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NORTH CAROLINA DESIGN - 11 ANALYSIS FOR ESTIMATING GENETIC PARAMETERS IN COTTON *(GOSSYPIUM HIRSUTUM* L.*)*

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Genetic information is very important in formulating effective plant breeding programmes. North Carolina Design - 11 analysis was used to determine general combining ability (GCA), specific combining ability (SCA) and additive and dominant genetic variances for six quantitative traits in Upland cotton. In *per se* hybrid performance, parents CRIS - 241 and CRIS - 121 when crossed with other parents formed higher bolls per plant and produced more yield and lint %. It is usually predicted that *per se* hybrid performance is also reflected to SCA of the parents. This assumption did not always hold true, however, parents CRIS - 241 and CRIS - 121 that were good in *per se* hybrids and in GCA also formed good SCA when crossed with CRIS - 134 and CIM - 448, respectively. These results thus suggested that CRIS - 241 and CRIS - 121 are better parents simultaneously for *per se* hybrids, GCA and SCA. Genetic variation due to males (GCA), females (GCA) and males x females (SCA) were significant for all the traits except females for boll weight which indicated that both additive and dominant genes were important for characters under study. Similar to genetic variation due to GCA and SCA, estimates of additive and dominant genetic variances were also substantial suggesting that these characters can be improved either by hybridization and selection or suitable for hybrid cotton. The proportional contribution of GCA and SCA combining ability variances to total genetic variance further revealed that about equal proportions of additive and dominant genetic variances were available for all the traits except boll weight where additive variance was much higher than dominant variance.

Key words: General and specific combining abilities, Genetic parameters, Cotton.

Introduction

Improvement in metrical characters is usually based on progeny performance. In quantitative genetics, only additive genes determine progeny performance. Dominant genes, on the contrary, are specific to only genotypic value of an individual (Falconer 1989), thus do not contribute to progeny performance. Plant breeders make number of crosses among inbred parents to determine type of gene actions and also proportions of genetic variances attributable to additive and dominant genes for various plant characters. In earlier breeding performances, large number of crosses were also attempted and potential parents based on progeny performance were identified. These approaches of locating potential parents and genes functioning for various plant characters require huge resources in terms of manpower, space and time.

Information on genetic control of plant traits is also important before any breeding strategy is launched. Various mating designs such as diallels (Hayman 1954), Design-1, Design-11 (Comstock & Robinson 1948) and others are being used to estimate general combining ability (GCA) and specific combining ability (SCA) of parents and additive and non-additive genetic variances. The GCA effects are used to characterize the functions of additive genes whereas SCA effects and non-additive genetic variances are considered as the functions of dominant genes. North Carolina Design-11 analysis was used in the present study to estimate GCA and SCA effects and genetic components of variances for various cotton characters.

Materials and Methods

Four female parents that involved all advanced strains developed at the Central Cotton Research Institute, Sakrand, Sindh, Pakistan and four male parents of which two were cotton leaf curl virus (clcv) resistant from Punjab (CIM - 448 and CIM-443), one clcv resistant exotic (LRA - 5166) and one advance strain of CCRI-Sakrand (CRIS - 134) were crossed in North Carolina Design - 11 fashion. Thus, 4 x 4 parents were crossed and 16 F_1 hybrids were developed during 1998 crop season. Enough number of crosses were attempted to produce sufficient quantity of F_1 hybrid seed to be tested in replicated progeny trials. Sixteen F_1 hybrids were planted during 1999 in a Randomized Complete Block Design with four replications. The plot size was 10 x 35 feet, where row-to-row and plant-to-plant distances were kept at 2.5 feet and 9.0 inches, respectively. Thinning was exercised after 25 days of planting for maintaining proper spacing. In-organic fertilizers, 1 bag of DAP per hectare was applied at sowing time whereas 100 kg per hectare of nitrogen was applied in three split doses, 25 kg at sowing time + 25 kg with 2nd irrigation + 50 kg at peak flowering. First irrigation was applied after 35 days of sowing whereas subsequent irrigations were given as and when required. The data on six quantitative traits such as yield per plant weighed in grams, average number of bolls counted on plant basis, average boll weight in grams, lint % calculated as the ratio of lint against cotton seed, fibre length measured in millimeters at 50% span length and seed index as the weight of 100 seeds in grams.

The general combining ability (GCA) and specific combining ability (SCA) effects were calculated by adopting Griffing's (1956) statistical procedures used by Singh and Choudhry (1979). The analysis of variance and genetic components of variances were determined as described by Comstock and Robinson (1948) adopted by Hallauer and Miranda (1986).

Results and Discussion

Genetic information to predict the relative contribution of desirable genes of parents to their offspring is very important in designing effective plant breeding programmes. Mating designs have been very useful in determining genetic control of various cotton characters. Diallel analysis has been used more than any mating designs in cotton breeding for determining general combining ability (GCA) and specific combining ability (SCA) of the parents.

The Design - 11 mating design as described by Comstock and Robinson (1948) is similar to diallel in obtaining genetic information. Two designs, however, are different in that the same parents are used as males and females in diallel, whereas, different sets of parents are used as males and females in design-11. Thus, design-11 uses more parents with small number of crosses as compared to that of diallel. Genetic information obtained from design-11, therefore, can be more reliable than diallel if same resources are to be used.

The *per se* performance of 16 F_1 hybrids for all six characters is shown in Table 1. In general, parents CRIS - 241 and CRIS - 121 when crossed with other parents gave more yield than the other parents in crosses. However, maximum yield of 155.0 gm was produced by the hybrid CRIS - 121 x CIM - 448. The next in the rank was CRIS - 241 x CIM - 443. Hybrids that gave higher yields generally set more bolls per plant but it did not always hold true because of variation in boll size. For instance, hybrids CRIS - 241 x CRIS - 134 which formed the highest number of bolls per plant (55.0) gave only 148.0 gm yield that actually ranked third in order. Boll weight, however, was found to be a contributing factor towards yield in that, as the boll weight increased, yields also increased with even less number of bolls set.

Though, boll weight varied from 2.3 to 3.8 gm, yet the best boll weight was 3.5 gm which gave maximum yield of (155.1 gm). These results thus suggested strong negative correlation between boll weight and number of bolls formed.

The *per se* hybrids' lint % varied from 34.6 to 40.0%, however, maximum lint was obtained from hybrid CRIS - 241 x CIM - 443. The next ginner hybrid was CRIS - 241 x CRIS - 134 that also

Table 1

Per se F_1 hybrid performance for yield, its components and fibre traits in cotton, *Gossypium hirsutum* L.

Hybrids	Yield per plant	Bolls per plant	Boll weight (gm)	Lint (%)	Staple length (mm)	Seed index (gm)
CRIS - 129 x CIM - 448	120.10	34.30	3.50	35.80	28.90	7.30
CRIS - 129 x CIM - 443	113.90	33.50	3.40	36.30	29.30	6.40
CRIS - 129 x LRA - 5166	139.90	37.80	3.70	34.60	30.60	6.90
CRIS - 129 x CRIS - 134	85.80	37.30	2.30	36.10	28.10	5.40
CRIS - 168 x CIM - 448	112.00	28.00	4.00	35.30	29.30	7.70
CRIS - 168 x CIM - 443	115.10	30.30	3.80	35.00	28.90	7.90
CRIS - 168 x LRA - 5166	134.60	40.80	3.30	35.10	26.90	6.10
CRIS - 168 x CRIS - 134	106.60	33.30	3.20	34.70	28.10	6.50
CRIS - 241 x CIM - 448	145.50	42.80	3.40	35.70	28.70	6.20
CRIS - 241 x CIM - 443	154.60	41.80	3.70	40.00	28.70	5.90
CRIS - 241 x LRA - 5166	107.20	33.50	3.20	36.10	27.80	5.80
CRIS - 241 x CRIS - 134	148.50	55.00	2.70	37.40	27.20	5.80
CRIS - 121 x CIM - 448	155.10	44.30	3.50	36.00	29.50	7.30
CRIS - 121 x CIM - 443	142.50	37.50	3.80	36.00	29.50	7.50
CRIS - 121 x LRA - 5166	113.40	37.80	3.00	35.70	29.10	6.10
CRIS - 121 x CRIS - 134	131.60	47.00	2.80	34.70	28.10	6.20
General mean	126.70	38.40	3.30	35.90	28.70	6.60

Table 2

North Carolina Design-11 analysis for yield, its components and fibre traits in cotton, *Gossypium hirsutum* L.

Source of variation	Degrees of freedom	Mean squares					
		Seed cotton yield	Bolls per plant	Boll weight (gm)	Lint (%)	Staple length (mm)	Seed index (gm)
Crosses	15	2066.20**	183.70**	0.77**	6.90**	3.58**	2.45**
Males (GCA)	3	423.40**	167.80**	2.69**	6.32**	5.41*	4.98**
Females (GCA)	3	4468.80**	372.10**	2.35	15.30**	4.87*	3.87**
Males x Females (SCA)	9	1817.60**	126.10**	0.28*	4.30**	2.55*	1.13**
Error	45	12.30	6.60	0.09	0.37	0.25	0.12
Genetic components of variances							
$^{i}d^{2}A$ (males)		347.90	10.408	0.604	0.505	0.716	0.963
$^{i}d^{2}A$ (females)		663.35	61.493	0.019	2.750	0.580	0.685
$^{i}d^{2}D$ (males x females)		1802.37	119.560	0.175	3.925	2.299	1.014
$^{i}d^{2}e$		12.25	6.580	0.099	0.373	0.248	0.116
Proportional contribution of males, females and their interaction to total variance							
Contribution of males (%)		4.10	18.27	69.87	18.32	30.22	40.65
Contribution of females (%)		43.25	40.50	9.09	44.35	27.21	31.59
Contribution of males x females (%)		52.69	41.19	21.82	37.39	42.73	27.67

**,*Significant at 1 and 5% probability levels, respectively.

ranked 3rd in yield (148.5 gm). For staple length, on an average, parents CRIS - 129 and CRIS - 121 when crossed with other parents gave longer fibre. The longest fibre of 30.6 mm however, was given by hybrid CRIS - 129 x LRA - 5166. The next in the rank were; CRIS - 121 x CIM - 448 and CRIS - 21 x CIM - 443, these produced 29.5 mm long fibre. The seed index of *per se* hybrids varied from 5.4 to 7.9 gm where maximum (7.9 gm) index was given by hybrid CRIS - 168 x CIM - 443. The three high yielding hybrids gave index value in the range of 5.8 to 7.9 gm. These results, therefore, indicate that for obtaining higher yields, index value should not exceed to 7.3 gm. Generally, seed index was positively correlated with boll weight, that means, as the boll weight increased, the index value also increased but the number of bolls reduced and as a consequence, yields decreased. The highest seed index (7.9 gm) giving hybrid CRIS - 168 x CIM - 443, however, gave less yield of only 115.1 gm that is even less than the general mean.

The mean squares of crosses (Table 2) for all the six characters were significant that allowed to further partition this factor into variation due to males (GCA), females (GCA) and males x females (SCA) components. The variation due to males, females and males x females were also significant for all the traits except only due to females for boll weight. For yield and number of bolls, the proportion of variance due to females was higher than males suggesting that female parents had more additive genes as compared to male parents. Males x females source of variation for both traits were also siginificant implying the importance of dominant genes for yield and bolls also. But small variation due to males x females compared to their respective males and females further indicated that both additive and dominant genes are functioning for these traits. Nevertheless, additive genes were more important than dominant genes in controlling yield and bolls per plant. Mean squares for boll weight due to females were non-significant but they were significant due to males suggesting that males retained more additive genes against females. Males x females factor for boll weight was also significant indicating the importance of non-additive genes controlling boll weight. Regarding lint %, the mean squares due to males, females and males x females were significant but the proportions of variations due to GCA were higher than SCA implying greater importance of additive genes than non-additive genes in expressing this trait. For staple length, variation due to males, females and males x females were all significant connoting the importance of additive as well as dominant genes for this trait. Baloch *et al* (2002) from line x tester analysis which is analogous to our Design - 11 analysis reported that mean squares due to GCA and SCA were significant implied that both additive and dominant genes were functioning for seed cotton yield, bolls per plant, boll weight, lint percent, and fibre length Table 2.

Baloch *et al* (2000) from diallel analysis also noted the importance of both additive and non-additive genes for seed cotton yield, bolls per plant, lint%, and staple length. In previous studies, Baloch *et al* (1999), however, observed that number of bolls, lint % and staple length were controlled by only additive genes. Additive genes predominantly controlled seed index, nevertheless, dominant genes were also important as reported by Tunio *et al* (2002). Bhutto *et al* (2001), nonetheless, observed that seed index was predominantly controlled by dominant genes.

The estimates of additive and dominant genetic variances were higher than environmental variances (Table 3) suggesting that inferences regarding genetic control of cotton traits in the present study are quite reliable. Similar to mean squares, predictions of additive and dominant genetic components for all the traits were substantial connotating that both additive and dominant genes are responsible for these traits. Results further suggested that all the characters under study could be improved by the selection in segregating generations or suitable for hybrid vigor, consequently, for hybrid crop development.

The proportional contribution of males (GCA), females (GCA) and males x females (SCA) variances to total genetic variance (Table 2) further revealed that about equal proportion of additive and dominant genetic variances is available for all the traits except boll weight. By using line x tester analysis, Baloch *et al* (1999), recorded controversial results where additive genetic variance for lint % was significantly higher than non-additive variance. Ubaidullah and Hussain (1997) however, did not find any significant genetic variance for cotton traits they studied. Genetic models, mating designs and material used in their studies, could explain these controversies.

Plant breeders generally prognosticate that parents, which perform well in hybrids *per se*, also perform similar for GCA and SCA as well. However, this divination did not always hold true (Srinivasan & Gururajan 1973; Baloch *et al* 1993,1995 & 1997). Our results for GCA estimates (Table 3) indicated that parents CRIS - 241 and CRIS - 121, which generally were based in hybrids *per se*, were also good general combiner for seed cotton yield and number of bolls. Surprisingly, both of these parents exhibited negative GCA estimates for boll weight, suggesting that boll weight was negatively correlated with yield and boll numbers. In other words, as the boll weight in-creases above certain point, the number of total bolls per plant drops-off, consequently yield per plant also reduces. In respect to lint %, parent CRIS - 121 formed the maximum GCA (1.400) and the next in the rank was CIM - 443 (0.913). The GCA estimates for staple length and seed index were not prominent, however, parents CIM - 443 and CIM - 448 were good general combiners for these traits and parent CRIS - 129 was good combiner for seed index only. Our GCA estimates, therefore, suggested that parents CRIS - 241 and CRIS - 121 are good general combiner simultaneously for yield, number of bolls and lint % and to improve these characters, the above three parents are good choices for hybridization and selection programmes. On the other hand, for staple length and seed index, parents CIM - 443 and CIM - 448 are desirable parents.

Specific combining ability estimates are presented in Table 4. Though good general combining ability parents, CRIS - 241 and CRIS - 121, were not always good specific combiners for

Table 3

General combining ability estimates for yield, its components and fibre traits in cotton, *Gossypium hirsutum* L.

Males	Yield per plant (gm)	Bolls per plant	Boll weight (gm)	Lint (%)	Staple length (mm)	Seed index (gm)
CIM - 443	- 0.940	- 2.660	0.344	0.913	0.441	0.369
CIM - 448	6.440	- 1.090	0.250	- 0.219	0.434	0.569
LRA - 5166	0.560	- 0.970	- 0.025	- 0.525	- 0.084	- 0.338
CRIS - 134	- 6.060	4.720	- 0.569	- 0.169	- 0.791	- 0.600
General mean	126.700	38.400	3.300	35.900	28.700	6.600
S.E (gi)	0.935	0.641	0.079	0.153	0.124	0.085
Females						
CRIS - 129	- 8.440	- 2.720	- 0.106	- 0.213	0.547	- 0.063
CRIS - 168	- 19.440	- 5.340	0.219	- 0.875	- 0.366	0.506
CRIS - 241	13.500	4.840	- 0.056	1.400	- 0.572	- 0.650
CRIS - 121	14.380	3.220	- 0.056	- 0.313	0.391	0.206
General mean	126.700	38.400	3.300	35.900	28.700	6.600
S.E. (gi)	0.940	0.640	0.079	0.153	0.123	0.085

Table 4

Specific combining ability estimates of yield, its components and fibre traits in cotton, *Gossypium hirsutum* L.

Hybrids	Yield per plant	Bolls per plant	Boll weight (gm)	Lint (%)	Staple length (mm)	Seed index (gm)
CRIS - 129 x CIM - 448	- 10.560	- 0.340	0.019	0.299	- 0.747	0.257
CRIS - 129 x CIM - 443	- 0.690	0.470	- 0.149	- 0.232	- 0.403	- 0.493
CRIS - 129 x LRA - 5166	30.560	3.030	0.469	- 0.569	1.497	0.763
CRIS - 129 x CRIS - 134	- 19.310	- 3.160	- 0.337	0.599	- 0.347	- 0.525
CRIS - 168 x CIM - 448	- 4.310	- 3.970	0.194	0.487	0.566	0.063
CRIS - 168 x CIM - 443	- 8.190	- 0.160	- 0.199	- 0.944	0.185	0.488
CRIS - 168 x LRA - 5166	12.560	- 8.660	- 0.231	0.619	- 1.340	- 0.606
CRIS - 168 x CRIS - 134	- 0.060	- 4.530	0.238	- 0.163	0.591	0.056
CRIS - 241 x CIM - 448	- 9.490	0.590	- 0.106	- 1.388	0.147	- 0.281
CRIS - 241 x CIM - 443	7.380	1.160	0.101	1.806	0.191	- 0.381
CRIS - 241 x LRA - 5166	- 24.130	- 8.780	- 0.031	- 0.681	- 0.234	0.199
CRIS - 241 x CRIS - 134	26.250	7.030	0.038	0.262	- 0.105	0.462
CRIS - 121 x CIM - 448	24.000	3.720	- 0.006	0.599	0.035	- 0.037
CRIS - 121 x CIM - 443	1.500	1.470	0.151	- 0.532	0.029	0.388
CRIS - 121 x LRA - 5166	- 18.990	- 2.910	- 0.206	0.631	0.079	- 0.376
CRIS - 121 x CRIS - 134	- 6.870	0.660	0.063	- 0.701	- 0.140	0.006
General mean	126.700	38.400	3.300	35.900	28.700	6.600
S.E. (Si)	1.750	1.280	0.158	0.305	0.249	0.170

yield with every other parents in crosses, yet both the parents, CRIS - 241 with CRIS - 134 and CRIS - 121 with CIM - 448 formed good SCA estimates. However, hybrid CRIS - 129 x LRA - 5166 formed the best SCA effect of 30.56. In respect of bolls per plant, the above-mentioned hybrids also ranked 2nd and 3rd for SCA estimates. These results thus concluded that some of the parents are simultaneously good in *per se* hybrid performance, GCA and SCA as in our case CRIS - 241 and CRIS - 121 are parents of better choice for hybridization and selection and also for hybrid cotton development.

Baloch *et al* (1997) also noted that some of the parents performed equally well either in *per se* hybrids, GCA or SCA. The high GCA and SCA estimates of some parents for yield, bolls per plant and lint % indicated that both additive and dominant genes are function for these characters.

References

Baloch M J, Bhutto H U, Lakho A R, Tunio G H 1993 Fertility restoration and combining ability studies of R lines crossed onto cytoplasmic male sterile cotton. *Pakphyton* **5** (1 - 4) 147-155.

Baloch M J, Bhutto H U, Rind R, Tunio G H 1995 Combining ability estimates in 5x5 diallel intra-*hirsutum* crosses. *Pak Jour Bot* **27**(1) 121-126.

Baloch M J, Bhutto H U, Lakho A R 1997 Combining ability estimates of highly adapted tester lines crossed with pollinater inbreds of cotton, *Gossypium hirsutum* L. *Pak J Sci Ind Res* **40**(5-12) 95-98.

Baloch M J, Lakho A R, Bhutto H U 1999 Line-tester analysis for estimating genetic components of some quantitative traits in *Gossypium hirsutum* L. *Sindh Balochistan Jour of Plant Sci* **1**(1) 28-34.

Baloch M J, Lakho A R, Bhutto H U, Memon A M, Panhwar G N, Soomro A H 2000 Estimates of combining ability and genetic parameter for yield and fibre traits in upland cotton *Pak Jour Biol Sci* **3**(7) 1183-1186.

Baloch M J, Lakho A R, Bhutto H U, Solangi M Y, Tunio G H 2002. Testcrosses an estimator of combining ability in upland cotton, *Gossypium hirsutum* L. *Sindh Balochistan Jour of Plant Sci* **4**(1) 86-92.

Bhutto H U, Baloch M J, Lakho A R 2001 Heterosis and combining ability estimates in intraspecific and interspecific diallel crosses of upland cotton. *Sindh Balochistan Jour Pl Sci* 3(Suppl.1&2) 78-86.

Comstock R E, Robinson H F 1948 The component of genetic variance in populations of bi-parental progenies and their use in estimating the average degree of dominance. *Biometrics* **4** 254-266.

Falconer D S 1989 *Introduction to Quantitative Genetics*, (3rd ed.). Longman Scientific and Technical Co, UK, pp 117.

Griffing B 1956 Concept of general and specific combining ability in relation to diallel analysis. *Aust Jour Biol Sci* **9** 483-493.

Hallauer A R, Miranda J B 1986 *Quantitative Genetics in Maize Breeding*, (1st ed & 2nd printing). Iowa State University Press, Ames, Iowa. pp 64-72.

Hayman B I 1954 The analysis of variance of diallel tables. *Biometrics* **10** 235-244.

Singh R K, Choudhry B D 1979 *Biometrical Methods in Quantitative Genetic Analysis*, (Revised ed. 1979), Haryana Agriculture University Hissar, India, pp 191-200.

Srinivasan K, Gururajan K N 1973 Heterosis and combining ability in intra-*hirsutum* crosses utilizing male sterile cotton. *Madras Agric Jour* **69** 1545-1549.

Tunio G H, Baloch M J, Lakho A R, Panhwar G N, Chang M S, Solangi M Y 2002 Diallel analysis for estimating combining ability in upland cotton. *Sindh Balochistan Jour Pl Sci* **4**(1) 108-111.

Ubaidullah S, Hussain I 1997 Evaluation of high potential parent for cross breeding American cotton (*Gossypium hirsutum* L.) *The Pak Cottons*, **41**(3&4) 12-22.