

ESTIMATION OF BEST PARENTS AND SUPERIOR CROSS COMBINATIONS FOR YIELD AND FIBER QUALITY RELATED TRAITS IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM* L.)

SHADAB SHAUKAT^{1*}, TARIQ MANZOOR KHAN¹, AMIR SHAKEEL¹ AND SIDDRA IJAZ²

¹Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan.

²Centre of Agricultural Biochemistry and Biotechnology (CABB), University of Agriculture, Faisalabad, Pakistan.

Abstract

Combining ability was studied for identification of potential cultivars and hybrids in upland cotton (*Gossypium hirsutum* L.) in a 6×6 set of diallel crosses among six genotypes of cotton, i.e., VH-232, CRS-2007, SB-149, GR-156, FH-207, and MARVI carried out on fiber length, fiber fineness, fiber elongation, fiber strength, ginning out turn (GOT) and seed cotton yield. Analysis of variance revealed highly significant ($p \leq 0.01$) differences among the genotypes for all traits. Combining ability studies showed that the mean squares, due to general combining ability (GCA), specific combining ability (SCA) and reciprocal effects were highly significant in F₁ generation. Genetic components, due to GCA and SCA, revealed that traits, such as, fiber length, strength and fineness, showed high proportion of additive type of gene action in F₁ generation because of greater GCA variances were greater than SCA variance. GR-156 was the best combiner for lint percentage and fiber length. FH-207 was the best combiner for fiber fineness. FH-207, MARVI and SB-149 were the best general combiners for fiber character and were suggested to be used in future breeding programme to improve fiber quality traits. CRS-2007 × GR-156, CRS-2007 × MARVI, SB-149 × MARVI and VH-232 × SB-149 had higher specific combining ability and reciprocal effects and they can be used for future breeding programme to improve fiber quality.

Keywords: *Gossypium hirsutum* L., Fiber quality, Genetic variability.

Introduction

Cotton (*Gossypium hirsutum* L.) occupies the high rank among all the available natural fibers in the world. It is also called the king of natural fibers and is the main stay of the economy of the many countries. In Pakistan, this crop is the mainstay of the economy. Cotton is a vital profitable crop for Pakistan and out of the total cultivated area of the country; 12% is covered by this crop (Khan et al., 2009). Cotton fiber quality is no longer an afterthought; it is becoming an increasingly important issue in modern textile industry. Fiber quality of a specific cotton genotype is a composite of various characteristics, including, staple length, fiber strength, fineness, maturity and fiber elongation. These traits have their individual importance in

spinning, weaving and dying units (Munro, 1987). To improve production, it is imperative to develop new high yielding varieties/hybrids possessing greater yield potential with desirable fiber quality traits. The information about genetic variability and the gene controlling this genetic variability is essential for crop improvement exercise (Naveed et al., 2004). The variation in genetic constitution in both domestic and extrinsic germplasm for the enviable characters may be utilised advantageously conferring in plant improvement strategy. The knowledge about combining ability effects helps the plant breeders in selection of suitable parents for hybridisation programme (Patil et al, 2011). Combining ability is the ability of a parent to produce superior offsprings when combined with

*Author for correspondence E-mail: shadab_uaf@hotmail.com

another parent. Any type of knowledge on the gene action and inheritance of various plant traits in addition to general and specific combining ability may assist the plant breeders in their strivings in that way. The mode of inheritance of economic characters is a pre-requisite for enhancing the progress in breeding new cultivars of cotton (Nadeem and Azhar, 2004).

On the basis of these backgrounds, a research experiment was conducted to determine the mode of gene action associated with fiber quality traits and to select potential parents and crosses for further improvement.

Material and Methods

In the first year, all crosses between parents were made (Pohlman, 1959) and in the second year 30 F₁ hybrids and their parents were grown in a randomised complete block design with three replications at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, during 2011-2012. For present study six different parents, namely, VH-232, CRS-2007, SB-149, GR-156, FH-207, and MARVI, were grown in earthen pots placed in the glass house during October 2011. The light and temperature were controlled to provide suitable conditions for germination and growth of plants. When the parents started to flower, these were crossed in all possible combinations. During emasculation and pollination, all precautionary measures were adopted to avoid contamination of the genetic material. The F₁ seed of 30 crosses alongwith the parents was planted in the field during the next growing season in randomised complete block design with three replications. Each genotype had 10 plants in each replication. The line-to-line and plant-to-plant distance was maintained 75 cm and 30 cm, respectively. All

recommended agronomic practices, like, plant protection, fertilisers, irrigation, and hoeing, were adopted. Fiber characteristics (staple length, fiber strength, fiber elongation and fiber fineness) were recorded from these samples, using Ustar HVI 900 S.A., in the Department of Fiber Technology, University of Agriculture, Faisalabad, Pakistan. The computerised instrument recorded staple length (mm), fiber strength (g/tex), fiber elongation in (millimeters, inches) and fiber fineness ($\mu\text{g}/\text{Inch}$) according to international standards.

Statistical Analysis

The data collected was subjected to analysis of variance after to determine significant differences among the genotypes under-study (Steel et al., 1997). Combining ability analysis parents, their hybrids and gene action of different traits were determined by subjecting the data to diallel analysis, using Griffing's approach model I, method I (Griffing, 1956).

Results

Analysis of variance carried out for studied traits showed that there were significant differences among genotypes; hence, later analysis for combining ability was possible. The data analysis of variance of each of the character and genetic analysis of the data are presented for interpretation (see Table 1). Analyses of variance showed that all type of genetic effects (additive, non-additive and cytoplasmic) were highly significant ($P \leq 0.01$). However, traits such as fiber length, fineness and strength showed high magnitude of additive effects while preponderance of non-additive effects were noted only for fiber elongation. High cytoplasmic effects were noted for lint percentage.

Table 1. Analysis of variance for combining ability of five traits in *Gossypium hirsutum* involving 6×6 diallel mating design

SOV	D.F	Fiber Length	Fiber Fineness	Fiber Elongation	Fiber Strength	Lint Percentage
GCA	5	2.40**	0.286**	1.46**	6.05**	88.59**
SCA	15	1.79**	0.138**	1.66**	4.07**	173.76**
Reciprocals	15	2.18**	0.131**	1.24**	3.44**	186.46**
Error	70	0.38	0.009	0.05	0.31	0.27
GCA/SCA		1.34	2.07	0.88	1.48	0.51

*Significant at 0.05

**Significant at 0.001

Ratio of GCA/SCA was also high for fiber length, fineness and strength showing high magnitude of GCA as compared to SCA effects. Thus additive effects were important in the inheritance of these traits. On the other hand, fiber elongation and lint percentage showed ratio lesser than unity showing high magnitude of non-additive genes. Rauf et al. (2005), Ahuja and Dhayal (2007) reported non-additive type of gene action, were important to fiber length.

In the present study, fiber length, fiber strength, fiber fineness, lint percentage (GOT) were conditioned largely by additive gene effects, suggesting the occurrence of transgressive segregants in segregating generation. Nimbalkar et al. (2004), Kansik and Kapoor (2006), and Iqbal et al. (2003) reported that the character controlled by additive gene action had high

narrow-sense heritability. Falconer and Mackay (1996) suggested that segregating population was amenable to selection pressure in early generation, such as, F_2 . Selection must be delayed in traits, showing high magnitude of non-additive effects till the genes are established in breeding programme, this confirms the finding of Godoy and Palomo (1999). Review of Table 2 showed that GR-156 was the best combiner for lint percentage and fiber length. FH-207 was the best combiner for fiber fineness. FH-207, MARVI and SB-149 were best general combiner for fiber character and are suggested to be used in future breeding programme to improve fiber quality traits. Crosses such as CRS-2007 \times GR-156, CRS-2007 \times MARVI, SB-149 \times MARVI and VH-232 \times SB-149 had higher specific combining ability and reciprocal effects (Table 3).

Table 2. Estimation of GCA effects of six parents for five traits in *Gossypium hirsutum* involving 6 \times 6 diallel mating design

Parents	Fiber Length	Fiber Fineness	Fiber Elongation	Fiber Strength	Lint Percentage
VH-232	-0.028	-0.014	-0.347	-0.33	3.135
CRS-2007	-0.219	-0.064	-0.147	-0.375	0.307
SB-149	0.122	0.294	0.569	-0.433	2.608
GR-156	-0.486	-0.064	0.128	-0.617	-4.087
FH-207	0.814	-0.156	0.128	0.117	-0.152
MARVI	-0.203	0.003	-0.331	1.342	-1.830

Table 3. Two top crosses of SCA for fiber quality characters.

Character	Crosses	SCA values
Fiber length	CRS-2007 \times MARVI	(1.778)
	SB-149 \times FH-207	(1.269)
Fiber Strength	SB-149 \times MARVI	(1.883)
	GR-156 \times FH-207	(1.842)
Fiber fineness	VH-232 \times SB-149	(0.497)
	VH-232 \times CRS-2007	(0.206)
Fiber elongation	CRS-2007 \times GR-156	(1.764)
	FH-207 \times MARVI	(1.097)
Lint percentage	VH-232 \times SB-149	(26.39)
	CRS-2007 \times MARVI	(6.26)

Conclusion

Traits related with fiber quality, such as, fiber fineness, length and strength had high magnitude of GCA effects showing preponderance of additive genes. Cultivar SB-149 was positive general combiner for all these traits and may be

used in hybridisation programme for the development of segregating populations. FH-207 was the best combiner for the fiber length and thus may also donate positive alleles for transgressive segregants. Crosses, SB-149 \times FH-207, SB-149 \times MARVI with good specific

combining ability effects may further utilised for the establishment of segregating populations.

Acknowledgment

Authors gratefully acknowledge Dr. Saeed Rauf, Assistant Professor, Department of Plant Breeding and Genetics, University College of Agriculture, University of Sargodha, Sargodha, for making corrections in this manuscript.

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