accounts for 83% of the world's supply (Devegowda *et al*., 2018) [2]. It is an important food legume in India as well as semi-arid regions of the world and is invariably cultivated as an annual crop. Pigeonpea is an important pulse crop that is adapted to the tropical and subtropical regions and it performs well in poor soils, low fertiliser input and regions where moisture availability is unreliable or inadequate, even under drought conditions. In India, it was estimated that 80-90% of the pigeonpea were intercropped, i.e., with cereals (sorghum, maize, pearl millet, finger millet and rain-fed rice), with legumes (groundnut, cowpea, mung bean, black gram, soybean), with long-season annuals (caster, cotton, sugarcane, and cassava), etc.

The distribution of pigeonpea is asymmetric over the globe. Worldwide, the pigeonpea area has recorded a 56% increase in the area since 1976. It is grown in different parts of the world covering more than twenty-two countries in mainly four continents namely, Asia, Africa, North and South America. (FAOSTAT, 2021) [3].

Heritability is the heritable portion of phenotypic variance which is a good index of the transmission of character from parents to their offspring. Since narrow sense heritability is estimated from additive genetic variance, the estimation of heritability and genetic advance will be important for selection of elite genotypes from segregating population of pigeonpea.

2. Materials and Methods

2.1 Site description

The present carried out to study narrow-sense heritability and genetic advance of seed yield and yield contributing traits in medium duration pigeonpea [*Cajanus cajan* (L.) Mill sp.] was evaluated out at two agro-climatic zones, *viz.*, Instructional farm, Department of Agronomy, Junagadh Agricultural University, Junagadh (South Saurashtra agro-climatic zone) and Cotton Research Station, Junagadh Agricultural University, Kukada (North Saurashtra agro-climatic zone) during 2019 to 2022 in *Kharif* season. Geographically, Junagadh is situated at 21.5º N latitude and 70º E longitude with an altitude of 60 meters above the Mean Sea Level (MSL) and Kukada is situated at 22.66º N latitude and 71.42º E longitude with an altitude of 108 meters above the Mean Sea Level (MSL). Junagadh's soil is medium black, alluvial in origin and poor in organic matter, while Kukada's soil is shallow, medium black and poor in organic matters. The climate of the area represents a tropical condition with semi-arid nature.

2.2 Experimental material and crossing pattern

The experimental material comprised five crosses each with six basic generations, *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2. Seeds of six parents *viz.*, GRG 152, GJP 1, AGT 2, JSP 6, BDN 711 and WRG 173 of pigeonpea were provided by Research Scientist, Pulses Research Station, Junagadh Agricultural University, Junagadh. The seeds of the F_1 generation of GRG 152 × GJP 1, GRG 152 × AGT 2, JSP 6 × GJP 1, JSP 6 × BDN 711 and WRG 173 × BDN 711 were developed by crossing all six parents during *Kharif* 2019-20 at Pulses Research Station, Junagadh Agricultural University, Junagadh. Seeds of F_1 of all five crosses, as well as six parents were used to developed F_1 (By crossing $P_1 \times P_2$), BC_1 (By crossing $F_1 \times P_1$), BC_2 (By crossing $F_1 \times P_2$) generations and F_2 (Selfed seed of F_1), P_1 (Selfed seeds of P_1) and P_2 (Selfed seeds of P_2) collected during *Kharif* 2020-21 the instructional farm, Department of Agronomy, Junagadh Agricultural University, Junagadh.

2.3 Experiment layout and character studied

The experimental material was evaluated during *Kharif* 2021-22 in Compact Family Block Design (CFBD) with three replications having each row of 2m of length and 90 × 20 cm inter and intra row spacing, respectively at two agro-climatic zones, *viz.*, instructional farm, Department of Agronomy, Junagadh Agricultural University, Junagadh (South Saurashtra agro-climatic zone) and Cotton Research Station, Junagadh Agricultural University, Kukada (North Saurashtra agro-climatic zone).

Each replication was divided into five compact blocks, each block consisting of a single cross and block accommodated eleven rows, *viz.*, one row of P_1, P_2 and F_1; four rows of F_2 and, two rows of BC_1 and BC_2 of six basic generations of each cross. The same experiment laid out at Junagadh and Kukada. All the recommended agronomical practised were adopted to raise a good crop.

The observations were recorded on selected and tagged five randomly plants from P_1, P_2 and F_1; twenty plants from F_2 and ten plants from BC_1 and BC_2 generations in each replication for days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, length of pod (cm), 100-seed weight (g) and seed yield per plant (g).

2.4 Statistical analysis

2.4.1 Heritability in narrow-sense

Heritability in narrow sense was estimated as per the method of Warner (1952) [20].

$$h^2 = \frac{2V_{F_2} - (V_{BC_1} - V_{BC_2})}{V_{F_2}}$$

Where

h^2 = heritability in narrow sense.

V_{F_2} = variance of the F_2.

V_{BC_1} = variance of the BC_1.

V_{BC_2} = variance of the BC_2.

Categorization of a range of heritability estimation was given by Robinson (1966) [16].

Less than 30% = Low.

30 to 60% = Medium.

Above 60% = High.

2.4.2 Genetic advance as % of mean

Expected genetic advance was calculated according to the formula given by Johnson *et al.* (1955) [6].

$$GA = k.h^2.\sqrt{V_{F_2}}$$

$$GA\ as\ \%\ of\ mean = \frac{GA}{\bar{X}} \times 100$$

Where

k = Selection coefficient at 5% selection intensity equal to 2.06

h^2 = Heritability narrow sense

$\bar{X}$ = Mean of the F_2 population

V_{F_2} = Variance of the F_2 generation

The range of genetic advance as per cent mean is given by Johnson *et al.* (1955) [6].

Less than 10% = Low

10 to 20% = Medium

Above 20% = High

Table 1: Heritability (NS) and genetic advance as % of means for all nine traits of five crosses in medium duration pigeonpea at Junagadh and Kukada

Crosses	Heritability (%) (NS)		Genetic advance as % of mean	
	Junagadh	Kukada	Junagadh	Kukada
	Days to flowering			
GRG 152 × GJP 1	49.62	(-)	0.89	(-)
GRG 152 × AGT 2	(-)	(-)	(-)	(-)
JSP 6 × GJP 1	(-)	39.55	(-)	1.31
JSP 6 × BDN 711	34.29	46.20	0.75	1.57
WRG 173× BDN 711	(-)	(-)	(-)	(-)
	Days to maturity			
GRG 152 × GJP 1	59.26	(-)	1.12	(-)

GRG 152 × AGT 2	(-)	60.55	(-)	1.37
JSP 6 × GJP 1	79.24	29.16	1.65	0.54
JSP 6 × BDN 711	67.20	(-)	1.14	(-)
WRG 173× BDN 711	48.62	53.92	0.96	0.93
	Plant height (cm)			
GRG 152 × GJP 1	54.04	40.90	1.01	1.07
GRG 152 × AGT 2	51.44	69.11	0.97	1.92
JSP 6 × GJP 1	30.10	17.17	0.70	0.45
JSP 6 × BDN 711	59.73	(-)	1.68	(-)
WRG 173× BDN 711	(-)	80.64	(-)	2.28
	Number of branches per plant			
GRG 152 × GJP 1	66.03	10.31	9.98	1.50
GRG 152 × AGT 2	62.23	(-)	13.93	(-)
JSP 6 × GJP 1	61.29	69.71	11.14	12.73
JSP 6 × BDN 711	47.20	(-)	6.68	(-)
WRG 173× BDN 711	(-)	42.93	(-)	7.22
	Number of pods per plant			
GRG 152 × GJP 1	(-)	52.90	(-)	1.33
GRG 152 × AGT 2	65.68	67.66	2.20	2.04
JSP 6 × GJP 1	(-)	61.95	(-)	1.88
JSP 6 × BDN 711	32.34	(-)	1.24	(-)
WRG 173× BDN 711	(-)	52.25	(-)	2.34
	Number of seeds per pod			
GRG 152 × GJP 1	(-)	69.46	(-)	16.03
GRG 152 × AGT 2	39.65	(-)	2.99	(-)
JSP 6 × GJP 1	(-)	20.79	(-)	2.27
JSP 6 × BDN 711	42.93	(-)	2.70	(-)
WRG 173× BDN 711	(-)	(-)	(-)	(-)
	Length of pod (cm)			
GRG 152 × GJP 1	(-)	(-)	(-)	(-)
GRG 152 × AGT 2	(-)	(-)	(-)	(-)
JSP 6 × GJP 1	(-)	(-)	(-)	(-)
JSP 6 × BDN 711	(-)	(-)	(-)	(-)
WRG 173× BDN 711	35.93	(-)	2.81	(-)
	100-seed weight (g)			
GRG 152 × GJP 1	(-)	(-)	(-)	(-)
GRG 152 × AGT 2	6.57	34.01	0.25	1.67
JSP 6 × GJP 1	(-)	8.35	(-)	0.49
JSP 6 × BDN 711	(-)	19.94	(-)	0.95
WRG 173× BDN 711	(-)	32.03	(-)	1.88
	Seed yield per plant (g)			
GRG 152 × GJP 1	(-)	69.16	(-)	10.20
GRG 152 × AGT 2	(-)	(-)	(-)	(-)
JSP 6 × GJP 1	(-)	(-)	(-)	(-)
JSP 6 × BDN 711	(-)	(-)	(-)	(-)
WRG 173× BDN 711	(-)	(-)	(-)	(-)

(-) indicates negative estimates of heritability (%) (NS) as well as genetic advance as % of mean

3. Results and Discussion

Narrow-sense heritability describes the ratio of additive genetic variance to total phenotypic variance. The breeder's ideal parameters for choosing desirable genotypes from the segregating material are heritability estimates in the narrow sense and genetic advance expressed as a percentage of the mean. Estimates of heritability that take genetic advances into account are typically better at forecasting the gain under selection than heritability estimates alone. Narrow sense heritability as well as genetic advance as % of mean of all nine quantitative traits for both locations are shown in Table 1.

In present investigation, higher heritability coupled with higher genetic advance was not observed for any of the trait. Higher heritability coupled with medium genetic advance was observed for number of branches per plant in JSP 6 × GJP 1 at both locations, whereas at Junagadh for number of branches per plant in GRG 152 × AGT 2 and at Kukada for number of seeds per pod and seed yield per plant (g) in GRG 152 × GJP 1.

High heritability coupled with low genetic advance was observed for number of pods per plant in GRG 152 × AGT 2 at both locations, while at Junagadh for days to maturity in JSP 6 × GJP 1 and JSP 6 × BDN 711, number of branches per plant in GRG 152 × GJP 1 and at Kukada for days to maturity in GRG 152 × AGT 2, Plant height (cm) in GRG 152 × AGT 2 and WRG 173 × BDN 711 and number of pods per plant in JSP 6 × GJP 1. High heritability estimates for different traits in pigeonpea have been reported by Vanniarajan *et al.* (2021) [18], Mula *et al.* (2019) [11], Bhut *et al.* (2019) [1], Kumar *et al.* (2018) [8], Pushpavalli *et al.* (2018) [14], Ranjani *et al.* (2018) [15], Verma *et al.* (2018) [19], Mallesh *et al.* (2017) [10] and Vanisree and Shreedhar (2014) [17].

Medium heritability with low genetic advance was observed for days to flowering in JSP 6 × BDN 711, days to maturity in WRG 173 × BDN 711, plant height (cm) in GRG 152 × GJP

1 at both locations, whereas at Junagadh for days to flowering as well as days to maturity in GRG 152 × GJP 1, plant height (cm) in GRG 152 × AGT 2, JSP 6 × GJP 1 and JSP 6 × BDN 711, number of branches per plant in JSP 6 × BDN 711, number of seeds per pod in GRG 152 × AGT 2 and JSP 6 × BDN 711, length of pod (cm) in WRG 173 × BDN 711 and at Kukada for days to flowering in JSP 6 × GJP 1, number of branches per plant in WRG 173 × BDN 711, number of pods per plant in GRG 152 × GJP 1 and WRG 173 × BDN 711, 100-seed weight (g) in GRG 152 × AGT 2 and WRG 173 × BDN 711. Medium heritability along with low genetics advance was also observed by Bhut *et al.* (2019) [1] for number of pods per plant for almost all crosses, length of pod (cm) in NTL 740 × BRG 14-1, 100-seed weight (g) in GJP 1 × BRG 14-1 and TRDG 107 × BDN 2010-1 and seed yield per plant (g) in GJP 1 × BDN 2010-1 as well as GJP 1310 × BSMR 853; Jadhav *et al.* (2019) [5] for days to flowering, number of primary branches per plant, pod length, number of seeds per pod and seed yield per plant (g); Pal *et al.* (2018) [12]; Ranjani *et al.* (2018) [15] and Kesha *et al.* (2016) [7].

Low heritability along with low genetic advance was observed for days to maturity as well as plant height (cm) in JSP 6 × GJP 1, number of branches per plant in GRG 152 × GJP 1, number of seeds per pod in JSP 6 × GJP 1 and 100-seed weight (g) in JSP 6 × GJP 1 and JSP 6 × BDN 711 at Kukada. Similar finding was observed by Bhut *et al.* (2019) [1] for number of seeds per pod, length of pod (cm) and 100-seed weight (g); Jadhav *et al.* (2019) [5]; Pandey *et al.* (2015) [13] and Kumar *et al.* (2014) [9].

Moreover, remaining all crosses for particular traits at particular locations have negative estimation of heritability as well as genetic advance because those have higher value of difference of variance of BC_1 and BC_2 generations than twice the value of variance of F_2 generation.

4. Conclusion

High heritability coupled with medium genetic advance was observed for number of branches per plant in JSP 6 × GJP 1 at both locations, whereas at Junagadh for number of branches per plant in GRG 152 × AGT 2 and at Kukada for number of seeds per pod and seed yield per plant (g) in GRG 152 × GJP 1, which indicates these crosses can be directly utilize for genetic improvement of these traits. Rest almost showed high to medium heritability with low genetic advance, so selection and improvement could be slow. We can use bi-parental mating or few cycles of recurrent selection for improvement in such traits.

5. References

1. Bhut NM, Monpara BA, Patel KP, Virani HB. Heritability and genetic advance for quantitative traits in medium duration pigeonpea [*Cajanus cajan* (L.) Mill sp.]. International Journal of Chemical Studies. 2019;7(5):2458-2461.
2. Devegowda SR, Singh OP, Kumari K. Growth performance of pulses in India. The Pharma Innovation Journal. 2018;7(11):394-399.
3. FAOSTAT. Agriculture data. https://fao.org/faostat/. 20 February, 2022.
4. Gowda CLL, Saxena KB, Srivastava RK, Upadhyaya HD, Silim SN. In Biodiversity in Agriculture: Domestication, Evolution and Sustainability (Gepts P, Bettinger RL, Brush SB, Famula TR, McGuire PE, Qualset CO and Damania AB eds.). Cambridge University Press. University of California, Davis, USA; c2011, p. 361-373.
5. Jadhav AG, Patil DK, Gite VK, Lokhande MR. Estimation of heritability in pigeonpea [*Cajanus cajan* (L.) Mill sp.]. International Journal of Chemical Studies. 2019;7(5):2679-2681.
6. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agronomy Journal. 1955;47(7):314-318.
7. Kesha R, Saxena K, Shrimali TM, Bisnoi G. A study on genetic variability, correlation and path analysis in pigeonpea [*Cajanus cajan* (L.) Mill sp.]. International Journal of Agricultural Science. 2016;8(51):2287-2289.
8. Kumar A, Singh A, Kumar R, Singh B. Genetic variability, character association and path analysis in pigeonpea [*Cajanus cajan* (L.) Mill sp.]. Bulletin of Environment, Pharmacology and Life Sciences. 2018;7(3):63-68.
9. Kumar S, Singh SS, Elanchezhian R, Shivani RE. Studies on genetic variability and inter-relationship among yield contributing characters in pigeonpea grown under rainfed lowland of eastern region of India. Journal of Food Legumes. 2014;27(2):104-107.
10. Mallesh P, Nanda HC, Durgaraju CH, Kumar SCV, Mohan N, Jake L. Variability, heritability and genetic advance for quantitative traits in pigeonpea [*Cajanus cajan* (L.) Mill sp.]. International Journal of Pure and Applied Bioscience. 2017;5(5):25-28.
11. Mula GM, Galian JL, Mula RP. Variability, heritability and genetic advance of medium to long duration pigeonpea [*Cajanus cajan* (L.) Mill sp.]. Green Farming. 2019;10(2):127-130.
12. Pal D, Verma SK, Panwar RK, Arora A, Gaur AK. Correlation and path analysis studies in advanced line of pigeonpea [*Cajanus cajan* (L.) Mill sp.] under different environments. International Journal off Current Microbiology and Applied Sciences. 2018;7(4):378-389.
13. Pandey P, Pandey VR, Tiwari DK, Yadav SK. Studies on direct selection parameters for seed yield and its component traits in pigeonpea [*Cajanus cajan* (L.) Mill sp.]. African Journal of Agricultural Research. 2015;6(10):485-490.
14. Pushpavalli SNCVL, Yamini KN, Anuradha R, Kumar G, Rani CS, Sudhakar C, *et al.* Genetic variability and correlation in pigeonpea genotypes. Electronic Journal of Plant Breeding. 2018;1(9):343-349.
15. Ranjani MS, Vanniarajan C, Saxena RK, Hingane AJ, Sudhagar R, Kumar CVS. Genetic variability and association studies for yield and its attributes in super-early pigeonpea [*Cajanus cajan* (L.) Mill sp.] genotypes. Electronic Journal of Plant Breeding. 2018;2(9):682-691.
16. Robinson HF. Quantitative genetics in relation to breeding on centennial of Mendelism. Indian Journal of Genetics. 1966;26(A):171-187.
17. Vanisree S, Sreedhar M. Genetic analysis of yield and yield components and determination of selection criteria in pigeonpea germplasm. Journal of Food Legumes. 2014;27(1):68-70.
18. Vanniarajan C, Magudeeswari P, Gowthami R, Indhu SM, Ramya KR, Monisha K. Assessment of Genetic Variability and Traits Association in Pigeonpea [*Cajanus cajan* (L.) Mill sp.] Germplasm. Legume Research-An

International Journal, 2021;44(2):1-8.

19. Verma SK, Bisht C, Gaur AK, Chandra D. Study on some genetic parameters for yield and related traits in pigeonpea [*Cajanus cajan* (L.) Mill sp.] genotypes. Chemical Science Review and Letters. 2018;7(25):70-76.
20. Warner JN. A method of estimating heritability. Agronomy Journal. 1952;44(8):427-430.