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### A study of heritability and genetic advance in pigeon pea. (*Cajanus cajan* (L.) Mill spp.)

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#### Abstract

The present investigation was conducted at Pulses and Castor Research Station, Navsari Agricultural University, Navsari during *Kharif* 2017-20 with a view to study heterosis of four crosses (each having P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations) in a Compact Family Block Design with three replications. Out of four crosses studied, high heritability coupled with high to moderate genetic advance for trait grain yield per plant in cross I and IV; days to flowering in cross I and II; days to maturity in cross II and IV; reproductive phase duration in cross I, III and IV; Plant height in cross II, III and IV; primary branches per plant in cross IV and pods per plant in cross II and IV. Simple selection method would be fruitful for improvement of various characters because they are predominantly inherited by genetic effect. Involvement of environment effect is very less in inheritance of above-mentioned traits.

**Keywords:** Heritability, genetic advance, pigeon pea, F<sub>1</sub>, F<sub>2</sub>, backcross generations

#### Introduction

Pigeon pea, a legume pulse crop, it is short lived woody perennial cultivated as annual crop in semi-arid tropical and subtropical regions of the world. Agronomically branching system in pigeon pea is classified as erect, semi-erect and spreading types. It originated in India and spread to Africa, where it formed secondary centre of biodiversity. *Cajanus cajanifolious*, is the only progenitor of pigeon pea. It has a seed strophiole which is only distinguishable morphological trait that differs it from cultivated pigeon pea. Pigeon pea is a diploid plant (2n = 22) with a genome size of 852 Mbp. Protein content in commonly grown pigeon pea cultivars ranges between 17.9 to 24.3 g per 100 g for whole grain samples (Salunkhe *et al.*, 1986). Regional name of pigeon pea in India are Toor in Hindi, Kandhi pappu in Telugu, thuvanan paruppu in Tamil, Togari bele in Kannada. Global perspective shows that pigeon pea could be considered a promising pulse crop that is cable of providing nutritional food security. After chickpea, pigeon pea is most important pulse crop which is widely grown in the country. Major pigeon pea growing states are Gujarat, Andhra Pradesh, Maharashtra, Uttar Pradesh, Madhya Pradesh, Karnataka and Bihar. India is leading in world production of pigeon pea, but still couldn't meet the country demand. Thus, it is a need to develop hybrids or varieties with high productivity. The major constraints that limit the production of pigeon pea are non-availability of quality seeds of improved varieties in adequate quantity, poor crop management, biotic and abiotic stresses prevalent in the pigeon pea growing areas, besides socio-economic factors and narrow genetic base. For yield improvement, selection of superior parents possessing better heritability and genetic advance for yield contributing traits is an essential prerequisite. Heritability along with genetic advance is more useful than heritability alone in the prediction of resultant effect of selection.

#### Materials and Methods

The present investigation was carried out during *Kharif* 2017-20, at Pulses and Castor Research Station, Navsari Agricultural University, Navsari. In this experiment six generations *viz.*, P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> of four crosses involving four diverse genotypes of pigeon pea were used to study the genetic analysis of quantitative traits. Randomly selected ten competitive plants from each of the P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, forty plants from F<sub>2</sub> and twenty plants from each of the BC<sub>1</sub> and BC<sub>2</sub> generations were utilized per replication and observations were recorded

on single plant basis for the following characters except days to maturity where, observations were made on plot basis

### Estimation of heritability

The narrow sense heritability, as suggested by Warner (1952) was calculated as follows:

$$h_{(n)}^2 (\%) = \frac{\sqrt{D}}{VF_2} \times 100$$

### Where

$h_{(n)}^2$  = Heritability in narrow sense

D = Additive genotypic variance

$VF_2$  = Phenotypic variance

Heritability percentage was categorized as demonstrated by Robinson *et al.* (1949) [19].

Sr. No.	Category	Percentage
1	Low	0-30%
2	Moderate	30-60%
3	High	60% and above

### Estimation of expected genetic advance under selection

The expected genetic advance at five percent selection intensity was estimated by using the following formula.

$$E.G.A. = k \cdot h_{(b)}^2 \cdot \sigma_p$$

Where,

$h_{(b)}^2$  = Heritability in broad sense

$\sigma_p$  = Phenotypic standard deviation

k = Selection differential

(k = 2.06 at 5 percent selection pressure)

Expected genetic advance as per cent of mean was estimated by the following formula.

$$E. G. A. (\text{per cent of mean}) = \frac{G.A.}{\bar{X}} \times 100$$

Where,

G. A. = Genetic advance

$\bar{X}$  = Mean of the character under study

### Result and Discussion

Heritability estimates along with genetic advance are important selection parameters and normally more helpful in predicting the gain under selection than heritability estimates alone. However, heritability estimates are influenced by the type of genetic material, sample size, method of sampling, type of experiment, method of calculation and effect of linkage. Genetic advance which refers to the improvement in the mean genotypic value of selected individuals over the parental population is influenced by the genetic variability, heritability, and selection intensity (Sharma, 2003) [15].

The results obtained on these aspects for different characters studied in four crosses of pigeon pea *viz.*, cross I (GNP-401 x NPMK-14-01), cross II (GNP-401 x GNP-1B), cross III (GNP-401 x NPMK-15-02) and cross IV (GNP-401 x NPKD-15-12) here after referred to as cross I, cross II, cross III and cross IV respectively are presented and discussed in the following paragraphs.

For trait grain yield per plant (Table 2), out of four crosses high heritability (101%) coupled with high genetic advance

(28.04%) was found in cross IV. High heritability (52.66%) coupled with moderate genetic advance (13.08%) was found in cross I. Similar results were reported by Patel *et al.* (2011) [10], Yerimani *et al.* (2013) [18], Saroj *et al.* (2014) [13], Niranjana Kumara *et al.* (2014) [8], Bhanu *et al.* (2016) [5], Mallesh *et al.* (2017) [7] and Bal *et al.* (2017) [3] for grain yield per plant. This estimate offers most suitable condition for selection. It also indicates the presence of additive gene effect in the trait and further suggests reliable crop improvement through selection of this trait

For trait days to flowering (table 1), high heritability coupled with moderate genetic advance was found in cross I (132.46%, 10.16%) and cross II (123.19%, 13.00%). Thus, days to first flowering trait could be improved via individual plant selection method.

Cross II (155.96%, 52.05%) and cross IV (151.57%, 20.04%) showed highly heritable and had high genetic advance value for trait days to maturity (table 1), cross II (160.02%, 54.49%) and cross IV (159.96%, 22.06%) reproductive phase duration (table 1) and pods per plant, cross II (138%, 63.80%) and cross IV (111%, 189%) (Table 1). Similar results were obtained by Udensi *et al.* (2011) [17] Patel *et al.* (2011) [10], Yerimani *et al.* (2013) [18], Saroj *et al.* (2014) [13], Niranjana Kumara *et al.* (2014) [8], Ram *et al.* (2016) [12], Bal *et al.* (2017) [3], and Pal *et al.* (2018) [9]. Thus, to improve traits with high heritability and high genetic advance, simple selection method would be most suitable.

High heritability couple with high genetic advance was found in cross II (123%, 84.68%) and cross IV (99.46%, 41.15%), for trait plant height (table 1). Similar results were obtained by Patel *et al.* (2011) [10], Sharma *et al.* (2012) [14] and Ram *et al.* (2016) [12] for plant height. Simple selection would be fruitful in improvement of trait plant height.

For trait primary branches per plant (table 1), showed high heritability with moderate genetic advance value in cross IV (125.40%, 12.69%) (Table 1). Similar results were obtained by Niranjana Kumara *et al.* (2014) [8], Mallesh *et al.* (2017) [7], Pal *et al.* (2018) [9] for days to flowering; Sharma *et al.* (2012) [14]. Individual plant selection method would be fruitful for improvement of this trait.

High heritability coupled with low genetic advance value was found in cross II (54.71%, 0.33%), III (50.50%, 7.67%) and IV(125.40%, 12.69%) for primary branches per plant (table 1); cross I (129.04%, 1.13%) and cross III(140.40%, 4.99%) for pod length (table 2); cross I (101.10%, 1.05%), cross II (49.22%, 0.25%), cross III(49.87%, 0.86%) and cross IV (155.20%, 1.66%) for seeds per pod(table 2); cross I (147.64%, 2.36%), cross II(139.76%, 1.52%), cross III(146.72%, 1.21%) and cross IV(154.25%, 1.74%) for 100 seed weight (table 2); cross II (41.12%, 5.99%), cross III (92.57%, 7.83%) and cross IV(65.54%, 2.29%) for leaf area (table 2); cross I(116.93%), cross II(122.72%, 5.17%) and cross III(166.24%, 9.79%) for harvest index (table 2); cross I(30.58%, 1.09%), cross II(42.01%, 0.07%) and cross IV(99.21%, 0.78%) for trait protein content (table 1). Similar results were obtained by Birhan *et al.* (2013) [6] for primary branches per plant; Bhanu *et al.* (2016) [5] and Pushpavalli *et al.* (2018) [11] for secondary branches per plant; Udensi *et al.* (2011) [17], Bhadr. (2011) [4] for pod length; Yerimani *et al.* (2013) [18] and Ram *et al.* (2016) [12] seeds per pod; Udensi *et al.* (2011) [17], Yerimani *et al.* (2013) [18] and Ram *et al.* (2016) [12] for pod length; Pushpavalli *et al.* (2018) [11] for 100 seed weight. Direct selection should be avoided for improvement of above-mentioned trait because influence of environment is more in expression of above-mentioned trait in mentioned crosses.

**Table 1:** Estimates of heritability and genetic advance in four crosses of pigeon pea for days to first flowering, days to maturity, reproductive phase duration, plant height, primary branches per plant, secondary branches per plant and pods per plant

Character and cross	Narrow sense heritability (%)	Genetic advance % mean
<b>Days to first flowering</b>		
GNP-401 X NPMK-14-01	132.46	10.16
GNP-401 X GNP-1B	123.19	13.00
GNP-401 X NPMK-15-02	185.31	4.99
GNP-401 X NPDK-15-12	90.29	7.45
<b>Days to maturity</b>		
GNP-401 X NPMK-14-01	8.10	9.38
GNP-401 X GNP-1B	155.96	52.05
GNP-401 X NPMK-15-02	32.79	8.39
GNP-401 X NPDK-15-12	151.57	20.04
<b>Reproductive phase duration (days)</b>		
GNP-401 X NPMK-14-01	78.51	11.16
GNP-401 X GNP-1B	160.02	54.49
GNP-401 X NPMK-15-02	23.18	8.48
GNP-401 X NPDK-15-12	159.96	22.06
<b>Plant height (cm)</b>		
GNP-401 X NPMK-14-01	66.29	3.71
GNP-401 X GNP-1B	123.00	84.68
GNP-401 X NPMK-15-02	59.68	20.82
GNP-401 X NPDK-15-12	99.46	41.15
<b>Primary branches per plant</b>		
GNP-401 X NPMK-14-01	79.74	2.45
GNP-401 X GNP-1B	54.71	0.33
GNP-401 X NPMK-15-02	50.50	7.67
GNP-401 X NPDK-15-12	125.40	12.69
<b>Secondary branches per plant</b>		
GNP-401 X NPMK-14-01	16.58	11.24
GNP-401 X GNP-1B	147.49	3.16
GNP-401 X NPMK-15-02	79.32	6.05
GNP-401 X NPDK-15-12	54.22	1.55
<b>Pods per plant</b>		
GNP-401 X NPMK-14-01	14.15	56.41
GNP-401 X GNP-1B	138.92	63.80
GNP-401 X NPMK-15-02	32.39	13.44
GNP-401 X NPDK-15-12	111.04	189

\*\* - significant at 1% level of significance \* - significant at 5% level of significance

**Table 2:** Estimates of heritability and genetic advance in four crosses of pigeon pea for pod length, seeds per pod, 100 seed weight, grain yield per plant, leaf area, harvest index and protein content

Character and cross	Narrow sense heritability (%)	Genetic advance % mean
<b>Pod length (cm)</b>		
GNP-401 X NPMK-14-01	129.04	1.13
GNP-401 X GNP-1B	57.21	0.85
GNP-401 X NPMK-15-02	140.40	4.99
GNP-401 X NPDK-15-12	28.67	2.13
<b>Seeds per pod</b>		
GNP-401 X NPMK-14-01	101.10	1.05
GNP-401 X GNP-1B	49.22	0.25
GNP-401 X NPMK-15-02	49.87	0.86
GNP-401 X NPDK-15-12	155.20	1.66
<b>100 seed weight (g)</b>		
GNP-401 X NPMK-14-01	147.64	02.36
GNP-401 X GNP-1B	139.76	01.52
GNP-401 X NPMK-15-02	146.72	01.21
GNP-401 X NPDK-15-12	154.25	01.74
<b>Grain yield per plant (g)</b>		
GNP-401 X NPMK-14-01	52.66	13.08
GNP-401 X GNP-1B	16.84	09.94
GNP-401 X NPMK-15-02	24.19	18.77
GNP-401 X NPDK-15-12	101.19	28.04
<b>Leaf area (cm<sup>2</sup>)</b>		
GNP-401 X NPMK-14-01	02.94	04.20
GNP-401 X GNP-1B	41.12	05.99
GNP-401 X NPMK-15-02	92.57	07.83
GNP-401 X NPDK-15-12	65.54	02.29

Harvest index (%)		
GNP-401 X NPMK-14-01	116.93	04.52
GNP-401 X GNP-1B	122.72	05.17
GNP-401 X NPMK-15-02	166.24	09.79
GNP-401 X NPDK-15-12	33.49	02.65
Protein content (%)		
GNP-401 X NPMK-14-01	30.58	01.09
GNP-401 X GNP-1B	42.01	00.7
GNP-401 X NPMK-15-02	27.58	02.14
GNP-401 X NPDK-15-12	99.21	00.77

\*\* - significant at 1% level of significance \* - significant at 5% level of significance

## Conclusion

High heritability coupled with high genetic advance was found in cross II and IV for trait days to maturity; cross II and IV reproductive phase duration; cross II and IV in plant height; cross I and IV for pods per plant; cross IV for grain yield per plant. High heritability coupled with moderate genetic advance was found in cross I and II for days to first flowering; cross I for reproductive phase duration; cross IV for primary branches per plant; cross II for leaf area. Thus, it could be concluded that maximum traits in many crosses showed high heritability along high, moderate and low genetic advance. Thus, to improve the overall population for all the traits biparental mating followed by pedigree method or cyclic breeding methods could be used for improvement of this trait. Traits with low genetic advance, selection for such traits could be delayed to latter generation.

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