

## Estimation of Heritability and genetic advance for Seed Cotton Yield and its Component Traits in Desi Cotton

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### ABSTRACT

A study was conducted to assess the extent of the heterosis for sixteen yield and yield-attributing traits in four cotton hybrids (each having  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  generations) obtained by crossing four inter-specific lines of *desi* cotton in a compact family block design with three replications during *kharif* 2017-18. The observations recorded for sixteen different char-

acters were subjected to generation mean analysis (each having  $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$  generations) to assess the gene effects controlling these traits to estimate the extent of heritability and genetic advance. In present study both additive and non-additive effect play important role in the expression of different characters under study. High heritability coupled with high genetic advance was recorded by cross III (GShv 362/12  $\times$  PA 812) followed by cross II (GBhv 2399/09  $\times$  DWDa 1502) and cross I (GBhv 618/09  $\times$  ARBa 1502) for seed cotton yield per plant revealed the role of additive gene action for this trait.

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### INTRODUCTION

Cotton is most important fiber crop of India being a raw material for textile industry and plays a key role in agricultural economy. There are four species of cotton, namely, *Gossypium hirsutum* L., *Gossypium barbadense* L., *Gossypium herbaceum* L. and *Gossypium arboreum* L. are cultivated all over the world.

India is the only country where all the four cultivated species being grown commercially. Cotton is grown in India in three distinct agro-ecological zones viz., north zone (Punjab, Haryana, Rajasthan and Western Uttar Pradesh), central zone (Gujarat, Madhya Pradesh, Maharashtra and Orissa) and south zone (Karnataka, Andhra Pradesh, Telangana and

Tamil Nadu). Among the cotton growing countries of the world, India ranks first in acreage of 125.84 lakh ha as well as in production of 360 lakh bales of with a productivity of 486.33 kg/ha (Anonymous 2020). Gujarat, Maharashtra and Telangana are the major cotton growing states contributing around 70% of the area and 67% of cotton production in India. During the year 2019-20 in Gujarat cotton was grown in 26.29 lakh ha area with production of 95 lakh bales and productivity of 614.30 kg/ha (Anonymous 2020).

In crop improvement, only the genetic component of variation is important since only this component is transmitted to next generation. Knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, there by helps the breeder to employ a suitable breeding strategy to achieve the objective quickly. Heritability estimate along with genetic advance is more useful in predicting the resultant effect of selecting the best individuals. GAM together with heritability estimates gives a relatively better picture of the amount of advance to be expected through selection (Johnson *et al.* 1955).

## MATERIALS AND METHODS

The present investigation was carried out to study the genetic parameters of four cotton crosses obtained by crossing four interspecific lines of *desi* cotton in a Compact Family Block Design with three replications at Main Cotton Research Station, Navsari Agricultural University, Athwa farm, Surat were obtained by crossing four interspecific lines of *desi* cotton. The hybrids were generated during late *kharif*-2017 from its respective parents. The observations recorded for sixteen different characters were subjected to generation mean analysis (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) to assess the gene effects controlling these traits to estimate the extent of heritability and genetic advance.

### Estimation of heritability and expected genetic advance under selection

$$\text{Narrow sense heritability } h^2_{(n)} (\%) = \frac{\frac{1}{2} D}{VF_2}$$

Expected G. A. (at five per cent selection intensity)  
 $= kh^2_{(n)} \sigma_P$

$$\text{Expected GA (as per cent of mean)} = \frac{GA}{\bar{X}}$$

Where,  $h^2_{(n)}$  = Heritability in narrow sense

D = Additive genotypic variance

VF<sub>2</sub> = Phenotypic variance

$\sigma_P$  = Phenotypic standard deviation

k = Selection differential (k = 2.06 at 5% selection pressure)

GA = Genetic advance

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

## RESULTS AND DISCUSSION

Both broad and narrow sense heritability estimates were important but when segregating generations are available, calculation of narrow sense heritability provide more precise result. Hence, in present investigation, narrow sense heritability may be more helpful in the selection of segregating populations and that is why the genetic advance was calculated on the basis of narrow sense heritability to ascertain more reliable results and improvement in the mean genotypic value of selected families over that of the base population.

High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson *et al.* 1949).

Low heritability (0 - 30 %),

Moderate heritability (30 - 60 %),

High heritability (> 60 %).

The value of expected genetic advance for various characters is demarcated into three categories

**Table 1.** Estimates of heritability and genetic advance for days to first flower, plant height (cm), monopodia per plant, sympodia per plant, leaf area (cm<sup>2</sup>), bolls per plant, average boll weight (g) and seed cotton yield per plant (g) in four crosses of *desi* cotton. \* and \*\*, significant at 5% and 1%, respectively and “ - “ represent negative value.

Particulars	Estimates (%)							
	Days to first flower	Plant height (cm)	Mono-podia per plant	Sym-podia per plant	Leaf area (cm <sup>2</sup> )	Bolls per plant	Average boll weight (g)	Seed cotton yield per plant (g)
Cross I (GBhv 618/09 × ARBa 1502)								
Heritability (NS) %	123.57	141.71	-	17.86	-	49.17	12.51	77.08
Genetic advance %	34.66	57.07	-	7.70	-	26.99	5.06	48.53
Cross II (GBhv 2399/09 × DWDa 1502)								
Heritability (NS) %	144.10	163.10	-	66.80	-	30.46	167.52	86.08
Genetic advance %	41.29	77.77	-	37.96	-	14.87	70.53	47.04
Cross III (GShv 362/12 × PA 812)								
Heritability (NS) %	154.31	53.37	-	41.80	47.17	141.17	153.36	156.63
Genetic advance %	52.13	23.25	-	19.89	10.08	99.06	48.76	148.96
Cross IV (GShv 385/12 × PA 812)								
Heritability (NS) %	157.61	143.29	-	41.35	129.08	-	130.65	18.89
Genetic advance %	56.88	64.53	-	18.59	28.70	-	46.48	8.72

viz., low, moderate and high, as follows (Johnson *et al.* 1955).

Low genetic advance (0–10%),

Moderate genetic advance (10–20 %),

High genetic advance (> 20 %)

The results obtained on these aspects for different characters studied in four crosses of *desi* cotton viz., cross I (GBhv 618/09 × ARBa 1502), cross II (GBhv 2399/09 × DWDa 1502), cross III (GShv 362/12 × PA 812) and cross IV (GShv 385/12 × PA 812) are presented and discussed in the following paragraphs.

### Heritability

If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the

genotype and phenotype due to relatively smaller contribution of the environment to phenotype. But for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects.

High to moderate narrow sense heritability was recorded for most of the characters in all the crosses, viz. days to flowering, plant height, bolls per plant, seed cotton yield per plant, lint yield per plant, ginning percentage, seed index, fiber fineness, fiber strength and oil percentage in cross I; days to flowering, plant height, sympodia per plant, bolls per plant, average boll weight, seed cotton yield per plant, lint yield per plant, seed index, lint index, 2.5 % span length, fiber strength and oil percentage in cross II ; days to flowering, plant height, sympodia per plant, leaf area, bolls per plant, average boll weight, seed cotton yield per plant, lint yield per plant, ginning percentage, seed index, lint index, fiber fineness and oil percentage in cross III; while

**Table 2.** Estimates of heritability and genetic advance for lint yield per plant (g), ginning percentage (%), seed index (g), lint index (g), 2.5 % span length (mm), fiber fineness (mv), fiber strength (g/tex) and oil percentage (%) in four crosses of *desi* cotton \* and \*\*, significant at 5% and 1%, respectively and “ - “ represent negative value.

Particulars	Lint yield per plant (g)	Ginning percentage (%)	Seed index (g)	Lint index (g)	2.5 % span length (mm)	Fiber fineness (mv)	Fiber strength (g/tex)	Oil percentage (%)
Cross I (GBhv 618/09 × ARBa 1502)								
Heritability (NS) %	76.67	119.82	52.58	11.51	-	105.16	112.19	186.37
Genetic advance %	49.58	18.02	12.82	3.40	-	21.64	7.32	6.98
Cross II (GBhv 2399/09 × DWDa 1502)								
Heritability (NS) %	89.54	-	118.00	64.90	148.74	-	162.20	131.50
Genetic advance %	48.59	-	35.31	21.86	15.59	-	20.50	2.51
Cross III (GShv 362/12 × PA 812)								
Heritability (NS) %	157.85	156.93	125.68	147.35	-	142.64	-	131.34
Genetic advance %	153.16	30.52	38.81	62.51	-	22.82	-	5.37
Cross IV (GShv 385/12 × PA 812)								
Heritability (NS) %	13.82	151.23	81.43	67.95	120.36	-	80.14	184.32
Genetic advance %	6.37	28.17	26.00	24.12	7.27	-	5.22	10.90

days to flowering, plant height, sympodia per plant, leaf area, average boll weight, ginning percentage, seed index, lint index, 2.5% span length, fibre strength and oil percentage in cross IV. The obtained results are in conformity with the results of Manimaran and Raveendran (2004), Ahmed *et al.* (2006), Abbas *et al.* (2013), Dhivya *et al.* (2014), Eswari *et al.* (2017), Gnanasekaran *et al.* (2018), Jarwar *et al.* (2018), Joshi and Patil (2018), Kumar *et al.* (2019), Shruti *et al.* (2019).

The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotype is good reflection of genotype and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these metric traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement.

### Genetic advance

In the present investigation, high to moderate genetic

advance was also recorded for many traits. Low genetic advance was recorded for sympodia per plant, average boll weight, lint index, fiber strength and oil percentage in cross I ; oil percentage in cross II and cross III, while seed cotton yield per plant, lint yield per plant, 2.5 % span length and fibre strength in cross IV. The results are in concordance with the findings of Manimaran and Raveendran (2004), Ahmed *et al.* (2006), El-Rafae and El-Razek (2013).

High genetic advance was recorded for days to flowering, plant height, bolls per plant, seed cotton yield per plant, lint yield per plant and fiber fineness in cross I ; days to flowering, plant height, sympodia per plant, average boll weight, seed cotton yield per plant, lint yield per plant, seed index, lint index and fiber strength in cross II ; days to flowering, plant height, bolls per plant, average boll weight, seed cotton yield per plant, lint yield per plant, ginning percentage, seed index, lint index and fiber fineness in cross III and days to flowering, plant height, leaf area, average boll weight, ginning percentage, seed index and lint index in cross IV. Shift in the gene

frequency towards selection pressure is termed as genetic advance. Johnson *et al* (1955) found it more useful to estimate heritability values together with genetic advance in predicting the ultimate choice of best individuals by selection.

### Heritability coupled with genetic advance

High to moderate heritability coupled with high genetic advance were observed in cross I for days to flowering, plant height, bolls per plant, seed cotton yield per plant, lint yield per plant and fiber fineness; in cross II for days to flowering, plant height, sympodia per plant, average boll weight, seed cotton yield per plant, lint yield per plant seed index, lint index and fibre strength; in cross III for days to flowering, plant height, bolls per plant, average boll weight, seed cotton yield per plant, lint yield per plant, ginning percentage, seed index, lint index and fiber fineness and in cross IV for days to flowering, plant height, leaf area, average boll weight, ginning percentage, seed index and lint index indicated that most likely the heritability was due to additive gene effects and selection in early generations may be effective.

High heritability coupled with moderate genetic advance was observed in cross I for ginning percentage; in cross II for 2.5 % span length; in cross IV for oil percentage indicated the presence of additive gene effects and selection may be effective for these traits. These results are similar to the findings of different scientists viz., Ahmad *et al.* (2003), Manimaran and Raveendran (2004), Ahmed *et al.* (2006), Abbas *et al.* (2013), El-Rafaey and El-Razek (2013), Iqbal *et al.* (2013), Dhivya *et al.* (2014), Kumar *et al.* (2016), Eswari *et al.* (2017), Gnanasekaran *et al.* (2018), Jarwar *et al.* (2018), Joshi and Patil (2018), Kumar *et al.* (2019), Shruti *et al.* (2019), AL-Hibbiny *et al.* (2020).

### CONCLUSION

In present study high to moderate heritability coupled with high genetic advance were observed in most of the traits, while high heritability coupled with moderate genetic advance was observed in cross I for ginning percentage; in cross II for 2.5% span length; in cross IV for oil percentage indicated

that most likely the heritability was due to additive gene effects and selection in early generations may be effective for these traits. However, low genetic advance was recorded for sympodia per plant, average boll weight, lint index, fiber strength and oil percentage in cross I; oil percentage in cross II and cross III, while seed cotton yield per plant, lint yield per plant, 2.5% span length and fiber strength in cross IV clearly indicated the characters are mainly under the control of non-additive types of genes, hence they need further confirmation and evaluation for their fixation and that could be possible through recurrent selection in the succeeding generations. Thus, biparental mating followed by reciprocal recurrent selection that take care of both additive and non-additive gene actions are more promising for the improvement of various characters studied.

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