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COMBINING ABILITY ANALYSIS AND SELECTION OF SUITABLE PARENTS FOR BREEDING HIGH YIELDING COTTON VARIETIES

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ABSTRACT

Following study was carried out to determine the nature of gene action for yield and fiber qualityrelated traits. F_1 progeny were obtained by following line × tester (6×3) mating design. The experiment was raised using randomized complete block design and replicated thrice. All F_1 hybrids and their respective parents mean showed significant differences for all the traits i.e. plant height, number of nodes to first monopodia, number of monopodia/plant, number of sympodia/plant, seed per boll, total number of bolls per plant, weight per boll, yield, ginning out turn %age, seed index, chlorophyll %age, staple length, micronaire value, uniformity index and fiber strength. Additive and non additive types of gene actions were observed for most of the traits. Lines showed greater contribution as compared to testers for all the traits except number of monopodial branches and yield. The parents AGC-339, FH-lalazar and CEMB-56 showed high GCA effect. Cross BS-52×FH-lalazarexhibited high SCA effect for yield and quality related traits.Cross combinations AGC-338×CEMB-56 and AGC-340×CEMB-56 showed high SCA effects for yield related traits. Line AGC-338 appeared as the best general combiner for fibre quality traits whereas the testers FH-Lalazar and CEMB-56 appeared as the best general combiner for plant height and ginning out turn %age. Tester FH-Lalazar also appeared as the best general combiner for number of bolls per plant, boll weight, seed cotton yield per plant and fiber quality traits. Conclusively, cotton yield and quality can be improved by utilizing above mentioned parents and crosses in breeding programs.

Keywords: gene action, additive, monopodia, tester, combining ability

INTRODUCTION

Cotton is an important crop which is grown in more than 80 countries across the world [1]. It is a significant agricultural product, almost 60 million farmers across the world directly emphasis on cotton crop for their livelihood [2].Cotton fiber is the main product for which the cotton is being grown. Fiber quality of a specific cotton cultivar is not a single character; it is a complex of numerous characteristics comprising fibre strength, staple length, fiber fineness, fiber elongation and maturity ratio. These attributes have their distinct significance in weaving, dying and spinning units[3]. Seed cotton yield and fiber quality are governed by quantitative inheritance therefore breeding for these traits is not an easy task.

To meet the needs of increasing world's population it is imperative to enhance the production of cotton. Therefore, development of cotton varieties which have greater potential for yield and fiber related traits seems obligatory [4]. The information regarding genetic variability and genes controlling quality and yield related traits is imperative for crop improvement [4]. To obtain desirable improvement in certain plant traits the information present in the genetic makeup of both local and foreign germplasm should be exploited.

To increase cotton production inheritance of yield and fiber related traits should be determined. Line × Tester analysis is a well documentedapproach being used extensively in determining the inheritance of important yield and fiber related traits. To improve the fiber quality and yield vast genetic resources should be explored therefore, breeding programs in which diverse parents are used for making crosses are more successful as compared to the parents having narrow genetic base [5].

Previously many researchers have used estimates of general combining ability and specific combining ability for various trait and determined prevalence of additive and non-additive type of gene actions [6, 7]. General combining ability is due to the prevalence of genes which are additive in nature whereas, specific combining ability is due to dominance or epistatic effect genes [8]. The study of general combining ability and specific combining is important because cotton breeders are interested in identifying the genetic potential of inbred parents for hybrid combinations. Specific combining ability (SCA) helps in identifying the specific combination having greater potential for a specific trait. Similarly, to identify broad range parents, general combining ability, (GCA) is practiced. Parents having greater value of SCA are useful in hybridization programs whereas, parents with greater GCA are useful in hybridization and selection in segregating populations. Information regarding combining ability helps a plant breeder to select suitable parents for hybridization program [9].

Keeping in view the importance of combining ability in selection of suitable parents following research work was conducted. Therefore, the study was conducted keeping in view following objectives i) to determine the inheritance of various economic traits ii) to determine general and specific combining ability iii) to find out best general and specific combiner that can be used in hybridization process in crop improvement program.

MATERIALS AND METHODS

The experiment was carried out at the research area of the Department of Plant Breeding and Genetics, Faculty of Agricultural Sciences and Technology, Bahauddin Zakariya University Multan. Nine parents and eighteen F1 hybrids of American cotton were evaluated during 2015. Line × Tester design was practiced using 3 testers (FH-Lalazar, CEMB-55 and CEMB-56) and 6 lines (AGC-337, AGC-338, AGC-339, AGC-340, BZU-85 and BS-52) to produce 18 F1 hybrids. Parents were sown in September, 2014 in glasshouse of the Department of Plant Breeding and Genetics. At the time of flowering, maximum numbers of crosses were made among six lines and three testers. At maturity, crossed bolls were picked and ginned. In the following year 2015, nine parents and their eighteen crosses were evaluated under field conditions. Nine seeds of each entry were sown on 2nd May 2015. Experiment was comprised of 3 replications using Randomized Complete Block Design (RCBD). Rows were distanced 30″ from each other similarly plants were distanced 9″ from each other. Standard agronomic practices were adopted throughout crop cultivation as recommended. At maturity, data was documented for following traits i.e, plant height, number of nodes to first monopodia, number of monopodia/plant, number of sympodia/plant, seed per boll, total number of bolls per plant, weight per boll, yield, ginning out turn %age, seed index, chlorophyll %age, staple length, micronaire value, uniformity index and fiber strength. Data recording and analysis of variance was performed according to [10]. GCA and SCA effects were determined by following [11] using MS-excel computer program.

RESULTS AND DISCUSSION

Data related to various yield and fibre related traits was subjected to analysis of variance (ANOVA). Significant variations were found among genotypes for the traits like plant height, number of nodes to first monopodia, number of monopodia/plant, number of sympodia/plant, number of bolls, weight per boll, plant yield, chlorophyll %age, number of seeds per boll, seed index, staple length , staple strength , micronaire and uniformity %age at 5% probability level (Table 1). Parents showed high significant differences for all the traits except uniformity index. Lines exhibited significant differences for plant height, number of sympodia/plant, number of bolls and all the fibre quality traits. Testers showed significant differences for number of monopodia/plant, weight per boll, plant yield, ginning out turn % and seed index. Line × tester interaction displayed highly significant differences for number of nodes to first monopodia, number of seeds per boll, ginning out turn %, seed index, staple length, micronaire, uniformity index and staple strength (Table 1).

The traits plant height, number of nodes to first monopodia, number of monopodia/plant, number of seeds per boll, boll per plant, plant yield, ginning out turn, chlorophyll percentagestaple length, micronaire, uniformity index %age, staple strength showed lower value of variance due to GCA effects as compared to the value of variances due to SCA effects which showed prevalence of non-additive type of gene action for these traits. Similarly, the traits number of sympodia/plant, weight per boll and seed index depicted greater value of variance due to GCA than variance due to SCA presenting the predominance of additive gene action (Table 2).

Karademir and Gencer [12] found the additive gene action for ginning out turn percentage and non-additive gene action for yield of seed cotton and uniformity ratio. Saravanan *et al*. [13 stated the non-additive gene action for all the fiber quality characters in cotton. Karademir*et al*. [14] found non-additive gene action for yield per plant, uniformity index and ginning out turn percentage. Larger values of SCA variances results in non-additive gene action. Under such conditions population should be enhancement by recurrent selection to gather required genes by hatching of un-desirable linkages in breeding programs [15].

The ratio of SCA/GCA was greater than unity for plant height, number of nodes to first monopodia, number of monopodia/plant, number of seeds per boll, boll per plant, plant yield, ginning out turn %age, chlorophyll %age, staple length, micronaire, uniformity index and staple strengthwhich showed involvement of over dominance of gene action for these traits, while partial dominance was observed for number of sympodia/plant and weight per boll because the ratio was less than unity. The degree of dominance was greater than unity for all the fiber quality traits, number of nodes to first monopodia, number of monopodia/plant, number of seeds per boll, ginning out turn percentage, seed index and chlorophyll percentage.

Testers showed high contribution for number of monopodia per plant, boll weight and yield of seed cotton but for remaining traits contribution of testers was not prominent. Lines (maternal genotypes) contribution was high for plant height, number of nodes to first fruiting branch, number of sympodia/plant, number of seed per boll, number of bolls per plant, ginning out turn percentage, chlorophyll percentage, staple length, miconaire, uniformity index and fiber strength. Interaction among line × tester was high for number of nodes to first fruiting branch, seed index, staple length and uniformity index (Table. 2).

Observations showed that Line AGC-337, AGC-339 and AGC-340 are best general combiner for plant height. Line AGC-339, AGC-340 and BZU-85 are the best general combiner for total number of bolls per plant. Combining ability observations showed that line AGC-337, AGC-339 and BZU-85 are best general contributor towards plant yield. Line AGC-338 is a best general combiner for quality traits in cotton (Table. 3). It is cleared from observations that testers FH-lalazar and CEMB-56 are the best general combiners for trait plant height and ginning out turn percentage. Tester FH-lalazar is a good general combiner for total number of bolls per plant, boll weight and seed cotton yield per plant. Tester FH-lalazar is also a good general combiner for cotton quality traits (Table. 4). Crosses AGC-337×CEMB-56, AGC-339×FH-lalazar and BZU-85×CEBM-55 are the good specific combiner for fiber quality traits in cotton. AGC-338×CEMB-55 is a good specific combiner for number of sympodia per plant, number of seed per boll, number of bolls per plant and plant yield. AGC-339×CEMB-55 is a specific combiner for trait number of seed per boll. AGC-340×CEMB-56 is a good specific combiner for number of seed per boll, seed cotton yield and chlorophyll %. BS-52×FH-lalazar is a good specific combiner for traits total number of bolls per plant and seed cotton yield per plant (Table. 5).

Traits number of sympodia/plant, weight per boll and seed index depicted greater value GCA effects presenting the predominance of additive gene action and can be transferred by mass selection. In present investigation, cultivars AGC-339,AGC-340, FH-lalazar and CEMB-56 have greater values of GCA for plant height, plant yield and quality traits, these should be used in the breeding program due their greater ability to transfer characters to their progeny and cultivars with greater yield can be obtained by using these varieties [16-18]. Based on SCA effects BS-52×FH-lalazar, AGC-338×CEMB-56 and AGC-340×CEMB-56 showed high values for yield contributing characters. So these can be part of research to improve the yield of cotton.

Table 1: Mean Square value of all parameters in Analysis of Variance

SOV	D.F	PHT	NFB	NMB	NSB	S/B	TNB	W/B	PY	GOT	SI	CH%	SL	MIC	UI%	SS
Replication	2	1312.83	0.97	2.87**	73.88	3.34	74.14	0.87**	384.64	1.46	0.03	4.52	5.37**	0.09	23.44	1.70
Genotypes	26	4489.94**	0.85*	0.84*	64.94*	39.52*	77.70*	0.55*	1128.64*	24.31**	1.03*	23.13*	3.56**	0.16*	5.65*	11.95**
Parents	8	7001.54**	0.64**	1.65**	107.65**	20.52**	142.65**	0.58**	1965.06**	28.12**	1.04*	25.25**	3.93**	0.17**	1.75	10.36**
Parents vs. crosses	1	216.62	0.82	0.03	22.91	5.17	6.06	0.63	0.06	36.55**	0.01	64.0**	13.18**	0.09	1.08	0.01
Crosses	17	3559.38**	0.94**	0.51	47.37**	50.49**	51.35**	0.54**	801.41**	21.79**	1.09**	19.17**	2.82**	0.15**	7.75**	13.41**
Lines	5	9088.06**	1.50	0.32	117.55**	85.30	103.59**	0.32	142.13	26.08*	1.01	20.89	4.58*	0.34**	10.21*	27.58*
Testers	2	1964.39	0.09	1.48*	24.99	43.48	54.79	2.80**	5218.27**	33.71*	1.10*	36.88	0.51	0.00	4.64	8.67
Line × testers	10	1114.03	0.84**	0.41	16.76	34.48**	24.54	0.19	247.68	17.27**	1.12**	15.71*	2.40**	0.09**	7.15**	7.27**
Error	52	800.51	0.24	0.32	14.21	3.31	21.52	0.17	152.60	4.19	0.49	8.17	0.22	0.03	1.17	1.29

SOV= Source of variance, d.f= Degree of freedom, *= Significant, **= Highly Significant, PHT= Plant Height, NFB= Number of Nodes to First Monopodia, NMB= Number of Monopodia/plant, NSB= Number of Sympodia/plant, S/B= Seed per Boll, TNB= Total Number of Boll per plant, W/B= Weight per Boll, PY= Plant Yield, GOT= Ginning Out Turn Percentage, SI= Seed Index, CH%= Chlorophyll percentage, SL= Staple Length, MIC= Micronaire Value, UI%= Uniformity Index, SS= Fiber Strength.

Table 2: Genetic components

Genetic components	PHT	NFB	NMB	NSB	S/B	TNB	W/B	PY	GOT	SI	CH%	SL	MIC	UI%	SS
□□GCA	73.32	0.00	0.00	0.92	0.48	0.80	0.01	16.6	0.13	0.00	0.12	0.01	0.00	0.02	0.18
□□SCA	104.51	0.20	0.03	0.85	10.39	1.01	0.01	31.69	1.22	0.00	2.52	0.23	0.02	1.99	1.99
□□GCA/□□SCA	0.70	0.02	0.10	1.08	0.05	0.8	1.57	0.52	0.10	0.32	0.05	0.03	0.11	0.01	0.09
□□SCA/□□GCA	1.43	63.28	9.73	0.93	21.66	1.25	0.64	1.91	9.73	3.15	20.9	30.53	9.00	110.28	10.82
□□A	146.63	0.01	0.01	1.84	0.96	1.61	0.02	33.2	0.25	0.00	0.24	0.02	0.00	0.04	0.37
□□D	104.51	0.20	0.03	0.85	10.39	1.01	0.01	31.69	1.22	0.00	2.52	0.23	0.02	1.99	1.99
$(□□D/□□A)^{1/2}$	0.84	5.62	2.21	0.68	3.29	0.79	0.56	0.98	2.21	1.26	3.23	3.91	2.12	7.43	2.33
Contribution of lines	75.10	46.63	18.45	72.98	49.69	59.33	17.6	5.22	42.8	32.71	31.15	44.17	66.34	38.72	60.5
Testers	6.49	1.08	34.34	6.21	10.13	12.55	61.6	76.6	16.1	11.04	21.99	2.58	0.22	7.03	7.61
Line × testers	18.41	52.28	47.21	20.81	40.18	28.12	20.9	18.18	41.1	56.26	46.86	53.25	33.44	54.25	31.89

PHT= Plant Height, NFB= Number of Nodes to First Monopodia, NMB= Number of Monopodia/plant, NSB= Number of Sympodia/plant, S/B= Seed per Boll, TNB= Total Number of Boll per plant, W/B= Weight per Boll, PY= Plant Yield, GOT= Ginning Out Turn Percentage, SI= Seed Index, CH%= Chlorophyll percentage, SL= Staple Length, MIC= Micronaire Value, UI%= Uniformity Index, SS= Fiber Strength.

Table 3: Values of General Combining ability of lines used in this experiment

Lines	PHT	NFB	NMB	NSB	S/B	TNB	W/B	PY	GOT	SI	CH%	SL	MIC	UI%	SS
AGC-337	19.51	0.76	0.22	-3.19	4.91	-3.97	-0.16	6.83	-2.87	-0.12	-1.04	-0.68	-0.06	-1.34	-0.39
AGC-338	-14.49	0.13	-0.01	-1.99	2.23	-0.71	0.15	-3.94	0.34	-0.53	0.65	1.14	-0.34	1.71	1.93
AGC-339	35.28	-0.16	0.15	6.01	-0.63	4.32	0.09	1.62	0.56	0.15	-1.90	0.05	0.10	0.61	-2.55
AGC-340	28.73	-0.10	0.09	2.15	-3.32	2.03	-0.19	-3.64	1.19	0.10	-0.40	0.34	-0.01	-0.40	1.68
BZU-85	-32.75	-0.30	-0.18	0.25	-2.53	2.10	-0.14	0.11	1.05	0.24	0.19	-0.37	0.08	0.04	0.64
BS-52	-36.27	-0.33	-0.26	-3.23	-0.66	-3.76	0.26	-0.98	-0.27	0.15	2.51	-0.47	0.23	-0.63	-1.31

PHT= Plant Height, NFB= Number of Nodes to First Monopodia, NMB= Number of Monopodia/plant, NSB= Number of Sympodia/plant, S/B= Seed per Boll, TNB= Total Number of Boll per plant, W/B= Weight per Boll, PY= Plant Yield, GOT= Ginning Out Turn Percentage, SI= Seed Index, CH%= Chlorophyll percentage, SL= Staple Length, MIC= Micronaire Value, UI%= Uniformity Index, SS= Fiber Strength.

Table 4: Values of general combining ability of testers for all traits used in this experiment

Testers	PHT	NFB	NMB	NSB	S/B	TNB	W/B	PY	GOT	SI	CH%	SL	MIC	UI%	SS
FH-lalazar	7.94	-0.01	0.31	0.04	1.41	2.01	0.45	19.11	0.67	0.21	0.59	0.19	0.01	0.36	-0.20
CEMB-55	-11.83	0.08	-0.06	-1.20	0.26	-1.11	-0.21	-5.56	-1.18	-0.12	1.04	-0.02	0.01	-0.58	-0.57
CEMB-56	3.89	-0.06	-0.25	1.16	-1.67	-0.90	-0.25	-13.55	0.51	-0.10	-1.63	-0.17	-0.01	0.21	0.77

PHT= Plant Height, NFB= Number of Nodes to First Monopodia, NMB= Number of Monopodia/plant, NSB= Number of Sympodia/plant, S/B= Seed per Boll, TNB= Total Number of Boll per plant, W/B= Weight per Boll, PY= Plant Yield, GOT= Ginning Out Turn Percentage, SI= Seed Index, CH%= Chlorophyll percentage, SL= Staple Length, MIC= Micronaire Value, UI%= Uniformity Index, SS= Fiber Strength.

Table 5: Values of specific combining ability for crosses for all traits
PHT= Plant Height, NFB= Number of Nodes to First Monopodia, NMB= Number of Monopodia/plant, NSB= Number of Sympodia/plant, S/B= Seed

Crosses	PHT	NFB	NMB	NSB	S/B	TNB	W/B	PY	GOT	SI	CH%	SL	MIC	UI%	SS
AGC-337×FH-lalazar	-22.39	-0.21	0.59	1.57	1.47	-4.22	-0.09	2.05	1.77	0.42	-0.95	-0.81	0.09	-0.39	-1.91
AGC-337×CEMB-55	16.72	-0.13	-0.70	-3.14	-0.67	2.28	-0.26	-1.12	-3.86	-0.64	0.76	0.13	-0.06	-1.41	0.39
AGC-337× CEMB-56	5.67	0.34	0.11	1.57	-0.79	1.94	0.35	-0.92	2.09	0.22	0.19	0.68	-0.03	1.80	1.52
AGC-338×FH-lalazar	31.61	0.25	-0.20	-4.64	-2.85	-3.11	0.45	-14.58	-0.65	-0.70	-0.35	0.93	0.00	1.16	-1.27
AGC-338× CEMB-55	-39.94	0.63	0.21	3.16	1.53	3.06	-0.19	12.47	1.39	0.44	0.01	-0.26	-0.08	0.14	1.01
AGC-338× CEMB-56	8.33	-0.88	-0.01	1.48	1.32	0.06	-0.26	2.11	-0.75	0.26	0.35	-0.67	0.08	-1.29	0.26
AGC-339×FH-lalazar	-5.72	0.05	-0.03	0.83	0.21	2.44	-0.19	4.48	-0.07	-0.04	1.86	1.36	-0.13	0.66	1.58
AGC-339× CEMB-55	7.06	-0.07	0.11	0.19	4.70	-3.06	0.18	-3.40	-0.31	0.21	1.27	-0.57	0.06	-1.33	-2.38
AGC-339× CEMB-56	-1.33	0.02	-0.08	-1.01	-4.91	0.61	0.01	-1.08	0.38	-0.17	-3.12	-0.78	0.08	0.67	0.81
AGC-340×FH-lalazar	-1.17	-0.52	-0.08	1.52	-1.90	1.44	-0.13	-0.96	-0.40	0.03	-3.01	0.27	-0.16	-0.50	-0.22
AGC-340× CEMB-55	5.94	0.32	0.07	-0.86	-2.81	-1.39	0.05	-9.39	0.04	0.07	-0.32	-0.09	-0.03	1.48	1.28
AGC-340× CEMB-56	-4.78	0.20	0.01	-0.66	4.71	-0.06	0.08	10.35	0.36	-0.10	3.34	-0.17	0.19	-0.98	-1.06
BZU-85×FH-lalazar	0.28	0.14	-0.14	0.29	2.71	1.33	-0.03	-1.23	0.04	-0.28	1.80	-0.69	0.15	-1.70	0.36
BZU-85× CEMB-55	4.39	-0.70	-0.11	-0.05	-3.27	-1.50	0.08	1.20	1.11	0.13	-2.70	0.58	0.18	2.15	0.13
BZU-85× CEMB-56	-4.67	0.56	0.25	-0.25	0.56	0.17	-0.05	0.03	-1.15	0.15	0.91	0.11	-0.33	-0.45	-0.48
BS-52×FH-lalazar	-2.61	0.28	-0.16	0.44	0.37	2.11	0.00	10.24	-0.70	0.57	0.66	-1.06	0.06	0.77	1.47
BS-52× CEMB-55	5.83	-0.04	0.43	0.70	0.52	0.61	0.14	0.25	1.63	-0.21	1.00	0.22	-0.07	-1.02	-0.43
BS-52× CEMB-56	-3.22	-0.24	-0.28	-1.14	-0.89	-2.72	-0.13	-10.49	-0.93	-0.36	-1.66	0.84	0.01	0.25	-1.04

per Boll, TNB= Total Number of Boll per plant, W/B= Weight per Boll, PY= Plant Yield, GOT= Ginning Out Turn Percentage, SI= Seed Index, CH%= Chlorophyll percentage, SL= Staple Length, MIC= Micronaire Value, UI%= Uniformity Index, SS= Fiber Strength

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