

Gene Action Studies in the Inheritance of Yield and Quality Attributing Traits in Diallel Cross of Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

A field experiment was conducted to evaluate the 45 F1 hybrids derived from 10×10 half diallel fashion along with ten parents and one standard check GN.Cot.Hy-14 were sown in randomized block design with three replications during kharif -2017 at Cotton Research Station, Junagadh Agricultural University, Junagadh. The genetic components of variation were determined for 12 characters viz., days to 50% flowering, days to 50% boll opening, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), ginning percentage (%), seed index (g), lint index (g) and oil percentage (%). The estimate of the components of variation revealed significant results for both additive (D) as well as dominance effects (H₁ and H₂) for all the characters except plant height non-significant H₂ component, but in majority of traits (except plant height, lint index) H₁ was higher than D indicating dominance components were important in the inheritance of seed cotton yield and its components. The average degree of dominance (H₁/D)^{1/2} was found to be more than unity for all the traits (except plant height, number of monopodia per plant and lint index indicating partial dominance) indicating over dominance. Asymmetrical distribution of positive and negative genes in the parents was observed for all the traits. High estimates of heritability in narrow sense was observed for days to 50% flowering, days to 50 % boll bursting, number of monopodia per plant, ginning percentage (%), lint index (g) and oil content (%) suggesting that selection based on these attribute would lead to rapid improvement. Due to preponderance of non-additive gene effects of seed cotton yield per plant and most of its component traits, heterosis breeding would also be practically feasible in cotton.

Keywords: Diallel Cross, Average degree of dominance, Heterosis breeding.

INTRODUCTION

Cotton is one of the most important commercial crop and popularly known as the

"White Gold". Cotton is a multipurpose crop that supplies five basic products viz., seed, lint, oil, hulls and linters.

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The seeds are being used for growing crop and also as feed for animal, lint is used in textile industry, linters for various industrial uses, refined cotton seed oil is used for human consumption and cotton seed meal as fertilizer as well as livestock feed. Cotton is commercially cultivated in nearly 77 countries across the globe with India, China, United States, Pakistan and Brazil being five of the largest producers of cotton. India is the only country where all the four cultivated species of cotton are grown on commercial scale and covers cultivated area about 122.35 lakh hectares. It occupies first position in production with 377.00 lakh bales (each of 170 kg) among all cotton producing countries. Average productivity of India is 524 kg per ha which is much lower as compared to the world average productivity of 792 kg per ha. Gujarat is the second largest cotton growing state with acreage of 26.18 lakh hectares and largest cotton producing state of India with production of 104.00 lakh bales. The average productivity of cotton in the state is 675 kg per ha which is higher than national productivity (Anon., 2017-18).

In India most of the local varieties which are grown by the cultivators have not been fully utilized in any genetic improvement programme. The development of cultivars with improved seed cotton yield per plant and quality for better market value, through breeding has received relatively little attention in cotton. For the improvement of cotton, one needs to elucidate the genetic nature and magnitude of quantitatively inherited traits and estimate prepotency of parents in combinations.

The information generated in the process can be used to understand the magnitude of heterosis. However, genetic control of different yield and quality related as well as agronomic traits has been studied extensively in cotton.

The direct selection for quality traits in cotton, same as in all other crops, will not be successful due to interaction of many genes with environment. Knowledge of the genetic controlling system of the character to be

selected and genetic variation are the prerequisite for viable breeding strategy.

Breeding objectives of cotton are higher yield, earliness, boll size, lint quality, higher number of sympodial branches and monopodial branches as per consumers preference, good quality oil, lower gossypol content, easy to harvest, upright sturdy plant free from lodging and resistance to diseases. Therefore, the present study entitled Gene action studies in the inheritance of yield and quality attributing traits in diallel cross of cotton (*Gossypium hirsutum* L.) is undertaken to understand the nature of gene effects involved in the expression of a character in interacting and non-interacting crosses. An assessment of these genetic parameters will allow for the development of efficient breeding strategies for cotton cultivar improvement.

MATERIALS AND METHODS

The experimental materials for the present study consisted of ten promising genotypes of *hirsutum* cotton used in half diallel crossing programme viz., G.Cot-10, GISV-267, GJHV-503, GJHV-515, GJHV-517, GJHV-522, GJC-101, Deviraj, GJHV-510, 76IH20. All the ten lines were crossed in all possible combination excluding reciprocals to obtain 45 F₁ hybrids for the study of gene action for seed cotton yield per plant and its contributing traits. A set of 56 entries comprising of 10 parents and their resultant 45 F₁ and standard check GN.Cot.Hy-14 were sown in Randomized Block Design with three replications at Cotton Research Station, Junagadh Agricultural University, Junagadh during late *kharif* 2017. Each entry was planted in a single row. Row to row and plant to plant distances were 120 cm and 45 cm, respectively. Recommended agronomical practices and plant protection measures were adopted as and when required to raise a good crop of cotton under irrigated condition. Fertilizers were applied at the rate of 160:000:120 N-P-K kg per ha. As per the recommendation for the non Bt-cotton, N was applied in four split of 25% and K₂O were applied in two split of 50% of the recommended dose.

Five competitive plants from each entry excluding border plants were randomly selected to record the observations on days to 50% flowering, days to 50% boll opening, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant (g), ginning percentage (%), seed index (g), lint index (g) and oil percentage (%). The mean values of each genotype were subjected to analysis of variance. The estimation of genetic components of variation was calculated for the analysis of numerical approach followed the method given by Hayman (1954).

RESULTS AND DISCUSSION

Genetic components of variances *viz.*, D, H₁, H₂, h², E, F along with value of t² for twelve characters in cotton are presented in Table 1. In addition to above mentioned components, mean degree of dominance (H₁/D)^{1/2}; proportion of positive and negative genes in the parents (H₂/4H₁); proportion of dominant and recessive genes in the parents (K_D/K_R); number of gene groups which control the character and exhibited the dominance (h²/H₂) and narrow sense heritability (per cent) for all the characters under studied are also presented in Table 1.

The estimate of the components of variation revealed significant results for both additive (D) as well as dominance effects (H₁ and H₂) for all the characters except plant height non-significant H₂ component, but in majority of traits (except plant height, lint index) H₁ was higher than D indicating dominance components were important in the inheritance of seed cotton yield and its components. Similar findings also were reported by Soomro et al. (2015), Muhammad et al. (2015) and Muhammad et al. (2013).

The average degree of dominance (H₁/D)^{1/2} was found to be more than unity for all the traits (except plant height, number of monopodia per plant and lint index indicating partial dominance) (Table 5.5) indicating over dominance which suggested that heterosis breeding might be advantageous to get higher

gain in cotton. The non-significant estimate of 'E' for the traits days to 50% flowering, days to 50% boll bursting, number of monopodia per plant, number of sympodia per plant, seed cotton yield per plant and oil content suggested that there was no considerable environment influence modifying their expression. The rest of the character are found significant for 'E' component.

The equal distribution of positive and negative genes in the parents helps the breeders in selecting desirable traits without losing other traits of interest. In the present study, asymmetrical distribution of positive and negative genes in the parental lines was revealed from the estimate, H₂/4H₁ for all the characters.

The negative sign of 'F' and K_D/K_R ratio less than unity for days to 50% flowering and number of monopodia per plant showed an excess of recessive gene in the parents, while positive sign of 'F' and K_D/K_R ratio more than unity for days to 50% boll bursting, plant height, number of sympodia per plant, number of bolls per plant, boll weight, seed cotton yield per plant, ginning percentage, seed index, lint index and oil content indicated that proportion of dominant gene were more frequent than recessive genes. Similar findings also were reported by Soomro et al. (2015), Muhammad et al. (2015) and Muhammad et al. (2013).

Knowledge of number of gene groups which exhibit dominance and are responsible for particular traits is important for the genetic progress through selection. In the present investigation, the value of h²/H₂ was low in case of days to 50% flowering, days to 50% boll bursting, plant height, number of monopodia per plant, boll weight and seed index indicating that one group of genes generally controlled the inheritance of a particular character. The rest of character was generally controlled by more than one group of genes.

High estimates of heritability in narrow sense was observed for days to 50% flowering, days to 50% boll bursting, number of monopodia per plant, ginning percentage

(%), lint index (g) and oil content (%) suggesting that selection based on these attribute would lead to rapid improvement. Moderate heritability was also observed for number of sympodia per plant, number of bolls per plant, boll weight (g), seed cotton yield per plant and seed index (g), whereas plant height (cm) displayed low heritability.

In general, narrow sense heritability was found to be less than 50 per cent for plant height, number of sympodia per plant, number of bolls per plant, boll weight, seed cotton yield per plant and seed index indicating major role of dominance gene action in the expression of this trait. High narrow sense

heritability for days to 50% flowering, days to 50 % boll bursting, number of monopodia per plant, ginning percentage, lint index and oil content indicated that major part of phenotypic variability was due to additiveness and possibility of fixing these traits by simple selection.

Therefore, the present study showed preponderance of dominance genes in the expression of seed cotton yield and other traits including quality parameters suggesting that hybrid breeding can be used efficiently to improve yield together with quality traits in cotton.

Table 1: Estimation of genetic components of variation for different characters in cotton

Components/ratios	Days to 50% flowering	Days to 50% boll bursting	Plant height (cm)	Number of monopodia per plant	Number of sympodia per plant	Number of bolls per plant
D	177.00*	146.74*	305.84*	1.07*	2.87*	94.44*
	± 32.89	± 37.94	± 23.40	± 0.12	± 0.98	± 11.84
H ₁	225.46*	272.60*	206.27*	1.07*	9.92*	204.01*
	± 70.01	± 80.77	± 46.26	± 0.27	± 2.09	± 25.22
H ₂	200.54*	245.72*	69.11	0.85*	9.07*	154.24*
	± 59.50	± 68.64	± 41.86	± 0.23	± 1.78	± 21.43
h ²	45.20	1.63	-3.28	0.10	21.21*	308.87*
	± 39.82	± 45.95	± 28.02	± 0.15	± 1.19	± 14.34
F	-17.54	3.99	402.73*	-0.42	0.86	82.96*
	± 75.89	± 87.55	± 53.40	± 0.29	± 2.27	± 27.34
E	1.35	21.57	64.88*	0.02	0.40	10.41*
	± 9.91	± 11.44	± 6.97	± 0.03	± 0.29	± 3.57
(H ₁ /D) ^{1/2}	1.12	1.36	0.82	0.99	1.85	1.47
H ₂ /4 H ₁	0.22	0.22	0.08	0.20	0.22	0.18
K _D /K _R	0.91	1.02	9.08	0.66	1.17	1.85
h ² /H ₂	0.22	0.007	-0.04	0.12	2.33	2.00
Heritability (ns) %	68.00	50.00	19.00	78.00	34.00	38.00
t ²	0.87	0.32	1.07	10.42	0.03	0.08

*,** significant at 5% and 1% levels, respectively.

Table 2: Estimation of genetic components of variation for different characters in cotton

Components/ratios	Boll weight (g)	Seed cotton yield per plant (g)	Ginning percentage (%)	Seed index (g)	Lint index (g)	Oil content (%)
D	0.17*	1071.11*	4.40*	0.84*	0.67*	0.12*
	± 0.03	± 213.63	± 0.40	± 0.14	± 0.05	± 0.01
H ₁	0.30*	3009.75*	5.25*	1.16*	0.40*	0.14*
	± 0.07	± 454.74	± 0.86	± 0.30	± 0.12	± 0.03
H ₂	0.24*	2463.38*	4.27*	0.65*	0.31*	0.11*
	± 0.06	± 386.47	± 0.73	± 0.25	± 0.10	± 0.02
h ²	0.23*	7930.34*	4.70*	0.18	0.48*	0.19*
	± 0.04	± 258.69	± 0.49	± 0.17	± 0.06	± 0.01
F	0.16*	465.52	0.99	1.09*	0.40*	0.06
	± 0.07	± 492.91	± 0.93	± 0.32	± 0.13	± 0.03
E	0.02*	96.17	0.36*	0.17*	0.07*	0.006
	± 0.01	± 64.41	± 0.12	± 0.04	± 0.01	± 0.004
(H ₁ /D) ^{1/2}	1.29	1.67	1.09	1.17	0.77	1.07
H ₂ /4 H ₁	0.20	0.20	0.20	0.13	0.19	0.19
K _D /K _R	2.07	1.29	1.23	3.47	2.29	1.61
h ² /H ₂	0.92	3.21	1.09	0.28	1.56	1.74
Heritability (ns) %	29.00	44.00	60.00	27.00	54.00	58.00
t ²	0.24	1.04	1.60	1.01	1.15	0.01

*,** significant at 5% and 1% levels, respectively.

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