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Original Article

Genetic analysis for yield and its components in okra (*Abelmoschus esculentus* (L.) Moench)

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Abstract

Combining ability variances and effects of yield and its components in okra (*Abelmoschus esculentus* (L.) Moench) were studied through half diallel analysis of 45 F_1 hybrids derived by crossing 10 nearly homozygous germplasm lines namely P_1(IC282248), P_2(IC27826-A), P_3(IC29119-B), P_4(IC31398-A), P_5(IC45732), P_6(IC89819), P_7(IC89976), P_8(IC90107), P_9(IC99716) and P_{10}(IC111443) during mid *kharif* (July-October), 2009, at the Vegetable Research Station, Rajendranagar, Andhra Pradesh, India. Both additive and non-additive variances were important for a majority of the characters except plant height, fruit and shoot borer infestation on fruits and shoots and yellow vein mosaic virus infestation on plants. Genetic analysis revealed a preponderance of non-additive gene action for plant height, internodal length, days to 50% flowering, first flowering and fruiting node, fruit length and weight, total number of fruits and number of marketable fruits per plant, total yield and marketable yield per plant and yellow vein mosaic virus infestation on fruits and plants and a preponderance of additive gene action for number of branches per plant and fruit and shoot borer infestation on fruits and shoots. The parents P_5(IC45732), P_6 (IC89819) and P_7(IC89976) were high general combiners for total and marketable yield per plant and their associated traits, which could be exploited for developing prolific pure line varieties of okra. The crosses C_{23}(IC29119-B × IC99716), C_{17}(IC 27826-A × IC111443), C_{42}(IC89976 × IC111443) were superior specific combiners for total and marketable yield per plant with the potential of being commercially exploited for the production of F_1 hybrids. The cross combinations C_{42} (IC89976 × IC 111443) and (IC27826-A × IC89819) having one of the parents with positively significant general combining ability effects for total yield and marketable yield per plant could be utilized in recombination breeding with single plant selection in the passing generations to capitalize additive gene action to develop high yielding lines or varieties in okra.

Keywords: combining ability effects, gene effects, germplasm lines, half diallel analysis, half diallel crosses

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1. Introduction

The cultivated okra is *Abelmoschus esculentus* (L.) Moench. It is native of Ethiopia (Vavilov, 1951). It is a warm season fruit vegetable in the tropical and subtropical countries of the world. Apart from nutritional and health importance, okra plays an important role in income generation and subsistence among rural farmers in developing countries like India. It is commercially grown in the Indian states of Gujarat, Maharashtra, Andhra Pradesh, Karnataka and Tamilnadu. In Andhra Pradesh, it is cultivated over an area of about 0.02 million hectares with an annual production of 0.409 million tonnes and productivity of 15.0 tonnes ha^{-1} (NHB, 2010). The productivity of okra in Andhra Pradesh (15.0 t/ha) is higher than the national average (10.5 t/ha), but lower than in Egypt (15.7 t/ha). In spite of its importance, no major breakthrough has been made in this crop and the farmers are still growing their own local varieties or open pollinated varieties. This has raised concerns to breeders on the breeding for better okra varieties and their subsequent introduction in the country. Hence, there is a need for restructuring this vegetable crop for increasing the productivity.

Hybridization has been the most successful approach in increasing the productivity in vegetable crops. Selection of genetically superior and suitable genotypes is the most important stage from the standpoint of hybridization of vegetable crops in order to develop new genotypes having desirable characters. One of the main problems of vegetable breeders for developing high yielding varieties through either heterosis breeding or pedigree breeding is to select good parents and crosses. In a systematic breeding programme, it is essential to identify superior parents for hybridization and crosses to expand the genetic variability for selection of superior genotypes (Inamullah *et al.*, 2006). The value of any population depends on its potential *per se* and its combining ability in crosses. Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may not lead to expected degree of heterosis in F_1 generation or throw superior transgressive segregants in segregating generations. Thus, any method which would help in choosing desirable parents for hybridization will be important for the vegetable breeders. Combining ability analysis is important to decide parents, crosses and appropriate breeding procedure to be followed to select heterotic F_1 hybrids or desirable segregants (Salgotra *et al.*, 2009). Diallel analysis is one of the most powerful tools for characterizing the genetic architecture of plant materials and estimating the general combining ability (GCA) of parents and selecting of desirable parents and crosses with high specific combining ability (SCA) for the exploitation of heterosis (Sarker *et al.*, 2002).

In okra, pod yield and related traits are polygenically determined. Availability of genetically based variation for yield and its component traits is a prerequisite for the development of new cultivars of okra. Okra breeders all over the world have been utilizing the available genetic resources to modify the varieties to meet the ever changing requirement of their society. To explore the gene pool regarding the presence of variability and its genetic basis, combining ability analysis provides very useful information. Several researchers have made combining ability analysis of single crosses generated by crossing elite and diverse genotypes from the germplasm of okra (Pathak *et al.*, 2001; Kumar and Thania 2007). Diallel mating design has been used extensively by several researchers to measure gene action and combining ability for yield and yield components in okra (Bendale *et al.*, 2004; Jindal and Ghai, 2005; Dahake and Bangar, 2006; Bhalekar *et al.*, 2006; Jindal *et al.*, 2009; Singh *et al.*, 2009). Several workers studied gene action of the yield and yield attributes and determined that additive and non-additive variance components are important in the genetic control of yield and its associated traits in okra (Kumar *et al.*, 2006; Jaiprakashnarayan *et al.*, 2008; Jindal *et al.*, 2009; Singh *et al.*, 2009).

The present investigation was, therefore, undertaken with a set of half-diallel crosses to elicit information about the nature and magnitude of gene action and combining ability effects for yield and its components in okra so as to formulate suitable breeding strategy and isolate potential parents and promising crosses for further exploitation.

2. Materials and Methods

Ten elite, intermediary diverse and nearly homozygous lines of okra namely P_1(IC282248), P_2(IC27826-A), P_3 (IC29119-B), P_4(IC31398-A), P_5(IC45732), P_6(IC89819), P_7 (IC89976), P_8(IC90107), P_9(IC99716) and P_{10}(IC111443) were crossed in all possible combinations excluding reciprocals (n(n-1)/2) to develop 45 half diallel crosses during summer, 2009. Forty five F_1s along with their 10 parents and one standard check (Mahyco Hybrid No.10) were evaluated in a randomized block design with three replications during mid *kharif* (July-October), 2009 at the Vegetable Research Station, Rajendranagar, Andhrapradesh, India. In each replication, each entry was grown in a double-row plot of 3.0 m length and 1.2 m width, maintaining a row-to-row spacing of 60 cm and a plant-to-plant spacing of 30 cm and accommodating 10 plants per row and 20 plants per plot and entry. The recommended package of practices was followed to raise a successful crop. Regular plant protection measures were carried out to safeguard the crop from pests and diseases. Biometric observations were recorded on five randomly selected competitive plants in each genotype in each replication for plant height (cm), number of branches per plant, internodal length (cm), first flowering node, first fruiting node, fruit length (cm), fruit width (cm) and fruit weight (g) and on whole plot basis for days to 50% flowering, total number of fruits per plant, number of marketable fruits per plant, total yield per plant (g), marketable yield per plant (g), fruit and shoot borer (FSB) infestation on fruits and shoots (%) and yellow vein mosaic virus (YVMV) infestation on fruits and plants (%). The mean replicated values of FSB infestation on fruits and shoots and YVMV infestation on fruits were subjected to square root transformation, while the mean replicated values of YVMV infestation on plants were subjected to arc sin transformation to restore the distribution to normality. The data were subjected to analysis of variance (Panse and Sukhatme, 1985). The characters showing significant differences were subjected to combining ability analysis. General combining ability effects and specific combining ability effects were calculated as per Griffing's Method-II and Model-I (Griffing, 1956) as elaborated by Singh (1973). The variances for general combining ability and specific combining ability were tested against their respective error variances derived from analysis of variance reduced to mean level. Significance test for GCA and SCA effects were performed using t-test as suggested by Cochran and Cox (1950) and Wynne *et al.* (1970).

3. Results and Discussion

3.1 Analysis of variance for combining ability

Analysis of variance for combining ability (Table 1) revealed that the variances due to GCA (Table 1) were highly significant (p<0.01) for all the characters except YVMV infestation on plants. Variances due to SCA were highly significant (p<0.01) for all the characters except plant height and FSB infestation on fruits and shoots. Significance of the variances due to GCA as well as SCA implies that both the additive and non-additive components of heritable variance are responsible for variation observed for number of branches per plant, internodal length, days to 50% flowering, first flowering node, first fruiting node, fruit length, fruit width, fruit weight, total number of fruits per plant, number of marketable fruits per plant, total yield per plant, marketable yield per plant and YVMV infestation on fruits. Significance (p<0.01) of the variances due to GCA alone for plant height, FSB infestation on fruits and shoots reveals that only additive component of heritable variance is solely responsible for the variation of these traits. These findings are in line with those of several researchers, who also indicated the importance of both additive and non-additive components of heritable variance conditioning these characters in okra. Involvement of both additive and non-additive components of heritable variance was also reported by Jindal *et al.* (2009) for plant height, number of branches per plant, internodal length, first flowering node and marketable yield per plant, Dahake and Bangar (2006) for days to 50% flowering and Kumar *et al.* (2005) for first fruiting node, fruit length and width, total number of fruits per plant and total yield per plant.

3.2 Gene action

The ratio of GCA variance to SCA variance (Table 2) was lower than unity (<1) for plant height (0.413), internodal length (0.315), days to 50% flowering (0.413), first flowering node (0.366), first fruiting node (0.366), fruit length (0.481), fruit weight (0.927), total number of fruits per plant (0.059), number of marketable fruits per plant (0.083), total yield per plant (0.289), marketable yield per plant (0.311), YVMV infestation on fruits (0.056) and YVMV infestation on plants

Table 1. Analysis of variance for combining ability in okra

Character	Source of variation		
	GCA (9)	SCA (45)	Error (108)
Plant height (cm)	242.9164**	106.0535	71.5069
Number of branches per plant	0.9384**	0.0743**	0.0399
Internodal length (cm)	0.6585**	0.3083*	0.1816
Days to 50% flowering	1.0086**	0.4127*	0.2625
First flowering node	0.3600**	0.0876**	0.0053
First fruiting node	0.3600**	0.0876**	0.0053
Fruit length (cm)	3.1892**	0.5644**	0.0158
Fruit width (cm)	0.02142**	0.00193**	0.00005
Fruit weight (g)	5.3777**	0.5159**	0.0360
Total number of fruits per plant	2.9715**	3.7743**	1.0177
Number of marketable fruits per plant	2.5757**	2.5881**	0.7683
Total yield per plant (g)	3261.9460**	1118.5205**	250.3374
Marketable yield per plant (g)	2173.9287**	719.1504**	185.8249
FSB infestation on fruits (%)	0.0923**	0.0148	0.0110
FSB infestation on shoots (%)	0.1273**	0.0088	0.0084
YVMV infestation on fruits (%)	0.0582**	0.0754**	0.0209
YVMV infestation on plants (%)	9.7845	29.3500**	9.4734

* , ** Significant at 5 and 1% levels, respectively
Values in parentheses denote degrees of freedom

Table 2. Components of heritable variation and their ratios for yield and its components in okra

Character	σ^2GCA	σ^2SCA	σ^2GCA / σ^2SCA
Plant height (cm)	14.284	34.547	0.413
Number of branches per plant	0.075	0.034	2.206
Internodal length (cm)	0.040	0.127	0.315
Days to 50% flowering	0.062	0.150	0.413
First flowering node	0.030	0.082	0.366
First fruiting node	0.030	0.082	0.366
Fruit length (cm)	0.264	0.549	0.481
Fruit width (cm)	0.002	0.002	1.000
Fruit weight (g)	0.445	0.480	0.927
Total number of fruits per plant	0.163	2.757	0.059
Number of marketable fruits per plant	0.151	1.820	0.083
Total yield per plant (g)	250.967	868.183	0.289
Marketable yield per plant (g)	165.675	533.325	0.311
FSB infestation on fruits (%)	0.007	0.004	1.750
FSB infestation on shoots (%)	0.0099	0.0005	19.800
YVMV infestation on fruits (%)	0.003	0.054	0.056
YVMV infestation on plants (%)	0.026	19.877	0.001

σ^2GCA = General combining ability variance;
σ^2SCA = Specific combining ability variance

(0.001). The greater magnitude of SCA variance than that of GCA variance suggests the predominance of the non-additive gene action. The ratio of GCA variance to SCA variance was more than unity (>1) for number of branches per plant (2.206), FSB infestation on fruits (1.750) and FSB infestation on shoots (19.800). For these characters, the greater magnitude of GCA variance than that of SCA variance suggests the preponderance of the additive gene action. The ratio of GCA variance to SCA variance is equal to unity (=1) for fruit width (1.000). For this trait, the equal magnitude of GCA and SCA variances suggests the equal role of the both additive and non-additive gene actions. This investigation, therefore, revealed that both additive and non-additive gene effects were important in the genetic control of majority of the traits under study. Similar results were also reported for yield and its components in okra by several researchers. Preponderance of the non-additive gene action was also reported by Kumar *et al.* (2005) for plant height, number of branches per plant, internodal length, first fruiting node, fruit length and width, total number of fruits per plant and total yield per plant, Jaiprakashnarayan *et al.* (2008a) for days to 50% flowering and fruit weight and Jindal *et al.* (2009) for first flowering node. In such a situation, a breeding procedure that would take cognizance of the two types of gene effects simultaneously would be most desirable. The efforts may be initiated on the superior general and specific combining lines by following population improvement through reciprocal recurrent selection, which in turn would give good transgressive segregants.

3.3 Combining ability effects

Number of parents and crosses with significantly positive and negative GCA and SCA effects, respectively are presented in Table 3. The direction and degree of combining ability effects of ten parents and forty five crosses varied greatly from trait-to-trait. None of the parents or crosses was found to be consistently superior for all the traits.

Significance of mean squares for GCA suggests significant differences among the GCA effects of ten parental lines for almost all the traits except YVMV infestation on plants (Table 4). From the results of the GCA effects, it is evident that the magnitude of GCA effects was relatively higher in some of the parental lines for certain characters like plant height, total yield per plant and marketable yield per plant. High GCA effects for some or all of these characters in okra were also reported by Jaiprakashnarayan *et al.* (2008), Jaiprakashnarayan *et al.* (2008a), Singh *et al.* (2009) and Jindal *et al.* (2009). High GCA effects are attributed to additive or additive x additive gene effects, which represent the fixable genetic components of variance (Griffing, 1956).

Parental line P_7 was the high general combiner for plant height. Parental line P_5, P_6, P_7 and P_6 were the high general combiners for number of branches per plant. For internodal length, P_2 was the high general combiner. For days to 50% flowering, P_6 and P_9 were the high general combiners. Parental lines P_1, P_2, P_3, P_4, P_5 and P_9 were the high general combiners for both first flowering and fruiting nodes. For fruit length, parents P_3, P_5, P_6, P_7 and P_8 were the high general

Table 3. Number of parental lines and cross combinations with significantly positive negative general and specific combining ability effects for yield and its components in okra

Character	No. of parents with significant GCA effects		No. of crosses with significant SCA effects	
	Positive	Negative	Positive	Negative
Plant height (cm)	1	1	1	3
Number of branches per plant	4	4	5	3
Internodal length (cm)	1	1	3	1
Days to 50% flowering	2	1	3	3
First flowering node	3	6	15	9
First fruiting node	3	6	15	9
Fruit length (cm)	5	4	21	14
Fruit width (cm)	5	3	13	17
Fruit weight (g)	4	5	17	10
Total number of fruits per plant	1	1	11	6
Number of marketable fruits per plant	1	2	8	6
Total yield per plant (g)	3	3	9	6
Marketable yield per plant (g)	3	5	8	6
FSB infestation on fruits (%)	4	3	1	2
FSB infestation on shoots (%)	2	4	-	1
YVMV infestation on fruits (%)	1	1	8	4
YVMV infestation on plants (%)	1	-	3	6

GCA= General combining ability; SCA= Specific combining ability

combiners. Parental lines P_3, P_4, P_5, P_9 and P_{10} were the high general combiners for fruit width. For fruit weight, parents P_5, P_6, P_7 and P_{10} were the high general combiners. Parental line P_7 was the high general combiner for total number of fruits per plant and number of marketable fruits per plant. Parental lines P_5, P_6 and P_7 were the high general combiners for both total and marketable yield per plant. Parental lines P_2, P_4 and P_8 were the high general combiners for FSB infestation on fruits, while P_2, P_4, P_8 and P_9 were the high general combiners for FSB infestation on shoots. Parental line P_4 was the high general combiner for YVMV infestation on fruits. These parental lines with high GCA effects may be used in a multiple crossing programme for isolating desirable lines in okra. The selected lines from such multiple crosses could be released as conventional varieties or used as improved parents for F_1 hybrid production.

Negative combining ability effect is highly desirable for the earliness attributes like days to 50% flowering, first flowering node and first fruiting node. The parental line P_9 was found to be the high general combiner for all of the three earliness attributes, indicating its potential for exploiting earliness in okra. Similar results were also reported by Arora (1993). Parental lines P_5, P_6 and P_7 were high general combiners for total yield and marketable yield per plant. Interestingly, of the three high combiners identified for both total and marketable yield per plant (P_5, P_6 and P_7), P_5 was also the high general combiner for number of branches per plant, first flowering and fruiting nodes, fruit length, width and weight, P_6 was also high combiner for number of branches per plant, days to 50% flowering, fruit length and weight and P_7 was also high combiner for plant height, number of branches per plant, fruit length and weight, total number and number of marketable fruits per plant. From these results, it is evident that parental lines showing high general combining ability effects for total yield per plant and marketable yield per plant might be due to their high general combining ability effects for some of the yield-contributing characters. These findings are in agreement with the earlier findings of Pathak *et al.* (1998), Kumar (2001) and Rewale *et al.* (2003).

Significant SCA effects were observed in forty five single crosses for all the traits except plant height, FSB infestation on fruits and shoots. The top five crosses with significant SCA effects in desirable direction for each of the traits for which the mean squares due to SCA are significant are presented in Table 5. In general, a relatively higher magnitude of SCA effects was observed in many crosses for plant height, total number and number of marketable fruits per plant, total and marketable yield per plant and YVMV infestation on plants, which may probably be due to the formation of superior gene recombinations (Singh *et al.*, 1989). The negative SCA effects observed in some of the crosses for different characters might be due to the presence of unfavorable gene combinations in the parents for the respective traits. Of the various high specific combiners identified for

Table 4. Estimates of general combining ability effects of ten parental lines for yield and its components in okra

Parental line									
P1	P2	P3	P4	P5	P6	P7	P8	P9	P10
Plant height (cm)									
-1.40^{L}	-9.32**^{L}	0.21^{L}	3.41^{L}	0.95^{L}	0.23^{L}	8.70**^{H}	-0.71^{L}	-2.11^{L}	0.04^{L}
Number of branches per plant									
-0.29**^{L}	0^{L}	-0.28**	-0.26**^{L}	0.30**^{H}	0.55**^{H}	0.12*^{H}	-0.05^{L}	-0.21**^{L}	0.12*^{H}
Internodal length (cm)									
-0.09^{L}	-0.56**^{H}	-0.04^{L}	0.17^{L}	0.06^{L}	0.2^{L}	0.04^{L}	-0.15^{L}	0.25*^{L}	0.12^{L}
Days to 50% ^{L}									
-0.18^{L}	0.13^{L}	-0.26^{L}	0.07^{L}	-0.26^{L}	0.41**^{L}	0.07^{L}	0.04^{L}	-0.46**^{H}	0.43**^{L}
First flowering node									
-0.11**^{H}	-0.07**^{H}	-0.08**^{H}	-0.11**^{H}	-0.17**^{H}	0.35**^{L}	0.18**^{L}	0.04^{L}	-0.16**^{H}	0.13**^{L}
First fruiting node									
-0.11**^{H}	-0.07**^{H}	-0.08**^{H}	-0.11**^{H}	-0.17**^{H}	0.35**^{L}	0.18**^{L}	0.04^{L}	-0.16**^{H}	0.13**^{L}
Fruit length (cm)									
0.04^{L}	-0.31**^{L}	0.10**^{H}	-0.16**^{L}	0.73**^{H}	0.55**^{H}	0.38**^{H}	0.20**^{H}	-0.97**^{L}	-0.55**^{L}
Fruit width (cm)									
-0.05**^{L}	0.01^{L}	0.02**^{H}	0.05**^{H}	0.02** ^{H}	0.01^{L}	-0.04** ^{L}	-0.08** ^{L}	0.04** ^{H}	0.03** ^{H}
Fruit weight (g)									
0.05^{L}	-0.86**^{L}	-0.42**^{L}	-0.52**^{L}	1.01**^{H}	0.79**^{H}	0.59**^{H}	-0.81**^{L}	-0.20**^{L}	0.39**^{H}
Total number of fruits per plant									
-0.37^{L}	0.29^{L}	0.13^{L}	0.27^{L}	0.22^{L}	-0.28^{L}	0.93**^{H}	-0.02^{L}	-0.93**^{L}	-0.24^{L}
Number of marketable fruits per plant									
-0.66**^{L}	0.34^{L}	0.04^{L}	0.46^{L}	0.16^{L}	-0.17^{L}	0.70**^{H}	0.15^{L}	-0.74**	-0.24^{L}
Total yield per plant (g)									
-4.88^{L}	-13.73**^{L}	-7.13^{L}	-6.77^{L}	24.65**^{H}	11.61**^{H}	27.08**^{H}	-17.42**^{L}	-18.29**^{L}	4.87^{L}
Marketable yield per plant (g)									
-9.13*^{L}	-10.13**^{L}	-7.44*^{L}	-2.29^{L}	20.55**^{H}	10.99**^{H}	21.32**^{H}	-12.54**^{L}	-14.74**^{L}	3.40^{L}
FSB infestation on fruits (%)									
0.13**^{L}	-0.10**^{H}	0.07*^{L}	-0.10**^{H}	0.06*^{L}	-0.01^{L}	0.02^{L}	-0.14**^{H}	0.004^{L}	0.06*^{L}
FSB infestation on shoots (%)									
0.20**^{L}	-0.07**^{H}	0.09**^{L}	-0.12**^{L}	0.05^{L}	0.03^{L}	-0.02^{L}	-0.14**^{H}	-0.06*^{H}	0.04^{L}
YVMV infestation on fruits (%)									
0.16**^{L}	0.02^{L}	0.03^{L}	-0.10*^{L}	-0.04^{L}	-0.03^{L}	0.03^{L}	0.01^{L}	-0.04^{L}	-0.05^{L}
YVMV infestation on plants (%)									
1.72*^{L}	0.52^{L}	0.76^{L}	-1.48^{L}	-0.38^{L}	-0.16^{L}	0.3^{L}	-0.4^{L}	-0.97^{L}	0.09^{L}

P_1 = IC282248; P_2 = IC27826-A; P_3 = IC29119-B; P_4 = IC31398-A; P_5 = IC45732; P_6 = IC89819; P_7 = IC89976; P_8 = IC90107; P_9 = IC99716; P_{10} = IC111443

* , ** Significant at 5 and 1% levels, respectively

^{H} denotes significant general combining ability effect in favorable direction

^{L} denotes non-significant general combining ability effects in favorable direction, significant and non-significant general combining abi^{L}ity effects in unfavorable direction

each of the traits studied (Table 5), the cross $C_{36}(P_6xP_7)$ for number of branches per plant, $C_{44}(P_8 \times P_{10})$ for internodal length, $C_{17}(P_2 \times P_{10})$ for days to 50% flowering, $C_4(P_1xP_5)$ for first flowering and fruiting nodes, $C_{35}(P_5 \times P_{10})$ for fruit length, $C_{22}(P_3 \times P_8)$ for fruit width, $C_4(P_1xP_5)$ for fruit weight, $C_{23}(P_3 \times P_9)$ for total number of fruits per plant, number of marketable fruits per plant, total yield per plant and marketable yield per plant and $C_{14}(P_2 \times P_7)$ for YVMV infestation on fruits and plants were the best specific combiners. These best specific combiners having the highest magnitude of significant SCA effects in a favorable direction are recommended for heterosis breeding. The inter-crossing of these materials could, therefore, generate a population with a large gene pool, where genetic linkages and genetic blocks could be broken.

For yield detriments such as FSB infestation on fruits and shoots and YVMV infestation on fruits and plants, nega-

Table 5. Top five specific combiners with high specific combining ability effects and general combining ability effects of their parents for yield and its components of okra

Character/ Cross	SCA effect	GCA effect of itsparents		Character/ Cross	SCA effect	GCA effect of itsparents	
		Female	Male			Female	Male
Number of branches per plant				Fruit weight (g)			
C36(P6xP7)	0.57**	0.55**^{H}	0.12*^{H}	C4(P1xP5)	1.19**	0.05^{L}	1.01**^{H}
C6(P1xP7)	0.55**	-0.29**^{L}	0.12*^{H}	C35(P5xP10)	1.15**	1.01**^{H}	0.39**^{H}
C24(P3xP10)	0.47*	-0.28**^{L}	0.12*^{H}	C39(P6xP10)	1.05**	0.79**^{H}	0.39**^{H}
C31(P5xP6)	0.46*	0.30**^{H}	0.55**^{H}	C42(P7xP10)	0.98**	0.59**^{H}	0.39**^{H}
C44(P8xP10)	0.37*	-0.05^{L}	0.12*^{H}	C21(P3xP7)	0.91**	-0.42**^{L}	0.59**^{H}
Internodal length (cm)				Total number of fruits per plant			
C44(P8xP10)	-1.26**	-0.15^{L}	0.12^{L}	C23(P3xP9)	4.76**	0.13^{L}	-0.93**^{L}
-	-	-	-	C24(P3xP10)	3.23**	0.13^{L}	-0.24^{L}
-	-	-	-	C36(P6xP7)	2.66**	-0.28^{L}	0.93**^{H}
-	-	-	-	C42(P7xP10)	2.51**	0.93**^{H}	-0.24^{L}
-	-	-	-	C17(P2xP10)	2.49**	0.29^{L}	-0.24^{L}
Days to 50% flowering				Number of marketable fruits per plant			
C17(P2xP10)	-1.21**	0.13^{L}	0.43**^{L}	C23(P3xP9)	4.34**	0.004^{L}	-0.74**^{L}
C25(P4xP5)	-1.13*	0.07^{L}	-0.26^{L}	C24(P3xP10)	2.81**	0.004^{L}	-0.24^{L}
C16(P2xP9)	-0.99*	0.13^{L}	-0.46**^{H}	C36(P6xP7)	2.43**	-0.17^{L}	0.70**^{H}
-	-	-	-	C17(P2xP10)	2.09**	0.34^{L}	-0.24^{L}
-	-	-	-	C15(P2xP8)	1.74**	0.34^{L}	0.15^{L}
First flowering node				Total yield per plant (g)			
C4(P1xP5)	-0.55**	-0.11**^{H}	-0.17**^{H}	C23(P3xP9)	65.87**	-7.13^{L}	-18.29**^{L}
C11(P2xP4)	-0.48**	-0.07**^{H}	-0.11**^{H}	C42(P7xP10)	65.06**	27.08**^{H}	4.87^{L}
C39(P6xP10)	-0.39**	0.35**^{L}	0.13**^{L}	C17(P2xP10)	53.56**	-13.73**^{L}	4.87^{L}
C41(P7xP9)	-0.35**	0.18**^{L}	-0.16**^{H}	C43(P8xP9)	43.24**	-17.42**^{L}	-18.29**^{L}
C15(P2xP8)	-0.30**	-0.07**^{H}	0.04^{L}	C13(P2xP6)	42.51**	-13.73**^{L}	11.61**^{H}
First fruiting node				Marketable yield per plant (g)			
C4(P1xP5)	-0.55**	-0.11**^{H}	-0.17**^{L}	C23(P3xP9)	16.22**	-7.44**^{L}	-14.74**^{L}
C11(P2xP4)	-0.48**	-0.07**^{H}	-0.11**	C17(P2xP10)	45.15**	-10.13**^{L}	3.40^{L}
C39(P6xP10)	-0.39**	0.35**^{L}	0.13**^{L}	C42(P7xP10)	33.78**	21.32**^{H}	3.40^{L}
C41(P7xP9)	-0.35**	0.18**^{L}	-0.16**^{H}	C43(P8xP9)	32.51*	-12.54**^{L}	-14.74**^{L}
C15(P2xP8)	-0.30**	-0.07**H	0.04^{L}	C13(P2xP6)	32.28*	-10.13**^{L}	10.99**^{H}
Fruit length (cm)YVMV infestation on fruits (%)							
C35(P5xP10)	1.87**	0.73**^{H}	-0.55**^{L}	C14(P2xP7)	-0.61**	0.02^{L}	0.03^{L}
C42(P7xP10)	1.18**	0.38**^{H}	-0.55**^{L}	C2(P1xP3)	-0.45**	0.16**^{L}	0.03^{L}
C4(P1xP5)	0.92**	0.04^{L}	0.73**^{H}	C30(P4xP10)	-0.43**	-0.10*^{H}	-0.05^{L}
C11(P2xP4)	0.86**	-0.31**^{L}	-0.16**^{L}	C5(P1xP6)	-0.29*	0.16**^{L}	-0.03^{L}
C23(P3xP9)	0.86**	0.10**^{L}	-0.97**^{L}	-	-	-	-
Fruit width (cm)YVMV infestation on plants (%)							
C22(P3xP8)	0.15**	0.02**^{H}	-0.08**^{L}	C14(P2xP7)	-11.40**	0.52^{L}	0.30^{L}
C42(P7xP10)	0.08**	-0.04**^{L}	0.03**^{H}	C2(P1xP3)	-7.83**	1.72*^{L}	0.76^{L}
C41(P7xP9)	0.06**	-0.04**^{L}	0.04**^{H}	C24(P3xP10)	-6.19**	0.76^{L}	0.09^{L}
C28(P4xP8)	0.06**	0.05**^{H}	-0.08**^{L}	C30(P4xP10)	-5.91*	-1.48^{L}	0.09^{L}
C16(P2xP9)	0.05**	0.003^{L}	0.04**^{H}	C4(P1xP5)	-5.72*	1.72*^{L}	-0.38^{L}

* , ** Significant at 5 and 1% levels, respectively

^{H} denotes significant general combining ability effect in favorable direction

^{L} denotes non-significant general combining ability effects in favorable direction, significant and non-significant general combining ability effects in unfavorable direction tive combining ability effect is desirable. Parental lines P_2, P_4 and P_8 were found to be high general combiners for FSB infestation on fruits and shoots. Parental line P_4 was the high general combiner for YVMV infestation on fruits. Since screening of genotypes for reaction to FSB and YVMV was carried out in the field under natural conditions with regular plant protection measures, interpretation of results on FSB and YVMV would lead to exaggeration of facts. Hence, the genotypes could be screened under artificial epiphytotic conditions to get the real reaction of genotypes to both FSB and YVMV in okra.

The parental lines of the various cross combinations displayed very critical trends in their GCA effects for different characters (Table 5). Of the top five cross combinations showing positively significant SCA effects for total yield per plant, two crosses $C_{42}(P_7 \times P_{10})$ and $C_{13}(P_2 \times P_6)$ involved high x low general combiners as parents, while the remaining three crosses $C_{23}(P_3 \times P_9)$, $C_{17}(P_2 \times P_{10})$ and $C_{43}(P_8 \times P_9)$ involved low x low general combiners as parents. Of the top five crosses showing significantly positive SCA effects for marketable yield per plant, two crosses $C_{42}(P_7 \times P_{10})$ and $C_{13}(P_2 \times P_6)$ involved high x low general combiners as parents, while the remaining crosses $C_{23}(P_3 \times P_9)$, $C_{17}(P_2 \times P_{10})$ and $C_{43}(P_8 \times P_9)$ involved low x low general combiners as parents. For other yield associated traits also, the top five cross combinations exhibiting significant SCA effects in desirable direction involved high x high, high x low and low x low general combiners as parents. From the perusal of the GCA status of the parents of high specific combiners for various traits, it is evident that the high specific combiners involved high x high, high x low and x low general combiners as parents, indicating that high specific combiners are not only obtained from the combination of high x high general combiners but also obtained from the combination of high x low and low x low general combiners. Thus, high GCA effects of the parents, therefore, do not seem to be a reliable criterion for the prediction of high SCA effects. High performance of these crosses may be attributed to additive x additive (high x high), additive x dominance (high x low) or dominance x dominance (low x low) epistatic interactions (Patil *et al*., 1996; Rewale *et al*., 2003). Superiority of the cross combinations involving high x low or low x low general combiners as parents may be attributed to the genetic diversity in the form of number of heterozygous loci of the parents involved in the cross combinations (Shukla and Gautam, 1990; Kumar *et al*., 2006). In some of the characters studied, parents with high GCA effects produced hybrids with low SCA effects (data not shown). This may be due to the lack of complementation of the parental genes. On the other hand, parents with low GCA effects produced hybrids with high SCA effects (Table 5) which can be attributed to complementary gene action.

Of the top five promising specific combiners identified for total yield per plant and marketable yield per plant, only two crosses $C_{42}(P_7 \times P_{10})$ and $C_{13}(P_2 \times P_6)$ had one of the parents with high GCA effects. These could be utilized in recombination breeding with single plant selection in the passing generations to capitalize the additive gene action to develop lines or varieties with higher total as well as marketable yield per plant. Ahmed *et al*. (1997) also noted that when parents with high and low GCA effects were involved in a cross, the parent with low GCA effect could throw up desirable transgressive segregates giving rise to a desirable population. This is only possible if the additive genetic system present in the good general combiner and the complementary epistatic effect present in the crosses act in a complementary fashion to maximize desirable plant attributes which could be exploited for further breeding.

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