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Estimates of Genetic Parameters from Line x Tester Mating Design for Some Quantitative Traits in Upland Cotton, *Gossypium hirsutum* L.

Muhammad Jurial Baloch*, Moula Bux Kumbher, Wajid Ali Jatoi and Nasreen Fatima
Department of Plant Breeding & Genetics, Sindh Agriculture University, Tando Jam, Sindh, Pakistan

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Abstract. Combining abilities of cotton varieties were evaluated using a line x tester design with eight lines and 4 testers. Good performance combination was found between the varieties CRIS-134 and BH-147. The former was a good candidate for fibre length improvement and the latter, a good parent for yield improvement. The specific combining ability suggested that both additive and dominant genes controlled the characters. Hybrid performance *per se* may be used to predict the parental performance for specific combining ability and thus for hybrid crop development.

Keyword: cross breeding, combining ability estimates, fibre length, *Gossypium hirsutum*

Introduction

In cotton breeding, some crosses make better combinations than the others in forwarding desirable genes to their offsprings. Richy and Mayer (1925) thus emphasized that due to lack of any definite association in the performance between the parents and their offspring, selection for combining ability must be based on the performance of the inbred parents in cross combinations rather than the inbred parents *per se*. Thus it is essential that those inbred parents may be identified which produce good individuals in specific combinations, commonly referred to as specific combining ability (SCA) of the inbred parents, and those parents may be marked which form good combinations with other parents in a series of crosses, referred to as general combining ability (GCA) of the parents (Sprague and Tatum, 1942). The former types of inbreds are useful for hybrid crop development whereas the latter are desirable to generate segregating populations for selection.

In quantitative genetics, genotypic value of an individual is determined by various types of gene actions such as additive, dominance and their interactions (Falconer, 1989). Theoretically, inbreds which show higher estimates of SCA are those which predominantly possess dominant genes; such genes are not transferable to their progenies. Whereas inbreds which perform well in general terms are referred to as general combiners; they posses predominantly additive genes. Baloch *et al*. (2002, 2000, 1997, 1995 and 1993) and Bhutto *et al*. (2001) observed that inbred parents were very inconsistent in their *per se* hybrid performance and GCA and SCA estimates. They pointedout that generally, parents which formed best GCA did not perform similarly for SCA estimates. However, Baloch (2004) and Baloch and Bhutto (2003) reported that not all but some parents perform equally well in hybrids *per se*, for GCA and also for SCA estimates. It was, hence, believed that combining ability is the property of an individual parent in hybrid combination rather than inbred parents, *per se*. It is, therefore, very essential for plant breeders that every inbred parent be specified for its potential in terms of GCA or SCA. Ever since cotton leaf curl virus (clcv) disease erupted in Pakistan during 1991, cotton breeders had no choice but to include one of the clcv resistant parents with other high yielding commercial varieties in their hybridization programme. Breeders are also aware of the phenomenon that making a large number of crosses between clcv resistant and high yielding parents and thereby separating potential inbreds based on progeny performance seems a chance game. This method of identifying desirable inbreds is eventually very laborious and expensive in terms of inbred selection and also requires vigorous selection in segregating populations. At present, though numerous clcv resistant inbreds have been evolved which do not require screening of segregated population in the clcv hot spots if both parents in crosses are resistant, yet not all the clcv resistant parents yield good harvest or other fibre traits. It is, thus, important for cotton breeders to determine the GCA and SCA estimates of the parents to be used in hybridization programme for producing potential progenies. In this way, more dependable hybridization programme could be launched. The essential objectives of conducting line x tester analysis is therefore to determine or predict the combining ability of the clcv resistant inbred parents, for knowing the types of gene actions controlling different traits. The general and specific combining ability effects of individual

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*Author for correspondence; E-mail: dr_mjr@hotmail.com parents further demonstrate the saturation of additive or dominant genes in the parents. So far, controversial results have been presented by many researchers on the type of genes controlling various traits in cotton and the types of genes present in individual parents. Baloch (2004), Baloch and Bhutto (2003) and Tang *et al*. (1993) reported that both additive as well as dominant genes were involved in the expression of seed cotton yield, bolls per plant, boll weight, lint percentage and the fibre length. They, however, observed that parents were still quite different in exhibiting general and specific combining ability effects for these traits. The results of above researchers are quite justifying in that F_1 hybrids do show heterosis or vigour due to dominant gene action but at the same time, much improvement in such characters have also been made by selection from segregating populations. Such results suggest that additive genes are also important for the above mentioned traits. It appears that types of gene action vary a little depending upon the mating design used; nevertheless, the general and specific combining ability are solely dependent on the individual parents. For this purpose, diallel analysis has been extensively used but line x tester mating design is still superior as it uses more number of crosses, thus providing more reliable estimates of genetic components of variance as compared to diallel analysis. Actually, it gives two estimates of GCA from both female lines and male testers. The objectives of the present research were to determine the GCA and SCA effects of clcv resistant parents and also genetic variations due to GCA and SCA, thereby knowing the importance of additive and dominant genes attributable to various quantitative traits in intra-hirsutum F_1 hybrids.

Materials and Methods

Eight commercially grown cotton leaf curl virus (clcv) resistant varieties from Punjab (CIM-707, CIM-499, CIM-506, FH-1000, FH-925, VH-142, NIAB-111/S and BH-147) were used as female lines and crossed with four pollinators (testers) from Sindh (CRIS-134, CRIS-342, CRIS-191 and CRIS-377) in a line x tester mating design during 2003-2004. Thus a total of 32 cross combinations were developed. The crossed bolls were grown as F_1 during crop year 2004-2005. The experiment was conducted in a randomized complete block design with four replications in a plot size of 35.0 × 7.5 feet (3 rows, each 35 feet long). The seeds were hand dibbled by putting only 3 seeds per hole. After 25 days of planting, the extra two plants per dibble were thinned leaving only one vigorously growing plant per dibble. The plant-to-plant and row-to-row distances were maintained at 9.0 inches and 2.5 feet, respectively. All the inputs like fertilizer, irrigation and pesticides were applied as and when required in the doses recommended for the local conditions. For recording the observations, 20 plants from each genotype per replication were randomly tagged and kept as index plants. The data was recorded on seed cotton yield per plant in g, number of bolls per plant, lint percentage (taken as the ratio of lint from seed cotton sample), fibre length (in mm measured with digital fibrograph at 2.5% span length) and earliness percentage (as the number of open bolls after 120 days of planting). The analysis of variance and general and specific combining ability estimates were determined according to the procedures of Singh and Choudhry (1979).

Results and Discussion

The hybrids' performance *per se*, the general combining ability (GCA), specific combining ability (SCA) estimates and mean squares from line x tester analysis are presented in Tables 1, 2, 3 and 4, respectively.

The mean performance of hybrids *per se* (Table 1) indicated that pollinator CRIS-342 when crossed with female lines BH-147, CIM-707 and CIM-499, pollinator CRIS-374 crossed with lines FH-1000 and CIM-506 and pollinator CRIS-134 crossed with lines VH-142 and NIAB-111/S gave higher yields. Yield results thus generally connoted that majority of pollinators formed good combinations for yield with at least one of the eight female lines used. Nevertheless, very interestingly, all of the pollinators produced higher yields when crossed with a female line BH-147. It means that female line BH-147 is the choice parent to be crossed with any of the pollinators to obtain maximum yields. It was also interesting to note that hybrids which gave higher yields *per se* also correspondingly produced more number of bolls per plant; this suggested that number of bolls and yield are parallel attributes and are highly correlated traits in cotton. As regards to lint percentage, pollinator CRIS-134, with a few exceptions, always ranked first when crossed with female lines. These results, therefore, indicated that if lint percentage is to be improved via selection from segregating populations, CRIS-134 is one of the best pollinator parents. Pollinator CRIS-134 always produced fibres of longer length when crossed with any of the female parents and thus may be considered as one of the best parents for the hybridization and selection programme.

In respect of earliness percentage, again pollinator CRIS-134 when crossed with any of the female lines, opened maximum number of bolls (Table 1) after 120 days of planting except female BH-147; with the latter, pollinator CRIS-342 opened maximum number of bolls (81.0%). Results regarding hybrids' performance *per se* suggested that in general pollinato CRIS-134 and line BH-147 may be given priority in hybridization programme with the

Table 1. Hybrid performance *per se* of cotton leaf curl virus resistant intra-hirsutum F_1 hybrids

F_1 hybrids	Seed cotton yield (g)	Number of bolls per plant	Lint (%)	Fibre length (mm)	Earliness (%) at 120 DAP*
CIM-707 x CRIS-134	194.50	52.38	37.80	29.30	82.13
CIM-707 x CRIS-342	195.50	54.00	33.90	28.20	71.80
CIM-707 x CRIS-191	126.50	35.68	34.80	28.70	74.87
CIM-707 x CRIS-377	115.75	31.00	35.50	27.70	82.50
CIM-499 x CRIS-134	151.50	40.18	38.10	28.70	86.30
CIM-499 x CRIS-342	177.00	44.75	35.80	27.70	65.70
CIM-499 x CRIS-191	134.25	36.13	37.60	27.10	82.30
CIM-499 x CRIS-377	116.50	30.88	35.90	26.70	79.70
CIM-506 x CRIS-134	145.00	38.13	36.10	28.50	93.40
CIM-506 x CRIS-342	132.00	34.75	34.70	27.20	87.50
CIM-506 x CRIS-191	152.25	39.50	34.60	27.03	76.00
CIM-506 x CRIS-377	160.13	42.75	35.90	26.50	69.00
FH-1000 x CRIS-134	158.50	41.75	37.90	28.20	75.50
FH-1000 x CRIS-342	119.75	32.63	39.70	26.40	75.00
FH-1000 x CRIS-191	164.50	43.00	36.30	26.30	60.70
FH-1000 x CRIS-377	216.50	57.88	35.80	25.70	67.50
FH-925 x CRIS-134	119.00	31.63	37.80	28.40	67.20
FH-925 x CRIS-342	122.25	33.25	36.40	27.20	46.50
FH-925 x CRIS-191	132.50	35.58	38.20	26.80	58.00
FH-925 x CRIS-377	131.25	35.75	35.30	26.90	53.70
VH-142 x CRIS-134	145.00	38.68	38.50	28.50	91.50
VH-142 x CRIS-342	116.50	30.88	36.50	27.50	87.13
VH-142 x CRIS-191	120.50	32.25	37.90	27.00	82.05
VH-142 x CRIS-377	132.00	35.05	36.30	26.50	83.90
NB-111/S x CRIS-134	132.25	35.42	36.70	27.80	83.50
NB-111/S x CRIS-342	121.25	40.00	35.50	27.20	67.00
NB-111/S x CRIS-191	108.00	29.00	36.10	26.40	61.00
NB-111/S x CRIS-377	121.25	32.00	34.50	27.70	77.20
BH-147 x CRIS-134	221.50	58.38	36.70	27.00	79.70
BH-147 x CRIS-342	236.00	62.63	35.80	26.50	81.00
BH-147 x CRIS191	204.00	53.83	36.40	26.00	72.70
BH-147 x CRIS-377	221.00	58.38	36.70	25.50	70.70
Avg.	152.32	40.56	36.43	27.80	74.78
LSD (5%)	1.17	0.74	0.33	0.28	1.57

DAP = days after planting.

prediction of improvement in yield and number of bolls of cotton.

Cotton breeders are aware that inbred parents are quite different in transferring the breeding value to their offsprings. Thus, Sprague and Tatum (1942) used the term “combining ability” to designate the ability of the parents to contribute favourable genes to their progenies.

It is generally predicted that parents which perform well in hybrids’ *per se* similarly exhibit good general combining ability as well as specific combining ability. (Baloch and Baloch, 2005; Baloch, 2004; Baloch and Bhutto, 2003; Baloch *et al*., 1997, 1995, 1993; Srinivasan and Gururajan 1973). However, in the present study, this assumption was not always found correct except some parents which performed well in hybrids *per se* also similarly exhibited good GCA and SCA. For example, tester CRIS-134 which formed good combinations in hybrids, also expressed maximum GCA estimates for all the traits studied whereas tester CRIS-342 ranked next for only yield and bolls but expressed negative estimates for the other three traits (Table 2). Among the female lines, BH-147, which gave maximum yields in hybrids’*per se*, performed similarly by giving the highest GCA values for yield (68.3g) and bolls (17.69). These

Table 2. General combining ability (GCA) estimates of lines and testers inbred parents for some quantitative traits in upland cotton

Variety	Seed cotton yield (g)	Bolls per plant	Lint (%)	Fibre length (mm)	Earliness (%)
Lines (females):					
CIM-707	5.738	2.70	-0.91	1.23	3.08
CIM-499	-7.512	-3.28	0.42	0.28	3.73
CIM-506	-4.980	-1.78	-1.13	0.01	6.67
FH-1000	12.488	3.25	0.99	-0.62	-5.10
FH-925	-26.074	-6.51	0.47	0.06	-18.41
VH-142	-23.820	-6.35	0.86	0.10	11.37
NB-111/S	-24.136	-6.46	-0.72	0.08	-2.60
BH-147	68.300	17.69	-0.02	-1.03	1.28
General mean	152.320	40.56	36.43	27.28	74.78
SE (gi)	0.209	0.132	0.058	0.05	0.279
SE (gi-gj)	0.295	0.187	0.082	0.07	0.395
Testers (pollinators/males):					
CRIS-134	6.080	1.50	1.02	1.02	7.62
CRIS-342	3.960	1.04	-0.39	-0.02	-2.07
CRIS-191	-9.510	-2.45	0.05	-0.37	-3.82
CRIS-377	-0.530	-0.11	-0.67	-0.61	-1.73
General mean	152.320	40.56	36.43	27.28	74.78
SE (gi)	0.147	0.093	0.041	0.035	0.198
SE (gi-gj)	0.209	0.132	0.058	0.050	0.279

SE = Standard error

results are coinciding with the results of Baloch and Baloch (2005) and Baloch (2004) who noted that not all but some parents exhibit equally good performance in hybrids' *per se* and in GCA, both. The GCA results thus suggested that CRIS-134 and CRIS-342 among the pollinators and BH-147, FH-1000 and CIM-707 among the female lines could be used in hybridization programme for significant improvement in all the traits through selection from segregating populations.

It is generally believed by the plant breeders that *per se* hybrid's performance is also reflected in specific combining ability estimates. This prediction does not hold true exactly; however, in the present study, some hybrids FH-1000 x CRIS-377, CIM-707 x CRIS-342, CIM-707 x CRIS-134 expressed maximum hybrid performance *per se* for yield per plant and correspondingly gave maximum SCA estimates (Table 3). These three high scoring specific combiners displayed similar SCA estimates for bolls per plant also.

The SCA results for lint percentage indicated that parents which performed better as *per se* hybrids, performed almost similar for SCA estimates except little change in rank orders. The SCA estimates of staple length in present research are in accordance with those of Baloch and Baloch (2005) and Baloch (2004) who noted that SCA estimates are not so prominent in cotton as compared to other parameters. Regarding SCA estimates for earliness; many hybrids gave fairly higher estimates, however the top three high scorers were CIM-506 x CRIS-342 (8.11%), CIM-499 x CRIS-191 (7.58%) and FH-1000 x CRIS-342 (7.39%). These results clearly indicated that inbred CRIS-342 is one of the best specific combiner among the pollinator parents.

The GCA variances for the traits like yield, bolls per plant and earliness were higher in lines (females) whereas among the testers/pollinators (males), the GCA variances were larger for lint percentage and fibre length, suggesting that these traits are controlled by additive genes and could successfully be improved through selection from segregating populations. The variances for SCA (line x tester) were also significant for all the traits (Table 3) indicating that dominant genes are also responsible for the expression of these traits hence insinuating the feasibility of hybrid crop development in the present material.

The analysis of variance presented in Table 4 reveal that mean squars of F_1 hybrids for all the traits were significant for further partitioning of this source of variation into other components such as line (estimates the GCA variances of

Table 3. Specific combining ability (SCA) estimates of lines and testers inbred parents for some quantitative traits in upland cotton

F_1 hybrids	Seed cotton yield (g)	Bolls per plant	Lint (%)	Fibre length (mm)	Earliness (%)
CIM-707 x CRIS-134	30.36	7.61	1.25	-0.23	-3.34
CIM-707 x CRIS-342	33.46	9.70	-1.19	-0.24	-3.91
CIM-707 x CRIS-191	-22.55	-5.14	-0.73	0.16	0.86
CIM-707 x CRIS-377	-41.78	-12.14	0.64	-0.15	6.40
CIM-499 x CRIS-134	0.61	0.69	0.19	0.12	0.16
CIM-499 x CRIS-342	28.23	5.73	-0.62	0.16	-10.69
CIM-499 x CRIS-191	-1.05	0.59	0.66	-0.09	7.58
CIM-499 x CRIS-377	-32.79	-6.92	-0.22	-0.20	2.97
CIM-506 x CRIS-134	-8.43	-0.55	-0.23	0.16	4.28
CIM-506 x CRIS-342	-20.44	-5.07	2.80	-0.10	8.11
CIM-506 x CRIS-191	14.41	3.17	-0.79	0.10	-1.64
CIM-506 x CRIS-377	13.30	4.08	1.23	-0.18	-10.73
FH-1000 x CRIS-134	-12.40	-3.56	-0.53	0.54	-1.81
FH-1000 x CRIS-342	-44.52	-12.23	2.71	-0.19	7.39
FH-1000 x CRIS-191	9.19	1.64	-1.21	-0.04	-5.11
FH-1000 x CRIS-377	52.21	14.17	-0.99	-0.30	-0.45
FH-925 x CRIS-134	-13.34	-3.93	-0.13	0.06	3.25
FH-925 x CRIS-342	-7.96	-1.84	-0.15	-0.07	-7.80
FH-925 x CRIS-191	15.76	3.97	1.26	-0.15	5.45
FH-925 x CRIS-377	5.52	1.81	-0.97	0.14	-0.89
VH-142 x CRIS-134	10.41	2.96	0.18	0.10	-2.28
VH-142 x CRIS-342	-20.96	-4.38	-0.39	0.16	3.04
VH-142 x CRIS-191	1.51	0.49	0.52	-0.01	-0.28
VH-142 x CRIS-377	4.02	0.95	-0.33	-0.27	4.53
NB-111/S x CRIS-134	-2.02	-0.18	0.02	-0.54	3.69
NB-111/S x CRIS-342	19.10	4.86	0.20	-0.03	-3.11
NB-111/S x CRIS-191	-10.68	-4.65	0.26	-0.56	-7.36
NB-111/S x CRIS-377	-6.41	-1.99	-0.49	1.06	6.80
BH-147 x CRIS-134	-5.20	-1.43	-0.73	-0.27	-4.48
BH-147 x CRIS-342	11.42	3.28	-0.35	0.27	7.01
BH-147 x CRIS191	-7.11	-2.03	-0.01	0.12	0.51
BH-147 x CRIS-377	0.92	0.19	1.08	-0.14	-4.12
General mean	152.32	40.56	36.43	27.28	74.78
SE (si)	0.417	0.264	0.116	0.100	0.559

SE = Standard error

Table 4. Line x tester analysis: Mean squares for some quantitative traits in upland cotton

Source of variation	Degree of freedom	Mean squares				
		Seed cotton yield (g)	Bolls per plant	Lint percentage	Fibre length (mm)	Earliness (%)
Replication	3	35.413	2.073	0.126	0.102	2.209
F_1 hybrids	31	5404.350*	373.109*	7.043*	3.581*	487.179*
Lines (females)	7	15463.205*	1066.801*	10.827*	6.966*	1304.064*
Testers (males)	3	1529.601*	99.604*	17.534*	16.595*	853.985*
Line x tester	21	2604.934*	180.950*	4.284*	0.593*	162.483*
Pooled error	93	0.696	0.279	0.054	0.040	1.249

* = significant at 1% probability level.

females), testers/pollinators (estimates the GCA variances of males) and lines x testers (estimates SCA variances of males x females) The importance of GCA and SCA variances, hence reflects the importance of additive and dominant gene actions, respectively.

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