

**Genetic variability and heritability in F₂ population of *Gossypium hirsutum* for seed cotton yield and its components**^a Muhammad Zahir Ahsan*, ^b Hafiz Tariq Mahmood^a Cotton Research Station, Sahiwal, ^b Directorate of Research (Headquarters) Pakistan Central Cotton Committee

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ABSTRACT	Digital Object Identifier (DOI): https://doi.org/10.33865/IJCRT.001.01.0245

Genetic variability, heritability and correlation for seed yield and its attributing components were estimated in the F₂ population of the cross Lalazar × SLH-33 at Cotton Research Station Sahiwal during Kharif season 2018. The segregating population was evaluated for eleven quantitative traits i.e. plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, number of seeds per boll, seed index, seed cotton yield per plant, ginning outturn, staple length and micronaire value. A wide range of variability was observed for all these traits. A high value of GCV, Heritability and genetic advance percentage over mean was recorded for number of bolls per plant, number of sympodia per plant, number of seeds per boll and staple length. The traits having high heritability coupled with moderate to high genetic advance could be utilized as indirect selection for yield improvement.

Key word: Genotypic variance, phenotypic variance, heritability, genetic advance as percent of mean, correlation.

INTRODUCTION: Major share in national economy comes from agriculture sector, especially from cotton crop as major export is textile products. Thus playing a key role in socio-economic position of the country. Within last few years a shear decline in cotton production was observed due to multiple reasons, one of that is a cultivar suitable in changing climatic scenario. Genetic information on different qualitative and quantitative traits is very much helpful for the breeders in order to develop high yielding cultivars (Nadeem and Azhar 2004, Ali and Khan, 2007 and Abbas *et al.*, 2008). The creation of new variability and its proper utilization in the breeding program along with its genetic understanding is of crucial importance in a breeding program (Basal and Tuegut, 2005, Abbas *et al.*, 2008, Ali *et al.*, 2008, Ali and Awan 2009). Heritability in itself did not provide any indication about the genetic gain that would result from selection, but in fixed selection pressure amount of genetic advance varies with the magnitude of the heritability. Genetic advance in a population cannot be predicted from heritability alone instead genetic gain at specific selection pressure has to be worked out. In *Gossypium hirsutum* genotypic and phenotypic variation, correlation for many quantitative and qualitative traits such as plant height, number of bolls, boll weight, number of squares, number of monopodial branches, number of sympodial branches, days taken to 50% bolls, number of seeds per boll, seed index, lint index, ginning turnout, staple length, micronaire and seed cotton yield has been studied (Sakthi *et al.*, 2007, Dhamayanathi *et al.*, 2010, Vrinda and Patil 2018).

OBJECTIVES: The present study was conducted with the objective of evaluating the variability among the *Gossypium hirsutum* hybrids for yield and other attributes and to analyze the heritable components of the variability for making suitable selection for breeding program.

MATERIAL AND METHODS: The material of the present study was generated during Kharif 2016 at Cotton Research Station Sahiwal by crossing high yield,

compact stature cultivar FH-Lalazar with medium stature spreading stature advance line of the station. F₂ seeds were harvested during 2017 and non-replicated F₂ material was sown during 2018. The experiment was carried out without replications as it is segregating material the row to row spacing was 75cm and plant to plant spacing was 30cm. recommended agronomic practices were carried out to raise the crop the observation was recorded for 20 plants from parents and 10% plants from F₂ populations for seed cotton yield per plant and its components viz, plant height, number of monopodia per plant number of sympodia per plant, number of bolls per plant, boll weight, seeds per boll, seed index, GOT%, staple length and micronaire value.

The mean and variances were statistically analyzed (Singh and Chaudhary, 1977).

Phenotypic Variance (V_p): The individual observation made for each trait on F₂ population calculating the phenotypic variance

Phenotypic variance = Variance of F₂ population

Environmental Variance (V_e): The average variance of the parents and their corresponding F₁ is used to work out environmental variance for single crosses

$$\text{Environmental Variance} = \frac{Vp_1 + Vp_2 + VF_1}{3}$$

Where, Vp₁ = Variance of parent 1, Vp₂ = Variance of parent 2, VF₁ = Variance of cross F₁

Genotypic Variance (V_g)

Genotypic Variance (V_g) = V_p - V_e. Where V_p = Phenotypic Variance, V_e = Environmental variance

Coefficient of Variability (CV): Genotypic (GCV) and Phenotypic (PCV) coefficient of variations were computed as suggested by Burton and Devane (1953).

$$GCV (\%) = \frac{\sqrt{Vg}}{\text{mean}} \times 100$$

$$PCV (\%) = \frac{\sqrt{Vp}}{\text{mean}} \times 100$$

GCV and PCV values were classified as low, moderate and high as suggested by Sivasubramanian and Menon (1973).

0 - 10%: Low, 11 - 20 %: moderate, 21% and above: High

Heritability h^2 (Broad Sense): The heritability percentage was estimated for all the traits under study as suggested by Lush (1949) and Henson (1956).

$$\text{Heritability } (h^2) = \frac{V_g}{V_p} \times 100$$

Heritability was classified as low, medium and high as suggested by Robinson et al., 1949.

0 - 30%: Low, 30 - 60 %: moderate, 60% and above: High

Genetic advance: The extent of genetic advance to be expected from the selecting five percent of the better progeny was calculated by using the formula suggested by Johanson et al., 1955.

$$\text{Genetic advance} = S \times \sqrt{V_p} \times h^2$$

Where value of S at 5% selection intensity was 1.755

Genetic advance over percentage of mean was calculated as

$$GA(\%) = \frac{GA}{Mean} \times 100$$

Genetic advance as percentage of mean was categorized as low, medium and high as follows;

Table-1: Mean, Range, Phenotypic and genotypic variances (V_p & V_g), Phenotypic and Genotypic Coefficient of Variances (GCV & PCV), heritability (h^2), Genetic advance (GA) and Genetic advance percent over mean (GA%) for yield attributes and fiber quality traits.

Traits	Mean	Range		V_g	V_p	GCV	PCV	h^2	GA	GA (%)
		Min	Max							
Plant height	137.8	75.67	189.76	503.18	638.96	16.28	18.34	79.0	34.94	25.35
Monopodia plant ⁻¹	2.36	1.00	3.45	0.20	0.29	18.95	22.82	69.0	0.65	27.62
Sympodia plant ⁻¹	13.78	7.56	21.34	15.53	19.85	28.60	32.33	78.0	6.12	44.39
Bolls plant ⁻¹	21.23	11.23	38.76	76.11	119.5	41.60	51.19	64.0	12.24	57.59
Boll weight	3.32	2.21	4.35	0.14	0.21	11.27	13.80	67.0	0.54	16.15
Seeds boll ⁻¹	18.25	14.35	21.34	57.08	102.31	41.40	55.42	56.0	9.90	54.27
Seed index	6.31	5.64	8.87	0.16	0.34	6.34	9.24	47.0	0.48	7.63
Seed cotton yield plant ⁻¹	125.98	78.56	189.45	402.15	636.6	15.93	20.03	63.0	28.0	22.23
GOT (%)	37.81	35.68	41.32	5.85	6.67	6.40	6.83	88.0	3.98	10.51
Staple length	27.92	25.60	29.31	105.42	123.87	36.77	39.86	85.0	16.62	59.54
Micronaire value	4.13	3.38	5.40	0.39	0.45	15.12	16.24	87.0	1.02	24.71

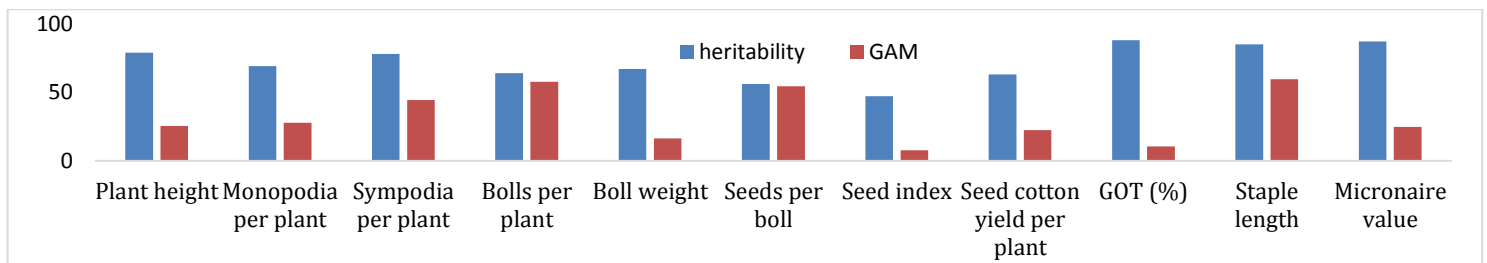


Figure 1: heritability and Genetic advance as percentage of mean in F_2 populations of cross FH-Lalazar×SLH-33.

Traits like plant height, number of monopodia per plant, boll weight, seed cotton yield per plant and micronaire value showed moderate PCV and GCV values. Seed index and ginning outturn showed low PCV and GCV values. Low PCV and GCV for these traits indicate a narrow range of variability for these characters and limited scope for selection. GCV values were invariably lower than the PCV values for all traits and were in line with the findings of Laxman and Ganesh 2003, Gururajan and Sundar 2004, Neelima et al., 2005, Kale et al., 2007, Alkudsi

0 - 10%: Low, 10 - 20 %: moderate, 31% and above: High

RESULTS AND DISCUSSION

Genetic Variability, heritability and Genetic advance as percentage of mean: The phenotypic co-efficient of variation (PCV) was recorded for plant height (18.34) number of monopodia per plant (22.82), number of sympodia per plant (32.33), number of bolls per plant (51.19), boll weight (13.80), number of seeds per boll (55.42), seed index (9.24), seed cotton yield per plant (20.03), GOT% (6.83), staple length (39.86) and micronaire value (16.24). The genotypic co-efficient of variation (PCV) was recorded for plant height (16.28) number of monopodia per plant (18.95), number of sympodia per plant (28.60), number of bolls per plant (41.60), boll weight (11.27), number of seeds per boll (41.24), seed index (6.34), seed cotton yield per plant (15.93), GOT% (6.40), staple length (36.77) and micronaire value (15.12). PCV and GCV were classified as suggested by the Sivasubramanian and Menon (1973) low (0-10%), moderate (11-20%) and High (>21%). Traits like number of sympodia per plant, number of bolls per plant, number of seeds per boll and staple length recorded high PCV and GCV, a very high PCV and GCV for these traits indicate greater scope for selection to improve seed cotton yield.

and genotypic co-efficient of variation, it also gives information regarding the relative variation in different populations. The co-efficient of variation does not discriminate the variability into heritable and non-heritable portion. Heritability in broad sense would suggest how much the variation is heritable and selection is effective. So the heritability estimate is the true indicator for genetic potential which can be used as tool for selection. Changes in heritability due to environment factors hurdle the total dependence on heritability, however heritability estimate in conjunction with the genetic advance as percentage of mean is reliable tool for selection. Broad sense heritability was recorded for plant height (79.0) number of monopodia per plant (69.0), number of sympodia per plant (78.0), number of bolls per plant (64.0), boll weight (67.0), number of seeds per boll (56.0), seed index (47.0), seed cotton yield per plant (63.0), GOT% (88.0), staple length (85.0) and micronaire value (87.0). The genetic advance as percentage of mean was recorded as plant height (25.35) number of monopodia per plant (27.62), number of sympodia per plant (44.39), number of bolls per plant (57.59), boll weight (16.15), number of seeds per boll (54.27), seed index (7.63), seed cotton yield per plant (22.23), GOT% (10.51), staple length (59.54) and micronaire value (24.71). The traits under study exhibited high heritability except number of seeds per boll and seed index which had moderate heritability percentage. High heritability provided the information that maximum portion of the phenotypic variance was attributed by the genotypic variance. And selection can be done on the basis of phenotypic expression. Most of the characters exhibited high genetic advance except boll weight, seed index and ginning turnout which had moderate genetic advance as percentage of mean. Traits plant height, number of monopodia, number of sympodia, number of bolls per plant and number of seeds per boll had high heritability coupled with high genetic advance so indirect selection through these traits can be utilized to maximize seed cotton yield.

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