

Combining Ability Estimates for Yield and Fiber Quality Parameters in *Gossypium Hirsutum* L. Hybrids

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Abstract: General and specific combining ability effects were discriminated in different parents and offspring to isolate the potential of genotypes used in diallel system to attain the genetic inheritance pattern ascertain with the nature of gene action. A six-by-six, *hirsutum* diallel excluding reciprocals, was analyzed for general and specific combining ability estimates and components of genetic variation to investigate the genetic retrospect and inheritance pattern of eleven quantitative and fiber quality characters. *Hirsutum* cultivars included CIM-506, BH-160, NIAB-111, CIM-497, NIAB-999 and RH-510. Some of the traits like boll number, boll weight and sympodia plant¹ did not reveal the highest GCA scoring parent for seed cotton yield. The ranking order for GCAs of the parents was not maintained from F₁ to F₂ diallel set and the ranking order of the hybrids with respect to their SCA values was also not maintainable from F₁ to F₂ diallel set. Thus the hybrids could not maintain their superiority (or inferiority) of their SCA values.

Keywords: Cotton, Diallel analysis, Fiber, GCA and SCA, quality, yield.

1. INTRODUCTION

Fiber quality improvement is one of the main economic goals in textile and commercial cotton [1, 2]. In Pakistan seed cotton yield and fibre quality is low as compared to developing countries [3]. Hence, breeding with good segregating recombinants in context to diallel mating design will lead to maximum experimental precision in selection of superior lines [4]. The availability of variation in the genotypes is more advantageous as controlled by significant genetic components. Simultaneously, plant characters directly employing to yield is the main target of the breeder to enhance productivity [5]. Breeding of superior qualitative characters has long enjoyed effective genetic guidance and has prospered accordingly; but the breeding of superior quantitative characters, to large extent, has been denied and has therefore been much less prosperous. The difficulty with quantitative characters is that they tend to be continuous in their variation. Distinguishing phenotypic traits is sometimes difficult or impossible applicability of classical Mendelian analysis. Hence, plant breeders synthesize selection of parents to regulate the manipulation of progenies and permit to predict and isolate superior genotypes/cultivars.

Combining ability demonstrates the performance or contribution of parent lines in different hybrid

combinations on average basis [5, 6]. Representing the inheritance pattern with the role of additive gene action conferring GCA (as parents with higher estimates) and non-additive gene action inferring SCA (higher interaction of hybrids) leads to the identification of superior genotypes [5, 7]. Hence, diallel analysis could be used to evaluate the potential of parents for their utilization in hybridization program for the improvement of a particular metrical character [8, 9]. Therefore segregating populations that contain most desirable genotypes are identified in early generations and inferior populations with limited promise are eliminated [10].

The aim of this study was to estimate gene action and the type of inheritance of investigated traits in cotton, evaluate GCA of parents and SCA of F₁ diallel crosses, and select the superior F₁ diallel crosses that can be used in breeding program of cotton.

2. MATERIALS AND METHODS

The experimental research work was conducted in the Botanical Garden area of Plant Breeding & Genetics Department of Sindh Agriculture University, Tando Jam during kharif in 2006. Six cultivars viz. CIM-506, BH-160, NIAB-111, CIM-497, NIAB-999 and RH-510 were utilized for this experiment. Five rows of each cultivar were planted to create F₁ hybrid seed through crossing/hybridization. All possible cross combinations excluding reciprocals were made in this case 15 direct cross combination were made. During 2007, selfed seed of parent varieties and crossed F₁s were planted in Randomized Complete Block Design with three

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replications. Selfing was continuously made to have sufficient selfed seed of parents for replicated trial in kharif 2008. After maturity, all the F₁ bolls along with selfed seed of parents were harvested to complete the experimental seed material for replicated trial of F₂s in kharif 2008.

2.1. Statistical Analysis

Griffing [11] method were used for the present study corresponding to half diallel method incorporating as one way crosses without reciprocals and with parental lines. The estimates of general combining ability (GCA) for parents and specific combining ability (SCA) of hybrids together with variances for GCAs and SCAs followed by the method of Griffing [11] method 2, mathematic model I was applied. The estimates were obtained using following formulae:

$X_{ij} = \mu + g_i + g_j + s_{ij} + e$, Where, X_{ij} = is the mean of $i \times j^{th}$ genotypes, μ = is the experimental grand mean, g_i and g_j = is the GCA effects of i^{th} female parent, effects of j^{th} male parent, s_{ij} = is the SCA effects specific to the hybrid of the i^{th} female line and the j^{th} male line, and e = is the experimental error.

3. RESULTS AND DISCUSSION

3.1. Mean Performance of F₁ and F₂ Populations and Parental Cultivars

The present study was aimed at evaluating a 6-parent half diallel cross (parents plus one way crosses) of upland cotton cultivars for the general and specific abilities to obtain an explanation of the genetic mechanism of agronomic and fiber characteristics. Accordingly, the analysis of variance for general and specific combining ability for 2007 F₁ and 2008 F₂ diallel sets for all the eleven quantitative characters under study was performed to estimate the variances for GCAs and SCAs which will pave way to target selection/isolation of desirable parents for further exploitation of their utility in the cotton breeding program. Analysis of variance for general and specific combining abilities together with the estimates of GCA and SCA variances are presented in Table 1. The estimates of GCA effects for parents and SCA effects from their one-way hybrids for 2007 F₁ diallel set are given in Table 2 and for 2008 F₂ diallel set in Table 3.

3.2. General and Specific Combining Ability in 2007 and 2008, F₁ and F₂ Crosses

The means of F₁ and F₂ hybrid and there parental lines tested through ANOVA showed highly significant

Table 1: Mean Squares from the Analysis of Variance of General and Specific Combining Ability of 6x6 F₁ and F₂ Cotton Diallele Cross for Seven Quantitative Traits During 2007 and 2008

Source of variation	D.F	Plant Height	Sympo-dia Plant ⁻¹	Bolls Plant ⁻¹	Boll Weight	Seed Index	Lint Index	Yield Plant ⁻¹
F₁ – 2007								
Replications	2	14.06	0.07	0.69	0.02	0.14	0.11**	1.51
GCA's	5	171.86*	9.38**	14.41**	0.29**	1.08**	0.10*	228.69**
SCA's	9	171.87**	4.49**	4.28**	0.17**	0.17*	0.16**	270.15**
Error	28	32.88	0.39	0.43	0.02	0.07	0.02	4.77
GCA Variances	-	14.32	0.78	1.20	0.02	0.09	0.01	19.06
SCA Variances	-	57.23	1.49	1.43	0.06	0.06	0.05	90.05
F₂ – 2008								
Replications	2	40.85	2.64	19.49**	0.01	1.39**	0.08*	9.61
GCA's	5	70.14	0.60	13.42**	0.26**	1.16**	0.07*	396.65**
SCA's	9	55.43*	4.10**	3.94**	0.16**	0.18**	0.14**	15.61**
Error	28	22.37	1.26	0.40	0.02	0.04	0.02	3.90
GCA Variances	-	5.85	0.05	1.12	0.02	0.10	0.01	33.05
SCA Variances	-	18.48	1.37	1.31	0.05	0.06	0.05	5.20

*= Significant at 5% probability level.

**= Significant at 1% probability level.

Table 2: Mean Squares for Combining Ability of Seven Cultivars of 6x6 F₁ and F₂ cotton diallele cross during 2007 and 2008

Character	Reps DF=02	Genotypes DF=20	Error DF=40	C.V. %
F₁ – 2007				
Plant Height	1.216	152.15**	19.94	4.91
Sympodia Plant ⁻¹	4.23	4.79**	0.99	5.67
Bolls Plant ⁻¹	15.87	14.51**	0.70	3.07
Boll Weight	0.028	0.497**	0.021	4.33
Seed Index	0.574	1.168**	0.096	3.93
Lint Index	0.111	0.273**	0.019	3.11
Yield Plant ⁻¹	2.339	480.751**	4.885	2.49
F₂ – 2008				
Plant Height	27.006	47.180**	18.110	4.75
Sympodia Plant ⁻¹	6.006	2.249	1.433	6.57
Bolls Plant ⁻¹	20.919	5.683**	0.363	2.91
Boll Weight	0.011	0.190**	0.026	4.95
Seed Index	1.862	0.500**	0.059	3.11
Lint Index	0.039	0.134**	0.019	3.15
Yield Plant ⁻¹	9.783	233.097**	4.183	2.37

*= Significant at 5% probability level.

**= Significant at 1% probability level.

differences ($P < 0.01$) for all the traits which attribute the genetic variations due to GCAs and SCAs (Tables 1; 2), whereas for GCAs in both generation was significant at $P < 0.05$ only for lint index. This suggests that almost all the characters displayed high magnitude of variation except lint index. This might be inconsistent due to genotypic and phenotypic variances and thus considered that the analysis of variance for GCAs and SCAs would be important having diverse genetic background. In our results, seed cotton yield and bolls per plant observed significant for mean squares due to GCA. Similarly, Baloch *et al.*, [12] and Hassan *et al.*, [13] revealed significant mean squares for both traits. Ali *et al.*, [14] and Baloch *et al.*, [15] for plant height, bolls per plant and seed cotton yield achieved significant mean squares due to SCA. For the same traits our results also revealed significant for SCA.

3.3. General Combining Ability

GCA components of genetic variation were observed to be greater and more significant in both the generations (Table 3). General combining ability mean squares for all the characters were significant at 5% level of probability in case of plant height and lint index, and were significant at 1% level for sympodial branches plant⁻¹, number of bolls plant⁻¹, boll weight,

seed index and seed cotton yield plant⁻¹. Since general combining ability reflects parental performance and is the result of additive gene effects and additive x additive type of gene effects, significance of GCAs mean squares for above mentioned seven quantitative characters show the importance of additive gene effects for these characters. And since the magnitude of GCA variances for all the quantitative characters was of lesser intensity, pedigree breeding method for selecting desired parental genotypes on the basis of significant additive gene effects would be more effective and fruitful. Since pedigree breeding especially emphasizes proper record maintenance from one generation to the other, it will help selecting the desired targeted parental genotypes in cases where GCA mean squares were non-significant also, for example, for fiber fineness and fiber strength in the present case. MA El-Hennawy.; M Zare-kohan and Bahram Heidari suggested [9, 16] for all the traits except seed cotton yield and bolls per plant influenced additive type of variance.

3.4. Specific Combining Ability

Mean squares for specific combining ability were highly significant ($P < 0.01$) for plant height, sympodial branches plant⁻¹, bolls plant⁻¹, boll weight, lint index and

Table 3: General and Specific Combining Ability Estimates from 6x6 F₁ Cotton Diallele Cross for Seven Quantitative Characters During 2007

Entries	Plant Height	Sympodia plant ⁻¹	Bolls Plant ⁻¹	Boll weight	Seed Index	Lint Index	Yield plant ⁻¹
General Combining Ability							
CIM-506	-058	0.99	0.08	0.01	0.42	-0.03	0.04
BH-160	0.55	0.35	-0.72	0.23	0.06	-0.01	6.70
NIAB-111	1.80	0.21	0.83	-0.25	0.28	0.17	-5.75
CIM-497	-6.99	-1.64	-1.79	0.06	-0.22	0.00	-2.55
NIAB-999	4.23	0.20	1.19	0.01	-0.29	-0.08	2.98
RH-510	0.99	-0.10	0.41	-0.06	-0.24	-0.05	-1.42
Specific Combining Ability							
CIM-506 x BH-160	6.78	0.77	-0.43	0.30	-0.49	-0.04	9.43
CIM-506 x NIAB-111	1.10	-0.62	-0.87	0.05	0.03	0.06	-2.14
CIM-506 x CIM-497	-6.05	-0.98	-0.23	-0.36	0.12	-0.09	-11.87
CIM-506 x NIAB-999	4.04	1.65	1.90	-0.05	0.16	-0.10	3.63
CIM-506 x RH-510	-5.87	-0.82	-0.37	0.06	0.17	0.16	0.95
BH-160 x NIAB-111	-9.34	-0.04	-0.33	-0.06	0.02	-0.25	-3.71
BH-160 x CIM-497	2.32	0.46	0.52	0.18	0.06	-0.08	6.40
BH-160 x NIAB-999	5.87	-0.18	0.83	-0.25	0.20	0.32	-1.57
BH-160 x RH-510	-5.63	-1.01	-0.58	-0.16	0.22	0.05	-10.54
NIAB-111 x CIM-497	7.03	1.00	0.71	0.18	-0.04	0.12	9.71
NIAB-111 x NIAB-999	-1.27	-0.19	0.00	0.03	0.03	0.24	2.01
NIAB-111 x RH-510	2.48	-0.15	0.49	-0.20	-0.04	-0.16	-5.87
CIM-497 x NIAB-999	-10.48	1.87	-2.09	-0.02	-0.08	-0.18	-11.89
CIM-497 x RH-510	7.18	1.39	1.09	0.01	-0.05	0.22	7.64
NIAB-999 x RH-510	1.84	0.59	-0.64	0.29	-0.31	-0.28	7.82

yield of seedcotton plant⁻¹ and fiber strength. SCA mean squares were significant at $P < 0.05$ for seed index. Since the specific combining ability reflects the average performance of hybrid progenies and is outcome of dominance and dominance x dominance gene action, significance of mean squares of SCAs for above mentioned characters reflects the importance of dominant gene effects, selection of desired hybrid progeny genotypes must be made considering dominant gene effects which are pronounced and preponderant for above mentioned significant characters under study. Pedigree record breeding would be the most appropriate selection procedure in selecting the desired hybrid progeny ideotypes on the basis of significant dominant gene effects for precise objectivity. In addition, since the magnitude of SCA variances was significantly high for plant height and seed cotton yield plant⁻¹, pedigree breeding would be even more meaningful if dominant gene effects are

further partitioned into dominance x dominance epistatic effects for these two characters to pin point the desired genotypes masking/epistating the effects of recessive alleles and expressing pronounced phenotypic attribute for that character.

The estimates of GCA of six parental varieties for seven characters studied from 2007 F₁ diallel set are given in Table 2. Since GCA estimates pertaining to a parental variety show the deviation of parental mean from the general mean, the sum of all deviations (that is all general combining ability effects) would be zero and this is also true in the present case which could also be regarded as the accuracy test of the model/data. Many of the parents and hybrid scored highest GCA value as NIAB-999 (4.23) for the trait plant height (cm). NIAB-111 x CIM-497 hybrid represented highest SCA, whereas lowest SCA value was revealed by CIM-497 x NIAB-999 (SCA = -10.48).

This shows that maximum positive GCA effects were due to best combiners desirable from breeding point of view. Maximum SCA was observed in the trait sympodial branches per plant, with the hybrid CIM-497 x NIAB-999 (1.87) and the least SCA values were observed in cross BH-160 x RH-510 (SCA = -1.01). With respect to number of bolls plant⁻¹, hybrid CIM-506 x NIAB-999 scored the highest value (SCA = 1.90) while the lowest SCA was recorded in hybrid CIM-497 x NIAB-999 (-2.09). These results reveal that numbers of bolls are consistent with number of sympodial branches and that they were controlled by dominance type of gene action. Highest SCA for boll weight, was scored by the progeny CIM-506 x BH-160 (SCA = 0.30), which revealed predominance of non-additive gene action for the inheritance of this trait. For seed index, hybrid BH-160 x RH-510 showed highest SCA (0.22) and the lowest SCA producing progeny being NIAB-999 x RH-510 (SCA = -0.31). Consequently, for the trait lint index, hybrid BH-160 x NIAB-999 gave the highest SCA value of 0.32 followed by hybrid NIAB-111 x NIAB-999 (SCA = 0.24) (Table 3). These results are similar with Hassan *et al.*, (2000) and Sheraz *et al.*,

(2015) [13, 17] who observed additive and non-additive gene action for Bolls per plant and Seed Cotton Yield per plant (g). Hence, the best parents and cross combinations could be effective for improving yield components and thus incorporated in further breeding programs. The overall study reveals the importance of both additive and non-additive genetic variability which suggests the use of integrated breeding strategies which can efficiently utilize the additive as well as non-additive genetic variability. Thus, the use of diallel mating selection could provide the better conditions for recombination and accumulation of desirable genes.

Estimates of general and specific combining ability effects in 2008 F₂ diallel set are presented in Table 4. The GCA components of genetic variance for the traits in plant height was maximum with the parents RH-510 (GCA = 3.04) followed by NIAB-999 (GCA = 1.97) and the lowest GCA scoring parent was CIM-497 (GCA = -4.11). Predominance and additive type of gene action was performed in this trait. The cultivars NIAB-999 and CIM-497 displayed positive GCA effects for sympodia and bolls per plant revealing that sympodia is positively

Table 4: General and Specific Combining Ability Estimates from 6x6 F₂ Cotton Diallel Cross for Seven Quantitative Characters During 2008

Entries	Plant Height	Sympodia plant ⁻¹	Bolls Plant ⁻¹	Boll weight	Seed Index	Lint Index	Yield plant ⁻¹
General Combining Ability							
CIM-506	0.46	0.12	0.04	0.01	0.43	-0.02	-9.16
BH-160	-0.10	-0.05	-0.62	0.21	0.12	0.00	-5.22
NIAB-111	-1.23	-0.27	0.88	-0.24	0.23	0.15	2.32
CIM-497	-3.93	0.12	-1.76	0.05	-0.11	-0.02	3.80
NIAB-999	1.89	0.31	1.11	0.01	-0.30	-0.07	3.79
RH-510	2.96	-0.22	0.35	-0.05	-0.37	-0.03	4.46
Specific Combining Ability							
CIM-506 x BH-160	1.48	0.80	-0.48	0.03	-0.27	-0.05	2.78
CIM-506 x NIAB-111	-1.23	-0.47	-0.91	0.05	-0.01	0.07	-1.59
CIM-506 x CIM-497	1.88	-0.45	-0.19	-0.34	0.26	-0.06	0.36
CIM-506 x NIAB-999	1.08	1.13	1.88	-0.05	0.10	-0.11	0.72
CIM-506 x RH-510	-3.21	-1.01	-0.30	0.05	-0.08	0.14	-2.26
BH-160 x NIAB-111	-5.06	-0.16	-0.05	-0.09	-0.12	-0.23	2.11
BH-160 x CIM-497	-2.57	-0.47	0.42	0.18	-0.15	-0.06	0.34
BH-160 x NIAB-999	5.85	-1.08	0.73	-0.24	0.30	0.30	-3.65
BH-160 x RH-510	0.29	0.91	-0.62	-0.16	0.25	0.04	-1.58
NIAB-111 x CIM-497	4.89	0.14	0.65	0.18	-0.09	0.04	-1.62
NIAB-111 x NIAB-999	0.61	-1.01	-0.08	0.03	0.03	0.25	0.79
NIAB-111 x RH-510	0.78	1.49	0.40	-0.16	0.19	-0.14	0.31
CIM-497 x NIAB-999	-6.95	1.56	-1.97	-0.02	-0.05	-0.16	-0.23
CIM-497 x RH-510	2.74	-0.79	1.09	0.00	0.03	0.24	1.15
NIAB-999 x RH-510	-0.60	-0.60	-0.56	0.27	-0.38	-0.28	2.38

correlated with bolls and seed cotton yield per plant. With respect to boll weight, parent BH-160 secured highest GCA value of 0.22, whereas the lowest GCA effects were scored by parent NIAB-111 (-0.26). The parent CIM-506 for seed index scored highest GCA (0.45) among the parents. With respect to lint index, parent NIAB-111 secured highest GCA value of 0.16. Ginning outturn percentage, lead to the highest GCA estimates with parent RH-510. The parent CIM-506 and NIAB-999 valued maximum GCA for staple length, both enhancing good quality parents. Seedcotton yield plant⁻¹ are correlated with yield traits. The parents RH-510 (GCA = 4.69) and CIM-497 (GCA = 4.00) conflict maximum yield. In case of qualitative traits, for fiber fineness, the parent CIM-506 revealed good quality. However, with respect to fiber strength, highest GCA score was obtained from parent NIAB-111 and NIAB-999 both giving 0.46 GCA.

4. CONCLUSIONS

The conclusions for the study 2008 F₂ diallel, on the pattern of 2007 F₁ diallel set combining ability analysis, can be drawn from the above gathered information giving example of yield of seedcotton plant⁻¹: (i) The highest yielding parent in 2007 F₁ diallel was CIM-506 and highest yielding hybrid was CIM-506 x BH-160 while the lowest yielding parent was NIAB-111 and lowest yielding hybrid was CIM-596 x CIM-497. Correspondingly, the highest yielding parent in 2008 F₂ diallel was NIAB-999 and lowest was CIM-506. Likewise, the highest yielding hybrid in 2008 was NIAB-999 x RH-510 and lowest was CIM-506 x NIAB-111. Therefore, it can be suggested that, highest yielding parent in 2007 F₁ diallel cannot maintain its superiority and out yielded in 2008 F₂ diallel. The same conclusion can also apply to low and high yielding hybrids. (ii) Highest mean performance of parents does not necessarily yield highest GCA effects.

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