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GENETIC STUDIES ON VARIATION FOR FIBER QUALITY TRAITS IN UPLAND COTTON

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ABSTRACT

Five cotton (*Gossypium hirsutum* L.) varieties namely SLH-41, F-281, COKER-3113, LA-85-52-1 and H-88-8-J.69-j.70 were studied in diallel cross experiment to evaluate genetic effects for various plant traits. The characters under consideration were Ginning out-turn, staple length, fiber fineness and strength All the genotypes were found to significantly differ from each other for the above mentioned traits. Joint regression analysis proved the validity of the data of all characters for additive-dominance model suggested by Hayman (1954) and Jinks (1954). Staple length, fiber fineness and fiber strength were controlled by additive gene action with partial dominance while Ginning out-turn revealed over dominance type of gene action. The predominance of additive gene action involved in the phenotypic manifestation of the traits suggested selection as an accurate procedure for character improvement.

Keywords: Genetic studies, fiber traits, Upland cotton, Gossypium hirsutum L.

INTRODUCTION

Cotton occupies a unique position in Pakistan's agrarian economy. Efforts on various aspects of the crop have been under way to increase its overall production of the country. Pakistan is an agricultural country and cotton crop is the backbone for earning foreign exchange of the country. The economy of Pakistan mainly depends upon cotton production, exportable surplus of cotton fiber and fiber made products. Share of cotton and cotton manufactures is about 69% of the total foreign exchange annually. It accounts for 7.5% of the value added in agriculture and about 1.6% to GDP. It accounts for 78% of domestic oil production. The crop not only meets the need of the fiber of the local industry but also provides edible oil for cooking purpose and low grade oil for the soap manufacturing industries. Residual seed cake is a valuable protein concentrate that is used for livestock feed. (Anonymous, 2008).

The most important factor in the process of crop production has always been a good variety in any crop. Cotton breeders managed to produce high yielding

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varieties through various genetic manipulations and breeding approaches and consequently a significant progress was achieved in this connection. As the improvement in yield and quality in agricultural crops is a continuous process, therefore, the breeders are busy all the time in adopting new techniques and approaches for improving the production of the crop.

To achieve desirable results, parents utilize in any breeding program, must be genetically diverse and physiologically efficient. Keeping this in view, an experiment was undertaken in the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad to study the gene action in F_1 hybrids to select suitable parents for the evaluation of high yielding hybrids, well adaptive to the prevailing climatic conditions and having better quality. The current research work was launched to analyze some important cotton cultivars to ascertain the relative performance regarding gene control for yield and its components.

The diallel analysis technique devised by Hayman (1954) and Jinks (1954) which was reviewed and studied by Mather and Jinks (1982) is a useful tool to obtain precise information about the type of gene action involved for the expression of various yield characters.

Diallel analysis provides a systematic approach for the detection of appropriate parents and crosses superior in terms of the investigated traits. The present research work was launched to obtain the genetic information for some economic cotton traits by using diallel technique, following Hayman (1954) and Jinks (1954).

MATERIALS AND METHODS

The present experiment was carried out at experimental area of Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the years 2007-08. The experimental material consisted of five parental genotypes namely SLH-41, F-281, COKER-3113, LA-85-52-1 and H-88-8-J.69-j.70 representing a range of yield and fiber quality traits, was sown in earthen pots placed in greenhouse during November 2007. During germination and growth environmental conditions were possibly controlled and required agronomic practices were followed. In glass-house, temperature was maintained at 35-40 °C throughout the period. At flowering, the parental lines were crossed in a complete diallel fashion (5 \times 5) to generate 20 F₁ crosses (direct and indirect) along with 5 selfs. At maturity, selfed and crossed bolls were picked and seed cotton was ginned with single roller ginning machine. The F₀ seed from all crosses along with their parents was sown in the field during June-2008 in Randomized Complete Block Design (RCBD) with three replications. In a replication 25 entries were planted each in a single row having 10 plants with a distance of 30cm and 75cm within and between rows respectively. All required agronomic practices and crop protection measures were carried out from sowing to harvesting of the crop. At maturity, the data were recorded for Ginning out-turn, staple length, fiber fineness and fiber strength on five guarded plants from each entry, both in field as well as laboratory on individual plant basis.

The data collected were subjected to standard techniques of analysis of variance (Steel *et al.*, 1997) to Table 1 Differences among genotypes for fiber strength

establish the level of genotypic differences for the plant traits under study. The characters showing significant genotypic differences were further analyzed genetically following additive-dominance model of genetic analysis developed by Hayman (1954) and Jinks (1954).

RESULTS AND DISCUSSIONS

The results of different characteristics from progeny plants are presented:

Ginning Out-Turn: Highly significant differences were observed among the genotypes for Lint % and thus permitting the data for further analysis. From Vr/Wr graph shown in Figure 1, absence of non-allelic interaction was confirmed, as the regression line did not deviate from unit slope. Gene action controlling the inheritance of GOT % was of over dominance type as the regression line intercepted the Wr axis below the point of origin (Figure 1). Similar findings have been reported by Keerio *et al.* (1995) and Ajmal *et al.* (2000) while Islam *et al.* (2001) reported additive-dominance and Saeed *et al.* (1996) and Larik *et al.* (1997) reported additive type of gene action and Sayal and Hussain (1997) and Yingxin and Xiangming (1998) reported non additive type of gene action for this character.

It was observed from the position of array points on the regression line that SLH-41 being closest to the origin had maximum dominant genes while H-88-8-J.69-J.70 got most of the recessive genes due to its farthest position from the origin (Figure 1).

Staple length: The analysis of variance for staple length indicated highly significant differences among the genotypes (Table 1). Results of joint regression analysis (Table 2) indicated that 'b' value (0.84 ± 0.15) deviated significantly from zero showing that the data were valid for additive-dominance model as suggested by Hayman (1954) and Jinks (1954). The Vr/Wr graph (Figure 2) indicated that this character is governed by additive gene action with partial dominance gene, as the regression line intercepted Wr axis below the origin.

Table 1. Differences among genotypes for inder strength.								
SOV	d.f.	Lint %age	Fiber fineness	Staple Length	Fiber strength			
Replication	2	12.063 NS	0.03 ^{NS}	0.13 ^{NS}	0.16 ^{NS}			
Genotypes	24	34.23**	8.87**	6.49**	8.10*			
Error	48							
Total	74							

The results are in accordance with the findings of Amin and Hussain (2000) studied that fiber length was governed by gene acting additively with partial dominance. While differ with Khan *et al.* (1995), Sayal and Sulemani (1996), Ahmad *et al.* (1997), Mukhtar *et al.* (2000), Ajmal *et al.* (2000) and Khan *et al.* (2001) who

reported over dominance type of gene action while Nadeem and Azhar (2005), Hendawy *et al.* (1999), Larik *et al.* (1997) and Ali *et al.* (2008) reported additive type of gene action in phenotypic manifestation of this character. The variety F-281 has maximum dominant genes as it is nearest to the origin whereas LA-85-52-1 has maximum recessive genes as it is the farthest from the origin (Figure 2). (Table-1) illustrated that the differences, between the parents and the F_1 hybrids were highly significant. Results of joint regression analysis (Table 2) showed fitness of data for additive-dominance model. The graphical representation (Figure 3) for fiber fineness indicated additive gene action with partial dominance is involved in the phenotypic expression of this character as the regression line intercepted the Wr-axis below the origin.

Fiber fineness: The results of analysis of variance Table 2. F-ratio for various traits in 20 crosses and 5 selfs.

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SOV	d.f.	Lint %age	Fiber fineness	Staple Length	Fiber strength
Replication	2	12.063 NS	0.03 ^{NS}	0.13 ^{NS}	0.16 ^{NS}
Genotypes	24	34.23**	8.87**	6.49**	8.10*
Error	48				
Total	74				
40 30-		• H-88-8-J.69-J.70	0.14-0.12-0.1-		• LA-85-52-1
20- Wr. 10		<i>,</i>	0.08-		
	I-41 5 20 30 LA-85-52-1	40 50 60	0.04- 0.02	-281• H-88-8-J.69-J.70	
10	F-281 • COKER-3113		0.02 0.02 0.02 0.02	0.04 0.06 0.08 0.3 41	1 0.12
	Vr			Vr	
Figure 1. GOT			Figure 2. Fiber fir	ieness	
1.2-			2.4-		
1-	/	• LA-85-52-1	2-		• SLH-41
0.8-			1.6-		• CORER-5115
Wr 0.6-	• COKE	H-41 R-3113	Wr 1.2-	• LA-85-5	52-1
0.4-			0.8-	• ₩-88-8-J.69-J.70 • F-281	
0.2	281		0.4-		
0- <mark>ľ</mark> 0 0.2	2 0.4 0.6 Vr	0.8 1 1.2	0-10).5 1 1.5 Vr	2

Figure 3. Staple length

Figure 4. Fiber strength

S. No.	Character	b	Remarks	Conclusions
1 Ginning out-turn	Cinning out turn	0.06+0.22	b value deviated significantly	The data were adequate for simple
	0.90±0.23	from zero but not from unity.	additive-dominance model.	
2 Staple length	0.84±0.16	b value deviated significantly	The data were not fit for genetic	
		from zero but not from unity	analysis	
3 Fiber fineness	1.0 ± 0.19	b value differed significantly	The data were fit for additive-	
		from zero but not from unity.	dominance model	
4 Fiber streng	Fibor strongth	n 0.97 ± 0.21	b value differed significantly	The data were not fit for genetic
	riber strength		from zero but not from unity.	analysis

Table 3. Results of Joint Regression Analysis.

The line did not deviate from the unit slope; the absence of epistasis was thus concluded. These results are in accordance with those already given by Ajmal *et al.* (2000), Khan *et al.* (2001), Ranjan *et al.* (1999) Pathak *et al.* (2003) and Ahmad *et al.* (1997). However Khan *et al.* (1995), Hendawy *et al.* (1999), Larik *et al.* (1997) and Ali *et al.* (2008) reported additive type of gene action controlling the inheritance of this trait. From the relative position of array points on the regression line, it was apparent that variety SLH-41 showed maximum dominant genes being closest to the origin while the variety LA-85-52-1 contained minimum dominant genes being farthest from the origin (Figure 3).

Fiber strength: Highly significant differences were observed among the genotypes for fiber strength (Table 1) and thus permitting the data for further analysis. The graphical representation confirmed the absence of non-allelic interaction, as the regression line did not deviate from unit slope. Gene action controlling the inheritance of fiber strength was of additive gene with partial dominance as the regression line intercepted the Wr axis below the point of origin (Figure 4).

Nadeem and Azhar (2005) obtained genetic information on fiber strength of *G. hirsutum* L. and it showed that it was influenced by additive type of gene action with partial dominance. While other results according to the findings of Liu *et al.* (1998), Mukhtar *et al.* (2000), Ajmal *et al.* (2000) and Khan *et al.* (2001) reported that it is under control of over dominance type of gene action and some scientist Pathak (2003), Larik *et al.* (1997), Hendawy *et al.* (1999) and Nadeem and Azhar (2005) reported additive type of gene action for this character. It was observed from the position of array points on the regression line that H-88-8-J.69-J.70 being closest to the origin had maximum dominant genes while SLH-41 got most of the recessive genes due to its farthest position from the origin (Figure 4).

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