

Genetic Analysis for Some Characteristics in Cotton (*Gossypium hirsutum* L.).

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Abstract: A wide range of average performance and genetic variability was estimated for F₁ crosses of nine commercial varieties of cotton viz., CIM443, MNH147, FH-682, N. Krishma, SLS-1, CIM-446, CIM448, FVH-53 and MNH552 for bolls and seed cotton yield per plant, boll weight, staple length, ginning out turn (%) and virus infestation (%). The highest genotypic variability was recorded for virus infestation (94.61%) followed by bolls per plant (29.84%). The highest estimates of heritability associated with highest genetic advance for bolls per plant (97.8 and 60.78), virus infestation % (95.0 and 189.9) and boll weight (97.39 and 10.99) suggested selection for improvement of these traits due to presence of sufficient genotypic variability. However, low estimates of these parameters for staple length showed slow progress through selection.

Key words: Cotton, varieties, yield, fibre characteristics, virus infestation

Introduction

Cotton (*Gossypium hirsutum* L.) can rightly be considered one of the most important cash crops in playing effective and vital role for boosting up Pakistan's economy. Cotton plant directly as well as indirectly provides food and feed to millions of human beings and animals. In the recent years, production of the crop has very encouraging due to release of high yielding, virus resistant varieties as well as application of proper package of production technology by the farmers of eco-zones especially in Multan division. Therefore, these varieties can further be utilized to get good combinations. So, through knowledge and complete understanding of inheritance pattern of economic traits is a pre requisite for enhanced progress in breeding new varieties of cotton. Sufficient variability of a character is a first step for plant breeder to channelize the breeding system. Because variability of a quantitative character is the result of genetic and of environmental causes. The proportion of total phenotypic variability of a character that arises from genetic differences is attributed as broad sense heritability, which is a major concern to plant breeder as it helps to predict response to select in a genetically segregate population. A pragmatic breeding programme aimed at improving the yielding ability of a crop species require information on the nature and magnitude of variability, heritability in cotton for seed cotton yield, bolls per plant, fibre length and boll weight. Both heritability and

genetic advance. In recent years several scientists (Esmail *et al.*, 1999; Kumaresan *et al.*, 2000) estimated high heritability and genetic advance were found high for seed cotton yield and its components (Saddique, 1997) and these were moderate for lint percentage (Jagtap and Mehtari, 1998).

Accordingly the present work was carried out to study on varietal performance, variability, heritability and genetic advance for some characteristics in cotton.

Materials and Methods

Nine cotton varieties constituted the genetic material for the present study. All the varieties were sown in a replicated randomized complete block design (RCBD) at Cotton Research Station, Multan. Beds were kept 75 cm apart and plant to plant distance was maintained as 30 cm. Later on nine single crosses achieved from the above varieties were sown on May, 2001 with 30 cm plant to plant and 75 cm row to row distance. Observations on 15 randomly selected plants from each row plot in both experiments were recorded for bolls per plant, seed cotton yield, boll weight, staple length, ginning out turn percentage and virus infestation (%). Ginning out turn percentage was calculated by using the following formula:

$$\text{Ginning out turn (\%)} = \frac{\text{Weight of lint (g)} \times 100}{\text{Weight of seed cotton (g)}}$$

For this purpose, the seed cotton for each plant was gained separately with a single roller electric gin. The lint thus obtained was weighed. Staple length was obtained by counting number of plants infected. Analysis of variance was carried out and parameters such as mean standard error, variability, heritability and genetic advance were computed according to Burton (1952) and Johnson *et al.* (1955).

Results and Discussion

Varietal performance

The differences among nine varieties were significant for all traits except staple length (Table 1).

The variety MNH552 had more number of bolls (40) and seed cotton yield ha⁻¹ (3282 kg) followed by CIM446 having 36 bolls per plant and 2833 kg seed cotton yield. However, maximum boll weight (3.4 g) was observed by CIM448 and minimum boll weight (2.10 g) was obtained by SLS-1. Similarly, staple length was also highest (27.0 mm) in CIM448 and lowest (25.6 mm) in CIM446. Maximum lint (41.8%) was estimated in variety CIM448 followed by MNH147 (Table 2). The researchers Soomro *et al.* (1986) and Khan *et al.* (1989) conducted such type of experiment in

different climates and recorded the performance of some old cotton varieties CIM446, CIM448 and MNH552 showed complete resistance to virus for these traits. However, FH-682, MNH147, NIAB Krishna and SLS-1 showed susceptibility to virus for these traits having infestation from 23 to 25 %. Perhaps it is the reason that these varieties are low yielding as compared to virus resistant varieties. Virus infestation varied in virus susceptible varieties of Cotton (Ahmad *et al.*, 2002) and it caused reduction in seed cotton yield upto 70% (Tarr, 1957; Idris, 1990).

Table 1: Mean squares of nine varieties of cotton for six characters

SOV	D.F	Bolls Plant ⁻¹	Seed cotton yield plant ⁻¹	Boll weight (g)	Staple length (mm)	Ginning out turn(%)	Virus infestation(%)
Replications	2	95.00	978	0.03	0.83	1.44	48.00
Varieties	8	199.00**	929713	0.62*	1.42ns	18.42**	411.00**
Error.	16	1.46	16447	0.12	0.49	1.55	7.00

*, ** = Significant at 0.05 and 0.01 probability levels, respectively

Table 2: Varietal performance of cotton for some traits under Multan conditions

Varieties	Bolls plant ⁻¹	Seed cotton yield kg ha ⁻¹	Boll weight (g)	Staple length (mm)	Ginning out turn(%)	Virus infestation
CIM443	26±5	2376±370.1	2±0.03	26±0.40	37±0.79	3±0.29
MNH147	34±2	1883±243.2	3±0.23	25±0.57	41±0.18	22±0.10
FH-682	19±2	1560±173.5	3±0.14	26±0.57	33±0.44	25±1.39
N-KRISHMA	25±4	2179±226.2	2±0.10	27±0.17	36±1.36	23±3.47
SLS-1	26±3	1837±771.1	2±0.18	27±0.56	36±0.50	25±4.11
CIM446	36±2	2833±312.1	3±0.27	25±0.35	38±0.27	-
CIM448	24±4	1874±85.8	3±0.12	27±0.23	41±0.33	-
FVH-53	21±1	1838±7.3	3±0.13	26±0.07	38±0.34	10±2.03
MNH552	40±4	3282±187.3	2±0.06	26±0.23	40±0.07	-
Cdl (5%)	2	222.0±135.6	0.60	1.21	2.16	4.59

Variability, heritability and Genetic advance

Phenotypic and genotypic coefficient of variations ranged from 3.36 to 97.05 and 2.09 to 94.61, respectively. In general, the trend of variation with different characters was almost similar in genotypic and phenotypic coefficient of variations were observed for virus infection, moderate for bolls and seed cotton yield per plant, boll weight and low for staple length and ginning our turn. Moderate to high genetic variability could be exploited by selection programmes and low genotypic variability in case of staple length indicated lack of inherent variations and limited scope for improvement by selection (Table 3). Same results were observed by Saddique (1997) in cotton for yield and its components.

The broad sense heritability was very high (75%) for bolls and seed cotton yield plant⁻¹, ginning out turn and virus infestation. It was moderate (60%) for boll weight and low (40%) for staple length. Component breeding becomes more effective when selection is based on the related characters with high heritability. Further more, high heritability was associated with high

genetic advance in the presence of sufficient genotypic variability worthy of exploitation. The low heritability and genetic advance for staple length did not mean that there would be no progress, but in this case the improvement would be slow and gradual for this trait. Yingxin and Xiangming, (1988); Esmail *et al.* (1999), Hendawy *et al.* (1999), Shanti and Raveendran (1999), Kumaresan *et al.* (2000) estimated moderate to high heritability and genetic variance for seed cotton yield, bolls per plant, boll weight staple length and lint percentage.

Table 3: Biometrical parameters in nine single crosses of commercial varieties

Characters	Mean \pm S.E.	Variance			Coefficient of variation			Genetic advance as per mean
		Genotypic	Environmental	Phenotypic	Genotypic	Phenotypic	h ² %	
No. of bolls plant ⁻¹	27 \pm 1.21	65.00	1.46	67.44	29.84	30.17	97	60.78
Seed cotton yield plant ⁻¹	49 \pm 5.80	6.00	9.37	7.21	37.36	38.36	97	10.00
Boll weight (g)	2 \pm 0.28	0.17	0.12	0.29	14.47	18.89	58	22.00
Staple length (mm)	26 \pm 0.57	0.31	0.49	0.80	2.09	3.36	38	2.00
Ginning out turn (%)	38 \pm 1.02	5.00	1.55	7.17	6.22	7.03	78	11.00
Virus infestation (%)	12 \pm 2.65	134.00	7	141.79	94.61	97.05	95	189.00

The varieties MNH552 and CIM446 were high yielding with better number of bolls. Big boll size, long staple length and high ginning out turn were observed in cultivar, CIM448. So including these cultivars in experiment for hybridization programme, would yield better hybrids which could be used for commercial purposes. Moreover these varieties did not exhibit virus infestation. Today virus infestation in cotton is a hybridization programme to evolve high yielding and virus resistant varieties.

Breeding strategy becomes more effective when selection is based on the related characters with high variability and heritability. Moreover, high estimates of heritability associated with high genetic advance in the percent of genotypic indicated sufficient improvement for their variability traits. However, low estimates of heritability and genetic advance for staple length did not mean that there would be no progress but comparatively improvement for this trait would be slow.

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