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Combining ability analysis for seed cotton yield related traits in upland cotton

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Abstract: Cotton (*Gossypium hirsutum* L.) is the one of the significant crop in the world as fiber crop. It is also worthy source of edible oil. To assess the genetics of yield and yield favoring characters an experiment were executed at field area of Plant Breeding and Genetics department, University of Agriculture Faisalabad from 2015-17. Five genotypes of cotton were sown in the glasshouse. At the flowering stage crosses were attempted in all potential combinations. The five parents and 20 F_1 crosses were sown in the field in randomized complete block design within three replications. Data on various traits was collected using standard procedures from field when crop is at maturity stage. Data found to be significant for most of the traits when subjected to RBCD. According to GCA estimates, the parent CIM595 verified to be the good general combiner for maximum characters such as seed index, lint index, seed weight per plant, number of bolls per plant and sympodial branches. The combination VH371×CIM595 had high SCA effects for most of the important traits of cotton i.e. fiber fineness and fiber length. the cross KEH×VH371 exposed good reciprocal effects for most of the cotton traits i.e. plant height, number of bolls per plant, ginning out turn, seed index, lint index, seed weight per boll, seed weight per plant, number of seed per boll, monopodial branches, number of bolls per plant and seed cotton yield by exposing data to diallel analysis by means of Griffing's approach model 1 and method 1.
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Key words: Upland cotton, Combining ability analysis, Seed cotton, Yield

Introduction

Cotton crop is a major agriculture product in the economy of world which is being produced in approximately 65 regions of the world. It is agricultural crop which is traded majorly. Cotton is believed to be the crux of agricultural economy of Pakistan as a cash crop. It is the foremost reason of earning i.e. more than 65% of the entire foreign exchange is raised up by the trade of its final products. This crop is believed to have 7.5% of value added in agriculture. Cotton is basically produce to get fiber but it also be responsible for the food such as edible oil for human feeding, food for animals as seedcake which is high in protein and fuel to burn fire in rural areas and for manufacturing of bricks. In 2015-16, cotton was sown on the area of 2917000 hectares of the country. There is decrease of 1.5 percent decrease in area as compared to last year. In 2015 cotton production was 10.07 million of bales it shows 27.8% decrease as compared to last year. In 2014 its production was 13.960 million of bales. This season crop faces number of hazardous situations. Above four hundred textile mills are working through the courtesy of cotton. Good variety plays key role in cotton production through its yield production. Evaluation of variation in number of traits such as yield of seed cotton, fiber quality characteristic and its contributing features can be done through the use of many biometrical approaches, Griffing approach model one method one can be used to find out potential parents that can be used for improvement of cultivars in breeding project. Progress of often cross pollinated crop like cotton influenced by the kind of gene action answerable for the expression of specific trait. These are mostly quantitative characters like seed cotton harvest and other related component. Type of gene action determination through diallel analysis is important, and this information in turn supports in identification of the parents to be consume in breeding program. Information obtained from this analysis is helpful in the development of improved varieties.

Materials and Methods

The studies were performed to evaluate the combining ability possessions for yield and yield contributing characters in G. *hirsutum* L. For this purpose five cotton cultivars namely VH3-71, FH-2015, KEH, CIM-595 and VH3-77 of upland cotton were selected from the existing germplasm at Department of Plant Breeding and Genetics, University of Agriculture Faisalabad in October 2016. Particular lines were sown in the earthen post in glass house. Temperature and light in the glasshouse were maintained between 70^0F and 100^0F by the utilization of steam as well as electric heaters. At bud development stage all the 5 varieties were crossed in full diallel method. Maximum crosses were attempted to develop plenty of F_1 seeds. The seeds of 20 crosses of F_0 generation and their parents were get together, ginned and sown in 2016-17 within Randomized Complete Block Design, (RCBD) in 3 replications. The seeds of parents and crosses were seeded in single rows comprising 10 plants spread out at 30 cm plant to plant and 75cm between the rows. All the recommended agronomic and plant defense practices were applied from sowing to harvest. At maturity data on following traits were taken from five randomly selected plant from each row. Data was taken on the traits like number of bolls per plant, ginning out turn, plant height, seed index, lint index, seed weight per boll, seed weight per plant, number of seed per boll, monopodial branches, seed cotton yield and number of bolls per plant etc. The data was exposed to analysis of variance given by Steel *et al*. (1997). Then Griffing approach was utilized to find out the combining ability.

Results and discussions:

Investigation of variance for number of bolls per plant specified significantly high difference ($P \leq 0.01$) among genotypes. Higher assessment of general combining ability (2.5) was seemed for genotype CIM595 having high mean value (45.53) for number of bolls per plant. For specific combining ability effects, high SCA value (2.985) was depicted by combination VH371×KEH followed by FH2015×CIM595. Higher value of reciprocal effects were found for KEH×FH2015 followed by CIM595×KEH. Higher reciprocal values indicated presence of maternal and non-additive gene effects. Significant results were also recorded by Ahmad *et al.* (2001), Murtaza *et al*, (2006), Khan and Qasim (2012) and the gene action of additive type controlling the number of bolls were also mentioned by Sarvanan *et al*, (2003), Azhar and Khan (2005), Iqbal *et al.* (2011), Ekinci and Basbag (2015) and Khan *et al.* (2015).

Analysis performed for monopodial branches for general and specific combining ability is 7.94 and 6.80 respectively. Higher number of monopodial branches is not a desirable character. Specific combining ability analysis showed highest value 1.54 for cross VH371×VH377 followed by FH-2015×CIM595 and VH371×CIM595 with values 0.73 and 0.43 respectively. Reciprocal crosses showed higher value for cross VH377×VH371 -2.06 CIM595×FH2015 -0.971 and VH377×CIM595 -0.67 rests of reciprocal crosses showed lower values but all the results are negative. Sympodial branches showed that there is significant difference among genotypes. General combining ability analysis showed value 4.26 and specific combining ability analysis depicted the value 0.82. Investigation of variance explore the significant variations ($P \leq 0.01$) among genotypes. This suggested that the data for plant height can be analyzed for combining ability analysis. It is clear that VH371 (5.35) is the best general combiner followed by CIM595 (2.98). Among direct crosses FH2015×CIM595 represented highest value 16.81 for SCA. Plant height is favoring character, the crosses showing high positive value exhibit dominant gene effect. KEH× VH371 showed highest value for all reciprocal crosses. Dominant variance for SCA was higher than that of GCA variance. Plant height was in the control of non-additive sort of gene action. Same outcomes have been declared by Sarvanan *et al.* (2003), Rauf *et al*. (2006), Ilyas *et al*. (2007), Rauf *et al*. (2005), Kaleem *et al.* (2016) and Memon *et al*. (2016). Boll weight showed significant difference among genotypes. General combining ability analysis showed value 6.62 and specific combining ability analysis indicated the value 2.970 both are significant showing that boll weight can be improved through general and specific combining ability. VH377 showed highest value for combining ability 0.29 and mean 3.262 for seed cotton yield. Seed weight per boll indicating that there is significant difference among genotypes. General combining ability analysis showed value 23.00 and specific combining ability analysis indicated the value 1.37. VH377 showed highest value for combining ability 0.59 and mean 3.26 for seed per boll. This is a yield favoring character parents with positive value are more important. It could be seen that VH377 and FH-2015 were good general combiner for improving number of seed weight per boll. Rest of the results are shown in the table.

Number of seeds per boll showed that there is significant difference among genotypes. General combining ability analysis showed value 5.06 and specific combining ability analysis indicated the value 3.87. It could be seen that VH377 was best general combiner for improving number of seed per boll. VH371×VH377 depicted the best specific combining ability, its value was 2.78. Reciprocal crosses with highest value are FH2015×VH371 and

VH377×CIM595 their SCA values are 3.2 and 2.716667 respectively. Seed cotton yield showed that there is significant difference among genotypes. VH377 showed highest value for combining ability 0.594 and mean 3.262 for seed cotton yield. VH371×VH377 exposed the best specific combining ability, its value was 0.15. Reciprocal crosses with highest value are KEH×VH371 0.31 and VH FH2015×VH371 their SCA values are 0.31 and 0.22 respectively. The greater values indicated effective maternal effect for dominant gene action for seed cotton yield. This study suggests that seed cotton yield was under the non-additive genetic action. Saravanan *et al.* (2003), Rauf *et al*, (2005), Rauf *et al* (2006), Imran *et al.* (2011) and Kaleem *et al.* (2016) also mentioned that seed cotton yield was under the non-additive genetic effect. Fiber fineness showed significant value in analysis of variance. FH2015 showed highest value for combining ability 0.05 and mean 4.47 for fiber fineness. VH371×CIM595 showed the best specific combining ability, its value was 0.65. Reciprocal crosses with highest value are CIM595×VH371 and CIM595×FH2015 their SCA values are 0.63 and 0.53 respectively. Fiber length showed that there is significant difference among genotypes. General combining ability analysis showed value 1.78 and specific combining ability analysis indicated the value 2.09. Fiber strength showed significant value in analysis of variance. KEH showed highest value 0.862 for combining ability and mean 22.21 for fiber strength. VH371×KEH showed the best specific combining ability, its value was 1.9128. Reciprocal crosses had greater value for SCA for fiber strength than that of GCA. Reciprocal crosses with highest value are VH377×KEH and FH2015×VH371 their SCA values are 1.741667 and 0.82 respectively. Similar finding of significant SCA mean squares and the gene action of non-additive type controlling this trait was also correlates with the findings of Imran *et al.* (2011), Saravanan *et al.* (2003) and Ali *et al.* (2016).

Table 1: Combining Ability effects of yield and related traits in Upland Cotton

	No. of bolls per plant	Monopodial Branches	Sympodial Branches	Plant Height	No. of seeds per Balls	Seed weight per Ball	Boll weight	Seed Cotton yield	Seed weight per plant	Ginning out turn (GOT)	Lint index	Seed index	Fiber fineness	Fiber length	Fiber strength
Parents	**GCA**														
VH371	1.32	0.46	-0.37	5.35	-0.71	-0.24	-0.24	-0.24	-0.61	0.17	0.08	0.08	-0.05	0.15	0.24
FH2015	-1.17	-0.39	-1.07	-1.16	-0.75	-0.38	-0.11	-0.38	-0.09	-1.41	-0.09	-0.09	0.05	-0.20	-0.49
KEH	-1.89	-0.47	0.06	-7.85	0.23	-0.25	0.08	-0.25	-2.09	1.61	-0.07	-0.007	0.04	0.31	0.86
CIM595	5.25	0.20	1.23	2.98	-0.43	0.28	-0.01	0.28	1.96	-0.38	0.15	0.15	-0.02	0.02	-0.56
VH377	-3.51	0.20	0.15	0.67	1.72	0.59	0.29	0.59	0.83	0.007	-0.13	-0.13	-0.01	-0.28	-0.03
SE (GCA)	1.01	0.13	0.36	0.36	0.41	0.07	0.07	0.07	0.74	0.59	0.08	0.08	0.08	0.16	0.19
Direct crosses	**SCA**														
VH371×FH2015	5.60	-0.91	0.09	-16.59	1.16	0.09	-0.55	0.09	-4.16	-2.15	0.15	0.15	-0.02	-0.06	-0.94
VH371×KEH	10.62	-0.57	-1.47	14.17	-3.64	0.02	0.06	0.02	2.94	1.00	-0.24	-0.24	0.46	-0.08	1.91
VH371×CIM595	-5.47	0.45	0.22	10.12	-2.20	0.49	-0.25	0.49	1.08	0.17	0.42	0.42	0.65	0.54	-0.13
VH371×VH377	0.79	1.54	0.90	0.26	2.78	0.08	0.15	0.08	0.23	-0.95	-0.48	-0.48	-0.49	-0.42	-0.44
FH2015×kEH	-3.57	-0.20	0.59	-10.36	1.69	-0.04	0.09	-0.04	1.42	0.14	0.12	0.12	0.04	-0.21	0.99
FH2015×CIM595	7.63	0.73	-0.93	16.81	0.35	-0.00	-0.11	-0.003	-1.77	-3.09	-0.27	-0.27	-0.35	0.33	-0.68
FH2015×VH377	3.61	-0.07	-0.55	-0.22	-2.71	-0.07	-0.06	-0.07	4.85	3.30	-0.19	-0.19	0.34	-0.95	1.27
KEH×CIM595	-8.61	-0.66	0.02	-29.86	0.67	-0.01	0.08	-0.01	-4.01	2.45	0.31	0.31	-0.09	0.17	0.09
KEH×VH377	-1.67	-0.15	0.934	10.94	0.32	0.11	0.07	0.11	0.005	-1.38	0.60	0.60	-0.44	0.42	-1.26
CIM595×VH377	-7.40	-0.85	-0.21	-7.97	-0.08	-0.09	0.09	-0.09	-3.85	-0.82	-0.32	-0.32	-0.01	-0.41	-0.73
SE (SCA)	1.01	0.36	1.03	1.03	1.17	0.22	0.20	0.22	2.11	1.69	0.23	0.23	0.23	0.46	0.54
Reciprocal crosses	**SCA**														
FH2015×VH371	2.36	-0.47	3.20	10.47	0.25	0.22	0.55	0.22	0.27	2.93	0.15	0.15	0.01	0.34	1.74
KEH× VH371	13.59	0.50	2.63	13.85	4.03	0.31	-0.05	0.31	6.21	1.27	0.48	0.48	-0.15	0.63	0.04
CIM595×VH371	-5.40	-0.48	-0.43	-4.06	1.94	0.03	0.33	0.03	-5.81	-1.07	-0.56	-0.56	0.63	-0.25	-1.05
VH377×VH371	-3.50	-2.06	-2.63	-15.96	0.08	-0.65	-0.06	-0.65	-3.32	-0.99	-0.18	-0.18	-0.20	0.10	-1.25
KEH×FH2015	1.03	-0.15	-1.40	12.81	-3.15	-0.06	0.05	-0.06	-3.38	-2.03	-0.91	-0.91	0.006	-0.38	0.50
CIM595×FH2015	-8.93	-0.97	-0.70	-3.23	-0.85	-0.51	0.15	-0.51	0.98	0.12	0.21	0.21	0.53	-0.53	-1.31
VH377×FH2015	-3.32	-0.50	-3.33	-18.20	-0.48	-0.77	-0.31	-0.77	-0.58	-6.05	-0.59	-0.59	0.04	-2.25	0.51
CIM595×KEH	0.30	-0.35	-0.73	2.93	0.13	-0.61	0.33	-0.61	0.96	0.58	-0.02	-0.02	0.05	-0.09	0.19
VH377×KEH	0.65	-0.43	-0.63	-0.70	0.27	-0.79	-0.18	-0.79	-2.78	-0.44	-0.35	-0.35	0.09	0.74	0.82
VH377×CIM595	-2.35	-0.67	2.71	-18.82	1.58	0	0.16	0	-2.78	0.01	0.39	0.39	0.04	-1.08	-0.46
SE (RCA)	1.01	0.36	1.03	1.03	1.17	0.22	0.20	0.22	0.22	1.69	0.23	0.23	0.23	0.46	0.54

Conclusion

It is also known as the sovereign of natural fibers and has a major role in the economy of many countries including Pakistan. The results verified that there is significant difference between all the traits. The five parents VH371, FH2015, KEH, CIM595 and VH377 and their all possible crosses were also evaluated for genetic variability. The results verified the presence of genetic variation among the parents and all their crosses for all the observed characters. According to GCA estimates, the parent CIM595 verified to be the good general combiner for many traits such as seed index, lint index, seed weight per plant, sympodial branches and number of bolls per plant. The combination VH371×CIM595 had high SCA effects for most of the important traits of cotton i.e. fiber fineness and fiber length. These genotypes can be further used in the breeding procedures to improve the crop yield and associated traits".

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5/24/2020