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Estimates of Combining Ability and Genetic Parameters for Yield and Fibre Traits in Upland Cotton

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Abstract: Two commercially grown cotton varieties and four advanced strains were crossed in 6×6 diallel mating design, involving F1s only. Study was made on the estimates of general and specific combining ability of the parents and also genetic components of variances for seed cotton yield, lint%, staple length and uniformity ratio. The *per se* hybrid performance generally revealed that parents Karishma and CRIS-134 formed the best hybrids for yield, lint% and uniformity ratio. It is also assumed that parents that perform well in *per se* hybrids will also perform similar for specific combining ability (sca) but this prediction did not hold true without few exceptions. The discrepancy between *per se* hybrid and sca value is not a good indicator to predict parental performance in hybrid combinations. However, hybrids *per se* result generally connoted that parents Karishma and CRIS-134 form good combinations with other parents for hybrid crop production. Specific combining ability estimates further indicated that hybrids NH-26×CRIS-78 for yield, CRIS-134×NH-26 for lint%, NH-26×CRI5-122 for staple length and CRIS-134×NH-26 for uniformity ratio are greatly preferred. Based on general combining ability (gca) estimates, parents NH-26 and CRIS-78 are preferred for yield, Karishma for lint%, CRIS-129 for staple length and CRIS-134 for uniformity ratio. These parents are expected to be improved for above characters through selection in segregating generations. The proportion of variance due to gca (based on the mean squares) is higher than sca for seed cotton yield, lint% and staple length suggested that these traits are predominantly controlled by additive genes whereas variation due to sca for only uniformity ratio is significant suggesting that this trait is entirely controlled by dominant genes. The higher proportion of dominant variance (δ^2D) for uniformity ratio also denoted the similar position as variation due to sca for this trait. The additive genetic variance (δ^2A) for yield, lint% and staple length were quite substantial insinuating the importance of additive genes for these traits.

Key words: Combining ability estimates, genetic variances, upland cotton

Introduction

In quantitative genetic terms, it is in fact the breeding value of an individual that advocates the average performance of its progeny (Falconer, 1989). Breeding value also referred as additive effect is the property of additive genes. On the contrary, dominant genetic variance is the result of interaction of genes within the specific locus also referred as genotypic value of an individual (Falconer, 1989) is important for hybrid vigour, consequently useful for hybrid crop development. The essential idea to consider a set of crosses among the parents is to determine as to what extent the variance among the crosses is attributed statistically to additive genes and what portion is due to dominance and their interactions. In cotton breeding, making huge number of crosses to identify potential parents based on progeny performance seems a chance game. This approach of identifying desirable parents naturally is very tedious and expensive in the sense of labour, time and space. To make large number of crosses also require effective and vigorous selection in the selfing generations. Diallel analysis is one of the mating designs where selected parents are crossed in certain order and is used in predicting combining ability of the parents. The gca, therefore designates additive genes and is used to determine the performance of parents in general terms whereas sca effect is determined by dominant genes and is used to designate the hybrid performance in specific terms. The objective of this study was to identify potential parents for hybridization and selection programmes. Knowing the type of gene actions through gca, sca and genetic variance will also help cotton breeders to formulate an effective

breeding strategy to improve various cotton characters.

Materials and Methods

Six parents that included two commercially grown cotton varieties from Punjab (Karishma and NH-26) and four advanced strains of Sindh (CRIS-129, CRIS-78, CRIS-122 and CRIS-134), developed at Cotton Research Institute, Sakrand, Pakistan were crossed in a diallel mating design. The 6×6 dialled crosses which excluded parents and reciprocals, thus formed 15 cross combinations. The crosses were made in large numbers so as to produce enough F1 seed to be grown in replicated progeny test during 1998. The F1 hybrid seeds of all 15 crosses were planted in a Randomized Complete Block Design arranged in Four replications of four rows each and 40.0 long. To avoid loss of valuable F1 seed, instead of drilling, dibbling with two to three seeds per hole was preferred. Where two to three seedlings germinated were later thinned leaving only one vigorously growing plant per hill with a distance of 2.5' row to row and 9.0" plant to plant. Normal inputs such as fertilizer, insecticide and irrigations were applied whenever required. For taking the observations, twenty five F1 plants from each progeny in each replicate were chosen at random and tagged as index plants. The data on four quantitative traits such as seed cotton yield per plant weighed in grams, lint% calculated as the ratio of lint from seed cotton sample, staple length (fibre length at 50% span length) measured in millimeters and uniformity ratio calculated from 2.5 and 50% span length. The estimates of general combining ability (gca) and specific combining ability (sca) and their variances were

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determined by adopting of Griffing (1956) statistical method-4 used by Singh and Chaudhary (1979) where parents and reciprocals were excluded from the experimental material. The analysis of variance for gca and sca was also calculated through method-4 so as to ascertain the relative importance of additive and dominant gene actions functioning for characters under study.

Results and Discussion

Cotton breeders are well known of the phenomenon that certain crosses form better combinations than the others in transmitting favourable alleles to their offspring. Mating designs that provide appropriate information regarding the potential of parents in both hybrid combinations and segregating generations therefore are very useful to the plant breeders. Diallel analysis as proposed by Sprague and Tatum (1942) is one of such mating designs that distinguishes the ability of the parents to contribute favourable alleles to the progeny.

The mean squares of the crosses (hybrids) for yield, lint%, staple length and uniformity ratio were highly significant that allowed to arbitrate the proportions of genetic variability due general combining ability (gca) and specific combining ability (sca) and also the importance of their effects on each hybrid.

The *per se* hybrid performance of 15 cross combinations for all the characters is presented in Table 1. For seed cotton yield, hybrid CRIS-134 × CRIS-129 produced the maximum yield per plant and the next in the rank was Karishma × CRIS-134. However, without few exceptions, Karishma and CRIS-134 when crossed with other four parents, gave higher yields than the other parents in hybrid combinations. Regarding *per se* hybrid performance for lint%, Karishma with CRIS-78 produced highest lint% of 38.20 and next in the order was Karishma × CRIS-122. In staple length, NH-28 with CRIS-122 developed the longest fibre of 29.75 mm whereas the next ranking was CRIS-129 × CRIS-122. The maximum uniform fibre of 66.10% was recorded by Karishma × NH-28, however, the second high scoring hybrid was CRIS-134 with NH-26. The hybrids' performance *per se* thus suggested that for yield, parents Karishma, CRIS-134 and CRIS-129; and for lint%, parents Karishma, CRIS-122 and CRIS-78; and for staple length, CRIS-122, CRIS-129 and CRIS-78 are parents of the choice. These results further suggested that selection of parents reckon on the preference of the character as none of the parents is simultaneously desirable for all the four traits except Karishma which is worthwhile for yield, lint% and uniformity ratio, based on *per se* hybrid performance.

The mean squares of the crosses (Table 2) for all the four traits were significant that allowed to further partition this factor into the variation due to gca and sca. For seed cotton yield, lint% and staple length, the proportions of variation due gca is higher than sca, suggesting the importance of additive genes functioning for these traits. Nonetheless, genetic variability due sca for seed cotton yield and lint% were also significant, thus further indicating that dominant genes were also responsible for these characters. Ubaidullah and Hussain (1997) also reported the importance of both additive and dominant genes for yield and lint%. For other characters, staple length and uniformity ratio either of the gene action was predominant where for staple length, only gca was significant and for

uniformity ratio, sca was important. Considerable portion of additive and dominant genetic variability (Table 2) for seed cotton yield and lint% however suggested that both the

Table 1: Performance of F1 hybrids for yield and fibre characters in Upland cotton

Crosses	Yield plant (gm)	Lint %	Staple length	Uniformity ratio
Karishma × CRIS-134	185.00	38.75	28.25	48.75
Karishma × NH-26	121.50	35.45	27.25	66.10
Karishma × CRIS-129	142.25	36.95	28.15	63.75
Karishma × CRIS-78	162.00	38.20	25.92	63.33
Karishma × CRIS-122	96.50	37.85	28.72	65.15
CRIS-134 × NH-26	100.75	36.50	27.37	65.57
CRIS-134 × CRIS-129	169.50	32.27	28.65	81.33
CRIS-134 × CRIS-78	130.00	34.80	27.47	63.60
CRIS-134 × CRIS-122	132.20	32.37	28.82	62.85
NH-26 × CRIS-129	76.75	33.57	27.95	58.00
NH-26 × CRIS-78	159.75	37.20	26.95	60.75
NH-26 × CRIS-122	99.50	35.30	29.75	55.83
CRIS-129 × CRIS-78	128.25	35.82	28.55	60.87
CRIS-129 × CRIS-122	126.75	32.85	29.07	58.87
CRIS-78 × CRIS-122	131.25	34.52	27.05	61.50
General Mean	129.93	35.33	27.85	60.91

traits could be improved through hybridization and imposing effective selection in segregating generations and have potential for hybrid crop production also. However, staple length can only be improved through selection whereas uniformity ratio by exploring hybrid vigour. Our results are very much in accordance with the results of Baloch *et al.* (1993, 1995, 1997, 1999). With our courage, we have also attempted to determine the genetic parameters such as additive (δ^2A) and dominance (δ^2D) variances, through the assumptions of no maternal effect, regular diploid segregation, no multiple alleles, random distribution of genes, no epistasis and no linkage effects that all may not have been met because of fewer selected parents under study. The trend regarding the importance of additive and dominance variances as indicated by the genetic variability due to ace for all the traits are very similar except the proportion of δ^2D is greater than δ^2A which is vice-versa in case of variability due to ace for yield only. These genetic components of variances further suggested that yield is controlled by both dominant and additive genes, lint and staple length by additive genes whereas uniformity ratio entirely by dominant genes hence completely agreeing with genetic variability due sca in the analysis of variance Table 2. Ubaidullah and Hussain (1997) however did not find significant genetic variances for any of the traits under our study.

Plant breeders generally predict that parents that perform better in hybrids *per se* will also perform similar for gca and definitely for sca effects. However, this type of prediction did not always remain true as reported by Srinivasan and Gururajan (1973) and Baloch *et al.* (1993, 1995, 1997). The results for gca estimates are presented in Table 3. For seed cotton yield, parent NH-26 scored the maximum, 22.25 gca and next in the rank was CRIS-78 (15.40). Regarding lint%, Karishma scored the highest and for staple length, CRIS-129 was among the top scoring parent. In general, parent CRIS-78 was the good general combiner simultaneously for yield, lint% and uniformity ratio thus, suggesting that this parent retains more additive genes than the others, therefore is more favorable for developing segregating population for selection.

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Table 2: Genetic analysis of yield and fibre characters in upland cotton

Source of variation	Degrees of freedom	Mean squares			
		Seed cotton Yield	Lint%	Staple length	Uniformity ratio
Replication	3	381.02	1.408	1.078	8.312
Crosses	14	3114.48**	15.389**	4.071**	93.819**
GCA	6	1022.46**	7.519**	1.726**	2.974
SCA	9	643.16**	1.807**	0.624	34.830**
Error	42	125.92	0.919	0.569	4.356

** Significant at 1% probability levels

Genetic Component of Variances

σ^2A	189.89	2.856	0.551	-15.928
σ^2D	517.24	0.888	0.055	30.474
σ^2e	126.92	0.919	0.569	4.356

Table 3: General combining ability estimates of yield and fibre characters in upland cotton

Parents	Seed cotton yield/plant	Lint%	Staple length	Uniformity ratio
Karishma	11.15	2.087	-0.737	0.035
CRIS-134	11.95	-1.044	0.281	1.164
NH-26	22.85	0.331	0.006	0.423
CRIS-129	0.09	-1.350	0.781	-0.527
CRIS-78	15.40	0.919	-0.825	1.373
CRIS-122	-15.85	-0.994	0.494	-0.139
General mean	129.93	35.335	27.850	60.91
S.E. (gi)	5.12	0.437	0.344	0.95

Table 4: Specific combining ability estimates of yield and fibre traits in upland Cotton.

Parents	Seed cotton	Lint%	Staple length	Uniformity ratio
Karishma x CRIS-134	11.97	0.327	0.856	-13.032
Karishma x NH-26	3.27	-2.353	0.131	4.730
Karishma x CRIS-129	7.96	0.860	0.256	2.967
Karishma x CRIS-78	5.52	0.465	-0.382	1.005
Karishma x CRIS-122	-28.70	1.377	-0.881	4.342
CRIS-134 x NH-26	-18.28	1.873	-0.762	5.405
CRIS-134 x CRIS-121	27.41	-0.665	-0.325	2.105
CRIS-134 x CRIS-78	-27.28	-0.610	0.170	2.480
CRIS-134 x CRIS-122	6.18	-0.922	0.000	3.042
NH-26 x CRIS-129	31.04	-0.747	-0.687	-0.807
NH-26 x CRIS-78	37.27	0.609	-0.081	-1.952
NH-26 x CRIS-122	8.28	0.622	1.400	-5.370
CRIS-129 x CRIS-78	-17.29	0.921	0.744	-0.882
CRIS-129 x CRIS-122	12.64	-0.341	-0.070	-1.370
CRIS-78 x CRIS-122	1.78	-0.735	-0.469	-0.645
General Mean	129.93	35.335	27.850	60.91
S.E. (si)	8.69	0.74	0.584	0.950

In *per se* hybrid performance (Table 1), parents karishma and CRIS-134 were better parents for yield in particular and other traits in general. It is nevertheless expected that *per se* hybrid performance of parents is correlated with at least sca. This prediction did not always hold true in our case as parents Karishma and CRIS-134 which almost always formed good hybrid combinations *per se* but their sca effects remained generally poor without few exceptions. The sca estimates of NH-26 x CRIS-78 and CRIS-134 x CRIS-122 were the first and second scoring hybrids respectively for yield, CRIS-134 with NH-26 was the highest scoring for lint%, NH-26 x CRIS-122, the highest scoring for staple length whereas CRIS-134 x NH-26

and Karishma x NH-26 the first and next maximum scoring specific combiner hybrids respectively for uniformity ratio. This discrepancy between *per se* hybrid performance and sca estimates is therefore not unusual. Our results are very coinciding with the observations obtained by Baloch *et al.* (1997) who noted that some of the parents perform equally better either in hybrids *per se* or for sca. These findings are also in consonance with the results of Soomro (1989) and Baloch *et al.* (1993, 1995). Specific combining ability estimates thus suggested that dominant gene action is very obvious in the parents for yield and uniformity ratio however, less important for lint% and staple length because without one exception

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in both later traits, sca estimates did not reach even a unit value. Baloch *et al.* (1997, 1999) also noted less importance of lint% and staple length based on gca and sca estimates (Table 4).

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