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EVALUATION OF GENETIC POTENTIAL OF INTRAHIRSUTUM F_2 POPULATIONS THROUGH LINE × TESTER ANALYSIS

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ABSTRACT

The objectives of research were to estimate the GCA, SCA and heritability for yield and fiber traits in F_2 populations. Four lines were crossed with 4 testers and 16 F_2 populations were obtained for evaluation for determining combining ability and heritability estimates. The trials were laid-out in RCBD with four replications during 2013 and 2014. Combined analysis revealed that genotypes performed differently over the years; however genotype × year interactions were non-significant for majority of the traits. Mean squares for lines and testers were significant, indicating the importance of GCA with additive genes while lines × tester interactions implied the importance of SCA with dominant genes. The lines, Sadori and CIM-573 and testers FH-113 and IR-1524 were good general combiners hence showed their suitability for hybridization and selection programmes. Degree of dominance was higher than unity which suggested the prevalence of dominant genes. The heritability estimates were generally low because of greater portion of dominant variances.

Key words: Combining ability; heritability; upland cotton.

INTRODUCTION

For any crop improvement program, knowledge on the nature of gene action and the inheritance pattern of various cotton traits essential in choosing suitable breeding material and methodologies (Vineela *et al.,* 2013). Identification of valuable inbred parents for successful hybridization programmes or hybrids in the form of higher specific combining ability is very important for launching successful breeding program. Such studies emphasize on the importance of evaluating the inbred lines for their general as well as specific combining ability because many times the higher yielding parents may not necessarily combine their genes very well to provide good segregants. Combining ability analysis is a powerful biometrical tool that discriminates between good and poor combiners hence help plant breeders choose appropriate parental material for their breeding programmes. The Specific combining ability (SCA) is useful for identification of potential hybrids with higher yields and reasonable level of stability (Ashokkumar and Ravikesavan, 2008). Line × tester analysis is one of the mating designs that efficiently evaluates the combining ability of genotypes and also provides information regarding genetic mechanisms controlling polygenic traits. The most desirable tester is the one which provides maximum information on the performance of a line in cross combinations while testers with broad genetic base involve heterogeneous cultivars or hybrids and provides information on GCA only in earlier generation. Several previous researchers like Hassan *et al.* (1999) reported the importance of non-additive type of gene action for different cotton traits while Baloch *et al*. (2000) and Khan *et al.* (2010) stressed upon the appreciable degree of variance attributable to GCA. Makhdoom (2011) observed significant mean squares due to GCA and SCA. However genetic variances for SCA were greater than GCA implying the preponderance of dominant genes controlling bolls per plant, seed cotton yield, ginning outturn% and seed index. It was noted that high × low and low × high and low × low GCA parents performed well in SCA determination (Makhdoom, 2011). Many commercial cotton cultivars despite their high or low agronomic performance, combined in a better or poor way when used as parental cultivars in cross combinations still remains controversial (Makhdoom *et al.,* 2010). Contradicting the findings of above researchers, Rokaya *et al.* (2005) and Soomro (2007) found significant GCA and SCA variances, suggesting the importance of additive as well as dominant genes, nevertheless the ratio of GCA/SCA was greater than unity indicating the preponderance of additive genes involved in the inheritance of seed cotton yield, bolls per plant, boll weight, seed index and lint%.

Genetic variability and heritability estimates for different yield traits are imperative for selection of potential parental lines in cotton breeding programs (Khan *et al.*, 2010). The yield is highly complex character and is directly influenced by various morpho-yield traits. Thus, a thorough knowledge about the genetic potential of different genotypes, inheritance pattern of various traits and the extent of transmissibility of seed cotton yield and other agronomic characters are crucial before launching any successful breeding programs (Ahmad *et al.,* 2008; Makhdoom *et al.,* 2010). It is generally believed that, higher the heritability estimates of given traits, the simpler will be the selection procedure and better will be the response (Baloch, 2004). Substantial genetic variances and higher heritability estimates implied that such characters are controlled by additive genes, thus, could be improved through selection from segregating populations (Baloch, 2004; Khan *et al.,* 2009; Baloch *et al.,* 2014a). The objectives of present research, therefore, were to estimate the potentiality of newly evolved lines and testers in terms of their general combining ability, specific combining ability and heritability from intrahirsutum F_2 populations by using line × tester analysis.

MATERIALS AND METHODS

A trial was conducted at the experimental field of the Department of Plant Breeding and Genetics, Sindh Agriculture University Tandojam, Pakistan. Four female lines CRIS-342, CRIS-134, Sadori and CIM-573 and four testers/pollinators FH-113, IR-1524, MG-06 and AA-802 of upland cotton (*Gossypium hirsutum* L.) were crossed in a line × tester mating design. Thus, 16 F_1 hybrids were developed. The seed of 16 F_2 populations was produced by allowing the F_1 plants to self-pollinate. The seeds of parents and their F_2 populations were sown in a randomized complete block design with four replications during the years 2013 and 2014. Each hybrid and parental lines were sown in four rows each 20 feet long with row to row and plant to plant distance of 75.0 and 45.0 cm, respectively. Sowing was done by dibbling and three seeds per hill were sown to ensure uniform stand; however after 25 days of sowing, seedlings were thinned and only one vigorous plant was allowed to grow. Forty plants per genotype were tagged at random from central rows excluding border plants for recording the data. All the cultural practices were followed according to the recommendations for cotton crop. On ha^{-1} basis, 100 kg P and 150 Kg N were applied. The observations were taken on bolls formed at 90 days after planting, plant height (cm), sympodial branches $plant^{-1}$, bolls $plant^{-1}$, bolls weight (g), seed cotton yield $plant^{-1}$ (g), seed index (100-seed wt. in g), ginning out-turn (%), staple length (mm) and micronaire (µg/inch). The data were statistical analyzed according to Gomez and Gomez (1984) so as to work-out the differences among the genotypes, parents and parents vs F_2 populations; while the genetic parameters such as general combining ability and specific combining ability were calculated according to methods developed by Kempthorne (1957) and adopted by Singh and Choudhry (1979). The additive (σ^2A) and dominance (σ^2D) variances were calculated by considering F=1 as suggested by Singh and Choudhry (1979) while σ^2heritability in narrow sense was determined by the quantitative genetic approach developed by Hallauer and Miranda (1987).

RESULTS AND DISCUSSION

Analysis of variance: The general and specific combining ability variances and their effects and heritability estimates were determined for different yield and fiber traits from a set of line × tester intrahirsutum F_2 populations developed from four female lines CRIS-342, CRIS-134, Sadori and CIM-573 crossed with four male testers FH-113, IR-1524, MG-06, AA-802 of upland cotton (*Gossypium hirsutum* L.) .

Though the experiments were carried-out for two years (2013 and 2014) and the combined analysis was carried-out accordingly, but when the genotype × year interactions were non-significant, then it was decided to average the data over the years and carry out the pooled genetic analysis (Table 1). The pooled analysis of variance indicated that genotypes (parents and their F_2 populations) were significantly different for all the studied traits. The mean squares for F_2 populations were split into lines, testers and line × tester interaction. The mean squares due to lines and testers both determined the general combining ability (GCA) variances which were significant for majority of the traits; however GCA variance of lines for boll weight and that of testers for bolls formed at 90 days after planting and staple length were non-significant. Similarly, the mean squares for lines × tester interactions, which designated specific combining ability (SCA) variance, were also significant for all the traits studied. These results suggested that both additive as well as dominant genes were important for the expression of all the traits. Significant mean squares for lines and testers allowed determining GCA and SCA effects and also the heritability estimates. Similar to our findings, Basal and Turgut (2003), Jatoi *et al.* (2011) and Alkuddsi *et al.* (2013) observed that both additive and dominance variances were important for GCA and SCA for sympodial branches per plant, bolls per plant, seed cotton yield and lint percentage, yet variances due to GCA were higher than SCA indicating greater importance of additive against non-additive genes, especially dominant ones in advocating these traits. Patel *et al.* (2012) estimated preponderance of non-additive genes for seed cotton yield and lint%, while Swamy *et al.* (2013) estimated pre-dominance of additive as well as non-additive genes involved in the inheritance of seed cotton yield and its attributes. Contrary to above findings, Deshpande and Baig (2003) also noted that though GCA and SCA variances were important, yet the magnitude of SCA was higher than GCA indicating the preponderance of dominant genes controlling number of bolls, ginning outturn%, seed index, lint index and seed cotton yield.

Mean performance of parental cultivars and F_2 populations: The performance (Table 2) of sixteen intrahirsutum F_2 populations along with their eight parental lines was evaluated for ten important quantitative characters of cotton. Most of the F_2 populations gave higher mean values against their parents (lines and testers) for all the traits. From lines, CIM-573 formed maximum bolls at 90 days after planting (19.2) and ranked 1st in staple length (29.45 mm). The tester AA-802 measured taller plants (136.7 cm) and IR-1524 recorded highest micronaire value (4.35 µg/inch); FH-113 recorded maximum seed cotton yield plant^{-1} (181.08 g), recorded bigger bolls (3.7 g), higher GOT% (43.60%) and gave more seed index (6.58 g); MG-06 produced maximum sympodial branches plant^{-1} (25.73) and set maximum bolls plant^{-1} (58.93) yet ranked second in seed cotton yield (172.34 g).

From F_2 progenies, Sadori × MG-06 gave tallest plants (136.7 cm) and recorded maximum bolls plant^{-1} (60.06) but gave next maximum seed cotton yield (181.21 g), while CIM-573 × MG-06 measured longer staple length (29.8 mm), ranked next in ginning outturn percentage (43.52%), formed 21.55 bolls at 90 days after planting. The F_2 populations Sadori × FH-113 gave maximum seed cotton yield and ranked1st (198.63 g) in seed cotton yield, yet produced next maximum bolls plant^{-1} (55.11). The hybrid CRIS-342 × AA-802 formed maximum bolls (23.81) at 90 days after planting; Sadori × AA-802 recorded maximum desirable micronaire value (4.42 µg/inch); CRIS-134 × FH-113 formed maximum sympodial branches plant^{-1} (25.18); CRIS-342 × FH-113 weighed maximum boll weight (3.75 g); CRIS-134 × IR-1524 gave highest seed index (6.61 g). Jatoi *et al.* (2010), Shakeel *et al.* (2012) and Alkuddsi *et al.* (2013) also recorded obvious superiority of hybrids over their parents.

General combining ability (GCA) and specific combining ability (SCA) effects: An ideal tester for revealing the GCA effects of entries may fulfill two criteria: 1) it should be representative of all the testers and 2) at the same time, it should be the most discriminating for the genotypes under evaluation (Yan and Kang, 2003; Malla *et al*., 2010). As far as GCA effects of female lines is concerned, Sadori expressed maximum desirable positive GCA effects for bolls formed at 90 days after planting (1.14), bolls per plant (3.04), boll weight (0.18), seed cotton yield per plant (25.28), yet moderately desirable effects for ginning outturn% (1.13). The line CRIS-134 exhibited maximum GCA effects for ginning outturn% (1.64) and negative but desirable GCA for plant height (-0.81), whereas CIM-573 expressed maximum GCA effect for staple length (0.89) and CRIS-342 for seed index (0.26). From the tester parents, FH-113 demonstrated exceptionally higher GCA effects for bolls formed at 90 days after planting (0.68); sympodial branches per plant (1.22); bolls per plant (4.42); boll weight (0.29); staple length (0.09) and seed cotton yield per plant (22.52). Whilst tester MG-06 recorded maximum GCA effects for GOT% (0.99) and IR-1524 for seed index (0.43) and micronaire value (0.22). Previous researchers suggested that *per se* performance of parents must not be taken as granted for their similar performance in GCA effects (Singh *et al*., 2010; Baloch *et al*., 2014b). Our overall results produced the same idea in that, among the four lines and four testers evaluated, only Sadori from lines and FH-113 from testers performed equally well as *per se* and in GCA effects for majority of the traits, particularly for seed cotton yield plant^{-1} (Table 3 and Fig. 1 a). Generally, the GCA effects of lines and testers suggested that if female line Sadori is crossed with tester FH-113, the creation of desirable segregates is expected for most of the important traits from segregating populations; hence these parents with additive genes deserve more attention in crossing and selection programmes as compared to other parents. It seems like out of eight parents evaluated; only two performed well in GCA effects, yet such parents also produced productive crosses. Likewise, Singh *et al.* (2010) reported that most of the hybrids were among the crosses of good × poor, average × poor and poor × poor general combiner parents for seed yield which indicated the involvement of additive, complementary and non-additive gene actions, respectively for such characters. Verma *et al.* (2004) also reported additive and non-additive gene action for such character. High SCA effect of any cross does not necessarily depend upon the GCA effects of the parents involved. The superiority of the cross may be due to complementary gene action, which can be exploited in the subsequent generations. Kalpande *et al.* (2008) carried out line × tester analysis and observed higher positive GCA estimates of some female lines for seed cotton yield per plant and other yield contributing characters. Whereas Kumar *et al.* (2010) noted that among the parents, some exhibited higher GCA estimates for bolls per plant, boll weight, seed cotton yield per plant; number of sympodia; ginning outturn and lint index; yet some were good general combiners for fiber quality traits.

With respect to SCA effects (Table 4), hybrid Sadori × MG-06 recorded maximum SCA estimates for sympodial branches per plant (2.13), bolls per plant (10.97) and seed cotton yield (20.26); hybrid CRIS-134 × FH-113 for staple length (0.61); Sadori × FH-113 for G.O.T% (11.29); CRIS-134 × IR-1524 for seed index (0.44) and CIM-573 × MG-06 for earlier maturity (2.81). Therefore, SCA effects are used in combination with hybrid means and GCA with corresponding parental performance. The cross combination with good mean, favorable SCA effects and at least one parent with significant GCA effects tend to increase favorable alleles (Alkuddsi *et al.*, 2013). Coinciding with this explanation, it is generally believed that *per se* hybrid performance will be reflected in their SCA effects but such assumptions did not always hold true, nonetheless several researchers have identified some hybrids those have performed equally well as *per se* hybrid performance and in SCA effects (Jatoi *et al.*, 2010). If two poor general combiners express higher SCA effects that means dominant genes were involved in the manifestation of SCA effects and when two good general combiners express higher SCA effects that may be attributable to the involvement of additive genes (Ahuja and Dhayal 2007; Singh *et al.*, 2010). From SCA estimates, it was observed that Sadori × MG-06 involved high × low general combiners, CIM-573 × AA-802 and CRIS-134 × IR-1524 involved low × low general combiners. This indicated that higher SCA effects of such hybrids were due to involvement of additive, complementary and dominant genes, respectively, (Figure 1b). These results suggested that above three hybrids may be given priority to improve different traits either through heterosis breeding or selection may be delayed till later segregating generations while giving the opportunity of recombination between desirable genes to occur. Kiani *et al.* (2007) identified some hybrids that were the best specific combiners for seed cotton yield; while Shakeel *et al.* (2012) reported that some hybrids displayed diligent specific combining ability for bolls per plant, seed cotton yield, lint percentage and fiber length.

Variances due to GCA and SCA, proportional contribution of lines, testers and their interactions: The additive variance (σ^2A), dominance variance (σ^2D) and degree of dominance (σ^2 SCA/σ^2GCA)$^{1/2}$ for different traits revealed that variances due to specific combining ability (σ^2 SCA) were higher than the general combining ability (σ^2 GCA) and degree of dominance over unity for all the traits studied suggested the importance of dominant genes controlling them. The ratio of σ^2 SCA/ σ^2GCA is was greater than unity which also confirmed the involvement of dominant genes advocating the expression of traits (Table 5).

The proportional contribution of lines, testers and their interactions from the total variances for different plant traits is given in Figure 2. The results revealed that the lines contributed fair portion of genetic variances for bolls formed at 90 days after planting (22.28%), plant height (43.14%), sympodial branches plant^{-1} (50.66%), staple length (68.43%) and GOT% (49.004%), thus, contributed reasonable amount of variance attributable to maternal effect (Fig. 2). If more lines are found to be giving superior crosses with a tester, then it is possible to initiate multiple crosses among such lines selected for combining ability and this can lead to creation of broad gene pool for recombination and variability and combining ability (Alkuddsi *et al.*, 2013). Similar to our findings, Karademir *et al.* (2009) obtained maximum contribution to total variance by female parents for most of the characters like seed cotton yield, ginning percentage, fiber length, and fiber fineness. Similarly, Basal *et al.* (2009) noted that the maximum contribution to the total genetic variance for seed cotton yield and fiber traits was made by the female parents. The testers/pollinators denoted normal portion of paternal effect over maternal for bolls plant^{-1} (20.83 %), boll weight (27.91%), and micronaire value (29.67%). Line ×tester interactions contributed higher portion of genetic variance as compared to either lines or testers for the traits like bolls formed at 90 days (69.23%), plant height (50.87%), bolls plant^{-1} (57.76%), boll weight (55.23%), seed cotton yield^{-1} (99.34%), seed index (54.73%), and micronaire value (57.66%). Similar to present findings that line × tester interaction took greater portion of variances; Alkuddsi *et al.* (2013) also reported higher contribution of line × tester interaction from total variance for sympodia per plant, seed cotton yield per plant, plant height, bolls per plant and mean boll weight. Contrary to our findings, Shaukat *et al.* (2013) stated that the traits such as fiber length, strength and fineness, showed high proportion of additive type of gene action in F_1 generation because of greater GCA variances over the SCA variance. These variances indicated that the traits studied were under the influence of both maternal and paternal effects with additive and dominant genes.

Heritability estimates: Heritability estimates provide information about genetic variation that is attributable to additive genes and is transferable to next generation (Baloch, 2004). The success of any breeding venture, therefore, depends mainly on the presence of the abundant genetic variability for a trait which is amenable to selection. A lot of work on genetic variability and heritability estimates has already been carried out, yet the differences always existed due to either material and methodology used or environments in which the material is tested (Baloch, 2004; Baloch and Bhutto, 2003). Heritability estimates remained variable depending upon the genetic nature of genotypes and the traits studied. In crop plants, generally, heritability estimates in broad sense are higher than narrow sense because narrow sense heritability uses only additive genetic variance as a numerator over the total phenotypic variance. The heritability estimates in F_2s varied from 0.07 to 8.00% (Table 5). These heritability estimates are lower which is due to higher portion of dominant variance and dominant genes against the additive variances and additive genes influencing quantitative traits. The lower heritability estimates for majority of the traits suggested that selection for such traits may be exercised in later filial generations while giving the opportunity of recombination between desirable genes to occur. Similar to our findings, Lu and Mayer (2011) observed low narrow sense heritability in the range of 0.15 to 0.79 %. They reported heritability for boll weight (0.5%), lint percentage (3.2%), seed index (1.3%), and lint index (0.2%).

Table 1. Combined analysis of variance over the years (2013 and 2014) and pooled genetic analysis from line × tester analysis for various characters in intra-hirsutum F$_2$ populations.

Source of variation	D.F.	Bolls formed at 90 DAP+	Plant height	Sympodial branches plant^{-1}	Bolls plant^{-1}	Boll weight	Staple length	Seed cotton yield plant^{-1}	GOT %	Seed index	Micro-naire value
Replications	3	0.97	2.22	3.4	15.3	0.19	0.26	45.68	0.68	0.017	0.019
Years (Y)	1	5.08*	110.23**	8.23*	85.62*	0.88**	1.66	366.87*	10.45*	0.77**	0.23
Rep / Year	6	1.05	4.37	1.08	12.39	0.06	0.42	55.61	2.45	0.09	0.06
Genotypes (G)	23	20.9**	611.4**	19.4**	127.2**	0.63**	2.03**	2263.20**	23.9**	1.010**	0.59**
G × Y	23	5.61	30.37**	1.44	7.56	0.18	0.44	45.91	0.55	0.28**	0.03
Parents (P)	7	16.5**	910.3**	23.7**	102.9**	0.70**	2.80**	2528.93**	35.14**	1.47**	0.74**
F$_2$ hybrids (H)	15	10.8**	280.06**	17.4**	143.7**	0.53**	1.77**	2290.06**	20.17**	0.76**	0.45**
P vs H	1	202.2**	3488.4**	19.4**	50.7**	1.58**	0.47	0.30	1.60*	1.55**	1.67**
Lines (GCA)	3	11.9*	604.4**	44.01**	155.4**	0.41	6.06**	5098.02**	53.75**	0.73**	0.37**
Testers (GCA)	3	4.5	83.8**	10.7**	151.14**	0.67*	0.09	4403.57**	11.78**	2.07**	0.87**
Line × Tester (SCA)	9	12.3*	237.5**	10.7**	139.7**	0.44*	0.90*	481767.55**	14.72**	0.33**	0.56**
Error	69	3.90	12.9	1.30	6.90	0.17	0.32	47.55	0.45	0.04	0.05

**,* Significant at 1 and 5 % probability levels, respectively, +DAP= days after planting, GOT= Ginning outturn (%)

Table 2. Mean performance of parents and their intrahirsutum F$_2$ hybrids for various yield and fiber traits over two years

Parents	Bolls formed at 90 DAP*	Plant height	Sympodial branches plant^{-1}	Bolls plant^{-1}	Boll weight	Staple length	Seed cotton yield plant^{-1}	GOT %	Seed index	Micronaire Value
Lines										
CRIS-342	16.92	107.1	22.43	51.18	2.69	27.55	138.51	35.46	5.32	3.47
CRIS-134	15.56	127.0	19.31	46.92	2.65	28.11	138.14	42.14	5.56	3.35
Sadori	15.7	99.6	18.5	42.06	2.41	28.25	105.77	38.62	4.70	2.85
CIM-573	19.2	112.5	18.93	50.25	3.4	29.45	167.68	42.12	5.61	3.5
Testers										
FH-113	13.5	107.8	20.12	47.93	3.7	29.35	181.08	43.60	6.58	3.25
IR-1524	12.73	120.3	19.3	47.5	2.85	29.11	129.64	38.01	5.68	4.35
MG-06	14.75	89.7	25.73	58.93	2.87	27.11	172.34	42.81	4.68	3.42
AA-802	14.5	136.7	21.66	54.0	2.83	28.77	154.76	43.05	5.23	3.22
Average	15.36	112.59	20.75	49.84	2.93	84.46	148.49	40.73	5.42	3.43
				F$_2$ Hybrids						
CRIS-342 × FH-113	17.0	129.9	23.31	50.93	3.75	28.2	164.26	38.13	6.26	3.25
CRIS-342 × IR-1524	18.56	133.4	24.3	51.62	2.79	28.5	115.41	38.24	6.33	3.77
CRIS-342 × MG-06	18.0	130.1	22.3	43.18	2.64	27.35	114.9	38.35	5.73	3.62

CRIS-342 × AA-802	23.81	126.4	23.9	55.03	2.56	28.51	147.16	39.12	5.49	3.52
CRIS-134 × FH-113	19.5	123.0	25.18	52.43	3.4	29.25	161.61	42.88	5.74	3.4
CRIS-134 × IR-1524	17.72	116.4	20.82	46.5	2.75	27.97	150.99	41.18	6.61	3.77
CRIS-134 × MG-06	15.0	108.3	20.56	39.15	3.31	28.58	127.78	43.47	5.31	3.7
CRIS-134 × AA802	18.35	117.6	21.66	46.41	3.35	28.44	148.77	42.67	5.30	4.07
Sadori × FH-113	21.37	124.9	23.0	55.11	3.47	28.22	198.63	42.58	5.68	3.35
Sadori × IR-1524	18.56	126.3	21.56	45.25	3.55	28.36	156.56	43.08	6.17	3.97
Sadori × MG-06	19.81	136.7	23.68	60.06	3.05	28.72	181.21	42.24	5.49	3.85
Sadori × AA-802	18.65	124.3	19.13	43.75	3.1	28.15	159.39	40.26	5.17	4.42
CIM-573 × FH- 113	18.67	126.5	20.18	51.18	3.09	29.27	159.04	37.00	5.71	3.65
CIM-573 × IR 1524	17.48	112.0	18.0	39.73	3.13	29.47	122.56	38.43	5.39	4.17
CIM-573 × MG-06	21.55	133.8	19.12	41.92	2.8	29.8	117.61	43.52	5.21	3.82
CIM-573 × AA-802	16.7	136.5	20.53	45.61	3.35	29.62	148.09	43.38	5.47	3.4
Average	18.97	125.70	21.89	47.99	3.17	28.70	148.98	40.97	5.71	3.75
LSD (5%)	2.789	5.058	1.620	3.705	0.584	0.795	9.727	0.951	0.282	0.325

*DAP= days after planting, GOT= Ginning outturn (%)

Table 3. General combining ability estimates from line × tester analysis for various characters of upland cotton over two years

Parents	Bolls formed at 90 DAP*	Plant height	Sympodial branches plant^{-1}	Bolls plant^{-1}	Boll weight	Staple length	Seed cotton yield plant^{-1}	GOT %	Seed index	Micro-naire value
Lines (females)										
CRIS-342	-0.48	4.57	1.75	2.21	-0.10	-0.51	-12.94	-2.45	0.26	-0.16
CRIS-134	-0.81	-9.06	0.35	-1.87	0.07	-0.09	-1.09	1.64	0.05	0.03
Sadori	1.14	2.65	0.14	3.04	0.18	-0.29	25.28	1.13	-0.07	0.10
CIM-573	0.15	1.84	-2.24	-3.38	-0.04	0.89	-11.54	-0.32	-0.25	-0.07
S.E (gi.)	0.87	1.57	0.71	1.02	0.05	0.25	3.02	0.44	0.09	0.10
Testers (males / pollinators)										
FH-113	0.68	0.69	1.22	4.42	0.29	0.09	22.52	-0.76	0.16	-0.029
IR-1524	-0.37	-3.34	-0.53	-2.22	-0.08	-0.08	-11.99	-0.68	0.43	0.22
MG-06	0.14	1.86	-0.29	-1.95	-0.19	-0.04	-13.00	0.99	-0.26	-0.08
AA-802	-0.45	0.79	-0.39	-0.25	-0.03	0.03	2.47	0.45	-0.33	0.151
S.E (gi.)	0.87	1.57	0.71	1.02	0.05	0.25	3.02	0.44	0.09	0.10

*DAP= days after planting, GOT= Ginning outturn (%)

Table 4. Specific combining ability estimates from line × tester analysis for various characters of upland cotton over two years

F_2 hybrids	Bolls formed at 90 DAP*	Plant height	Sympodial branches plant^{-1}	Bolls plant^{-1}	Boll weight	Staple length	Seed cotton yield plant^{-1}	GOT %	Seed index	Micro-naire value
CRIS-342 × FH-113	-1.65	-0.77	-1.36	-3.69	0.52	-0.029	6.30	0.43	0.15	-0.002
CRIS-342 × IR-1524	0.96	-6.83	1.38	3.63	-0.07	0.44	-8.02	0.46	-0.05	0.011
CRIS-342 × MG-06	-0.11	-1.69	0.87	-5.21	-0.11	-0.75	-7.54	-1.101	0.03	0.16
CRIS-342 × AA-802	0.79	-4.37	0.86	5.27	-0.35	0.34	9.26	0.21	-0.13	-0.17
CRIS-134 × FH-113	1.17	5.98	1.91	1.89	-0.09	0.607	-8.19	1.09	-0.16	-0.05
CRIS-134 × IR-1524	0.45	3.43	-0.69	2.59	-0.37	-0.51	15.71	-0.69	0.44	-0.18
CRIS-134 × MG-06	-2.78	-9.87	-1.21	-5.02	0.29	0.19	-6.49	-0.06	0.10	0.043
CRIS-134 × AA-802	1.16	0.45	-0.0031	0.53	0.17	-0.15	-1.02	-0.33	-0.11	0.19
Sadori × FH-113	1.09	-3.83	-0.06	-0.35	-0.13	-0.23	2.16	11.29	-0.1	0.013
Sadori × IR-1524	-0.67	1.57	0.25	-3.57	0.32	0.078	-5.39	1.71	0.11	0.15
Sadori × MG-06	0.07	6.79	2.13	10.97	-0.08	0.39	20.26	0.88	0.12	0.03
Sadori × AA-802	-0.50	-4.54	-2.33	-7.05	-0.11	-0.25	-17.02	-1.108	-0.13	0.37
CIM-573 × FH- 113	-0.61	-1.39	0.49	2.15	-0.29	-0.35	-0.27	-2.82	0.11	0.3
CIM-573 × IR 1524	-0.75	-11.84	2.68	-2.66	0.11	-0.007	-2.29	-1.47	-0.49	0.42
CIM-573 × MG-06	2.81	4.76	-1.55	-0.74	-0.11	0.299	-6.23	1.95	0.02	-0.23
CIM-573 × AA-802	-1.45	8.46	-0.14	1.25	0.28	0.057	8.79	2.35	0.36	-0.39
S.E (si.)	1.73	3.13	1.005	2.04	0.09	0.50	6.04	0.87	0.17	0.20

*DAP= days after planting, GOT= Ginning outturn (%)

Table 3. General combining ability estimates from line × tester analysis for various characters of upland cotton over two years

Parents	Bolls formed at 90 DAP*	Plant height	Sympodial branches plant^{-1}	Bolls plant^{-1}	Boll weight	Staple length	Seed cotton yield plant^{-1}	GOT %	Seed index	Micro-naire value
Lines (females)										
CRIS-342	-0.48	4.57	1.75	2.21	-0.10	-0.51	-12.94	-2.45	0.26	-0.16
CRIS-134	-0.81	-9.06	0.35	-1.87	0.07	-0.09	-1.09	1.64	0.05	0.03
Sadori	1.14	2.65	0.14	3.04	0.18	-0.29	25.28	1.13	-0.07	0.10
CIM-573	0.15	1.84	-2.24	-3.38	-0.04	0.89	-11.54	-0.32	-0.25	-0.07
S.E (gi.)	0.87	1.57	0.71	1.02	0.05	0.25	3.02	0.44	0.09	0.10
Testers (males / pollinators)										
FH-113	0.68	0.69	1.22	4.42	0.29	0.09	22.52	-0.76	0.16	-0.029
IR-1524	-0.37	-3.34	-0.53	-2.22	-0.08	-0.08	-11.99	-0.68	0.43	0.22
MG-06	0.14	1.86	-0.29	-1.95	-0.19	-0.04	-13.00	0.99	-0.26	-0.08
AA-802	-0.45	0.79	-0.39	-0.25	-0.03	0.03	2.47	0.45	-0.33	0.151
S.E (gi.)	0.87	1.57	0.71	1.02	0.05	0.25	3.02	0.44	0.09	0.10

Table 5. Estimates of σ^2 GCA, σ^2 SCA, additive (σ^2 A), dominance (σ^2 D), heritability and degree of dominance (σ^2 SCA/ σ^2 GCA) $^{1/2}$ of inta-hirsutum F_2 populations

Character	σ^2 GCA	σ^2 A	σ^2 SCA	σ^2 D	σ^2 e	Heritability (h^2 ns; %)	(σ^2 SCA / σ^2 CA)$^{1/2}$
Bolls formed at 90 DAP*	0.042	0.084	0.073	0.073	1.513	5.03	1.318
Plant height	1.1104	2.221	71.499	71.499	4.900	2.83	8.024
Sympodial branchesplant $^{-1}$	0.173	0.346	4.813	4.813	0.510	6.11	5.274
Bolls plant^{-1}	0.141	0.282	34.990	34.990	2.089	0.73	15.754
Boll weight	0.001	0.002	0.121	0.121	0.005	1.56	11.018
Staple length	0.027	0.054	5.488	5.488	0.128	0.95	14.260
Seed cotton yield plant^{-1}	4968.924	9937.848	30975.027	30975.027	18.220	0.24	2.495
GOT %	0.188	0.376	6.180	6.180	0.381	5.42	5.730
Seed index	0.011	0.022	0.238	0.238	0.015	8.0	4.650
Micronaire value	0.00059	0.001	1.562	1.562	0.020	0.07	51.450

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