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Combining ability analysis for different morphological traits in diallel crosses of upland cotton (*Gossypium hirsutum* L.)

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ABSTRACT : A diallel analysis was carried out to study combining ability for different morphological traits in upland cotton (*Gossypium hirsutum* L.). Nine parental genotypes were involved in this study and these were crossed in half diallel mating design during *kharif,* 2016. The F_1crosses along with their parents were sown during *kharif,* 2017 to study combining ability analysis for different morphological traits. For inheritance of traits both additive and non additive gene actions are important but in the present study there was pre ponderance of non additive gene action for all the characters studied. On the basis of GCA estimates parents H 1353 and H 1098i were the best general combiners for seed cotton yield/plant, whereas on the basis of SCA estimates best specific combiners for seed cotton yield/plant were H 1465 × H 1226, H 1300 × H 1226 and H 1490 × H 1464.

Key words : Combining ability, diallel cross, gene action, *Gossypium hirsutum* L.

Cultivation of cotton, a leading natural fibre crop, constitutes 85 per cent raw material of our textile industry. The major cotton growing states in India are Karnataka, Maharashtra, Gujarat, Haryana, Punjab, Andhra Pradesh, Telangana, Madhya Pradesh, Rajasthan and Tamil Nadu. Cotton is grown in more than 100 countries in the world. In India it is grown in nearly 12.2 million hectares which is almost 34.6 per cent of the world cotton acreage with a total production and productivity of 37.7 million bales and 524 kg/ha, respectively. Whereas, in Haryana its area, production and productivity is 6.56 lakh ha, 25 lakh bales and 648 kg/ha, respectively (Anonymous, 2018).

The choice of parents is the most decisive step in hybridization programmes since certain combinations create much superior offsprings than others involving apparently equally promising parents. Combining ability analysis helps in selecting parents which when crossed would produce more desirable segregants. Experimental evidence on GCA *vs* SCA was provided by Sprague and Tatum and Carnahan also suggested that GCAcould include additive effects as well as additive x additive interactions. The major breakthrough in this field came from the work of Griffing. Who gave a comprehensive account of combining ability analysis in diallel considering four different methods and four different models. In the present study we used Griffing Method 2 Model 1.

MATERIAL AND METHODS

The present investigation was carried

out at Cotton Research Area, Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar. The experimental materials comprised of nine promising parental lines (H 1098i, H 1300. H 1316, H 1353, H 1465, H 1476, H 1226, H 1490 and H 1464) which were grown during *kharif,* 2016. Hand emasculation was performed for crossing in Half diallel mating design excluding reciprocal crosses to obtain 36 F_1 crosses.A complete set of all entries comprising of nine parents and their 36 F_1s were sown in *kharif* 2017. The trial was conducted in a randomized block design (RBD) with three replications in a single row of 7.2m length adopting a spacing of 67.5 cm between rows and 60 cm between the plants. Five random and competitive plants excluding border plants were selected from each row in each replication to record the observations *viz.*, days to first flower, plant height (cm), monopods/plant, sympods/plant, bolls/plant, boll weight (g), seed cotton yield/plant (g), ginning outturn (%), seed index (g), lint index (g).The combining ability analysis for different characters was carried according to procedure detailed by Griffing Model I (fixed effect model) Method II (parents and one set of F_1s excluding reciprocals), where parents and F_1s were included without reciprocals.

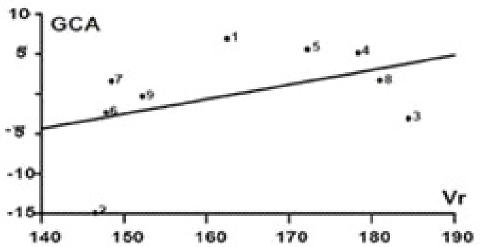
RESULTS AND DISCUSSION

Analysis of variance for combining ability unveiled the presence of considerable variability in parents and their hybrids for different characters under study.Combining ability is the ability of a line to give superior progeny consequent to hybridization with other lines. The magnitude of GCA variance was less than SCA variance indicating the preponderance of non additive gene action which is useful for exploitation of heterosis through hybrid breeding. Several researchers namely, Khan *et al.,* (2009) and Vekariya *et al.,* (2017) noticed supremacy of SCA variance in upland cotton for yield and its contributing characters.The term general combining ability is used to designate the mean or average performance of a genotype in cross combinations involving a set of other genotypes. The GCA effects emulate the breeding value of parental genotypes and it facilitates in finding the genotypes to be used for developing better or superior populations. The best combiner recorded for seed cotton yield was H 1353 whereas, best general combiner for traits *viz.*, boll weight, days to first flower (earliness), monopods/plant and lint index was H 1490. Among nine parents H 1300 was the poorest combiner for most of the traits studied (Table 1).

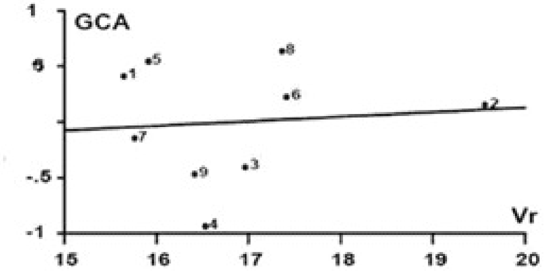
The results revealed that high negative SCA effects for days to first flower in negative direction (desirable) were recorded in crossed H 1098i × H 1226 (-3.83), H 1098i × H 1476 (-2.89), H 1316 × H 1465 (-2.64), H 1300 × H 1465 (-2.45) and H 1316 × H 1226(-2.43). Among these cross combinations crosses H 1316 × H 1465 and H 1316 × H 1226 includes H 1316 which is a poor combiner for this character, showing that additive and non additive both types of gene actions are important for this trait. Similar types of results were also reported by Reddy *et al.,* (2006), Lingaraja *et al.,* (2017) and Vekariya *et al.,* (2017). For plant height SCA effects were also reported in negative direction in the crosses H 1300 x H 1465 (-35.45) followed by H 1316 x H 1353.

Table 1. Best and poor general combiners for different morphological characters

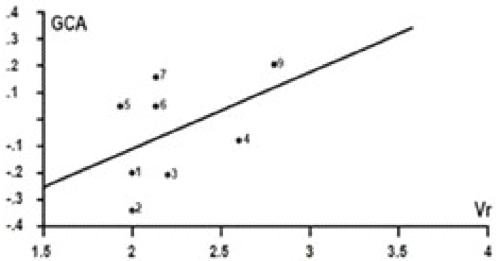
Character	Best combiners	Poor combiners
Seed cotton yield/plant (g)	H 1353 and H 1098i	H 1300
Bolls/plant	H 1226	H 1300
Boll weight (g)	H 1490	H 1465
Monopods/plant	H 1490 and H 1464	H 1300
Plant height (cm)	H 1098i and H 1465	H 1300
Days to first flower	H 1490	H 1316
Lint index	H 1490	H 1226



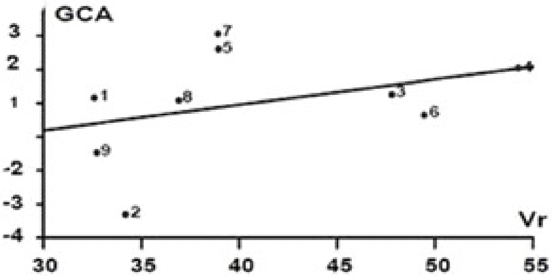
Graph 1. Plant height



Graph 2. No. of Sympods



Graph 3. No. of Monopods



Graph4. No. of balls

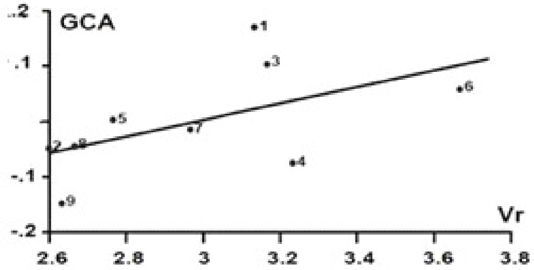
Maximum SCA effects for number of bolls were recorded in cross combinations H 1465 × H 1226 (good × good) and H 1098i × H 1300 (good × poor), while the high SCA effects for boll weight were reported in cross combinations H 1300 × H 1226 (good × poor) and H 1300 × H 1316 (good × poor). These results revealed the involvement of additive and non additive gene action with significant SCA effects for number of bolls and boll weight.

A concise description of the most promising cross combinations having high SCA effects for seed cotton yield and its attributing traits are given in Table 2. Out of 36 cross combinations 14 crosses were reported with positive significant results for seed cotton yield per plant. Most prominent among these combinations were H 1465 × H 1226 (41.88), H

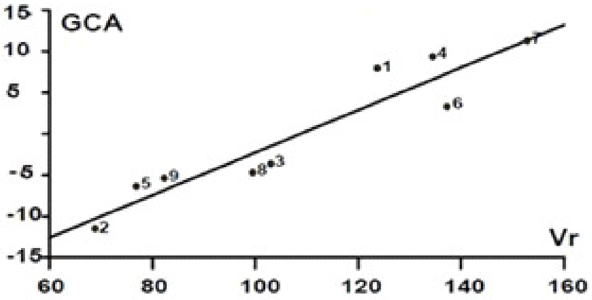
Table 2. Best and poor specific cross combinations for seed cotton yield and its attributing characters along with their *per se* performance

Characters	Best cross combinations		**Mean performance**		Poor cross combinations		**Mean performance**	
	1st	2nd	**1st**	**2nd**	1st	2nd	**1st**	**2nd**
Seed cotton yield/ plant (g)	H 1465 × H 1226 (41.88*)	H 1490 × H 1464 (27.54*)	**153.50**	**137.33**	H 1300 × H 1353 (-38.33*)	H 1476 × H 1226 (-29.17*)	**69.0**	**76.97**
Bolls/plant	H 1465 × H 1226 (18.33*)	H 1098i × H 1300 (11.06*)	**60.67**	**46.40**	H 1316 × H 1465 (-10.79*)	H 1476 × H 1490 (-9.81*)	**29.53**	**28.40**
Boll weight (g)	H1300 ×H 1226 (0.55*)	H 1300 × H 1316 (0.54*)	**3.47**	**3.57**	H 1300 × H 1353 (-0.47*)	H 1465 × H 1490 (-0.32*)	**2.60**	**2.73**

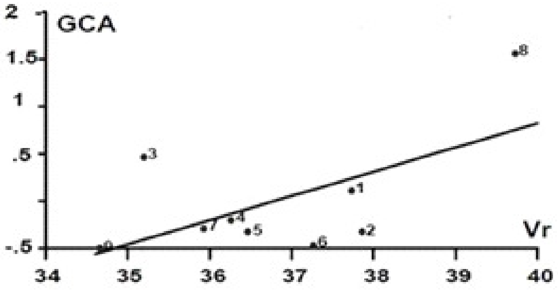
*Significant at 5%



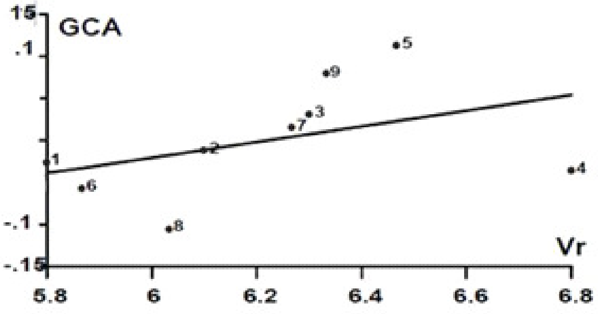
Graph 5. Boll weight



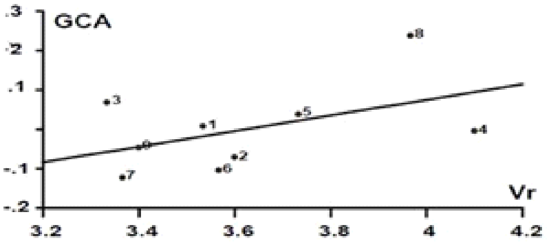
Graph 6. Seed cotton yield



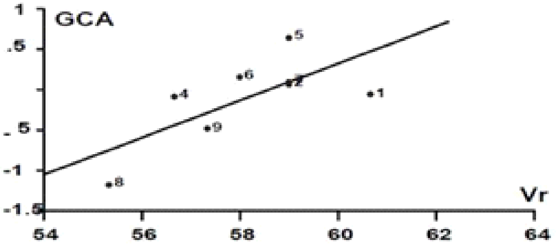
Graph 7. Ginning out turn



Graph 8. Seed index



Graph 9. Lint Index



Graph 10. Days to first flower

1490 × H 1464 (27.54) and H 1300 × H 1226 (25.36). It is also interesting to note that parallelism existed between SCA estimates for this best cross H 1465 × H 1226 also observed significant sca effects in case of number of boll per plant which found its suitability for increased seed cotton yield.These results confirm the findings of Rajamani *et al.,* (2014), Arbad *et al.* (2016) and Vekariya *et al.,* (2017).

The traits under study were also plotted on Wr - Vr graph to study the relationship between the parents. Wr/Vr graph is shown in Fig. 1-10. TheWr/Vr graph for the characters shown in Fig. 1-10, displayed that regression line passing through the Wr axis above the origin for all the observed traits except ginning out turn thus, indicating partial dominance with additive type of gene action. Significant positive correlation coefficient for plant height (r = 0.444), number of monopods (r = 624), no of sympod per plant (r = 0. 551), ball weight (r = 414), seed cotton yield (r = 512) and lint index (r= 0.411) between (Wr+Vr) and parental means, indicated that the parents containing dominant genes were responsible for the increased traitpercentage in F_1 generation. This position indicates genotype '3' (H 1316) has the highest plant height,genotype '5' (H 1465) has the highest no. of monopods, Genotype '2' (H 1300) has the highest no. of sympods, genotype '8' (H 1490) has highest ball weight and genotype '4' (H 1353) has highest seed cotton yield and lint index with most dominant genes. From the position of array points on regression line, genotype'1' (H 1098i) had maximum dominant genes by having dominance proportion for traits plant height, ball weight and seed cotton yield. Genotype'2' (H 1300) had maximum dominant genes by having dominance proportion for traits number of monopods and number of balls. Genotype'4' (H 1353) had maximum dominant genes for traits number of sympods and ball weight. Genotype'6' (H 1472), '7' (H 1226) and '8' (H 1490) had maximum dominant genes by having dominance proportion for traits lint index, GOT and seed index, respectively being nearer to the origin.

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