

## DIALLEL ANALYSIS IN UPLAND COTTON OVER THE ENVIRONMENTS FOR YIELD, EARLINESS, FIBER QUALITY TRAITS AND COTTON LEAF CURL VIRUS

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### ABSTRACT

A combining ability study conducted to evaluate 10 parents and 45 hybrids at two locations in Sindh province of Pakistan during 2017 revealed that general combining ability (GCA) variance was higher than specific combining ability (SCA) with greater than unity ratio for all the traits, indicating the role of additive gene action for inheritance of traits. Selection could therefore be performed in early segregating generation. Among the parents, CRIS-129 and Baghdadi were found good general combiners for yield and its components, CIM-602 for lint index, GOT and earliness. USD16-3058, NIAB-824 and FH-142 contributed for staple length, micronaire value and fiber strength, respectively. MAC-7 showing a significant positive GCA effects for healthy plant percentage and a negative effect for diseased plant percentage was measured as resistant against cotton leaf curl virus (CLCV). Genotypes expressing maximum positive GCA effects for different traits could be preferred for selection and utilization in breeding program. Based on SCA effects, cross MNH-886 x Baghdadi was the best specific combiner for plant height, seed and lint indices and staple length, MNH-886 x CIM-602 for bolls plant<sup>-1</sup> and bolls open at 90 DAP. FH-142 x CEMB-33 for boll weight, CRIS-129 x NIAB-824 for seed cotton yield plant<sup>-1</sup>, and CRIS-129 x MNH-886 for days to 1<sup>st</sup> flower, bolls formed at 120 DAP and uniformity index. The hybrids NIA-Noori x CIM-602, Baghdadi x CIM-602, NIA-Noori x USD16-3058, MNH-886 x FH-142 that gave significant positive SCA effects for the bolls formed at 90 DAP, bolls open at 120 DAP, micronaire value and fiber strength are suggested for hybrid development programs.

**Keywords:** Cotton, Diallel analysis, gene action, combining ability, environment, cotton leaf curl virus

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### INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is one of the important cash crops of Pakistan that plays a significant role in the national economy. Country's economic development depends upon the production of cotton and the related textile sector. The cotton crop is cultivated over an area of 2214.95 thousand hectares in Pakistan. The annual production of cotton in Pakistan is 10671 thousand bales with an average yield of 819 kg hectare<sup>-1</sup> (Anon., 2013). The country is largest exporter of raw cotton and cotton yarn. The cotton crop particularly grown for source of fiber, whereas other byproduct the seed cotton is important for its edible oil.

Cotton leaf curl virus (CLCV) is an important disease transmitted by whitefly and considered as major threat to the production of cotton in the country (Ahmad *et al.* 2010). Around 2.3 million bales were affected due to cotton leaf curl virus incident reported in the country (Anon., 2013).

Keeping in view the significant role of cotton in economy, the breeders are making efforts to improve genetic pattern of cotton crop by exploiting available genetic resources to evolve cotton varieties with high yielding, early maturing, cotton leaf curl virus resistance and better fiber traits. Diallel is one of the methods that is usually applied for assessing the additive and non-additive gene action of the parents; it facilitates in selecting appropriate parents for the utilization in hybridization and selection program to maintain the desirable traits. The general combining ability (GCA) in the average performance of strains in a series of crosses assessed by additive gene action, whereas specific combining ability (SCA) is the performance of parents in specific cross combinations measured by non-additive gene action (Sprague and Tatum, 1942). Dhamayanthi and Rathivanvel (2017) and Swetha *et al.* (2018) observed highly significant GCA and SCA variance for yield, its components and fiber traits in cotton and suggested the role of additive and non-additive gene effects for inheritance of these traits.

The purpose of this study was to estimate the gene action and nature of legacy for seed cotton yield, its components, fiber traits and cotton leaf curl virus disease percentage through evaluation of general and specific combining ability (GCA & SCA) of the parents and F<sub>1</sub> hybrids which can be exploited in future breeding program.

## MATERIALS AND METHODS

The present research was conducted to evaluate the genetic potential through combining ability of parents and  $F_1$  hybrids. Forty five  $F_1$  hybrids were produced through crossing 10 genotypes *viz.*, CRIS-129, MNH-886, FH-142, NIA-Noori, Baghdadi, CIM-602, NIAB-824, CEMB-33, MAC-7 and USD16-3058. The seed of parents and  $F_1$  hybrids were sown during the Kharif season 2017 in randomized complete block design with three replications at two locations *viz.*, Sakrand and Mirpurkhas in the province of Sindh, Pakistan. A 60 square feet plot was arranged for each treatment. The inputs i.e. di-ammonium phosphate (DAP) and nitrogen (Urea) fertilizers were applied @ 57 kg and 170 kg hectare<sup>-1</sup>, respectively. However, the plant protection measures i.e. nitenpyram 250mL and imidachlopride 125mL acre<sup>-1</sup> were applied for the control of jassids and thrips. At maturity, five plants from each replication were tagged for the collection of data on plant height (cm), number of sympodial branches, bolls plant<sup>-1</sup>, boll weight (g), seed index (g), lint index (g), seed cotton yield plant<sup>-1</sup> (g), ginning outturn (GOT %), days to first flower, bolls formed at 90 and 120 days after planting, bolls opened at 90 and 120 days after planting, staple length (mm), micronaire value ( $\mu\text{g inch}^{-1}$ ), fiber strength (g tex<sup>-1</sup>), uniformity index (%) and percentage of plants affected by cotton leaf curl virus (CLCV) disease by using disease rating scale suggested by Akhtar *et al.* (2010) and Farooq *et al.* (2011).

The data of both the locations were combined and employed for analysis of variance (ANOVA). The LSD (least significance difference) was examined for mean separation. The general combining ability and specific combining ability were estimated according to Diallel Method-II described by Griffing (1956) by using the statistical software Plant Breeding Tool 1.4 and Statistix 8.1.

## RESULTS AND DISCUSSION

The combined analysis of variance (ANOVA) showed a significant effect of environments for all the characters except boll weight, lint index, GOT, days to 1<sup>st</sup> flower, bolls opened at 90 days after planting and micronaire value (Table 1) that suggests that the genotypes have potential to perform in multi-environments. The results of parents and hybrids performance were highly significant for all the characters. The mean square due to genotypes was found highly significant in combined environments which suggests that enough genetic diversity and variability is present in the breeding material. Hence, the later analysis for interaction of parents, hybrids and genotypes with the environment was significant for all the characters studied. The analysis of variance mean squares of general combining ability (GCA) and specific combining ability (SCA) were highly significant for the all characters that indicates the involvement of additive and non-additive gene action for controlling these traits, whereas the interaction of environment with GCA and SCA was also significant for all the traits. The significant differences were also observed for GCA x environment and SCA x environment for all the characters which shows that both the GCA and SCA effects diverged in environments. Thus, the selection of genotypes (parents and hybrids) should be according to environments (Table 1). These findings are in accordance with Khan (2013), Sorour *et al.* (2013), Khan *et al.* (2017), Reddy *et al.* (2017), Patil *et al.* (2018) and Swetha *et al.* (2018) who found significant differences in GCA and SCA effects, GCA x environments and SCA x environments for various traits. Kumar *et al.* (2017) reported higher GCA significant effects than SCA for yield and its component traits.

The genetic variance for yield and its components, earliness and fiber traits are presented in Table 2. The GCA variance was found greater than the SCA variance for all the traits except fiber strength, which specifies the role of additive gene action. The proportion of gca/sca variance was more than unity that excelled the preponderance of additive gene action which is fixable and selection in early generation can be executed. The SCA variance was higher than the GCA whereas gca/sca variance unity ratio was less than zero indicating the role of non-additive gene action for inheritance of fiber strength only. The heritability was analyzed in combined environments, the broad sense heritability was found higher from the narrow sense heritability. The range of broad sense heritability ranged from 48-87% for all the characters studied. The present findings are in accordance with Kumar *et al.* (2017) who reported higher GCA variance than the SCA and greater than zero unity ratio for the traits *viz.*, seed cotton yield, boll weight, number of sympodial branches, bolls plant<sup>-1</sup>, ginning outturn, seed index and lint index. Swetha *et al.* (2018) found higher GCA variance for plant height, ginning outturn, seed index, lint index, sympodial branches, fiber length and micronaire value with grater ratio of unity.

Table 1. Analysis of variance (ANOVA) mean square values of various traits studied.

Source of Variation	D.F	PH	NOSB	BPP	BW	SI	LI	SCYPP	GOT	DFE	BF-90 DAP
Replications (R)	2	286.31	0.273	0.553	0.0147	0.2787	0.1414	27.78	0.6707	17.903	51.092
Environments (E)	1	1971.53*	213.93***	358.59***	0.0175 <sup>ns</sup>	11.2019***	0.0068 <sup>ns</sup>	4226.54**	0.6110 <sup>ns</sup>	0.7280 <sup>ns</sup>	244.068*
Parents (P)	9	1568.71**	42.12**	543.34***	1.7437**	7.9236**	2.3174**	2743.51**	30.4638**	109.109**	67.0127**
Crosses (C)	44	2821.47**	158.51**	2821.47**	2.4617**	14.7762**	3.0093**	5832.43**	53.1415**	105.172**	84.824**
Genotypes (G)	54	2891.19**	152.77**	778.79**	2.3706**	13.3793**	2.9455**	5250.86**	49.2065**	112.4232**	81.5399**
GCA	9	1257441**	765.31**	3622.95**	11.4334**	61.3883**	13.5684**	2567.97**	217.332**	530.864**	405.094**
SCA	44	954.55**	30.26**	209.96**	0.5580**	3.7775**	0.8209**	1247.44**	15.5814**	28.7349**	16.8291**
P x E	9	239.23*	10.61**	161.85**	0.09711 <sup>ns</sup>	0.2308 <sup>ns</sup>	0.1626 <sup>ns</sup>	945.33**	5.4278**	7.764 <sup>ns</sup>	21.2737**
C x E	44	415.16**	8.04**	99.44**	0.0529 <sup>ns</sup>	1.0786**	0.2894**	530.68**	6.8559**	9.927**	9.750*
G x E	54	379.44**	12.37**	110.71**	0.1292*	0.9221**	0.2630**	595.93**	6.4912**	9.4035**	11.7390**
GCA x E	9	456.83**	18.28**	168.41**	0.2857**	1.0864**	0.2694*	1437.35**	11.99**	16.6476**	34.8230**
SCA x E	44	363.96**	11.19**	99.16**	0.0979 <sup>ns</sup>	0.8892**	0.2617**	427.64**	5.16**	7.9546**	7.1222 <sup>ns</sup>
Error	216	73.12	1.20	16.05	0.1054	0.3896	0.1290	142.98	1.0310	3.0930	6.4002

Table 1. Continue

Source of Variation	D.F	BF-120 DAP	BO-90 DAP	BO-120 DAP	SL	MV	FS	UI	CLCV	DP%	HP%
Replications (R)	2	73.754	4.3064	21.761	0.6478	3.2202	0.6503	1.2323	243.53	243.87	
Environments (E)	1	774.947**	5.2694 <sup>ns</sup>	244.240**	9.1334*	0.0019 <sup>ns</sup>	82.1005**	34.5644**	1753.529*	1752.146*	
Parents (P)	9	236.870**	3.2965**	84.523**	20.0693**	1.2509**	29.1752**	36.0013**	3561.40**	3561.29**	
Crosses (C)	44	312.754**	3.2751**	126.581**	19.0311**	0.8918**	43.4321**	18.5731**	5072.76**	5073.14**	
Genotypes (G)	54	294.543**	3.2183**	117.151**	18.8553**	0.9393**	40.5428**	21.8627**	4822.899**	4823.176**	
GCA	9	1420.353**	15.7478*	555.643**	89.3824**	3.8162**	155.254**	90.2313**	84.10**	84.07**	
SCA	44	69.3819**	0.7124*	29.4528**	4.7498**	0.3639**	17.6005**	8.1709**	190.12**	190.04**	
P x E	9	69.744**	1.06785*	29.4834**	0.8763 <sup>ns</sup>	0.1719 <sup>ns</sup>	3.6701**	4.9337**	171.394**	171.330**	
C x E	44	41.069**	0.6038 <sup>ns</sup>	18.538**	1.1619 <sup>ns</sup>	0.1505 <sup>ns</sup>	3.3790**	3.3130**	25536.970**	25537.840**	
G x E	54	45.0924**	0.6760 <sup>ns</sup>	20.0193**	1.0943 <sup>ns</sup>	0.1514 <sup>ns</sup>	3.3810**	3.5255**	680.084**	680.242**	
GCA x E	9	117.336**	2.0349**	64.4479**	1.1914 <sup>ns</sup>	0.3256 <sup>ns</sup>	2.9777**	6.4794**	144.351**	144.406	
SCA x E	44	30.6435**	0.4042 <sup>ns</sup>	11.136**	1.0749 <sup>ns</sup>	0.1166 <sup>ns</sup>	3.4627**	2.9347**	176.803**	176.714**	
Error	216	15.1670	0.8439	6.9081	0.8375	0.2029	1.5901	1.6854	67.335	67.330	

\*, \*\* significant at 5% and 1% level respectively; PH-Plant Height, NOSB-Number of sympodial branches, BPP-Bolls Plant<sup>-1</sup>, BW-Boll Weight, SL-Seed Index, LI-Lint Index, SCYPP-Seed-cotton Yield Plant<sup>-1</sup>, GOT-Ginning Output, DFE-Days to 1<sup>st</sup> Flower, BF-Boll Formed, DAP-Days After Planting, BO-Boll Opened, SL-Straple Length, MV-Micronaire value, FS-Fiber Strength, UI-Uniformity Index, CLCV-Cotton Leaf Curl Virus, DP-Disease plant and HP-Healthy Plant

Table 2. Estimation of genetic variance components of the traits studied.

Source of Variation	$\sigma^2$ GCA	$\sigma^2$ SCA	$\sigma^2$ A	$\sigma^2$ D	$h^2$	$H^2$	$\sigma^2_{gca}/\sigma^2_{sca}$
Plant height	160.10	98.43	640.39	393.72	0.43	0.69	1.63
No. of sympodial branches	10.11	3.17	40.44	12.72	0.59	0.79	3.19
Bolls plant <sup>-1</sup>	46.44	18.46	185.70	110.81	0.47	0.65	2.52
Boll weight	0.15	0.08	0.59	0.31	0.57	0.87	1.93
Seed index	0.80	0.48	3.19	1.93	0.51	0.82	1.66
Lint index	0.18	0.09	0.71	0.37	0.51	0.77	1.90
Seed cotton yield plant <sup>-1</sup>	319.59	136.26	1278.37	546.53	0.51	0.74	2.35
Ginning outturn	2.70	1.71	10.82	6.84	0.42	0.70	1.58
Days to first flower	6.85	3.46	27.41	13.85	0.52	0.79	1.98
Bolls formed at 90 DAP	5.01	1.62	20.03	3.08	0.54	0.71	3.10
Bolls formed at 120 DAP	17.56	6.46	70.24	9.63	0.49	0.67	2.72
Bolls opened at 90 DAP	0.19	0.05	0.74	0.21	0.37	0.48	3.62
Bolls opened at 120 DAP	6.57	3.05	26.27	5.92	0.46	0.67	2.15
Staple length	1.17	0.61	4.70	2.45	0.56	0.85	1.92
Micronaire value	0.05	0.04	0.18	0.16	0.31	0.60	1.09
Fiber strength	1.92	2.36	7.67	9.43	0.36	0.80	0.81
Uniformity index	1.09	0.87	4.37	3.49	0.37	0.67	1.25
CLCV DP%	345.685	83.880	1382.741	335.520	71%	88%	4.12
CLCV HP%	345.693	83.921	1382.772	335.685	71%	88%	4.12

The general combining ability (GCA) is presented as the average performance of lines in a series of crosses, the GCA effects of combined environments of the parents are presented in Table 3. The parent MNH-886 exhibited significant positive GCA effects for plant height and uniformity index. The CEMB-33 showed significant positive effect for Sympodial branches plant<sup>-1</sup>. The CRIS-129 gave significant effect for bolls plant<sup>-1</sup> and maximum bolls formed at 120 DAP. The Baghdadi also excelled significant positive GCA effect for boll weight, seed index and seed cotton yield plant<sup>-1</sup>. Among the parents, CIM-602 performed extremely well for lint index, GOT and earliness traits which manifested it a good general combiner and showed significant positive GCA effects for lint index, GOT, days to 1<sup>st</sup> flower, bolls formed at 90 DAP and bolls opened at 90 and 120 DAP. USD16-3058 was found good general combiner for staple length, NIAB-824 for micronaire value and FH-142 for fiber strength.

The study suggested that the parents which exhibited maximum positive significant GCA effects for various traits i.e. yield, its components, earliness and fiber characteristics could be utilized in cotton improvement program. The genotypes CRIS-129 and Baghdadi have the potential for bolls plant<sup>-1</sup>, boll weight, seed index and seed cotton yield plant<sup>-1</sup>. CIM-602 proved to be a good general combiner for lint index, GOT and earliness traits. The positive GCA effects showed by USD16-3058, NIAB-824 and FH-142 for staple length, micronaire value and fiber strength over both the environments that may be attributed to additive gene action and was fixable. It would suggest that crossing of these parents will probably improve these traits. Similar results were obtained by Sorour *et al.* (2013), Reddy *et al.* (2017), Parkash *et al.* (2018) and Patil *et al.* (2018) who reported that genotypes found to be good general combiner with positive GCA effects for various traits could be exploited in hybridization program. Choudhary *et al.* (2016), Khan *et al.* (2017) and Vekariyal *et al.* (2017) also found positive GCA effects of various traits and suggested that high GCA for yield, its components, and earliness and fiber traits may possess considerable genes for these characters and can be used extensively in breeding program.

Specific combining ability (SCA) effects will generally help the cotton breeders to explore best cross combinations during hybrid production. The combined SCA effects of hybrids over the environments are depicted in Table 4 which revealed that among the 45 cross combinations, top three hybrids MNH-886 x Baghdadi, Baghdadi x NIAB-824 and CRIS-129 x FH-142 showed highest significant positive SCA effect for plant height in descending order.

Similarly, the highest significant positive SCA in descending order were shown the hybrids NIA-Noori x CEMB-33, MNH-886 x Baghdadi and CRIS-129 x FH-142 for sympodial branches plant<sup>-1</sup>, by MNH-886 x CIM-602, FH-142 x NIA-Noori and CRIS-129 x NIAB-824 for bolls plant<sup>-1</sup>. The best specific combiners for the boll weight were FH-142 x CEMB-33, FH-142 x Baghdadi and MNH-886 x Baghdadi. The crosses MNH-886 x Baghdadi, Baghdadi x CEMB-33 and CRIS-129 x CEMB-33 were reliable for seed index. The highest SCA effect for lint index was observed in cross MNH-886 x Baghdadi followed by CRIS-129 x CEMB-33 and CRIS-129 x CIM-602, respectively. The hybrids which manifested utmost significant positive SCA effects for seed cotton yield were CRIS-129 x NIAB-824, MNH-886 x FH-142 and Baghdadi x CIM-602, respectively.

Table 3. General Combining Ability (GCA) effects of 10 parents under two environments.

Parents	PH	NOSB	BPP	BW	SI	LI	SCY	GOT	DFB
CRIS-129	4.76**	1.63**	5.62**	-0.09*	0.14*	0.03	13.20**	0.15	1.54**
MNH-886	10.45**	1.26**	4.23**	0.15**	0.32**	0.20**	10.01**	0.40**	1.72**
FH-142	8.05**	1.35**	2.33**	0.31**	0.94**	0.25**	9.01**	0.78**	1.60**
NIA-Noori	2.39**	0.11	1.67**	-0.25**	-0.88**	-0.16**	-4.68**	0.91**	-0.32
Baghdadi	5.23**	2.22**	1.54**	0.48**	1.11**	0.32**	14.37**	0.65**	0.37
CIM-602	2.01*	1.10**	5.46**	-0.11**	-0.21**	0.41**	9.98**	1.54**	2.80**
NIAB-824	8.66**	1.68**	4.77**	-0.07*	0.15*	0.14**	10.83**	1.47**	1.38**
CEMB-33	7.54**	2.75**	0.41	0.39**	0.82**	0.20**	5.01**	0.44**	0.65**
MAC-7	-24.74**	-5.93**	-12.29**	-0.92**	-1.92**	-1.07**	-38.33**	-3.55**	-5.40**
USD16-3058	-24.37**	-6.16**	-13.75**	0.11**	-0.47**	-0.30**	-29.39**	-2.79**	-4.34**
S.E (gi.)	0.96	0.15	0.45	0.04	0.07	0.04	1.43	0.11	0.20
CD @5%	2.81	0.45	1.31	0.11	0.20	0.12	3.32	0.33	0.57

\*, \*\* significant at 5% and 1% level, respectively

Table 3. Continue.

Parents	BF90	BF120	BO90	BO120	SL	MV	FS	UI	CLCV	
									DP%	HP%
CRIS-129	1.79**	4.31**	0.05	2.06**	-0.37**	-0.21**	-1.20**	0.02	1.74	-1.74
MNH-886	1.94**	2.44**	0.21*	1.33**	0.70**	0.05	0.55**	0.77**	3.53**	-3.53**
FH-142	0.80**	2.06**	0.28**	1.86**	0.44**	0.16**	1.38**	0.28	-1.08	1.08
NIA-Noori	0.18	-1.16**	0.15	-0.40	-0.17	0.05	0.41**	0.24	6.27**	-6.27**
Baghdadi	0.32	1.66**	0.20	1.38**	0.43**	0.09	0.54**	0.41**	1.66	-1.66
CIM-602	2.69**	4.13**	0.55**	2.54**	-0.03	0.18**	-0.01	0.41**	5.77**	-5.77**
NIAB-824	0.93**	1.32**	0.22*	0.87**	0.38**	0.24**	0.59**	0.61**	4.47**	-4.47**
CEMB-33	-0.33	0.89*	0.03	0.40	0.54**	0.04	0.41**	0.52**	2.96**	-2.96**
MAC-7	-4.06**	-6.69**	-0.84**	-4.84**	-2.94**	-0.55**	-3.71**	-3.09**	-49.74**	49.74**
USD16-3058	-4.27**	-8.96**	-0.85**	-5.21**	1.03**	-0.05	1.02**	-0.17	24.42**	-24.42**
S.E (gi.)	0.25	0.44	0.10	0.29	0.10	0.05	0.14	0.16	0.91	0.91
CD @5%	0.83	1.28	0.30	0.86	0.30	0.14	0.41	0.43	2.69	2.69

\*, \*\* significant at 5% and 1% level, respectively

Table 4. Specific Combining Ability (SCA) effects of 45 F<sub>1</sub> hybrids under two environments.

Crosses	PH	NOSB	BPP	BW	SI	LI	SCY	GOT	DFE
CRIS-129 x MNH-886	10.96**	-0.09	5.54*	0.17	0.67**	0.01	0.12	1.48**	3.12**
CRIS-129 x FH-142	15.90**	3.00**	0.91	0.17	0.91**	0.35**	14.51**	-0.17	2.32**
CRIS-129 x NIA-Noori	-9.81**	-3.09**	-1.03	-0.11	-1.20**	-0.66**	-10.66**	-2.18**	0.16
CRIS-129 x Baghdadi	10.87**	-0.60	0.16	0.10	0.78**	0.37**	1.86	1.32**	0.71
CRIS-129 x CIM-602	-0.65	1.78**	5.66**	0.05	-0.08	0.62**	16.75**	1.88**	2.36**
CRIS-129 x NIAB-824	1.67	2.23**	6.03**	0.32**	-0.20	0.34**	21.87**	1.41**	-1.48*
CRIS-129 x CEMB-33	-7.53**	1.61**	3.53**	0.34**	1.26**	0.63**	11.04**	1.24**	-0.20
CRIS-129 x MAC-7	12.67**	-1.12**	-1.77	0.08	-1.24**	-0.18	-15.77**	0.53	0.03
CRIS-129 x USD16-3058	3.37	1.55**	-0.38	-0.39**	0.29	0.03	-9.51**	-2.77**	-3.07**
MNH-886 x FH-142	12.15**	1.64**	4.82**	0.19	0.05	-0.16	20.27**	0.16	1.31*
MNH-886 x NIA-Noori	1.40	-0.64	-2.44	0.31**	-0.66**	0.25*	-8.43*	1.46**	-0.89
MNH-886 x Baghdadi	16.43**	3.31**	0.64	0.45**	1.53**	0.73**	17.69**	2.16**	2.52**
MNH-886 x CIM-602	2.89	1.37**	8.12**	-0.13	-0.03	0.26*	1.38	-0.63	-2.91**
MNH-886 x NIAB-824	8.19**	-1.13*	4.92**	-0.42**	-0.61**	-0.25*	11.51**	-1.36**	0.61
MNH-886 x CEMB-33	12.40**	1.68**	2.14	0.09	-0.08	-0.20	-7.05	0.42	2.04**
MNH-886 x MAC-7	-12.34**	-2.45**	-1.81	-0.17	-1.22**	-0.16	-12.58**	-1.70**	0.63
MNH-886 x USD16-3058	0.18	-2.36**	-3.66**	0.06	-0.07	-0.03	-5.50	-0.49	-1.92**
FH-142 x NIA-Noori	6.28*	0.17	6.05**	-0.35**	-0.30	-0.27*	12.28**	-1.47**	0.27
FH-142 x Baghdadi	4.64	1.60**	5.71**	0.48**	0.41*	0.05	15.62**	-0.08	-1.05
FH-142 x CIM-602	8.61**	-2.36**	5.80**	0.02	-0.58**	0.33**	7.36	2.22**	2.01**
FH-142 x NIAB-824	-2.46	0.23	3.88**	0.02	0.75**	0.19	-15.37**	0.27	2.07**
FH-142 x CEMB-33	11.67**	1.92**	5.66**	0.48**	0.30	0.51**	9.08*	1.41**	1.39*
FH-142 x MAC-7	-8.94**	-0.66	-4.53**	-0.38**	-0.61**	-0.20	-14.88**	-0.93*	-0.38
FH-142 x USD16-3058	-10.37**	-0.57	-3.35**	0.15	0.38	0.38**	-11.16**	1.28**	-1.57**
NIA-Noori x Baghdadi	-2.42	0.72	2.77*	0.39**	-0.20	0.11	1.04	0.94**	1.84**
NIA-Noori x CIM-602	10.00**	-0.03	2.63	-0.04	0.56**	0.32**	-1.56	2.11**	1.99**
NIA-Noori x NIAB-824	6.09*	2.50**	3.42*	-0.12	0.44*	-0.37**	13.80**	0.73*	0.76
NIA-Noori x CEMB-33	15.87**	3.41**	1.05	0.01	0.60**	0.21	-5.47	1.64**	1.41*
NIA-Noori x MAC-7	-6.15*	-0.05	1.38	0.02	0.88**	0.02	4.62	0.02	-0.52
NIA-Noori x USD16-3058	4.52	-1.08*	1.83	0.37**	-0.37	0.01	0.83	0.88**	-0.45
Baghdadi x CIM-602	1.23	2.55**	5.56**	-0.01	-0.25	0.11	19.05**	-0.10	2.02**
Baghdadi x NIAB-824	16.00**	1.99**	2.00	0.05	-0.28	0.33**	-10.93**	-0.49	-0.76
Baghdadi x CEMB-33	13.00**	2.13**	4.91**	0.43**	1.46**	-0.08	6.45	0.20	1.22*
Baghdadi x MAC-7	7.75**	0.36	-0.31	-0.37**	-0.34	-0.08	-5.58	-0.58	-0.28
Baghdadi x USD16-3058	-2.03	-2.06**	0.05	0.06	-0.76**	-0.18	-10.23*	-0.13	-1.00
CIM-602 x NIAB-824	9.52**	0.56	5.06**	0.15	0.11	-0.13	0.84	1.45**	3.03**
CIM-602 x CEMB-33	4.59	0.45	1.15	0.01	0.05	0.10	16.44**	-0.01	1.99**
CIM-602 x MAC-7	7.48**	-1.11*	-1.33	0.03	0.33	-0.37**	-13.24**	-0.24	-1.35*
CIM-602 x USD16-3058	-0.09	-1.95**	-6.75**	0.15	0.28	-0.15	-17.43**	-3.00**	-1.87*
NIAB-824 x CEMB-33	-1.15	0.74	-0.74	0.13	0.44*	-0.03	17.63**	1.89**	0.57
NIAB-824 x MAC-7	-1.40	0.56	-4.37**	-0.01	-0.64**	-0.11	-6.87	-0.41	-0.19
NIAB-824 x USD16-3058	-6.90*	-1.48**	-1.50	-0.09	0.32	0.15	-10.74**	-1.09**	-0.58
CEBM-33 x MAC-7	-4.51	-1.54**	-0.11	-0.31**	-1.31**	-0.19	-7.48	-0.84*	-0.79
CEBM-33 x USD16-3058	-0.13	-2.69**	2.31	-0.30**	-1.22**	-0.19	-5.89	-2.99**	-0.69
MAC-7 x USD16-3058	-3.41	0.46	2.45	0.27*	0.26	-0.41**	3.41	0.65	-2.04**
S.E (Sij)	2.88	0.47	1.35	0.11	0.21	0.12	4.03	0.34	0.59
CD @5%	7.94	1.28	3.72	0.30	0.57	0.33	11.11	0.94	1.63

\*, \*\* significant at 5% and 1% level, respectively

Table 4. Continue

Crosses	BF90	BF120	BO90	BO120	SL	MV	FS	UI	CLCV	
									DP%	HP%
CRIS-129 x MNH-886	1.42	6.21**	0.15	2.41**	0.44	0.22	-1.19**	2.08**	3.71	-3.71
CRIS-129 x FH-142	1.26	0.89	0.16	0.83	-0.45	-0.17	-0.18	1.12**	5.39	-5.39
CRIS-129 x NIA-Noori	-0.10	-2.86*	0.05	0.21	0.01	-0.23	-0.09	-1.09*	-1.69	1.69
CRIS-129 x Baghdadi	0.29	1.94	0.15	-0.10	-0.66**	0.13	-0.14	-1.13**	-3.78	3.78
CRIS-129 x CIM-602	0.33	2.92*	-0.13	-0.81	0.03	0.05	-0.62	-1.21**	2.81	-2.81
CRIS-129 x NIAB-824	1.07	5.28**	0.17	3.11**	0.01	0.05	-0.11	-0.03	-2.43	2.43
CRIS-129 x CEMB-33	2.85**	0.81	0.10	-1.01	1.10**	0.17	0.57	1.66**	-3.15	3.15
CRIS-129 x MAC-7	-1.79*	-4.09**	-0.11	-2.45**	-0.01	-0.08	0.76	0.24	-7.27**	7.27**
CRIS-129 x USD16-3058	-0.99	-1.34	-0.22	0.90	-0.49	-0.07	-0.57	-0.23	-2.05	2.05
MNH-886 x FH-142	0.21	4.11**	0.26	3.65**	1.09**	-0.03	4.49**	0.92*	-2.34	2.34
MNH-886 x NIA-Noori	2.88**	0.60	0.30	1.10	-0.60	0.28	-1.68**	-1.32**	3.11	-3.11
MNH-886 x Baghdadi	-1.01	-3.20*	-0.10	-1.79*	2.12**	0.10	1.01*	0.25	-5.3	5.3
MNH-886 x CIM-602	1.80*	1.93	0.62**	0.51	-0.46	0.15	-0.26	-0.87*	-3.62	3.62
MNH-886 x NIAB-824	0.75	-1.22	0.01	-0.33	-0.90**	-0.12	1.99**	1.26**	-0.99	0.99
MNH-886 x CEMB-33	1.29	-3.97**	0.40	-3.96	1.71**	-0.06	0.27	-0.78	-5.95*	5.95*
MNH-886 x MAC-7	-0.57	-4.80**	-0.32	-1.29	-0.40	-0.13	-1.16**	-0.67	-9.06**	9.06**
MNH-886 x USD16-3058	-1.52	-2.07	-0.50*	-1.59	-1.20**	-0.21	-0.35	0.65	12.09**	-12.09**
FH-142 x NIA-Noori	-0.55	1.98	-0.06	0.67	-0.10	-0.01	2.78**	0.42	7.95**	-7.95**
FH-142 x Baghdadi	2.26**	-1.05	0.01	-1.29	0.05	-0.21	-0.20	1.52**	-4.21	4.21
FH-142 x CIM-602	-0.01	1.21	0.03	-0.27	-0.18	0.21	-1.43**	-1.81**	3.34	-3.34
FH-142 x NIAB-824	0.62	-0.13	0.07	1.32	1.80**	0.28	0.28	-2.19**	-1.95	1.95
FH-142 x CEMB-33	0.38	1.94	0.06	1.99*	-1.16**	0.17	-3.96**	0.17	-0.12	0.12
FH-142 x MAC-7	-0.18	1.61	0.17	-0.39	-0.65*	0.44**	-1.84**	-0.59	-4.44	4.44
FH-142 x USD16-3058	-0.22	-2.31	-0.11	-2.29**	0.97**	-0.43**	1.67**	1.42**	9.90**	-9.90**
NIA-Noori x Baghdadi	-1.86*	-4.42**	-0.16	-2.08*	-0.26	0.01	-1.07*	-1.03*	4.42	-4.42
NIA-Noori x CIM-602	3.09**	3.00*	0.48*	2.48**	0.30	-0.33*	3.95**	0.47	1.18	-1.18
NIA-Noori x NIAB-824	-3.14**	-4.06**	-0.38	-3.10**	0.26	0.17	-1.87**	0.63	-9.02**	9.02**
NIA-Noori x CEMB-33	-0.68	-0.85	-0.39	-1.83*	0.80**	-0.52**	1.76**	-0.07	-3.86	3.86
NIA-Noori x MAC-7	-0.37	-1.47	-0.26	-0.23	-1.17**	0.00	-1.10**	1.22**	-11.8**	11.8**
NIA-Noori x USD16-3058	0.10	1.95	-0.43*	0.24	0.50	0.83**	0.74	-0.38	8.38**	-8.38**
Baghdadi x CIM-602	1.72*	4.18**	0.48*	4.55**	0.65*	-0.07	-1.46**	0.91*	-3.2	3.20
Baghdadi x NIAB-824	0.75	4.79**	0.15	2.29**	-0.36	-0.19	0.90*	-1.03*	9.11**	-9.11**
Baghdadi x CEMB-33	1.42	0.11	0.13	2.22*	1.06**	0.34*	1.33**	1.85**	-3.12	3.12
Baghdadi x MAC-7	-1.52	2.19*	-0.60**	-0.62	-0.19	-0.07	-1.13**	1.18**	-7.19**	7.19**
Baghdadi x USD16-3058	0.72	-2.92**	-0.04	-2.42**	-0.82**	0.05	-0.06	-0.69	11.27**	-11.27**
CIM-602 x NIAB-824	1.97*	3.87*	0.31	1.83*	-0.17	0.30*	-1.46**	0.63	9.03**	-9.03**
CIM-602 x CEMB-33	-0.22	2.81**	-0.14	2.98**	0.30	-0.28	3.83**	1.32**	-0.5	0.5
CIM-602 x MAC-7	-1.52	4.54*	-0.36	-2.52**	-1.12**	-0.11	0.14	1.30**	-11.31**	11.31**
CIM-602 x USD16-3058	-1.68*	-3.22*	-0.42*	-2.76**	-0.42	0.22	0.48	0.34	13.0**	-13.0**
NIAB-824 x CEMB-33	-2.31**	-2.72	-0.31	0.08	-1.02	-0.31*	-0.02	1.23**	10.32**	-10.32**
NIAB-824 x MAC-7	1.90*	-0.93	-0.30	-1.85*	-0.33	0.02	0.28	-0.17	-10.01**	10.01**
NIAB-824 x USD16-3058	-0.75	-3.35**	-0.26	-2.26**	0.57	-0.25	1.01*	1.42**	4.28	-4.28
CEBM-33 x MAC-7	0.63	0.36	0.10	0.04	0.48	0.20	0.08	-0.50	-8.50**	8.50**
CEBM-33 x USD16-3058	0.61	0.43	0.27	0.20	-1.29**	0.18	-2.04**	-1.62**	16.38**	-16.38**
MAC-7 x USD16-3058	0.26	0.50	-0.17	-0.25	0.65*	-0.12	0.31	0.24	-8.81**	8.81**
S.E (Sij)	0.85	1.31	0.21	0.89	0.31	0.15	0.43	0.44	2.76	3.08
CD @5%	2.35	3.62	0.85	2.44	0.85	0.41	1.17	1.21	7.62	7.62

\*, \*\* significant at 5% and 1

It was observed that the hybrids which expressed maximum positive significant SCA effects for yield and its components were produced from crosses involving either one or both good general combiner parents. Such similar results have been reported by Sorour *et al.* (2013), Choudhary *et al.* (2016), Khan *et al.* (2017), Vekariyal *et al.* (2017), Patil *et al.* (2018) and Reddy *et al.* (2017) who also found high SCA effects for yield and its components in hybrids produced by one or both of good general combiner parents.

Early maturity is an important trait of cotton which is being suggested to growers as the crop matures earlier and harvested (picking of seed cotton) quicker. Among the 45 hybrid combinations (Table 4), CRIS-129 x MNH-886 excelled highest significant positive SCA effect for days to first flower (DFF) followed by CIM-602 x NIAB-824 and MNH-886 x Baghdadi, respectively. The hybrids NIA-Noori x CIM-602, MNH-886 x NIA-Noori and CRIS-129 x CEMB-33 showed highest significant positive SCA effect for bolls formed at 90 days after planting. Similarly, the crosses CRIS-129 x MNH-886, CRIS-129 x NIAB-824 and Baghdadi x NIAB-824 expressed significant positive SCA effect for bolls formed at 120 DAP trait. The hybrids MNH-886 x CIM-602, NIA-Noori x CIM-602 and Baghdadi x CIM-602 contributed significant positive SCA effect for bolls opened at 90 DAP. In case of bolls opened at 120 DAP, the hybrids Baghdadi x CIM-602, MNH-886 x FH-142 and CRIS-129 x NIAB-824 showed highest significant SCA effect in descending order.

High SCA effects for earliness indicated the combinations of positive alleles of good general combiner. The fiber quality parameters illustrated in Table 4 show the maximum positive significant SCA effect for staple length was shown by hybrid MNH-886 x Baghdadi followed by FH-142 x NIAB-824 and then by MNH-886 x CEMB-33. The crosses NIA-Noori x USD16-3058, FH-142 x MAC-7 and Baghdadi x CEMB-33 revealed significant positive SCA effect for micronaire value. For the fiber strength, the highest SCA effects were shown by the crosses MNH-886 x FH-142, NIA-Noori x CIM-602 and CIM-602 x CEMB-33. Similarly, the hybrids CRIS-129 x MNH-886, Baghdadi x CEMB-33 and CRIS-129 x CEMB-33 produced high SCA effects for uniformity index. These findings are in accordance with the results of Sorour *et al.* (2013), Choudhary *et al.* (2016), Dhamayanthi and Rathivanvel (2017), Khan *et al.* (2017), Kumar *et al.* (2017), Vekariyal *et al.* (2017), Chinchane *et al.* (2018), Patil *et al.* (2018), Reddy *et al.* (2017) and Swetha *et al.* (2018) who reported significant positive SCA effects for earliness and fiber traits with at least one of the good general combiners in cross combinations.

The genotypes that express maximum positive GCA effects are considered as superior general combiner who may unite the important genes for the development of traits and these can be preferred for selection and utilization in hybridization program. The general combining ability (GCA) effects of cotton leaf curl virus are presented in Table 3. The parent MAC-7 was found good general combiner, since it contributed significant positive GCA effects for healthy plant percentage (49.74), whereas it was a negative combiner for diseased plant percent (-49.74). It was followed by the genotype USD16-3058 that contributed higher significant positive GCA effects for diseased plant percentage (24.42) and higher negative GCA effect for healthy plant (-24.42) which is considered as highly susceptible against cotton leaf curl virus disease. The genotype MAC-7 that exhibited positive GCA effect for CLCV is designated as resistant/highly tolerant.

The specific combining ability (SCA) effects depicted in (Table 4) show that among the hybrids combinations, CRIS-129 x MAC-7, MNH-886 x MAC-7, FH-142 x MAC-7, NIA-Noori x MAC-7, Baghdadi x MAC-7, CIM-602 x MAC-7, NIAB-824 x MAC-7, CEMB-33 x MAC-7, MAC-7 x USD16-3058 excelled high SCA positive effects for healthy plant percentage and negative SCA effect for diseased plants. It was noted that cross combinations exhibited high SCA effect for healthy plants, confirmed the combination of average x good and poor x good general combiner with significant SCA effect was due to complementary gene action which produce desirable transgressive segregants. Therefore, single plant selection based on disease symptoms in early generation would be helpful in a plant breeding program.

The genetic variance components of CLCV illustrated in Table 2 shows that the GCA variance was higher than the SCA variance which indicates the role of additive gene action. The proportion of GCA / SGA variance for CLCV diseased and healthy plants percentage was more than unity which also indicates the predominant role of additive genes. Therefore, selection in early segregating generation could be performed for evolving the cotton leaf curl virus resistant/highly tolerant inbred lines. Khan (2013) and Khan *et al.* (2017) also reported that parents and hybrids with positive GCA and SCA effects in CLCV epidemic conditions could be utilized for further breeding and selection program.

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