ISSN NO. 2320-5407

Journal homepage: http://www.journalijar.com

INTERNATIONAL JOURNAL OF ADVANCED RESEARCH

RESEARCH ARTICLE

COMBINING ABILITY ANALYSIS IN DIALLEL CROSS OF UPLAND COTTON

Munaiza Baloch

Department of Plant Breeding and Genetics, Sindh Agriculture University, Tandojam, Pakistan

Manuscript Info

Manuscript History:

Received: 29 August 2014
Final Accepted: 26 September 2014
Published Online: October 2014

Key words:

genotypes analysis, upland, cotton

Corresponding Author

Munaiza Baloch

Abstract

Combining Ability (GCA and SCA) was studied in 6 × 6 F_1 diallel crosses of upland cotton during 2009 at Sindh Agriculture University, Tandojam, Pakistan. The breeding material consisted of six *Gossypium hirsutum* genotypes viz: CRIS-134, CRIS-342, Sindh-1, NIAB-78, Sadori and BH-160 and their F_1 diallel hybrids. Highly significant differences were observed among genotypes for all the variables. General combining ability (GCA) mean squares were highly significant for plant height, sympodia plant^{-1} and seedcotton yield plant^{-1} implying the importance of additive gene effects but non-significant for bolls plant^{-1}, boll weight, ginning outturn and staple length. Specific combining ability (SCA) mean squares were highly significant for all the parameters prioritizing hybrid combinations in selection based on their SCA values. Regarding GCA estimates, cultivar CRIS-342 showed positive and highest estimates for all the parameters followed by CRIS-134 which manifested positive estimates also for all the parameters except ginning outturn and staple length. Other four cultivars revealed negative GCA effects for almost all the characters. The highest positive SCA effects were recorded for hybrid CRIS-134 × Sindh-1 and its reciprocal. The SCA estimates in the hybrid combinations were almost higher than their respective reciprocal crosses. Cultivars CRIS-134 and CRIS-342 were found good general combiners due to maximum GCA estimates, hence could further be utilized in future breeding program aimed at improving the studied parameters.

Introduction

In order to select appropriate parents and their hybrids, and to determine the combining abilities of various parents in early generations, diallel analysis has been widely used by plant breeders. Diallel technique was successfully applied to improve self- and cross-pollinated crops (Jinks and Hayman, 1953; Hayman, 1954a and 1954b; Jinks, 1956; Griffing, 1956; Hayman, 1960), which is one of the conventional and powerful approaches used in quantitative genetics to obtain adequate information regarding the inheritance pattern of various quantitative traits. The procedure involves crossing a set of parental lines in all possible combinations, including their reciprocals in order to obtain an estimation of the magnitude of genetic variability ascribable to differences among the parental lines and their hybrids.

The GCA is used to explore the average contribution of a parental line in hybrid combinations (Sprague and Tatum, 1942), while Falconer and Mackay (1996) defined it as the mean performance of the line in all crosses expressed as deviation from the mean of all crosses. The SCA is used to isolate those cases in which certain combinations relatively perform better or worse, than would be expected based on their average performance of lines involved (Sprague and Tatum, 1942). It is roughly the deviation, to a greater/ lesser extent, from the sum of the GCAs of its two parents. SCA consists of dominance and all types of epistatic variances which are also regarded as effects of non-additive gene interactions (Falconer and Mackay, 1996). Relative contribution of GCA and SCA variances to the total phenotypic variance of population is very important in interpreting genetic structure of a breeding population and consequently in deciding the breeding methodology. High estimates of GCA variances indicate predominance of additive gene action, while SCA promising variances reveal predominance of non-additive and dominance gene action. Combining ability analysis of cultivars and their filial populations is thus important to exploit the relevant type of gene action for various traits.

Kiani, *et al* (2007) reported studied combining ability of six cotton cultivars for various traits evaluated in diallel crosses and cultivars. Siokra-324 was the best general combiner for yield, monopodial branches and plant height. Both additive and non-additive components of genetic variances were important for yield and yield related traits. However, non-additive gene effects were observed for earliness and sympodial branches.

Khan, *et al*. (2009) reported that mean squares due to GCA and SCA were significant in F_1 and F_2 generations. Genetic components of variation due to GCA and SCA revealed that most of the traits were controlled by additive gene effects in both the generations because of greater GCA variances. However, seeds per boll and cottonseed oil percentage in F_1 gained preponderance of SCA variances with non additive type of gene action. Ahuja and Dhayal (2007) also advocated improvement of fiber quality traits in line-tester crosses in *G. hirsutum*.

Soomro (2010) mentioned that highest GCA of the parents did not always tend to produce the highest SCA estimates of their hybrids. The diallel generations influenced GCA and SCA estimates for all the traits, however, highest SCA scoring hybrid in the F_1 diallel set, for a particular character and in a particular irrigation treatment, did not necessarily gave the highest SCA in the F_2 diallel set for that corresponding character and in that particular corresponding irrigation treatment. Therefore, the present studies were conducted to explore GCA and SCA estimates in upland cotton under environmental conditions of Tandojam, Sindh, Pakistan.

Material and Methods

The six upland cotton parental cultivars were crossed in a complete diallel fashion during 2008 at Sindh Agriculture University, Tandojam, Pakistan. The crossed seed referred as F_0 generation of all the combinations along with their parental lines was harvested and preserved. During May 2009 six upland cotton genotypes (CRIS-134, CRIS-342, Sindh-1, NIAB-78, Sadori and BH-160) and their 30 F_1 hybrids were sown in a randomized complete block (RCB) design replicated 4 times. All the cultural and agronomic practices were equally performed to minimize the environmental effects. Three seeds were dibbled per hill spaced at 30 cm and the rows were distanced at 75 cm apart. Thinning was performed after 15 to 20 days to have one healthy plant per hill. Three rows with 15 feet length were provided to each entry in each replication. Ten consecutive plants were randomly selected per entry per replication and treated as index plants for recording observations. These ten plants were; four consecutive plants from first row leaving two first plants as border effects; three plants from second row leaving first three plants as border effects and three plants from third row leaving first four plants in that row as border effects.

Data were recorded on seven parameters i.e. plant height, sympodial branches plant^{-1}, bolls plant^{-1}, seed cotton yield plant^{-1}, boll weight, ginning outturn percent, and staple length. All the data were subjected to analysis of variance differences according to Falconer (1989). Analysis was performed using “Statistix” version 8.1.1 (developed in Tallahassee, Florida, USA). Combining ability analysis was carried out according to Griffing (1956) Method-1, based on Eisenhart's Model-II to assess the genetic variances due to GCA and SCA and maternal effects.

Result and Discussion

Results indicated that genotypes showed highly significant differences for all the parameters under study establishing their behavioral differences for respective metrical traits (Table-1). The magnitude of coefficient of variability (C.V.%) was not high implying that the genotypes have developed relatively more adaptability to cope with the changing environments though the manifestation of their phenotypic behavior was there, but may be to lesser extent.

As regards to mean performance of parents and their hybrids (Table-3), CRIS-342 was recorded as the tallest genotype with 129.87 cm plant height followed by CRIS-134 which attained the height of 125.75 cm. The minimum plant height of 107.75 cm was recorded in BH-160, followed by Sindh-1 (111.65 cm). For number of sympodial branches, CRIS-342 produced maximum branches (25.975), followed by Sindh-1 (20.725). Minimum branches (18.025) were recorded in cultivar Sadori followed by NIAB-78 (19.175). Number of bolls plant^{-1} is very important trait and has direct impact on the productivity of any cultivar. Maximum bolls (43.59) were produced by the genotype CRIS-134 followed by CRIS-342 (41.23). Minimum number of bolls plant^{-1} (32.65) was produced by Sindh-1 followed by BH-160 (34.50). For seed cotton yield plant^{-1}, CRIS-342 yielded maximum (138.7 gm) followed by CRIS-134 (135.1 gm). The lowest yielding genotype recorded was Sindh-1 which produced 101.2 gm seed cotton followed by BH-160 (109.4 gm), while maximum boll weight of 3.338 gm was observed in CRIS-342, whereas minimum (3.028 gm) in NIAB-78. In respect of ginning outturn, maximum GOT of 36.22% was recorded from BH-160 followed by CRIS-134 (35.829%). The lowest ginning outturn (34.089%) was observed in NIAB-78 followed by Sadori (35.337%), while longest staple length was measured in CRIS-342 (28.881 mm) followed by CRIS-134 (28.846 mm). The shortest staple length (27.162) was noted in NIAB-78 followed by Sadori which measured 28.241 mm staple length.

Coming to the mean performance of hybrids, it was observed that maximum plant height of 134.35 cm was observed in hybrid CRIS-342 × CRIS-134 followed by its reciprocal which attained the height of 133.25 gm. Lowest plant height (110.70 cm) was noted in hybrid Sindh-1 × Sadori followed by its reciprocal (110.47 cm). For number of sympodial branches plant^{-1}, hybrid BH-160 × CRIS-342 produced maximum branches (24.4) followed by CRIS-342 × CRIS-134 (24.375), while minimum branches (16.4) were produced by the hybrid NIAB-78 × Sadori followed by Sadori × NIAB-78 (16.725). Regarding number of bolls plant^{-1}, maximum bolls (41.39) were produced by the hybrid CRIS-342 × CRIS-134 followed by Sadori × CRIS-342 (41.34), while minimum number of bolls (32.87) was observed in hybrid Sadori × BH-160 followed by its reciprocal (33.13). For seed cotton yield, highest yielding hybrid was CRIS-342 × CRIS-134 producing 146.2 gm yield followed by its reciprocal (145.1 gm). The lowest yielding hybrid was Sadori × BH-160 with 111.4 gm seed cotton yield followed by its reciprocal (113.5 gm). Heavier bolls (3.749 gm) were observed in the hybrid NIAB-78 × CRIS-342 followed by hybrids CRIS-342 × Sindh-1 and CRIS-342 × NIAB-78 (3.676 gm), while minimum boll weight of 3.28 gm was recorded in the hybrids NIAB-78 × BH-160, Sindh-1 × CRIS-134, Sadori × CRIS-342 and Sadori × NIAB-78. For ginning outturn percent, maximum GOT (36.913%) was noted in hybrid CRIS-134 × CRIS-342 followed by NIAB-78 × CRIS-342 (36.683%). The lowest ginning outturn percent of 33.99% was observed in hybrid Sadori × CRIS-134 followed by NIAB-78 × BH-160 (34.417%). Finally, the longest staple length (29.285 mm) was measured by the hybrid CRIS-134 × BH-160 followed by the hybrids CRIS-134 × CRIS-342 and CRIS-134 × Sadori (29.184 mm).

Analysis of variance of combining ability revealed that mean squares for GCA were highly significant ($P \leq 0.01$) for plant height, sympodia plant^{-1} and seed cotton yield plant^{-1}, but were non-significant for bolls plant^{-1}, boll weight, ginning outturn and staple length (Table-2). Significant GCA mean squares variances imply importance of additive gene effects and emphatically suggest selecting parental lines based on their high GCA values for particular character under selection. On the other hand, it has often been reported (Soomro, 2010) that parents with high GCA effects do not necessarily and always produce hybrids with high SCA values and therefore selection of parents should be done after verifying the pedigree record of the particular hybrid, promising combinations may be forwarded in the cultivar development programme. Mean squares of SCA were highly significant ($P \leq 0.01$) for all the parameters under study (Table-2). Similarly, mean squares for reciprocal crosses were also highly significant ($P \leq 0.01$) for bolls plant^{-1}, seed cotton yield plant^{-1}, boll weight, ginning outturn and staple length and non-significant for plant height and sympodia plant^{-1}. Significant mean squares due to SCA of F_1 hybrids and their reciprocals prioritize hybrid combinations in selection based on their SCA values, and after following them for couple of generation selections; these could be finalized for homogeneity through pedigree selection and bulked for cultivar development programme.

The GCA estimates of six parental cultivars for all the traits under study are depicted in Table-4 which revealed that highest and positive GCA estimates for plant height (10.33) were shown by cultivar CRIS-342 followed by CRIS-134 (1.36), while Sadori showed negative and lowest GCA (-3.72) followed by BH-160 (-3.41) for this trait. For sympodial branches, highest positive GCA (3.55) was exhibited by the cultivar CRIS-342 followed by CRIS-134 (1.84), while lowest negative GCA (-1.62) was manifested by Sadori followed by NIAB-78 (-1.02). Regarding bolls plant^{-1} highest positive GCA (2.21) was shown by CRIS-342 followed by CRIS-134 (1.48), while lowest GCA (-1.69) was manifested by BH-160 followed by NIAB-78 (-1.02). In respect of seed cotton yield, highest positive GCA (13.08) was given by cultivar CRIS-342 followed by CRIS-134 (5.34), while lowest GCA (-

5.91) was exhibited by BH-160 followed by NIAB-78 (-4.68). For boll weight, highest positive GCA (0.15) was given by genotype CRIS-342 followed by CRIS-134 (0.01), while lowest GCA (-0.09) was given by Sadori followed by Sindh-1 (-0.04). For ginning outturn, highest GCA (0.32) was shown by cultivar CRIS-342 followed by Sindh-1 (0.19), while lowest GCA (-0.23) was given by Sadori followed by BH-160 (-0.17). For staple length, highest GCA (0.18) was exhibited by CRIS-342 followed by Sindh-1 (0.06), while lowest GCA (-0.13) was manifested by Sadori followed by NIAB-78 (-0.10). Overall, two cultivars mostly CRIS-342 and CRIS-134 exhibited positive GCA for all the parameters, whereas remaining four cultivars showed negative GCA values for almost all the traits under study.

With respect to SCA estimates of the F_1 hybrids including their reciprocals (Table -4), maximum SCA value for plant height was scored by F_1 hybrid CRIS-134 × BH-160 (2.51) followed by F_1 hybrid BH-160 × CRIS-134 giving second highest plant height SCA value (2.39) whereas the lowest SCA value of -4.81 was provided by F_1 hybrid (CRIS-342 × BH-160) followed by its reciprocal BH-160 × CRIS-342 (-4.58). The ten F_1 hybrids manifested positive SCA values and five hybrids revealed negative SCA values for plant height while reciprocals also shown same range of positive/ negative SCA values. For sympodial branches plant^{-1}, F_1 hybrid CRIS-342 × BH-160 scored the maximum SCA effects (1.63) followed by its reciprocal BH-160 × CRIS-342 (1.55), whereas F_1 hybrid Sindh-1 × BH-160 scored the lowest SCA value (-1.40) followed by its reciprocal cross BH-160 x Sindh-1(1.33). Overall, one way hybrids and their reciprocal crosses, respectively gave seven positive values of SCA and eight negative values. For bolls plant^{-1}, F_1 hybrid CRIS-342 × BH-160 gave the highest SCA value of 2.91 followed by second highest value of 2.77 given by its reciprocal F_1 hybrid BH-160 × CRIS-342, whereas the lowest SCA of -3.24 was scored by F_1 hybrid CRIS-134 × BH-160 followed by F_1 hybrid BH-160 × CRIS-134 (-3.09). Nine one-way and reciprocal hybrids, respectively gave positive values of SCA effects while six revealed negative values for boll number. For seed cotton yield plant^{-1}, the F_1 hybrid CRIS-342 × BH-160 exhibited the highest SCA value (8.04) followed by its reciprocal cross BH-160 × CRIS-342 (7.66), whereas F_1 hybrid CRIS-134 × BH-160 ranked with lowest value (-9.07) followed by its reciprocal cross BH-160 × CRIS-134 (-8.64). Out of fifteen each one-way and reciprocal crosses, nine and six F_1 hybrids, respectively provided positive and negative SCA values for seedcotton yield plant^{-1}. For boll weight, maximum SCA value of 0.15 was scored by F_1 hybrid CRIS-342 × NIAB-78 followed by its reciprocal NIAB-78 × CRIS-342 (0.14), whereas the lowest ranking hybrid was CRIS-342 × Sadori (-0.14) followed by its reciprocal cross Sadori × CRIS-342 (-0.13). For boll weight, eight hybrids and their reciprocals individually presented positive SCA values, while seven showed negative SCA estimates. With respect to ginning outturn, hybrid CRIS-342 × NIAB-78 ranked highest with SCA value 0.42 followed by its reciprocal NIAB-78 × CRIS-342 (0.40), whereas NIAB-78 × BH-160 scored lowest SCA value of -0.43 followed by two hybrids simultaneously CRIS-342 × Sindh-1 and BH-160 × NIAB-78 (-0.41). Overall, eight F_1 hybrids and eight reciprocals revealed positive SCA values while seven showed negative SCA values for ginning outturn. In case of staple length, CRIS-134 × Sindh-1 ranked with highest SCA (0.33) followed by its reciprocal Sindh-1 × CRIS-134 (0.31), whereas lowest SCA scoring hybrid was CRIS-342 × Sindh-1 (-0.38) followed by its reciprocal cross Sindh-1 × CRIS-342 (-0.36). Nine hybrids and reciprocals respectively provided positive SCA values while six exhibited negative values. Khan *et al*. (2009) also reported significant mean squares for GCA and SCA and mentioned that most of the traits were controlled by additive gene effects because of greater GCA variances. Ahuja and Dhayal (2007) also advocated improvement of fiber quality traits in line-tester crosses using similar Griffing's procedure in upland cotton.

Table-1: Mean squares for various traits in 6 × 6 F_1 diallel cross of upland cotton.

Character	**Replications DF=03**	**Genotypes DF=35**	**Error**	**C.V.%**
Plant height	146.13	826.37**	4.18	1.80
Sympodial branches	10.806	83.794**	0.53	4.13
Number of bolls plant^{-1}	4.30	263.36**	1.78	4.14
Seedcotton yield plant^{-1}	36.8	4148.7**	14.5	3.66
Boll weight	0.02333	0.35521**	0.00412	1.99

Ginning outturn	0.4060	1.9274**	0.0173	0.38
Staple length	0.5417	0.9026**	0.0103	0.36

**Significant at P<0.01

Table-2: Mean squares due to GCA and SCA for various traits in 6 × 6 F$_1$ diallel cross of upland cotton.

Source of variation	**D.F.**	**Plant height**	**Sympodia plant^{-1}**	**Bolls plant^{-1}**	**Seed-cotton yield plant^{-1}**	**Boll weight**	**Ginning outturn**	**Staple length**
Replications	3	3.63	0.76	2.06	1.95	0.02	0.01	0.03
GCA	5	924.32**	117.80**	73.35^{ns}	1844.64**	0.20^{ns}	1.48^{ns}	0.41^{ns}
SCA	9	61.46**	8.98**	41.51**	240.09**	0.07**	0.77**	0.45**
Reciprocals	15	6.01^{ns}	0.31^{ns}	3.47**	5.25**	0.02**	2.33**	1.58**
Error	87	4.87	0.36	0.68	1.94	0.00	0.02	0.02

**Significant at P<0.01 NS= Non Significant

Table-3: Mean performance of parents and their F$_1$ hybrids for various traits in 6 × 6 F$_1$ diallel cross of upland cotton.

Parents and F$_1$ hybrids	**Plant height (cm)**	**Sympodia plant^{-1}**	**Bolls plant^{-1}**	**Seed cotton yield plant^{-1} (g)**	**Boll weight (g)**	**Ginning outturn (%)**	**Staple length (mm)**
Parents							
CRIS-134	125.75	19.375	43.59	135.1	3.100	35.829	28.846
CRIS-342	129.87	25.975	41.23	139.7	3.388	35.534	28.881
Sindh-1	111.65	20.725	32.65	101.2	3.100	35.304	28.308
NIAB-78	115.42	19.175	36.64	110.9	3.028	34.089	27.162
Sadori	119.60	18.025	36.14	114.6	3.172	35.337	28.241
BH-160	107.75	19.825	34.50	109.4	3.172	36.223	28.274
Hybrids (Direct crosses)							
CRIS-134 × CRIS-342	133.25	24.275	40.25	145.1	3.604	36.913	29.184
CRIS-134 × Sindh-1	119.77	20.550	37.91	129.8	3.424	36.158	29.049
CRIS-134 × NIAB-78	114.07	19.475	37.18	130.0	3.496	36.190	28.544
CRIS-134 × Sadori	114.55	19.750	38.09	127.6	3.352	36.355	29.184
CRIS-134 × BH-160	119.20	19.500	32.66	115.4	3.532	36.355	29.285
CRIS-342 × Sindh-1	127.60	21.675	35.40	130.1	3.676	35.764	29.016
CRIS-342 × NIAB-78	129.00	22.850	35.54	130.6	3.676	35.895	28.780
CRIS-342 × Sadori	125.90	21.050	38.77	134.1	3.460	35.599	28.915
CRIS-342 × BH-160	120.75	24.325	39.90	140.8	3.532	35.599	28.915
Sindh-1 × NIAB-78	113.00	19.000	35.25	116.8	3.316	35.961	28.342
Sindh-1 × Sadori	110.70	18.075	35.04	118.7	3.388	35.698	28.443
Sindh-1 × BH-160	113.27	17.025	35.38	121.0	3.424	35.928	28.544
NIAB-78 × Sadori	115.35	16.400	34.44	116.7	3.388	34.483	27.971
NIAB-78 × BH-160	114.40	18.150	34.47	113.1	3.280	34.417	28.342
Sadori × BH-160	113.65	17.900	32.87	111.4	3.388	35.402	28.207
Hybrids Reciprocal crosses							

CRIS-342 × CRIS-134	134.35	24.375	41.39	146.2	3.532	35.238	28.611
Sindh-1 ×CRIS-134	120.25	21.175	39.94	131.0	3.280	34.975	28.746
NIAB-78 × CRIS-134	115.10	19.575	39.41	130.7	3.316	35.008	27.836
Sadori × CRIS-134	115.55	19.675	35.79	125.1	3.496	33.990	26.960
BH-160 × CRIS-134	119.70	19.125	33.24	116.2	3.496	34.680	27.701
Sindh-1 × CRIS-342	128.32	21.925	34.58	125.9	3.640	35.665	27.769
NIAB-78 × CRIS-342	130.17	22.825	34.75	130.3	3.749	36.683	28.645
Sadori × CRIS-342	126.77	21.825	41.34	135.6	3.280	35.665	28.611
BH-160 × CRIS-342	121.45	24.400	39.77	140.5	3.532	35.698	28.308
NIAB-78 × Sindh-1	113.57	19.775	35.33	117.2	3.316	35.698	28.679
Sadori × Sindh-1	110.47	18.625	35.50	117.7	3.316	35.928	28.814
BH-160 × Sindh-1	113.45	16.975	35.18	120.5	3.424	35.829	28.611
Sadori × NIAB-78	114.40	16.725	35.64	116.9	3.280	35.764	28.645
BH-160 × NIAB-78	114.00	18.150	33.88	114.8	3.388	35.468	28.679
BH-160 × Sadori	112.80	18.125	33.13	113.5	3.424	35.369	28.780

Table-4: General and specific combining ability estimates for various traits in 6 × 6 F_1 diallel cross of upland cotton.

Parents and F_1 hybrids	Plant height	Sympodia plant^{-1}	Bolls plant^{-1}	Seed cotton yield plant^{-1}	Boll weight	Ginning outturn	Staple length
GCA effects							
CRIS-134	1.36	0.08	1.48	5.34	0.01	-0.03	-0.02
CRIS-342	10.33	3.55	2.21	13.08	0.15	0.32	0.18
Sindh-1	-2.44	-0.79	-0.56	-3.20	-0.04	0.19	0.06
NIAB-78	-2.11	-1.02	-1.02	-4.68	-0.03	-0.07	-0.10
Sadori	-3.72	-1.62	-0.43	-4.64	-0.09	-0.23	-0.13
BH-160	-3.41	-0.93	-1.69	-5.91	0.00	-0.17	0.01
SCA effects (Direct crosses)							
CRIS-134 × CRIS-342	0.62	-0.14	0.73	1.76	-0.03	0.17	0.21
CRIS-134 × Sindh-1	2.10	0.74	1.60	2.84	-0.07	-0.20	0.33
CRIS-134 × NIAB-78	-3.65	-0.36	1.43	4.23	-0.02	0.09	-0.21
CRIS-134 × Sadori	-1.58	0.42	-0.52	0.24	0.05	-0.17	-0.31
CRIS-134 × BH-160	2.51	-0.67	-3.24	-9.07	0.06	0.11	-0.02
CRIS-342 × Sindh-1	1.08	-1.08	-3.06	-7.33	0.08	-0.41	-0.38
CRIS-342 × NIAB-78	2.37	0.19	-2.45	-3.41	0.15	0.42	0.10
CRIS-342 × Sadori	0.74	-0.61	1.87	0.94	-0.14	-0.07	0.18
CRIS-342 × BH-160	-4.81	1.63	2.91	8.04	-0.06	-0.11	-0.11
Sindh-1 × NIAB-78	-1.16	1.09	0.47	-0.56	-0.06	0.10	0.03
Sindh-1 × Sadori	-2.24	0.65	-0.15	0.62	0.03	0.25	0.04
Sindh-1 × BH-160	0.22	-1.40	1.14	4.43	0.02	0.25	-0.02
NIAB-78 × Sadori	1.71	-0.91	0.08	0.66	0.00	-0.19	0.01
NIAB-78 × BH-160	0.72	-0.01	0.48	-0.93	-0.08	-0.43	0.07
Sadori × BH-160	1.36	0.45	-1.28	-2.47	0.05	0.18	0.08
SCA effects (Reciprocal crosses)							
CRIS-342 × CRIS-134	0.59	-0.13	0.70	1.68	-0.03	0.16	0.20
Sindh-1 ×CRIS-134	2.00	0.71	1.52	2.71	-0.07	-0.19	0.31
NIAB-78 × CRIS-134	-3.48	-0.34	1.36	4.03	-0.02	0.09	-0.20
Sadori × CRIS-134	-1.51	0.40	-0.50	0.23	0.05	-0.16	-0.30
BH-160 × CRIS-134	2.39	-0.64	-3.09	-8.64	0.06	0.10	-0.02
Sindh-1 × CRIS-342	1.03	-1.03	-2.92	-6.99	0.08	-0.39	-0.36
NIAB-78 × CRIS-342	2.26	0.18	-2.33	-3.25	0.14	0.40	0.10
Sadori × CRIS-342	0.71	-0.58	1.78	0.90	-0.13	-0.07	0.17
BH-160 × CRIS-342	-4.58	1.55	2.77	7.66	-0.06	-0.10	-0.10

NIAB-78 × Sindh-1	-1.11	1.04	0.45	-0.53	-0.06	0.10	0.03
Sadori × Sindh-1	-2.13	0.62	-0.14	0.59	0.03	0.24	0.04
BH-160 × Sindh-1	0.21	-1.33	1.09	4.22	0.02	0.24	-0.02
Sadori × NIAB-78	1.63	-0.87	0.08	0.63	0.00	-0.18	0.01
BH-160 × NIAB-78	0.69	-0.01	0.46	-0.89	-0.08	-0.41	0.07
BH-160 × Sadori	1.30	0.43	-1.22	-2.35	0.05	0.17	0.08

References

Ahuja, S. and S. Dhayal (2007). Combining ability estimates for yield and fiber quality in 4×13 line × tester crosses of *Gossypium hirsutum*, L. Euph., 153: 87-98.

Falconer, D. S (1989). Introduction to quantitative genetics. Longmans Green Scientific and Technical, Harlow, Essex, U.K. pp: xii+438.

Falconer, D. S, and T. F. C., Mackay (1996). Introduction to Quantitative Genetics, 4th Edition. Longmans Green, Harlow, Essex, UK. 464pp.

Griffing, B (1956). Concept of general and specific combining ability in relation to diallel crosses system. Aust. J. Biol. Sci., 9: 463-493.

Hayman B. I (1954a). The analysis of variance of diallel tables. Biometrics. 10: 235-244.

Hayman B. I (1954b). Theory and analysis of diallel crosses-I. Genetics. 39: 789-809.

Hayman, B. I (1960). Theory and analysis of diallel crosses-III. Genetics, 45: 155-172.

Jinks, J. L (1956). The F_2 and backcross generation from a set of diallel crosses. Heredity, 10: 01-30.

Jinks, J. L. and B.I. Hayman (1953). The analysis of diallel cross. Maize Genetics Newsletter, 19: 21-27.

Kiani, G., G. A. Nematzadeh, S. K. Kazemitabar and O. Alishah (2007). Combining ability in cotton cultivars for agronomic traits. Int. J. Agric. Biol., 9 (3): 521-522.

Khan, N. U., G. Hassan, K. B. Marwat, Farhatullah, M. B. Kumbhar, A. Parveen, U. Aiman, M. Z. Khan, and Z. A. Soomro (2009). Diallel analysis of some quantitative traits in *Gossypium hirsutum* L. Pak. J. Bot., 41(6): 3009-3022.

Soomro, M. H (2010). Genetic analysis of drought tolerance in *Gossypium hirsutum* L. Ph.D. dissertation. Deptt. of Botany, Shah Abdul Latif Univ., Khairpur, Pakistan. 317pp .

Sprague, G. F and L. A. Tatum (1942). General *versus* specific combining ability in single crosses of corn. J. Am. Soc. Agron., 34: 923-952.