

**ESTIMATION OF GENE ACTION FOR THE SELECTION OF SUPERIOR PARENTS AND THEIR CROSS COMBINATIONS FOR YIELD AND FIBER ASSOCIATED ATTRIBUTES IN AMERICAN COTTON (*GOSSYPIUM HIRSUTUM* L.)**

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**Abstract:** Cotton is very important crop regarding the global trade. It is grown for its fiber and edible oil in Pakistan. It contributes 1.5 percent to GDP and 69 percent in foreign exchange. There is need to enhance the yield per unit area of cotton by developing high yielding and stress tolerant varieties. In breeding program the parents and their crosses are selected on the basis of their combining ability. Combining ability analysis is performed to identify the general and specific combiner for yield attributed traits. This research was performed for evaluation of four lines as female parents (C-1, CIM-616, TIPO-1 and CYTO-608) and three testers as male parents (NIAB-1048, CYTO-124 and CIM-600) of cotton (*Gossypium hirsutum* L.). The traits such as plant height, first fruiting node, seed cotton yield, monopodial branches, sympodial branches, ginning out turn percentage, number of bolls per plant, height to node ratio and cotton seed yield was tested. The general combining ability of parental lines and specific combining ability of the F1 cross will be determined for yield related traits. The genotypes with good general combining ability and specific combining ability further exploited for hybrid/variety development programs. For most of the traits like number of monopods per plant, boll weight per plant, seed cotton yield, number of nodes per plant, 1st fruiting node, intermodal distance, ginning out turn percentage, cotton seed yield, seed index, plant height, fiber strength, fiber length, fiber uniformity and fiber fineness value had more value for dominance variance. The higher effects of GCA and SCA indicated that there is the role of additive and non-additive gene action for inheritance of traits.

**Keywords:** genetic variability, line × tester, *Gossypium hirsutum*, combining ability, gene action

### Introduction

When compared to percutaneous coronary Cotton is cultivating for its oil, fiber and livestock feed grown in hundred plus countries in all over the worlds (Hassan et al., 2021). It contributes 0.8% in GDP and 4.5% in agriculture value addition and cultivated on the area of 2373 thousand hectares. In 2019 it is grown for 33 million hectares worldwide. In Asia *Gossypium hirsutum* L. contributes 80% of total production of cotton (Zafar et al., 2022). Agriculture sector provides a key role to the economy of Pakistan. Agriculture sector contributes 19.2 percent to the GDP (Zafar et al., 2022ab). The majority of the population 65-70 percent depends directly on agriculture. Cotton contributes in agriculture sector as well as in textile sector. Cotton contributes 0.6 percent to gross domestic product (GDP) and 3.1

percent to agriculture (Manan et al., 2022). Pakistan is at 5th position in cotton production after China, USA and India and it is at 3rd position in the consumption of cotton in the world. The economy of Pakistan heavily depends upon on the cotton. Cotton contributes 4.8% in value addition and 0.8% share in GDP. It is cultivated on 2.489 million hectares with production of 10,671 million bales and average seed cotton yield is 730 kg per ha in Pakistan (Razzaq et al., 2021).

Breeder maintain the genetic diversity so many years by utilizing breeding methods includes pedigree selection, random mating, composite selection and back crossing methods during breeding history (Farooq et al., 2020). It is very important to identify the correlation of yield and yield related components

with other plant characters for selection (Zhang et al., 2022). Heritability is the extent of transfer of traits from parents to offspring. It is useful to check the environmental influence of biotic and abiotic stress on cotton crop. It is associated with genetic advance and genetic variability for proper selection (Hafeez et al., 2021ab).

The general combining ability variance possesses additive gene action while specific combining ability variance governs non-additive gene action. Line into tester analysis is mostly used for the analysis of combining abilities. In advanced breeding program it gives the information to understand the relationship between yield and yield related components (Hassan et al., 2021). In a breeding program, knowledge of the combining ability and how characters are transferred to the next generation is important to develop good breeding material. Line  $\times$  tester analysis is a biometrical tool that provides information about the combining ability variances and effects of the genotypes (Chaudhry et al., 2022). Line  $\times$  tester analysis gives information regarding parents and their crosses which could be useful for a future breeding program (Mudasir et al., 2021). The plant researchers widely used line  $\times$  tester for early generation selection (Ijaz et al., 2021). Through combining ability gene of action can be determined. For the genetic analysis of the traits research work was done for the analysis of various traits related to cotton yield. The main objective of this study was to check the gene action of parental traits using the line into tester analysis. The primary purpose is to identify the gene action regarding the traits that is responsible for the inheritance of traits in upland cotton.

The primary objective is to identifying the gene action which is responsible for inheritance of traits. Select the best general and specific combiner for yield and fiber related traits.

#### Materials and Methods

This experiment was carried out in order to find out the inheritance of selected attributed genotypes namely C-1, CIM-616, CYTO-608, TIPO-1, NIAB-1048, CIM-600 and CYTO-124. This research was conducted in the Cotton Research Station in AARI Faisalabad in kharif season. Suitable conditions of light and temperature were maintained in green house for the seedling emergence. Above cotton genotypes were sown in the earthen pots in glass house. The present research was conducted in order to find out the gene action and combining ability of different traits for different attributes of (*Gossypium hirsutum* L.) at the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad during the year of 2021. At flowering stage, maximum number of crosses will developed by selfing of buds in greenhouse. To get the maximum

number of seeds of  $F_1$  need to develop maximum number of crosses. The  $F_1$  seeds of hybrids with parental lines were sown in field with two replications in randomized completely block design. For data collection 5 plants were tagged from each row of replication. The row-to-row distance was maintained at 74 cm. The distance between rows ( $R \times R$ ) was 74 cm and plant to plant distance ( $P \times P$ ) 46 cm maintained respectively.

#### Statistical analysis

To check the differences among the genotypes for the evaluation of all above parameters analysis of variance (ANOVA) was used with the help of Statistix 8.1. Line into tester analysis use to evaluate the GCA and SCA of parents and their crosses respectively by using XLSTAT.

#### Results

The analysis of variance was significant for following traits that is number of monopodial branches per plant, boll weight, seed cotton yield, number of nodes per plant, internodal distance, ginning out turn percentage, seed index, fiber strength and fiber fineness as presented in table 1. The mean square for replications was not significant for all traits indicating that blocking do not affect the experimental error. Results revealed that for traits like monopodial branches per plant, boll weight, seed cotton yield, internodal distance, ginning out turn percentage, seed index, fiber strength, fiber length and fiber fineness had non-additive gene action. Number of nodes per plant and number of bolls per plant had additive type of gene action. It is suggested that plant traits which is controlled by additive type of gene action could be improved by simply selecting procedure in the upcoming generation. Testers performance was better than lines as shown in figure 1.

Tester CYTO-124 was best general combiner for the monopodial branches. C-1 was the positively highly significant line for seed cotton yield similar result was presented by (Rani Chapara & Satish, 2020; Abbas et al., 2016; Ali et al., 2013). For boll weight CIM-616  $\times$  NAIB-1048 had best specific combining ability for boll weight. Line CIM-616 and tester NIAB1048 performed best for sympodial branches and it was also reported by (Mahmood et al., 2021). The tester contribution was 42% for sympodial branches similar findings was found by Khokhar et al., (2018). The only little contribution of line  $\times$  tester was only 2%. C-1 was the good general combiner for the trait like 1<sup>st</sup> fruiting node. CYTO608  $\times$  CIM600 was good specific combiner for sympodial branches. For variance the contribution of lines was more than about 60%. The tester contribution was 26% for number of nodes per plant. The only little contribution of  $L \times T$  was only 14%. CYTO-608 was the good general combiner for fiber strength. TIPO-1

× CIM-600 was the best specific combiner for fiber fineness. When greater value of SCA as compared to GCA effects than non-additive type of gene action was influenced for fiber fineness similar results was found by Sultan et al., (2018); Ali et al., (2014). For most of the traits like number of monopods per plant, boll weight per plant, seed cotton yield, number of nodes per plant, 1<sup>st</sup> fruiting node, intermodal distance, ginning out turn percentage, cotton seed yield, seed index, fiber uniformity, plant height, fiber strength, fiber length and fiber fineness had more value for dominance variance same results was also found by Gnanasekaran et al., (2019) and Puspito et al., (2015). The values of the GCA and SCA was indicated that there was great chance to selection of genotypes for different traits like number of bolls per

plant, number of monopodial branches, boll weight, number of nodes per plant, internodal distance, ginning out turn percentage, seed index, plant height, fiber strength, fiber length fiber uniformity and fiber fineness (table 2,3).

**Conclusion**

Overall, the line CIM-616 and tester NIAB-1048 performed best as a good general combiner. Among the crosses CIM-616 × NIAB-1048 proved to best specific combiner for most of the traits. It is purposed that plant features affected by the additive gene action that can be enhanced by selection into several generations. In heterosis breeding the non-additive type gene action in plants is helpful for the enhancement of cotton and fiber production.

Table 1. Analysis of variance of quantitative and qualitative traits

SOV	MB	BW	SCY	SB	NNPP	FN	ID	GOT%	SI	PH	NBP	FS	FL	FU	FF
Rep	0.003	0.11	53.289	6.233	8.245	0.003	0.013	7.605	0.711	104.54	1.28*	0.93	0.84	1.56	13.88
Gen	0.413*	0.437*	326.187*	40.520*	26.028*	1.136	0.603*	63.46*	0.833	219.43*	1.95*	96.05*	11.23	10.04	21.56*
Crosses	0.911*	0.610*	391.233*	58.623*	24.39*	1.069	0.67*	82.89*	1.245	264.31*	2.03*	84.35*	11.59	8.42	12.93
Line	0.087*	0.317	839.152*	98.632*	53.89*	1.41	1.39*	77.16*	1.213	284.27*	6*	119.93*	8.51	14.32	11.72
Tester	0.262*	0.437*	276.541*	111.78*	34.66*	0.19	0.82*	110.29*	1.298	207.59*	0.041*	39.55*	8.53	3.26	2.21
L×T	0.219*	0.814*	205.482*	20.89*	6.21	1.185	0.26*	76.62*	0.115	273.27*	0.7	81.49*	14.13	7.1	17.11
Parents	0.077*	0.18	255.66*	11.25	23.41*	1.44	0.42*	31.57*	0.151	165.27*	1.452	58.03*	11.12	13.48	29.76*
Cross vs Parents	0.061*	0.021	33.910*	16.97	59.71*	0.03	0.928*	41.05*	0.628	50.78*	4.21*	452.94*	13.82	7.26	7.36*
Error	0.027	0.114	85.233	13.337	5.251	1.06	0.108	20.32	0.929	59.09	0.56	18.266	6.51	6.325	6.35*

Figure 1: Proportional Contribution of lines, testers and interaction to the total variance for various characters

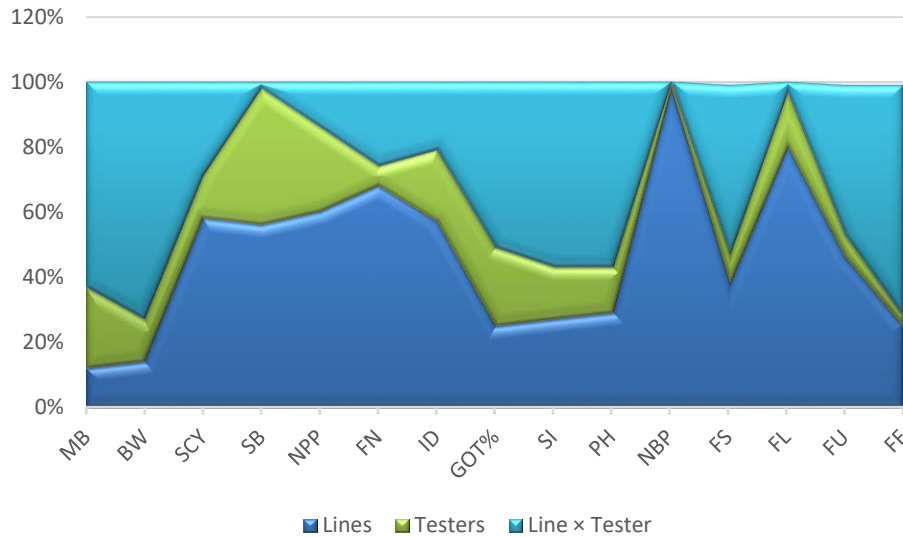


Table 2: GCA effects of parents for various traits in upland cotton

	MB	BW	SCY	SB	NPP	FN	ID	GOT%	SI	PH	NBP	FS	FL	FU	FF
C-1	-0.15	-	13.71**	-	2.87**	2.87**	-3.09*	-0.42*	-	-4.52	0.5	-0.74	1.27	0.48	1.02
CIM-616	0.14	0.03	6.04*	3.83*	0.11	0.11	0.06	-4.92*	0.58	3.53	1.17**	-2.32	-0.34	1.41	1.24
CYTO-608	0.02	-	-10.13*	-0.59	-	-	0.66**	2.58	0.12	7.87*	-	6.50**	-	-	-
TIPO-1	0.01	0.31	-9.63*	2.19	1.18	1.18	-0.32*	2.75*	-	-6.88	-0.83*	-3.43	0.55	0.32	-0.52

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									0.28							
NIAB-1048	-0.1	-0.1	1.42	3.09*	-1.67*	-1.67*	0.19	4.17*	-	1.65	0.04	1.34	-1.17	0.73	0.52	
CYTO-124	0.21**	0.16	-6.46*	4.15**	-0.67	-0.67	0.18	-1.12	0.43	4.06	0.04	1.23	0.79	0.27	0.01	
CIM-616	-0.11	0.27	5.04*	1.06	2.33**	2.33**	-0.37*	-2.96	-0.2	-5.71	-0.08	-2.57	0.38	0.46	-0.53	

Table 3: SCA effects of crosses for various traits in upland cotton

	MB	BW	SCY	SB	NPP	FN	ID	GOT%	SI	PH	NBP	FS	FL	FU	FF
C-1 × NIAB-1048	0.03	0.09	8.42	1.13	0.3	0.3	-0.25	-4.83	-	-6.65	0.13	-	-0.96	1.84	0.46
C-1 × CYTO-124	0.01	0.39	5.29	-0.11	-0.9	-0.9	0.15**	2.04	1.12	4	0.63	9.64*	2.43*	-	0.25
C-1 × CIM-600	-0.04	-0.48	-	-	0.6	0.6	0.1	2.79	0	2.64	-	2.87	-	-	-0.71
CIM-616 × NIAB1048	0.19	0.80**	-6.42	3.81*	-0.63	-	0.3	3.17	0.18	6.74	0.46	7.34	3.14*	0.65	1.79
CIM-616 × CYTO-124	0.33*	-0.52	0.46	3.76	0.57	0.57	0.58	-8.46*	-	-	-	-4.29	1.44	-1.3	1.24
CIM-616 × CIM600	-0.14	-0.29	5.96	0.04	0.07	0.07	0.28	5.29	-	10.25	0.08	-3.05	1.71	0.64	-3.04
CYTO-608 × NIAB-1048	-0.28	-0.1	3.25	0.68	2.33	2.33	0.01	2.17	0.75	6.76	-	2.92	-1.11	0.07	1.76
CYTO-608 × CYTO-124	-0.01	-0.14	1.13	-3.72	-0.17	-	0.24	5.04	-	4.44	0.04	-1.69	1.42	1.17	-1.73
CYTO-608 × CIM600	0.29*	0.23	-4.38	-3.03	2.63*	-	-0.25	-7.21	-	-11.22	0.08	-1.22	0.31	-	-0.03
TIPO-1 × NIAB-1048	-	-	-5.5	1.99	-2	-2	-0.06	-0.5	0.2	-6.85	-	-0.62	3.0*	-	-
TIPO-1 × CYTO124	0.33**	0.80**	-6.88	0.07	0.5	0.5	0.19	1.38	-	17.18*	0.04	-0.79	-	1.69	0.24
TIPO-1 × CIM600	-0.11	0.26	-6.88	0.07	0.5	0.5	0.19	1.38	0.57	17.18*	0.04	-0.79	2.45*	1.69	0.24
	0.99	0.53	12.13*	-2.07	1.5	1.58	-0.13	-0.88	0.37	10.15	0.58	1.41	-0.55	0.88	3.78*

**Conflict of interest**

The authors declared no conflict of interest.

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