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Heritability and genetic advance for quantitative traits in medium duration pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract
Six generations, namely P_1, P_2, F_1, F_2, BC_1 and BC_2 of five crosses of pigeonpea were grown in Compact Family Block Design with three replications in *kharif* 2018 at Pulses Research Station, Junagadh Agricultural University, Junagadh. The observatiosns were recorded on five randomly selected 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 ten characters. High heritability coupled with high genetic advance was observed for number of primary branches per plant in GJP 1 × BDN 2010-1, TDRG 107 × BDN 2010-1 and GJP 1310 × BSMR 853 and number of secondary branches per plant in cross GJP 1310 × BSMR 853 which indicated that the predominance of additive gene action in the expression of these characters which could be utilized through selection for the genetic improvement of these characters. Rest of the traits showed high to low heritability estimates coupled with moderate to low genetic advance as percentage of mean indicated the role of non-additive genetic variance in their expression.

Keywords: Heritability, genetic advance, pigeonpea [*Cajanus cajan* (L.) Millsp.]

Introduction
Pigeonpea [*Cajanus cajan* (L.) Millsp.] is an important leguminous short lived perennial shrub cultivated as annual crop in semi-arid tropical and subtropical regions of the world. Presently, pigeonpea is known by several trade names such as Arhar, Redgram, Tur, Angola pea and Congo pea *etc*. Pigeonpea (2n=2x=22) is a perennial member of the family Leguminosae (Fabaceae). Pigeonpea dal is mainly traded for food use. It is a rich source of protein, carbohydrate, and certain minerals. The residual nitrogen was estimated to be approximately 40 kg N per ha (Rao *et al*. 1980). Allantoin, one of the nitrogen transport compounds associated with nodulated legumes, appears to be a useful indicator of nitrogen-fixing activity of pigeonpea. Pigeonpea ranks sixth in global grain legume production and worldwide it is cultivated in above 4.70 million hectares area with an annual production of 3.69 million tonnes with productivity around 783 kg/ha. India ranks first in annual pigeonpea production with 4.42 million hectares area with an annual production of 3.68 million tonnes with productivity around 832 kg/ha followed by Myanmar (0.9 million tonnes), Malawi (0.23 million tonnes), Tanznia (0.20 million tonnes) and Kenya (0.09 million tonnes) (Anon., 2018a) [1]. In Gujarat, it is cultivated on 0.255 million hectares area with an annual production of 0.329 million tonnes with productivity around 1288 kg/ha (Anon., 2018b) [2].

Materials and Methods
Plant materials
Six generations, namely P_1, P_2, F_1, F_2, BC_1 and BC_2 of five crosses of pigeonpea *viz*., GJP 1 × BRG 14-1 (Cross 1), GJP 1 × BDN 2010-1 (Cross 2), NTL 740 × BRG 14-1 (Cross 3), TDRG 107 × BDN 2010-1 (Cross 4) and GJP 1310 × BSMR 853 (Cross 5) were grown *kharif* 2018 at Pulses Research Station, Junagadh Agricultural University, Junagadh. The experiment was laid out during *kharif*-2018 in Compact Family Block Design with three replications having each row of 4m length and 90 cm × 20 cm inter and intra row spacing, respectively. Each replication was divided into five compact blocks, each consists of single cross and blocks were consisted of six plots comprised of six basic generations of each cross. The crosses were assigned to each block and six generations of a cross were relegated to individual plot within the block. The single plot of one row for P_1, P_2, F_1, BC_1 and BC_2 generation and two rows for

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each F_2 generation was accommodated. All the recommended agronomical practiced were be adopted to raise good crop. The observations were recorded on five randomly selected 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 ten characters *viz.*, days to flowering, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, length of pod, 100-seeds weight and seed yield per plant.

Statistical analysis
1. Heritability in narrow sense
Heritability in narrow sense was estimated as per method of Warner (1952)

$$h^2 = \frac{2V_{F_2} - \left[V_{BC_1} + V_{BC_2}\right]}{V_{F_2}}$$

Where

h^2 = heritability in narrow sense

V_{F_2} = variance of the F_2 generation

V_{BC_1} = variance of the backcross one generation,

V_{BC_2} = variance of the backcross two generation.

2. Genetic advance (GA)
Expected genetic advance (GA) was calculated according to the formula given by Johnson *et al.* (1955).

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

$$GA \text{ as (\%) of mean} = \frac{GA}{\overline{X}} \times 100$$

Where

K= selection coefficient at 5% selection intensity equal to 2.06

h^2 = heritability narrow sense

$\overline{X}$ = mean of F_2 population

V_{F_2} = variance of F_2 generation

Results and Discussion
The relative amount of heritable portion of variation is assessed with the help of heritability estimates and genetic advance expressed as percentage of the mean (genetic gain). Narrow sense heritability indicates the proportion of additive genetic variance to the total phenotypic variance. Additive variance is always fixable. Hence, naturally more the additive genetic variance is always desirable to get more gain. Heritability estimates in narrow sense and genetic advance expressed as per cent of mean are ideal parameters to the breeder for selecting desirable genotypes from the segregating material.

Heritability estimates along with genetic advance are normally more useful in predicting the gain under selection than that of heritability alone. However, it is not necessary that a character showing high heritability will also exhibit high genetic advance (Johnson *et al.* 1955). An attempt has been made in the present investigation to estimate heritability in narrow sense and categorized as low (<50%), moderate

(50% to 70%) and high (>70%) as suggested by Robinson (1966) [9].

In present investigation the high heritability was recorded for the character days to flowering in all the crosses except cross GJP 1310 × BSMR 853; days to maturity in all the crosses except cross NTL 740 × BRG 14-1; plant height in all the crosses except cross GJP 1 × BRG 14-1; number of primary branches per plant in cross GJP 1 × BDN 2010-1, cross TDRG 107 × BDN 2010-1 and cross GJP 1310 × BSMR 853; number of secondary branches per plant in the all crosses; number of pods per plant in cross NTL 740 × BRG 14-1; number of seeds per pod in cross GJP 1 × BDN 2010-1; length of pod in cross GJP 1310 × BSMR 853 and seed yield per plant in cross GJP 1 × BRG 14-1, cross NTL 740 × BRG 14-1 and cross GJP 1310 × BSMR 853.

The moderate heritability was observed for days to flowering in cross GJP 1310 × BSMR 853; number of primary branches per plant in cross GJP 1 × BRG 14-1 and NTL 740 × BRG 14-1; number of pods per plant in cross GJP 1 × BDN 2010-1 and TDRG 107 × BDN 2010-1; number of seeds per pod in cross NTL 740 × BRG 14-1 and cross TDRG 107 × BDN 2010-1; length of pod in cross NTL 740 × BRG 14-1 and seed yield per plant in cross GJP 1 × BDN 2010-1 and cross GJP 1310 × BSMR 853 suggesting possibility of both additive and non-additive effects.

The low heritability was observed for days to maturity in cross NTL 740 × BRG 14-1; plant height in cross GJP 1 × BRG 14-1; number of pods per plant in cross GJP 1 × BRG 14-1 and cross GJP 1310 × BSMR 853; number of seeds per pod in cross GJP 1 × BRG 14-1 and GJP 1310 × BSMR 853; length of pod in cross GJP 1 × BRG 14-1, cross GJP 1 × BDN 2010-1 and cross TDRG 107 × BDN 2010-1 and 100 seed weight in all the crosses suggesting the impact of environment on these traits. High heritability estimates for different characters in pigeonpea have been reported by Patel and Patel (1992) [10], Saxena and Kataria (1993) [12], Pansuriya *et al.* (1998) [11], Venkateswarlu (2001) [13], Gohil (2006) [15], Kalaimagal *et al.* (2008) [14], Vanisree and Sreedhar (2014) [16], Mallesh *et al.* (2017) [18], Kumar *et al.* (2018) [19], Verma *et al.* (2018) [17] and Pushpavalli *et al.* (2018) [21]. Moderate heritability estimates for yield have been reported by Kalaimagal *et al.* (2008) [14] and moderate to low heritability estimate for number of primary branches per plant and number of secondary branches per plant by Sarsamkar (2008) [20].

The magnitude of genetic advance as percentage of mean was categorized as low (< 10%), moderate (10% to 30%) and high (> 30%). Genetic advance as percentage of mean was observed high for number of primary branches per plant in cross GJP 1 × BDN 2010-1, cross TDRG 107 × BDN 2010-1 and cross GJP 1310 × BSMR 853 and number of secondary branches per plant in cross GJP 1310 × BSMR 853 suggest that these characters are govern by additive genes and selection will be worthwhile for further improvement of these traits. Genetic advance as percentage of mean was recorded as moderate for number of primary branches per plant in cross GJP 1 × BRG 14-1 and cross NTL 740 × BRG 14-1 and number of secondary branches per plant in cross NTL 740 × BRG 14-1 and cross TDRG 107 × BDN 2010-1 while rest of the characters showed low genetic advance as percentage of mean suggesting influence of environment and hence selection for these traits would be worthwhile in later generation. High genetic advance for various traits in pigeonpea was reported by earlier workers. Prasad *et al.* (2013) [22] observed for the traits, number of primary branches

per plant; number of secondary branches per plant; number of pods per plan and grain yield, Saroj *et al.* (2013) [23] observed for plant height; days to 50% flowering; number of primary branches per plant; number of secondary branches per plant; pods per plant; 100-seed weight and grain yield per plant and Kesha Ram *et al.* (2016) [24] observed for number of primary branches per plant. While Takalkar *et al.* (1998) [25] observed low genetic advance for branches per plant; seeds per pod and 100-seed weight.

High heritability coupled with high genetic advance was observed for number of primary branches per plant in cross GJP 1 × BDN 2010-1, cross TDRG 107 × BDN 2010-1 and cross 5 and number of secondary branches per plant in cross GJP 1310 × BSMR 853 which indicated that the predominance of additive gene action in the expression of these characters which could be utilized through selection for

the genetic improvement of these characters. Similar result supported by Patel and Patel (1992) [10], Saxena and Kathiria (1993) [12], Mahamad *et al.* (2006) [26], Bhadru (2010) [27], Bhadru (2011) [28], Sreelakshmi *et al.* (2011) [32], Ajay *et al.* (2014) [29], Kumar *et al.* (2014), Galian *et al.* (2015), Pandey *et al.* (2015) [34] and Rajani *et al.* (2018) [21]. Rest of the traits showed high to low heritability estimates coupled with moderate to low genetic advance as percentage of mean indicated the role of non-additive genetic variance in their expression. High heritability coupled with moderate genetic advance was found in the number of secondary branches per plant in cross NTL 740 × BRG 14-1 and cross TDRG 107 × BDN 2010-1. Similar results were also obtained by Saxena and Kataria (1993) [12], Kumar *et al.* (2014) [31] and Pandey *et al.* (2015) [34].

Table 1: Heritability (narrow sense) and genetic advance as per cent of means for days to flowering, days to maturity, plant height (cm), no. of primary branches per plant, no. of secondary branches per plant, no. of pods per plant, no. of seeds per plant, length of pod (cm), 100 seed weight (g) and seed yield per plant (g) of five crosses in medium duration pigeonpea

Crosses	Heritability (%) (NS)	Genetic advance as % of mean	Heritability (%) (NS)	Genetic advance as % of mean
	Days to flowering		**Days to maturity**	
GJP 1 x BRG 14-1 (cross 1)	94.01	4.75	82.82	2.35
GJP 1 x BDN 2010-1 (cross 2)	78.99	2.75	82.56	2.10
NTL 740 x BRG 14-1 (cross 3)	76.77	3.94	24.26	0.85
TDRG 107 x BDN 2010-1 (cross 4)	76.71	3.23	91.79	2.95
GJP 1310 x BSMR 853 (cross 5)	57.81	3.18	94.20	2.93
	Plant height (cm)		**No. of primary branches per plant**	
GJP 1 x BRG 14-1 (cross 1)	25.40	0.72	54.09	21.89
GJP 1 x BDN 2010-1 (cross 2)	98.11	3.08	85.70	33.65
NTL 740 x BRG 14-1 (cross 3)	79.18	2.61	61.92	22.09
TDRG 107 x BDN 2010-1 (cross 4)	98.15	3.01	79.38	39.67
GJP 1310 x BSMR 853 (cross 5)	74.20	2.50	78.65	52.93
	No. of secondary branches per plant		**No. of pods per plant**	
GJP 1 x BRG 14-1 (cross 1)	73.97	15.33	45.00	0.68
GJP 1 x BDN 2010-1 (cross 2)	80.75	16.13	57.27	0.83
NTL 740 x BRG 14-1 (cross 3)	75.82	21.56	85.33	1.84
TDRG 107 x BDN 2010-1 (cross 4)	77.51	22.29	50.42	1.02
GJP 1310 x BSMR 853 (cross 5)	99.24	34.78	27.30	0.76
	No. of seeds per pod		**Length of pod (cm)**	
GJP 1 x BRG 14-1 (cross 1)	21.05	4.40	25.17	2.90
GJP 1 x BDN 2010-1 (cross 2)	89.64	18.50	14.15	1.77
NTL 740 x BRG 14-1 (cross 3)	58.82	10.99	57.88	7.99
TDRG 107 x BDN 2010-1 (cross 4)	68.16	13.43	12.17	2.52
GJP 1310 x BSMR 853 (cross 5)	14.23	2.66	75.37	12.85
	100 seed weight (g)		**Seed yield per plant (g)**	
GJP 1 x BRG 14-1 (cross 1)	47.97	9.41	82.10	4.57
GJP 1 x BDN 2010-1 (cross 2)	21.03	4.68	53.57	2.39
NTL 740 x BRG 14-1 (cross 3)	24.88	4.78	96.99	5.60
TDRG 107 x BDN 2010-1 (cross 4)	30.64	6.09	81.76	4.29
GJP 1310 x BSMR 853 (cross 5)	19.02	4.48	50.76	3.63

Conclusion

High heritability coupled with high genetic advance was observed for number of primary branches per plant in GJP 1 × BDN 2010-1 (cross 2), TDRG 107 × BDN 2010-1 (cross 4) and GJP 1310 × BSMR 853 (cross 5) and number of secondary branches per plant in cross GJP 1310 × BSMR 853 (cross 5) which indicated that the predominance of additive gene action in the expression of these characters which could be utilized through selection for the genetic improvement of these characters. Rest of the traits showed high to low heritability estimates coupled with moderate to low genetic advance as percentage of mean indicated the role of non additive genetic variance in their expression.

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