



Research Article

DIALLEL ANALYSIS FOR SEED COTTON YIELD AND FIBER QUALITY TRAITS IN UPLAND COTTON [*Gossypium hirsutum* (L.)] TESTED OVER SET OF ENVIRONMENTS

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Abstract: Crop improvement deals essentially with selection of superior individuals within genetically heterogeneous populations. The basic objective of upland cotton genotypes is sought that meet the needs of three sectors of the economy viz., cotton growing community, the ginning industries and the textile complex. The ten upland cotton (*Gossypium hirsutum* L.) genotypes were crossed in complete diallel (10x10) excluding reciprocals to obtain the forty five F1 hybrid combinations were evaluated in two sets of environments on experimental farm of the Cotton Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS). The experimental design was randomized block design with three replications with repetition over two sets of environments.

The analysis of variance was performed to test the significance of difference between the progenies for all the traits under investigation. The mean sum of squares due to GCA and SCA were highly significant for all the characters indicating the importance of both additive and non – additive gene effects in expression of these characters. The predictability ratio indicated that all most all the characters were found to be governed by additive components of genetic variance whereas plant height, seed cotton yield per plant, seed index and fibre strength were found to be controlled by additive as well as non-additive genetic components of genetic variance. In the present investigation the parents AKH-84635 and LRA-5166 expressed favorable GCA effects for most of the characters over the environments. Most of the cross combinations showed positive and significant specific combining ability effects for seed cotton yield per plant. Maximum positive significant SCA effects were recorded for seed cotton yield per plant in the cross by KH-118 x AKH-62 (17.15) followed by AKH-84635 x LRA-5166 (11.68) and JLH-1594 x AKH-24 (8.83). The crosses viz., AKH-44 x LRA-5166 and JLH-1594 x LRA-5166 may be advanced in further generations for development of superior genotypes.

Keywords: Combining ability, Cotton, Diallel, General and Specific Combining Ability

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Introduction

Cotton, one of the world's leading agricultural crops, plays an important role in Indian Economy. The basic objective of cotton (*Gossypium hirsutum* L.), genotypes are sought that meet the needs of three sectors of the economy viz., cotton growing community, the ginning industries and the textile complex. The cotton production in India during 2019-20 is expected around 360 lakh bales of 170 kg from 125.84 lakh hectares with a productivity of 486 kg lint/ha [2]

Cotton being a member of Malvaceae family, comprising genus *Gossypium* has more than fifty native species in arid and semi-arid regions of the Asia, America, Africa and Australia, of which about forty-five are diploid (2n=26) and five allotetraploids (2n=52) [8,18]. The species *G. hirsutum* has shown higher levels of genetic variability than the other three species [30,1]. Cultivation of cotton is more than eight million hectares in India and ranks first in the world in the area but third in production. Cotton refers to those species of genus *Gossypium* that bears the spinnable seed coat fibres. Since long, cotton workers are seriously attempting to improve the cotton productivity to bridge the gap between demand and supply but a spectacular success is still awaited. However, India is credited to be the first country where hybrid cotton was on commercial scale way back in 1970 based on seed production by hand emasculation and pollination. But the productivity barriers are yet to heal up [28].

Crop improvement deals essentially with selection of superior individuals within genetically heterogeneous populations. The populations used for exploration of potential by way of selection may be land races, germplasm (indigenous/exotic) or

products of the crossing of selected genotypes. In such crossings, favorable allele combinations are expected to originate new commercial cultivars highly adapted to range of environmental regimes. The steps during this process are of paramount importance, such as: selection of parents with identification of the best hybrid combinations; the advance of generations without the loss of favorable gene combinations and finally the selection of pure superior lines with maximum experimental precision.

In view of preciseness in selection of parents in cotton, diallel crosses are of great value, as provides the valuable information about parental genotypes and the segregating generations that follow crosses derived. The analyses of diallel crosses contain further information like the nature of the predominant gene action in traits of economic importance, besides estimates of both GCA&SCA combining ability. Among the different commonly used methods of choosing parents and identifying promising hybrid combination [9]. In this method the sums of squares for the effects of general and specific combining ability are estimated as well as the effects themselves. It is thus necessary to survey the variation present in the germplasm as the hybrids between diverse lines displays a greater heterotic effect than those between the closely related [29]

The present investigation is planned with objective to evaluate the general and specific combining ability and heterosis and to discover information on the genetic control of seed cotton yield and fiber quality traits in the hybrid combinations obtained by all possible crosses of ten elite upland cotton cultivars in 10x10 diallel excluding reciprocals over two sets of environments.

Table-1 Pooled combined Analysis of variance for fourteen morphological characters of cotton

Source of variation	d.f.	Mean sum of squares [MSS]						
		Days to 50% flowering	Plant height (cm)	No. of monopodia per plant	No. of sympodia per plant	No. of bolls per plant	Boll weight (g)	No. of seeds per boll
Environments	1	2272.594**	20447.345**	0.7380 ^{NS}	3050.099**	3869.711**	7.5217**	10.7431*
Replication	2	18.2393 ^{NS}	689.9358**	4.1440**	757.0779**	1594.9875**	3.0983**	18.4897**
Genotypes	54	37.4721 ^{NS}	433.4648 ^{NS}	1.1766**	28.9697**	93.2533**	1.1095**	87.0741**
Parents	9	20.6664*	174.8075 ^{NS}	0.7303**	4.6587**	50.2950**	0.2153 ^{NS}	19.6542**
Crosses	44	20.5342**	251.4269**	0.8231**	13.5011**	48.8141**	0.7924**	48.0350**
Crosses x Par	1	19.9641 ^{NS}	116.2771 ^{NS}	0.4642 ^{NS}	1.2275 ^{NS}	74.7812**	0.1476 ^{NS}	95.5451**
Env x Repl	2	27.6939**	109.8754**	6.3677**	367.020**	75.8713**	3.1618**	39.0364**
Env x Genoty	54	6.7976 ^{NS}	67.8226 ^{NS}	0.3737*	2.0364**	5.8296 ^{NS}	0.2977**	1.6787 ^{NS}
Env x Parents	9	6.3995 ^{NS}	141.082 ^{NS}	0.1237 ^{NS}	8.692**	19.371**	0.0351 ^{NS}	0.3350 ^{NS}
Env x Crosses	44	7.3520 ^{NS}	147.765*	0.0398 ^{NS}	6.534**	33.7645**	0.0591 ^{NS}	1.874 ^{NS}
Env x Cross x Parnt	1	20.8092 ^{NS}	0.008 ^{NS}	0.1161 ^{NS}	1.398 ^{NS}	161.2032**	0.292 ^{NS}	2.537 ^{NS}
Pooled Error	216	9.4883	105.3974	0.2549	0.4908	6.2462	0.1693	2.7082

Source of variation	d.f.	Mean sum of squares [MSS]						
		Ginning outturn (%)	Seed Index (g)	Lint Index (%)	2.5% span length (mm)	Fibre Strength (g/tex)	Micronaire value (mg/in)	Seed yield per plant (g)
Environments	1	2019.947**	17.9379**	95.2879**	117.6913**	4412.492**	220.745**	31784.02**
Replication	2	1027.160**	5.1330**	40.5678**	90.1002**	725.352**	34.4357**	4865.718**
Genotypes	54	58.3354**	2.0457**	2.5526**	12.1196**	24.7883**	0.5607**	253.538**
Parents	9	13.5540**	0.4742**	0.7571**	1.6841**	20.3452**	0.6981**	63.3074**
Crosses	44	31.6105**	1.3950**	1.4621**	6.8142**	14.1782**	0.3154**	169.7052**
Crosses x Parents	1	58.9332**	2.3252**	0.2761 ^{NS}	3.1214**	1.5486 ^{NS}	12.1715**	194.0089**
Env x Replication	2	130.9431**	10.8084**	19.2373**	388.4436**	456.044**	33.8074**	2630.718**
Env x Genotypes	54	0.8936**	0.0507 ^{NS}	0.0961**	0.1306**	5.6639**	0.2264**	49.6464**
Env x Parents	9	1.535**	1.6723**	1.535**	3.2020**	2.1076**	0.095 ^{NS}	130.190**
Env x Crosses	44	0.190 ^{NS}	0.9876**	0.540**	1.9503**	2.4348**	0.1956**	363.689**
Env x Crosses x Parent	1	9.648**	0.799*	0.049 ^{NS}	0.605**	9.0485*	0.0079 ^{NS}	301.927**
Pooled Error	216	1871	0.1622	0.2593	0.0707	1.8907	0.0666	12.4843

*, ** Significant at 5% and 1% level of significance

Table-2 Pooled analysis of Combining Ability over Environments

Source of variation	d.f.	Mean sum of squares [MSS]						
		Days to 50% flowering	Plant height (cm)	No. of monopodia per plant	No. of sympodia per plant	No. of bolls per plant	Boll weight (g)	No. of seeds per boll
GCA	9	27.4645**	136.3080**	0.7112**	11.7192**	49.1967**	0.5712**	48.5547**
SCA	45	9.4938**	146.1191**	0.3284**	9.2442**	27.4614**	0.3276**	25.1192**
Environment	1	757.344**	6815.510**	0.2459 ^{NS}	1016.716**	1289.873**	2.5089**	3.5999*
GCA x environment	9	2.6099 ^{NS}	31.9283 ^{NS}	0.2387**	0.7451**	2.3565 ^{NS}	0.1118*	0.7909 ^{NS}
SCA x environment	45	2.2011 ^{NS}	20.7493 ^{NS}	0.1017 ^{NS}	0.6651**	1.8613 ^{NS}	0.0967**	0.5128 ^{NS}
Error	216	3.1627	35.1324	0.0849	0.1636	2.0821	0.0564	0.9027

Source of variation	d.f.	Mean sum of squares [MSS]						
		Ginning outturn (%)	Seed Index (g)	Lint Index (%)	2.5% span length	Fibre Strength (g/tex)	Micronaire value	Seed yield per plant (g)
GCA	9	23.7872**	0.5437**	1.1551**	4.6160**	4.5063**	0.2246**	71.6029**
SCA	45	18.5755**	0.7097**	0.7901**	3.9237**	9.0142**	0.1793**	87.0934**
Environment	1	673.229**	5.9834**	31.7635**	39.1820**	1470.843**	73.5814**	10594.661**
GCA x environment	9	0.5134**	0.0153 ^{NS}	0.0505**	0.0352 ^{NS}	2.6851**	0.0894**	19.3449**
SCA x environment	45	0.2567**	0.0171 ^{NS}	0.0283**	0.0463**	1.7282**	0.0726**	15.9908**
Error	216	0.0623	0.0541	0.0086	0.0235	0.6302	0.0222	4.1614

*, ** Significant at 5% and 1% level of significance

Table-3 General Combining Estimates of parents over the environments

SN	Parents	Days to 50 per cent flowering	Plant Height (cm)	No. of monopodia per plant	No. of sympodia per plant	No. of bolls per plant	Boll weight (g)	No. of seeds per boll	Ginning outturn (%)	Seed Index (g)	Lint Index	2.5% span length	Fibre strength (g/tex)	Micronaire Value (inch)	Seed cotton yield per plant(g)
1	AKH-84635	-2.36**	0.72	0.01	0.18**	1.22**	0.28**	29**	18*	0.08*	0.08*	0.08*	0.08*	0.08*	0.08*
2	JLH-1594	-0.65**	1.88*	0.15**	1.36**	-2.96**	0.05*	17*	0.80*	0.02*	0.02*	0.02*	0.02*	0.02*	229*
3	KH-118	-0.25*	-3.70**	0.09*	0.13*	1.72**	-0.11**	0.89*	0.08*	0.03*	0.03*	0.03*	0.03*	0.03*	0.03*
4	NH-545	1.49**	0.5	-0.14**	-0.62**	-0.41*	-0.08**	1.16*	0.08*	0.03*	0.03*	0.03*	0.03*	0.03*	123*
5	AKH-91	-0.51*	-2.39**	0.24**	-1.09**	-1.76**	0.06*	1.79**	0.05*	0.08*	0.08*	0.08*	0.08*	0.08*	0.08*
6	AKH-62	0.2	2.93**	-0.32**	-0.72**	-0.14	-0.16**	0.30*	0.09*	0.08*	0.08*	0.08*	0.08*	0.08*	-143*
7	AH-107	0.74**	3.42**	-0.14**	0.63**	0.59**	0.01	0.12*	0.09*	0.05*	0.05*	0.05*	0.05*	0.05*	-383*
8	AKH-44	1.07**	-2.59**	0.18**	0.09*	0.02	0.12**	0.1	0.02*	0.08*	0.08*	0.08*	0.08*	0.08*	103*
9	AKH-24	0.06	-0.72	-0.04*	-0.01	0.66**	-0.26**	0.93**	1.44*	0.05*	0.03*	0.03*	0.03*	0.03*	-088*
10	LRA-5166	0.21	-0.04	-0.03	0.04	1.06**	0.09**	0.01	0.08*	0.02*	0.08*	0.08*	0.08*	0.08*	107*
	S.E.(g) 6	0.344	1.148	0.564	0.078	0.279	0.046	0.184	0.048	0.045	0.018	0.03	0.154	0.029	0.395
	C.D.(5%)	0.242	0.807	0.04	0.006	0.02	0.003	0.013	0.003	0.003	0.001	0.002	0.011	0.002	0.028
	C.D.(1%)	0.631	2.104	1.034	0.144	0.512	0.084	0.337	0.089	0.083	0.033	0.054	0.282	0.053	0.724

*, ** Significant at 5% and 1% level of significance

Table-4 SCA effects of cross combinations for fourteen morphological traits in cotton over environments

SN	Cross Combinations	DF	PH	No.MON	SYMP	BOLLS	BW	SPP	GOT	SI	LI	2.5% SP	FS(g/tex)	MV (/inch)	SCY (g)
1	AKH-84635 x JLH-1594	0.68	7.03**	-0.23*	-0.76**	0.05	-0.02	1.78**	5.29**	0.82**	1.50**	1.70**	-2.33**	0.04	7.00**
2	AKH-84635 x KH-118	-0.39	-4.21*	0.14*	-0.64**	0.48	0.16*	-2.31**	1.53**	0.05	0.30**	-0.10*	0.06	-0.08*	-2.02*
3	AKH-84635 x NH-545	0.38	1.12	-0.08	0.84**	1.28*	-0.47**	6.39**	6.06**	0.74**	1.56**	-0.41**	-0.74*	-0.04	3.24**
4	AKH-84635 x AKH-91	-2.46**	-2.4	-0.31*	1.22**	3.44**	0.15*	0.61*	-5.40**	-0.32**	-1.19**	-1.69**	-0.77*	0.03	-10.93**
5	AKH-84635 x AKH-62	1.33*	1.89	-0.03	-0.24**	-0.63	-0.19*	-6.87**	-4.85**	0.11*	-0.94**	1.94**	1.88**	-0.01	-6.63**
6	AKH-84635 x AH-107	-1.21*	4.09*	-0.08	-0.14	0.53	0.85**	-1.97**	-5.39**	0.31**	-0.83**	-2.81**	-0.08	0.09*	-2.36**
7	AKH-84635 x AKH-44	-0.38	3.14*	0.42**	0.18*	-4.52**	0.47**	1.32**	3.33**	-0.18*	0.51**	2.69**	1.93**	-0.15*	-1.26*
8	AKH-84635 x AKH-24	0.64	-0.29	0.15*	0.42*	2.16**	0.06	-2.66**	-0.01	-0.85**	-0.47**	-0.03	-0.1	0.15*	-1.44*
9	AKH-84635 x LRA-5166	-0.69	8.79**	-0.04	-0.16	4.72**	-0.29**	-3.13**	1.55**	-0.25**	0.17**	0.22**	-0.87**	-0.12*	11.68**
10	JLH-1594 x KH-118	-1.44*	12.38**	-0.06	0.85**	1.07*	0.12*	1.04**	-1.73**	-0.72**	-0.67**	-0.86**	-0.59*	0.17**	-1.90*
11	JLH-1594 x NH-545	0.5	9.84**	-0.17*	1.33**	6.39**	0.1	1.76**	2.83**	-0.27**	0.23**	1.95**	1.59**	-0.33**	5.73**
12	JLH-1594 x AKH-91	-0.84*	-4.70*	-0.82**	-0.33*	0.43	-0.28**	-4.06**	-2.07**	-0.51**	-0.56**	1.13**	1.32**	0.48**	1.04*
13	JLH-1594 x AKH-62	-2.21**	-15.13**	-0.29*	-0.37*	0.71*	0.01	5.23**	-1.25**	-0.46**	-0.41**	-0.37**	2.18**	-0.08*	-5.29**
14	JLH-1594 x AH-107	-0.92*	-5.71*	-0.09	0.60**	-3.27**	0.48**	0.3	1.93**	0.55**	0.59**	-1.60**	1.94**	0.14*	-3.03**
15	JLH-1594 x AKH-44	-1.25*	-1.21	0.54**	0.98**	2.12**	-0.33**	3.24**	-2.47**	0.98**	0	-1.47**	5.30**	-0.14*	6.99**
16	JLH-1594 x AKH-24	-1.74*	7.26**	0.62**	0.06	0.16	-0.06	-3.62**	-0.89**	0.15*	-0.14**	1.12**	-0.75*	0.16**	8.83**
17	JLH-1594 x LRA-5166	2.61**	-8.76**	0.74**	0.82**	-3.23**	0.30**	1.91**	0.75**	-0.50**	-0.09*	-2.08**	-2.54**	-0.26**	7.82**
18	KH-118 x NH-545	-0.74	-10.76**	0.25*	1.21**	-2.52**	-0.34**	0.42*	-4.94**	0.18*	-0.79**	-0.54**	-1.94**	0	-10.30**
19	KH-118 x AKH-91	0.1	-0.89	0.13*	0.02	0.33	0.59**	0.87*	0.58**	0.01	0.09*	0.60**	-2.09**	-0.15*	1.83*
20	KH-118 x AKH-62	0.72	3.00*	0.62**	-0.61**	1.57*	-0.23*	-3.70**	3.10**	0.64**	0.89**	1.24**	2.45**	0.25**	17.05**
21	KH-118 x AH-107	-2.58**	4.39*	-0.54**	-0.96**	2.95**	-0.11*	2.34**	-0.58**	0.18*	-0.03	1.72**	-0.19	-0.38**	6.08**
22	KH-118 x AKH-44	1.85*	3.88*	-0.66**	-1.19**	0.41	-0.19*	-1.81**	-2.03**	0.01	-0.33**	-1.91**	-0.88**	-0.35**	5.42**
23	KH-118 x AKH-24	3.70**	4.10*	1.04**	0.87**	0.70*	-0.16*	-1.19**	-1.53**	-0.71**	-0.63**	-1.00**	0.72*	-0.13*	-4.11**
24	KH-118 x LRA-5166	1.23*	13.52**	-0.09	-0.36*	0.43	0.1	-2.65**	-0.15**	-0.08	-0.05*	0.08*	1.50**	0.30**	3.05**
25	NH-545 x AKH-91	1.19*	6.68**	0.42**	-0.41*	1.49*	0.1	-5.08**	-2.06**	-1.12**	-0.86**	0.52**	-1.28**	0.50**	4.40**
26	NH-545 x AKH-62	-0.35	2.07	-0.66**	-1.59**	-2.35**	0.56**	3.83**	6.64**	-0.78**	0.83**	2.00**	-0.76*	-0.10*	3.32**
27	NH-545 x AH-107	-1.72*	3.25*	0.03	-0.59**	-4.14**	-0.45**	-4.79**	-0.89**	-0.16*	-0.25**	-1.63**	1.84**	-0.03	2.11*
28	NH-545 x AKH-44	-1.73*	-21.41**	-0.22*	-0.78**	-0.75*	0.46**	-1.91**	-2.07**	0.07	-0.34**	-0.79**	2.70**	-0.39**	3.66**
29	NH-545 x AKH-24	-3.38**	-1.2	-0.04	-0.01	3.66**	0.29**	-0.08	-2.64**	0.93**	-0.07*	0.70**	3.63**	-0.25**	-1.56*
30	NH-545 x LRA-5166	3.47**	0.35	0.06	-0.96**	-4.60**	-0.47**	2.92**	-2.09**	0.57**	-0.12**	-1.49**	-1.53**	0.57**	1.22*
31	AKH-91 x AKH-62	2.49**	17.48**	-0.05	-0.87**	-3.06**	-0.19*	5.76**	0.12*	0.13*	0.08*	0.16*	-0.89**	-0.33**	-4.78**
32	AKH-91 x AH-107	2.28**	-1.66	0.76**	1.01**	1.12*	0.27**	-1.77**	0.70**	0.56**	0.38**	-0.76**	-0.42*	0.05	-4.23**
33	AKH-91 x AKH-44	0.44	1.26	-0.06	-1.15**	-4.71**	-0.47**	1.76**	-2.80**	0.10*	-0.40**	-0.20**	1.82**	-0.46**	6.21**
34	AKH-91 x AKH-24	-0.88*	-6.91**	-0.73**	-1.18**	-2.28**	-0.32**	2.27**	1.45**	0.16*	0.34**	0.81**	-0.05	-0.32**	7.50**
35	AKH-91 x LRA-5166	-4.03**	-1.99	0.26*	0.29*	1.20*	0.24*	3.90**	2.55**	1.58**	1.26**	1.89**	-1.84**	0.11*	-5.56**
36	AKH-62 x AH-107	-1.44*	4.31*	-0.05	-0.87**	-5.31**	-0.44**	5.52**	-0.15*	0.70**	0.28**	0.84**	-3.18**	-0.32**	-1.03*
37	AKH-62 x AKH-44	-1.43*	0.71	0.25*	2.01**	6.28**	0.68**	2.12**	0.63**	0.14*	0.19**	-1.24**	-2.74**	-0.45**	-1.07*
38	AKH-62 x AKH-24	1.08*	-0.27	-0.17*	-0.53**	-4.14**	-0.22*	-2.45**	-2.08**	-0.19*	-0.46**	-2.28**	-1.16**	0.08*	-1.18*
39	AKH-62 x LRA-5166	0.6	3.24*	-0.24*	1.11**	2.24**	-0.34**	-0.18	-5.70**	0.54**	-0.70**	-1.17**	-0.36*	0.20**	-6.57**
40	AH-107 x AKH-44	1.20*	2.24	0.13*	0.18*	-0.78*	0.24*	0.17	1.71**	-0.62**	0.01	0.64**	-3.01**	0.01	-5.74**
41	AH-107 x AKH-24	-1.80*	-0.13	-0.09	0.65**	7.52**	-0.27**	0.28	3.86**	-0.46**	0.51**	-0.03	0.09	-0.08*	-5.95**
42	AH-107 x LRA-5166	4.22**	14.84**	0.19*	-0.86**	-5.53**	-0.63**	2.99**	-1.55**	-0.13*	-0.29**	1.80**	1.21**	-0.19**	-4.81**
43	AKH-44 x AKH-24	-1.47*	4.06*	-0.29*	-0.04	4.91**	-0.27**	2.24**	-1.07**	0.26**	-0.06*	1.93**	-0.56*	0.02	1.99*
44	AKH-44 x LRA-5166	-1.95**	5.30*	-0.04	-0.09	2.61**	0.93**	-0.65*	-1.21**	-0.49**	-0.38**	1.42**	2.87**	0.07*	-7.84**
45	AKH-24 x LRA-5166	-2.27**	-10.34**	0.05	0.50**	5.19**	0	6.03**	0.27**	0.86**	0.49**	-0.74**	2.91**	0.05	1.26*
	S.E.(Sij)	1.1584	3.8607	0.1899	0.2635	0.9398	0.1548	0.6189	0.1627	0.1515	0.0606	0.1	0.5171	0.0971	1.3287
	C.D. (5%)	0.7877	2.6252	0.1291	0.1792	0.6391	0.1052	0.4208	0.1106	0.103	0.0412	0.068	0.3516	0.066	0.9035
	C.D. (1%)	1.9414	6.4704	0.3356	0.4656	1.5752	0.2594	1.0372	0.2727	0.2538	0.1015	0.1676	0.8667	0.1627	2.2269

*, ** Significant at 5% and 1% level of significance

Material and Methods

The 10x10 diallel excluding reciprocals was planned with the ten-upland cotton (*Gossypium hirsutum* L.) genotypes (AKH-84635, JLH-1594, KH-118, NH-545, AKH-91, AKH-62, AH-107, AKH-44, AKH-24 and LRA-5166) and the forty-five F1 hybrid combinations were evaluated in two sets of environments on experimental farm of the Cotton Research Unit, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola (MS) in Randomized Block Design (RBD) fashion with three replications. Moreover, the data were collected from each plot for important morphological and fibre quality traits viz., days to 50 per cent flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), number of seeds per boll, ginning outturn (%), seed index (g), lint index (%), 2.5% span length, fibre strength (g/tex), micronaire value (µg/inch) and seed cotton yield per plant (g).

The analysis of variance was performed to test the significance of difference between the progenies for all the traits under investigation. The analysis of variance was carried out as per standard method [13, 23]. The mean squares were tested against error variance (Me) by using 'F' test. The standard error of difference for comparing any two progeny means along with critical differences were estimated. The analysis of combining ability effects were performed by the Method-2 and Model-I of Griffing [9]

Result and Discussion

Analysis of Variance over Environments

The analysis of variance for the experimental design showed significant differences for the genotypes for all the fourteen traits under the environments E1 and E2. Further partitioning of the genotypic variances revealed significant differences in the parents for all the traits except for number of monopodia per plant and seed index in E1, whereas except for boll weight in environment E2.

The variance due to crosses was significant for all the traits in both environmental conditions [Table-1]. Parents vs crosses were significant for plant height, number of bolls per plant, number of seeds per boll, ginning outturn, seed index, lint index, 2.5 per cent span length, fibre strength and micronaire value. This indicated significant differences among the parents and crosses. Pooled analysis of variance showed significant differences among the parents and crosses for all the traits except plant height and boll weight in respect of parents. This indicated that substantial genetic variability exists among the parents for most of the characters, which is a pre-requisite in any breeding programme.

Combining Ability Variance Analysis

The analysis of variance for combining ability for fourteen traits over environments along with GCA vs SCA ratios are presented in [Table-2]. The mean sum of squares due to GCA and SCA were significant for all the traits indicating the importance of both additive and non-additive genetic variance. It was revealed from table that mean sum of squares due to general combining ability were higher in magnitude than the corresponding specific combining ability for all the traits, except for those of seed index, fibre strength, micronaire value and seed cotton yield per plant in E2 environments.

The general predictability ratio (GCA vs SCA) ranged from 0.61 for seed index to 0.82 for number of seeds per boll while from 0.46 for plant height to 0.89 for days to 50 per cent flowering in E1 and E2 environments respectively. This indicated that the importance of dominance type of gene action than the additive type in the inheritance of these characters. The importance of dominance genetic variance over additive have been also reported by [10, 4, 5, 19, 31].

In pooled data, the mean sum of squares due to general and specific combining ability were significant for all the fourteen traits. The plant height, seed index, fibre strength and seed cotton yield per plant were exception, where mean sum of

squares due to general combining ability were high in magnitude than the corresponding specific combining ability indicating the important role of additive genetic variance than dominance. The variance GCA x environment was non-significant for all the traits except for number of monopodia per plant, number of sympodia per plant, boll weight, ginning outturn, lint index, fibre strength, micronaire value and seed cotton yield per plant. Whereas the SCA x environment variance was significant for traits viz., number of sympodia per plant, boll weight, ginning outturn, lint index, 2.5 per cent span length, fibre strength, micronaire value and seed cotton yield per plant and non - significant for rest of the characters [Table-1].

The general combining ability effects were less influenced by environmental variation, whereas specific combining ability effects were much influenced by environmental interaction[17]. However, several workers have reported significant GCA x environment and SCA x environment interaction for several traits including seed cotton yield. The significant interaction of GCA x environment and SCA x environment for these characters showed that they are influenced by the environment and their performance therefore varies from environment to environment. It is therefore, necessary to test the material at different locations and location specific selection should be done. The results of present investigation were supporting to those reported in cotton by [26, 16, 6,7,15, 25,33,34].

GCA Effects Analysis

The general combining ability effects of parents are indicative of heritable variation transmitted from parents to the progeny and helps for selection of parents to be used in hybridization programs. The significant GCA effects in desirable direction [Table-2].

The parent LRA-5166 exhibited high mean performance for seed cotton yield per plant with good general combining ability effects, it has also shown significant GCA effects in desirable direction for plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, number of seed per boll, seed index and fibre strength. The results revealed that the parent LRA-5166 is one of the parents in two hybrids included in top seven yielding cross combinations over environments. The parent JLH-1594 has also shown significant positive GCA effects for seed cotton yield along with for most of yield contributing traits and also a parent involved in five top yielding hybrids.

The parent NH-545 and KH-118 also identified as good general combiners having positive significant general combining ability effects for seed cotton yield per plant in desirable direction. Both the parents also exhibited significant GCA effects for most of the characters in the study. These parents also involved in seven top cotton yielding crosses. The parental lines having high GCA effects for seed cotton yield and other related characters can be suitably used in the hybridization programs as it is possible to get the transgressive segregants of gene action and additive x additive type of epistasis. Similar type of results and prediction have been reported [3, 26, 21,19].

SCA Effects Analysis

Specific combining ability is an indicative of heterosis in the cross combinations. The top crosses, which exhibited best per se performance for seed cotton yield are listed in [Table-4]. It can be revealed from the table that all these selected crosses showed significant and positive specific combining ability effects for seed cotton yield per plant and other characters studied.

The cross KH-118 x AKH-62 ranked first in per se performance for cotton yield. This cross exhibited significant specific combining ability effects for yield in positive direction in E1, E2 and pooled environments. The cross has also shown significant SCA effects for most of the traits studied over the set of environments. The cross AKH-84635 x LRA-5166 ranked second in case of yield performance, showed significant SCA effects in positive direction along with most of the yield contributing characters over the environments. Thus, these hybrids can be considered as promising and suggested to be exploited for hybrid breeding programme.

The crosses were pointed out, which exhibits high significant specific combining ability also showed good per se performance [3]. The importance of both additive and non-additive gene effects for yield and yield contributing characters in cotton

and indicated the superior crosses can be used in the breeding program for development of superior genotypes along with the heterosis breeding has been reported in various studies [11,14, 15, 26, 20,22, 17, 12, 7, 27,19,32,33].

Conclusion

The mean sum of squares due to GCA and SCA were highly significant for all the characters indicating the importance of both additive and non-additive gene effects in expression of these characters. The predictability ratio indicated that all most all the characters were found to be governed by additive components of genetic variance whereas plant height, seed cotton yield per plant, seed index and fibre strength were found to be controlled by additive as well as non-additive genetic components of genetic variance.

In the present investigation the parents AKH-84635 and LRA-5166 expressed favorable GCA effects for most of the characters over the environments. Most of the cross combinations showed positive and significant specific combining ability effects for seed cotton yield per plant. Maximum positive significant SCA effects were recorded for seed cotton yield per plant in the cross by KH-118 x AKH-62 (17.15) followed by AKH-84635 x LRA-5166 (11.68) and JLH-1594 x AKH-24 (8.83). Whereas on average basis, the crosses viz., AKH-62 x AKH-44, AKH-84635 x LRA-5166 and KH-118 x AKH-62 having high specific combining ability may be identified for the exploitation of heterosis. The crosses viz., AKH-44 x LRA-5166 and JLH-1594 x LRA-5166 may be advanced in further generations for development of superior genotypes.

Implication

The crosses showing high mean performance, high heterosis, high SCA may be suitably evaluated for yield performance and utilize for the exploitation of the heterosis, while the crosses having good per se performance and good GCA effects should be advanced into F2 generation to isolate superior transgressive segregants. It can conclude from the present study that, the crosses AKH-44 x AKH-62, AKH-84635 x LRA-5166 and KH-118 x AKH-62 may be used for exploitation of heterosis; and the crosses AKH-44 x LRA-5166 and JLH-1594 x LRA-5166 may be utilized for development of superior genotypes.

Application of research: Estimation of Combining Ability of genotypes for utilization in Cotton Heterosis Breeding

Research Category: Plant Breeding, Cotton Hybrid Development

Abbreviations: GCA-General Combining Ability
SCA-Specific Combining Ability

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References

- [1] Abdurakhmonov Y., Kohel R.J., Yu J.Z., Pepper A.E., Abdullaev A.A., Kushanov F.N., Salakhutdinov I.B., Buriev Z.T., Saha S., Scheffler B.E., Jenkins J.N. and Abdurakimov A. (2008) *Genomics*, 92 (2), 478-487.
- [2] Anonymous (2020) Annual Report 2020, AICRP on Cotton, ICAR-CICR, Coimbatore (TN)
- [3] Bhatade S.S. (1982) *Cotton Develop.*, 11 (4), 31-34.
- [4] Chaudhari P.N., Borole D.N., Patil S.S. and Deshmukh M.P. (1993) *J. Maharashtra agric. Univ.*, 18(3), 418-420.
- [5] Deshpande L.A., Baig K.S. and Nagare V.P. (2003) *J. Maharashtra agric. Univ.*, 28(1), 36-39.
- [6] El Adl A.M., El Diasty Z.M., Awad A.A., Zenia A.M. and El Bary A.M.A. (2001) *Egyptian J. Agril. Res.*, 79(2), 625-646.
- [7] El Debaby A.S., Kassem M.M., Awaad M.M., Hemaida G.M. (1997) *Egyptian J. Agril. Res.*, 75(3), 753-757.
- [8] Fang D.D., Hinze L. L., Percy R.G., Li P.D. and Dewayne T.G. (2013) *Euphytica*, 191(3), 391.
- [9] Griffing B. (1956) *Aust. J. Biol. Sci.*, 9, 463-493.
- [10] Jagtap D.R. and Kolhe A.K. (1987) *Indian Soc. Cotton Improv. J.*, 12(1), 5-10.
- [11] Kaushik L.S., Singh D.D. and Paroda R.S. (1984) *Theor. Appl. Genet.*, 68(6), 487-491.
- [12] Nirania K.S., Chhabra B.S., Dutt Y. and Jain P.P. (2005) *J. Cotton Res. Dev.*, 19(1), 21-26.
- [13] Panse V.G. and Sukhatme P.V. (1967) *Statistical method for agricultural workers*, ICAR Publication, New Delhi.
- [14] Patel U.G. and Mehta N.P. (1989) *Cotton Dev.*, 18(3-4), 37-40.
- [15] Patil R.A., Chopde P.R. and Goud J.V. (1987) *Indian J. Agric. Sci.*, 57(6), 402-406.
- [16] Patil U.G., Patel K.G., Maisuria A.T. and Chhimpi B.G. (1997) *Gujarat Agric. Res. J.*, 23(1), 11-15.
- [17] Pavasia M.J., Shukla P.T. and Patel U.G. (1999) *J. Indian Soc. Cotton Improv.*, 24(1), 14-17.
- [18] Tyagi P., Gore M.A., Bowman D.T., Campbell B.T., Udall J.A., Kuraparthi V. (2014) *Theor Appl Genetics*, 127(2), 283-295.
- [19] Rakshe M. B., V. V. Ujjainkar and Pallavi Yergude (2019) *Multilogic in Science*, VIII (XXVIII) 131-135.
- [20] Sandhu B.S., Bhatia R.S., Singh A., Singh A., Verma M.M. and Virk D.S. and Chahal G.S. (1993) *Heterosis breeding in Deshi cotton. Crop Improvement Society of India, Ludhiana, India.*
- [21] Satange I. V. (1997) MSc Thesis, Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola, 444 104, Maharashtra, India.
- [22] Shummungavalli N. and Das L.D.V. (1995) *Madras Agric. J.*, 82(6-8), 449-452.
- [23] Singh R.K. and Chaudhary B.D. (1985) *Biometrical methods in Quantitative Genetics Analysis*, Kalyani Publication, Ludhiana.
- [24] Sprague G.F. and Tatum L.A. (1942) *J. Amer. Soc. Agron.*, 4 (2), 296-305.
- [25] Bharad S. (2004) PhD Thesis, Dr Panjabrao Deshmukh Krishi Vidyapeeth, Akola, 444 104, Maharashtra, India.
- [26] Tomar S.K. and Singh S.P. (1993) *Indian J. Genet.*, 53 (1), 40-46.
- [27] Tuteja O.P. (2014) *J. Cotton Res. Dev.*, 28(1), 1-6.
- [28] Ujjainkar V.V. and Patil V.D. (2020) *International Journal of Agriculture Sciences*, 12(12), 9991-9994.
- [29] Ujjainkar V.V., Patil V. D. and Moharil M.P. (2020) *International Journal of Genetics*, 12(6), 740-744.
- [30] Wendel J.F. and Albert V.A. (1992) *Systematic Botany*, 17(1), 115-143.
- [31] Xiaoli G., Yujie Q., Yinhua J., Shoupu H., Zhaoe P., Liru W. and Xiangming D. (2021) *BMC Genomics*, 22, 123.
- [32] Zareen Sarfraz, Muhammad Shahid Iqbal, Xiaoli Geng, Muhammad Sajid Iqbal, Mian Faisal Nazir, Haris Ahmed, Shoupu He, Yinhua Jia, Zhaoe Pan, Gaofer Sun, Saghir Ahmad, Qinglian Wang, Hongde Qin, Jinhai Liu, Hui Liu, Jun Yang, Zhiying Ma, Dongyong Xu, Jinlong Yang, Jinbiao Zhang, Zhikun Li, Zhongmin Cai, Xuelin Zhang, Xin Zhang, Aifen Huang, Xianda Yi, Guanyin Zhou, Lin Li, Haiyong Zhu, Baoyin Pang, Liru Wang, Junling Sun and Xiongming Du (2021) *Frontiers in Plant Science*, 12, 1-20.
- [33] Zhang Zheng Sheng, Li XianBi, Xiao YueHua, Luo Ming, Liu DaJun, Hunag Shun Li, Zhang FengXin (2003) *Agricultural Sciences in China*, 2(1), 13-18.
- [34] Zhou H., Zhang Y., Dong W.Q., Xu X.M. and Tang C.M. (2020) *Photosynthetica*, 59(1), 106-115.