

## HERITABILITY AND SELECTION RESPONSE IN SEGREGATING GENERATIONS OF UPLAND COTTON

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**ABSTRACT:** Heritability (b.s), genetic advance, phenotypic and genotypic variance for different quantitative traits is important in determining the effectiveness of selection. In this study the potential effectiveness of selection in parents and their  $F_2$  and  $F_3$  progenies of *Gossypium hirsutum* for plant height, sympodia/plant, bolls/plant, boll weight, seed index and seed cotton yield/plant was determined. It was found that all the populations alongwith parents differed significantly ( $P \leq 0.01$ ) and exhibited genetic variability among the genotypes for all the traits except sympodia/plant. Genetic parameters computed through variance components method show that all the traits were highly heritable in  $F_2$  and  $F_3$  generations except sympodia/plant, indicating quantitative pattern of inheritance, offering better chances of selection for these traits in  $F_2$  and  $F_3$  generations. The traits namely plant height, bolls/plant and seed cotton yield/plant displayed high heritability (72.97 - 75.55%) with remarkable genetic advance (112.46 - 357.01%) indicating that these traits were predominantly governed by additive gene effects and direct selection may be effective. Boll weight and seed index exhibited low genetic advances irrespective to their high heritability estimates, probably due to non-additive gene effects, developing transgressive segregants through hybridization is suggested. However, hybridization system, which exploits both fixable and non-fixable components, simultaneously, could be useful in the genetic improvement of yield and yield components in upland cotton.

*Key Words:* *G. hirsutum*; Heritability; Genetic Advance; Segregating Generation; Pakistan.

### INTRODUCTION

Success in crop improvement programme depends on the amount of genetic variability and its utilization. In population improvement it is important to determine the extent of genetic variation for traits to be improved. The genetic information on broad sense (b. s.) heritability and genetic advance are very important to predict the behavior of the parents to be utilized in breeding programme for selecting high yielding cultivars. High genetic advance coupled with high heritability estimates offers a most effective response to selection (Larik et al. 1997). Khan et al. (2002) and Soomro et al. (2005) observed additive type of gene action for seed cotton yield and some yield components of *Gossypium hirsutum* due to high heritability and selection response. Considering the

importance of this type of research, it was contemplated to ascertain heritability and genetic gain in upland cotton genotypes. The information so obtained shall be useful in formulating a sound future breeding programme in this crop for tangible advancement.

### MATERIALS AND METHODS

Five cotton (*Gossypium hirsutum* L.) cultivars namely TH-3/83, NIAB-78, CIM-109, Mc-Nair-3150 and Reshmi were crosses in all possible combinations. The five parental cultivars and their 20  $F_2$ 's and 20  $F_3$ 's were grown in a RCB design with four replications at Sindh Agriculture University, Tandojam, Pakistan in 2005-06. Seeds were dibbled in rows 75 cm apart @ of 3.5 kg ha<sup>-1</sup>. Before first irrigation seedlings were thinned to maintain plant to

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plant distance of 30 cm. A 3.75 m x 14.2 m plot size was maintained. All required cultural operations were adopted uniformly in all the plots throughout growing season. Ten competitive plants in parents, F<sub>2</sub> and F<sub>3</sub> progenies were selected for recording observation on plant height, sympodia/plant, bolls/plant, boll weight, seed index and seed cotton yield/plant.

Genetic selection parameters were determined through variance component method (Breese, 1972; Larik et al. 1997) as follows:

$$\begin{aligned} \text{Genetic variance} &= \hat{\sigma}^2_g = (\text{MSG} - \text{MSE})/r \\ \text{Phenotypic variance} &= \hat{\sigma}^2_{ph} = \text{MSG}/r \\ \text{Heritability (h.w)} &= \hat{\sigma}^2_g / \hat{\sigma}^2_{ph} \\ \text{Selection index (s)} &= k \times \hat{\sigma}_{ph} \\ \text{Genetic advance (Gs)} &= hw \times s \\ \text{Genetic advance} &= \frac{GA \times 100}{\text{percent of population mean } \bar{X}} \end{aligned}$$

Where, MSG and MSE=are genotypic and error mean squares, respectively from analysis of variance

r= Number of replications

$\bar{X}$ = Population mean and

K= 2.06 at 5% selection intensity (Kang et al., 1983).

**RESULTS AND DISCUSSION**

**Performance of Parents, F<sub>2</sub> and F<sub>3</sub> Hybrids**

Analysis of variance (Table 1) exhibited that the genotypes differed significantly (P=0.01) for all the traits, indicating the presence of considerable genetic variability among parents, F<sub>2</sub>'s and F<sub>3</sub> progenies for further evaluation. Results revealed that in F<sub>2</sub> generation (Table 1) the cross TH-3/83 x Reshmi produced taller plants (111.3 cm), while Mc-Nair-3150 x NIAB-78 had the shortest plants (77.6 cm), while in F<sub>3</sub> generation, cross NIAB-78 x Mc-Nair-3150 produced tallest plants (88.34 cm). The parent CIM-109 and TH-3/83 manifested shortest plants of 53.48 and 53.43 cm, respectively as compared to the other genotypes. For sympodia/plant NIAB-78 x CIM-109 displayed highest number of fruiting branches (22.18) and Reshmi x Mc-Nair-3150 expressed lowest number of fruiting branches (17.07) per plant in F<sub>2</sub> generation. In F<sub>3</sub>'s

the cross CIM-109 x NIAB-78 displayed 17.93 sympodia/plant, while parent TH-3/83 expressed lowest number (12.25) of sympodia/plant. For bolls/plant, parent NIAB-78 expressed maximum bolls/plant (33.9) as compared to other genotypes, while low values for bolls/plant were expressed by cross TH-3/83 x Reshmi (17.4) in F<sub>2</sub> generation. In F<sub>3</sub>'s cross CIM-109 x TH-3/83 produced maximum bolls/plant (20.14) and the lowest number of bolls/plant were shown by parent TH-3/83 (8.56). The cultivar Reshmi gave maximum boll weight (3.55 g) and the lowest boll weight was shown by Mc-Nair-3150 (2.36 g) in F<sub>2</sub>'s. In F<sub>3</sub>'s NIAB-78 x Mc-Nair-3150 produced maximum boll weight (3.22 g) and the lowest boll weight was shown by the parent NIAB-78 (2.19 g). Maximum seed index was manifested by the cross Mc-Nair-3150 x Reshmi (6.77 g) and lowest (5.17 g) by the cross NIAB-78 x CIM-109 in F<sub>2</sub>'s. In F<sub>3</sub> generation cross NIAB-78 x Mc-Nair-3150 displayed maximum (7.65 g) seed index and TH-3/83 x Reshmi gave minimum seed index (5.62 g). The cross Reshmi x TH-3/83 provided maximum seed cotton yield of 91.18 g plant<sup>-1</sup>, while cross Mc-Nair-3150 x NIAB-78 gave lowest (51.01 g) seed cotton yield plant<sup>-1</sup> in F<sub>2</sub> generation. In F<sub>3</sub> generation, NIAB-78 x Mc-Nair-3150 produced highest seed cotton yield plant<sup>-1</sup> (50.14 g), whereas the parent TH-3/83 and CIM-109 expressed lowest (21.45 g) seed cotton yield plant<sup>-1</sup>. Generally the two hybrids NIAB-78 x Mc-Nair-3150 and CIM-109 x NIAB-78 displayed better performance for six quantitative traits as compared to other genotypes. It was further noticed that F<sub>2</sub> generation excelled the F<sub>3</sub> generation for all the quantitative traits which may be due to deterioration of heterosis in F<sub>3</sub> generation.

**Heritability and other Genetic Parameters**

Genetic parameters computed through variance components method in F<sub>2</sub>'s and F<sub>3</sub>'s demonstrate that all the characters were highly heritable except sympodial branches per plant in F<sub>2</sub> generation whereas, seed index in F<sub>3</sub> generation (Table 2). Seed index displayed maximum (88.13%)

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**Table 1. Mean performance and ANOVA (mean squares) of 5 parents and 20 crosses of cotton (*Gossypium hirsutum* L) for yield and yield components in F<sub>2</sub> and F<sub>3</sub> generations**

Parents and Crosses	Plant height (cm)	Sympodial/plant	No of bolls/plant	Boll weight (g)	Seed index (g)	Seed cotton yield/plant (g)	
<b>F<sub>2</sub> generation</b>							
TH-3/83	94.45 feg	18.72	26.07 bcd	2.812 c-f	6.264 c-f	72.24 b-e	
NIAB-78	98.45 d-h	20.05	33.90 a	2.597 d-g	5.398 jk	87.03 ab	
CIM-109	90.16 hi	20.63	22.06 c-h	2.626 d-g	5.514 ij	56.33 efg	
Mc-Niar-3150	83.12 ij	19.39	23.27 c-h	2.367 g	5.667 hij	54.56 fg	
Reshmi	110.6 ab	19.34	18.06 gh	3.556 a	6.576 ab	65.52 c-g	
TH-3/83 x NIAB-78	97.83 e-h	19.14	33.64 a	2.517 efg	5.472 j	84.69 ab	
TH-3/83 x CIM-109	110.7 ab	19.71	23.95 c-g	2.570 d-g	5.796 ghi	61.52 d-g	
TH-3/83 x Mc-Niar-3150	104.4 a-e	18.96	27.18 bc	2.664 c-g	6.087 efg	72.14 b-e	
TH-3/83 x Reshmi	111.3 a	19.5	17.40 h	2.799 c-f	6.165 ef	49.37 g	
NIAB-78 x CIM-109	110.3 ab	22.18	23.10 c-h	2.566 d-g	5.173 k	58.8 d-g	
NIAB-78 x Mc-Niar-3150	98.28 d-h	19.98	23.38 c-h	2.592 d-g	5.667 hij	57.92 d-g	
NIAB-78 x Reshmi	103.9 a-e	17.74	22.56 c-h	2.861 c-f	6.559 abc	63.70 c-g	
CIM-109 x Mc-Niar-3150	96.65 e-h	19.89	26.32 bcd	2.677 c-g	6.509 a-d	70.87 b-f	
CIM-109 x Reshmi	94.32 gh	18.84	20.55 d-h	2.827 c-f	6.025 fg	57.25 efg	
Mc-Niar-3150 x Reshmi	102.1 b-g	17.21	21.37 c-h	3.066 bc	6.775 a	64.11 c-g	
NIAB-78 x TH-3/83	93.45 gh	18.44	25.09 cde	2.432 fg	5.409 jk	61.31 d-g	
CIM-109 x TH-3/83	100.6 c-g	20.78	25.75 cde	2.940 cde	6.353 b-e	74.77 a-d	
Mc-Niar-3150 x TH-3/83	107.0 a-d	19.63	22.75 c-h	2.694 c-g	5.949 fgh	58.91 d-g	
Reshmi x TH-3/83	109.4 ab	20.14	32.04 ab	2.867 cde	6.198 ef	91.18 a	
CIM-109 x NIAB-78	99.62 c-g	20.08	24.53 c-f	2.575 d-g	5.534 ij	62.35 c-g	
Mc-Niar-3150 x NIAB-78	77.60 j	20.30	19.92 e-h	2.612 d-g	5.513 ij	51.01 g	
Reshmi x NIAB-78	103.3 a-f	18.96	24.75 c-f	3.456 ab	6.095 efg	84.85 ab	
Mc-Niar-3150 x CIM-109	95.67 e-h	20.51	26.96 bc	2.525 efg	5.489 ij	64.72 c-g	
Reshmi x CIM-109	107.4 abc	19.68	18.74 fgh	2.694 c-g	6.238 def	52.97 g	
Reshmi x Mc-Niar-3150	99.02 c-h	17.07	25.07 cde	2.981 cd	5.572 ij	79.57 abc	
<b>Source of variation</b>	<b>DF</b>	<b>Mean squares</b>					
Replication	3	733.761	25.288	93.947	0.258	0.441	236.764
Genotypes	24	289.128**	5.264	73.098**	0.321**	0.792**	557.580**
Error	72	70.688	3.356	18.792	0.093	0.094	150.707
<b>F<sub>3</sub> generation</b>							
TH-3/83	53.437 e	12.250 d	8.562 f	2.707 abc	6.360 bcd	21.450 f	
NIAB-78	60.750de	14.687a-d	12.437 b-f	2.197 c	6.812 abc	27.807 c-f	
CIM-109	53.488 e	12.500 cd	9.406 ef	2.641 abc	6.822 abc	21.450 f	
Mc-Niar-3150	71.598 a-e	16.696 ab	18.652 ab	2.427 bc	6.657 a-d	42.161 a-d	
Reshmi	73.087 a-d	15.562 a-d	13.75 a-f	2.794 abc	6.906 abc	37.809 a-f	
TH-3/83 x NIAB-78	67.656 b-e	16.210 ab	11.884 b-f	2.949 ab	6.652 a-d	31.861 b-f	
TH-3/83 x CIM-109	65.750 b-e	13.719 bcd	10.859 def	2.376 bc	6.574 a-d	25.533 def	
TH-3/83 x Mc-Niar-3150	69.865 b-e	15.883 abc	11.608 b-f	2.848 abc	6.527 bcd	31.896 b-f	
TH-3/83 x Reshmi	66.313 b-e	15.375 a-d	11.094 c-f	2.721 abc	5.623 d	28.663 c-f	
NIAB-78 x CIM-109	70.250 a-e	15.805 a-d	10.888 def	2.850 abc	6.301 bcd	30.638 b-f	
NIAB-78 x Mc-Niar-3150	88.348 a	17.792 a	16.091 a-e	3.216 a	7.653 a	50.141 a	
NIAB-78 x Reshmi	77.537 a-d	15.650 a-d	13.112 b-f	2.897 abc	7.293 ab	37.998 a-f	
CIM-109 x Mc-Niar-3150	62.130 cde	15.214 a-d	11.428 c-f	2.401 bc	6.561 a-d	27.303 c-f	
CIM-109 x Reshmi	75.531 a-d	15.438 a-d	15.562 a-f	2.854 abc	6.625 a-d	43.958 abc	
Mc-Niar-3150 x Reshmi	64.656 b-e	14.904 a-d	8.798 f	2.910 abc	6.920 abc	25.896 def	
NIAB-78 x TH-3/83	77.563 a-d	17.500 a	17.358 a-d	2.482 bc	6.224 bcd	43.959 abc	
CIM-109 x TH-3/83	76.015 a-d	16.594 ab	20.141 a	2.428 bc	6.065 cd	47.121 ab	
Mc-Niar-3150 x TH-3/83	61.525 cde	15.800 a-d	11.162 c-f	3.033 ab	6.905 abc	33.501 a-f	
Reshmi x TH-3/83	61.928 cde	15.247 a-d	11.250 c-f	2.586 abc	6.486 bcd	28.549 c-f	
CIM-109 x NIAB-78	82.419 ab	17.934 a	18.153 abc	2.808 abc	6.575 a-d	50.116 a	
Mc-Niar-3150 x NIAB-78	78.331 a-d	15.181 a-d	13.031 b-f	2.430 bc	6.835 abc	31.418 b-f	
Reshmi x NIAB-78	82.101 ab	17.750 a	15.791 a-f	2.480 bc	6.397 bcd	39.982 a-e	
Mc-Niar-3150 x CIM-109	63.375 cde	13.844 bcd	10.00 ef	2.511 abc	6.613 a-d	23.894 ef	
Reshmi x CIM-109	73.699 a-d	16.886 ab	14.313 a-f	2.722 abc	6.706 a-d	39.035 a-f	
Reshmi x Mc-Niar-3150	79.910 abc	14.896 a-d	10.746 def	2.821 abc	6.871 abc	28.853 c-f	
<b>Source of variation</b>	<b>DF</b>	<b>Mean squares</b>					
Replication	3	1700.671	59.846	10.894	0.170	1.656	1142.325
Genotypes	24	323.116**	8.774**	40.679**	0.239**	0.612**	299.766**
Error	72	69.241	2.616	10.332	0.10	0.24	63.795

*Means followed by same letters do not differ significantly at P ≤ 0.05*

**Table 2. Estimation of phenotypic and genotypic variance, heritability (b.s), genetic advance or seed cotton yield and its quantitative and qualitative characters in *Gossypium hirsutum* in F<sub>2</sub> and F<sub>3</sub> generations**

Characters	Genotypic variance	Phenotypic variance	Heritability (h <sup>2</sup> )% b.s	Selection index (S) at 5%	Genetic advance	G.A. % of mean
<b>F<sub>2</sub> generation</b>						
Plant height (cm)	54.61	72.282	75.5513	148.9009	112.496	112.506
Sympodia/plant	0.477	1.316	36.246	2.7109	0.9825	5.05219
No. of bolls/plant	13.5765	18.2745	74.292	37.645	27.9672	114.9187
Boll weight	0.057	0.08025	71.028	0.1653	0.1174	4.26134
Seed index	0.1745	0.198	88.1313	0.40788	0.3594	6.0709
Seed cotton yield/plant	101.71825	139.395	72.97123	287.1537	209.5395	316.0093
<b>F<sub>3</sub> generation</b>						
Plant height (cm)	63.468	80.779	78.5699	166.4047	130.744	185.9668
Sympodia/plant	1.5395	2.1935	70.1846	4.5186	3.17136	20.36513
No. of bolls/plant	7.58675	10.16975	74.6011	20.9496	15.6286	119.82366
Boll weight	0.03475	0.05975	58.1589	0.123	0.071535	2.665735
Seed index	0.093	0.153	60.7843	0.3151	0.19153	2.885139
Seed cotton yield/plant	58.9927	74.9415	78.7183	154.3794	121.5248	357.011119

heritability followed by bolls per plant (74.29%) in F<sub>2</sub> while in F<sub>3</sub> generation seed cotton yield/plant and plant height displayed (78.72%) and (78.57%) heritability respectively.

There was a wide range of genotypic and phenotypic variances among the characters. The highest phenotypic and genotypic variances of 139.395 and 101.72 respectively were recorded for seed cotton yield per plant followed by plant height (72.28 and 54.61) in F<sub>2</sub> generation. Seed cotton yield per plant displayed highest genetic advance (209.54), selection index (287.15) and G.A% of mean (316.01) followed by number of bolls per plant. Heritability estimates alongwith genetic advance are very useful in predicting expected gain under selection instead of heritability alone. High heritability estimates with high GA indicated that due to additive gene effects direct selection may be effective in F<sub>2</sub> and F<sub>3</sub> for these traits. All the traits though displayed high estimates of heritability (b.s.), yet the magnitude of other genetic parameters were quite low in F<sub>2</sub> generation. In F<sub>3</sub> generation highest genotypic and phenotypic variances 80.78 and 63.47 also showed by plant height followed by seed

cotton yield/plant (74.94 and 58.99). Plant height also showed highest genetic advance (130.74), selection index (166.40) and G.A% of mean (185.97) followed by seed cotton yield/plant (Table 2). All the traits though displayed high estimates of broad sense heritability, yet the magnitude of other genetic parameters were quite low except in plant height and seed cotton yield/plant.

Comstock and Moll (1963) reported that more diverse the environmental population the smaller the estimates of genetic variance which supports the present results of low estimates of genetic variance in F<sub>2</sub> population. The knowledge of the genetic and phenotypic variances for each parameter is necessary to construct a definite selection index (Sprague, 1966). Considering the broad sense heritability estimates, plant height, bolls per plant, boll weight, seed index, and seed cotton yield were ranked as high heritable. Rehman et al. (1991), Larik et al. (1992, 1997 & 2000), Yankun et al. (1998) and Hendaway et al. (1999) also reported high heritability for these traits. High heritability suggests that the parents could be used to develop better genotypes in early generations. The high heritability

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estimates also indicated that the additive/additive x additive effect were more effective than dominance/dominance x dominance effects. High heritable characters were least affected by environmental fluctuations. Hence simple selection method would be effective for these traits. The said traits displayed considerable amount of expected genetic advance percentage and the presence of non-allelic interaction played a major role in decreasing  $h^2$  estimates for these traits. Furthermore sympodia is polygenically controlled. Cumulative environmental effects on this polygenically controlled trait gave poor heritabilities for this trait.

Seed cotton yield exhibited 81.14% heritability (b.s.) coupled with genetic advance of 60.18%. Although the yield is a complex polygenic character, its inheritance has been characterized as the most fluctuative showing high heritability and genetic advance, indicating the importance of additive type of gene effects for its inheritance (Larik et al., 1997 and 2000). High phenotypic and genotypic variance of this trait resulted in high heritability and GA values which suggested the improvement of these traits by simple selection method. Therefore, the selection based on plant height, seed cotton yield per plant and bolls/plant could be exploited for the improvement of yield in cotton. However, the traits boll weight and seed index also displayed high heritability estimates but failed to express higher estimates of genetic advance expected through selection. Higher estimates of heritability (b.s) do not necessarily provide high values of genetic advance and hence heritability alone provides no indication for the amount of genetic progress in the trait that can be achieved through selection (Ansari et al., 2002, Hussain et al., 1999, Larik et al., 1997). High heritability associated with low genetic advance for these traits was probably due to non additive gene (dominance and epistasis) effects (Sharma and Tyagi, 1990, 1991) in  $F_2$  s while in  $F_3$  generation seed cotton yield exhibited 78.72% broad sense heritability coupled with 121.52% genetic

advance indicating the contribution of additive type of gene effects for its inheritance (Gomaa et al., 1999). Hendaway et al. (1999), Yuan et al. (2002) and Baloch (2004) explained that genetic variance in most cases however, were equal to that of phenotypic variances consequently giving high heritability estimates and significant genetic gain. Therefore, the selection based on seed cotton yield and bolls/plant, and plant height could be exploited for the improvement of yield and fibre quality in  $F_3$  generation.

Low estimates of broad sense heritability accompanied with low GA in respect of sympodia/plant in  $F_2$  generation suggested that the characters are poorly heritable and may be due to non-additive gene action and presence of GxE interaction, simple selection may not be rewarding (Kumar et al., 2002) and in such cases breeders can go for selecting desirable transgressive segregants. The successful breeding methods will be the ones, which will exploit the non-additive gene effects. The methods which mop-up the non-additive effects are restricted recurrent selection by the way of intermating the most desirable segregants followed the selection (Joshi, 1979) and diallel selective mating (Jensen, 1978). Hybridization system may therefore be useful in genetic improvement of yield and yield components in upland cotton.

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