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Diallel Analysis for Yield and its Components in Okra (*Abelmoschus esculentus* (L.) Moench)

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ABSTRACT

Gene action and combining ability effects for yield and its components of okra (*Abelmoschus esculentus* (L.) Moench) were studied through 10 × 10 half-diallel analysis. Forty five single crosses were developed by crossing 10 lines of okra *viz*., 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) in a half-diallel manner during summer. All 45 F_1s along with their 10 counterpart parental lines were evaluated in a randomized block design with three replications during early *kharif* (June to September) of the same year at the Vegetable Research Station, Rajendranagar, Andhra Pradesh, India. Combining ability analysis following Method-II and Model-I of Griffing's approach revealed the preponderance of non-additive gene action for plant height, internode length, days to 50% flowering, first flowering node, first fruiting node, fruit length, fruit weight, total number of fruits/plant, number of marketable fruits/plant, total yield/plant, marketable yield/plant, fruit and shoot borer infestation on fruits and shoots and *Yellow vein mosaic virus* infestation on fruits and plants and additive gene action for number of branches/plant and equal importance of both additive and non-additive gene action for fruit width. The parental lines P_5(IC45732), P_6(IC89819) and P_7(IC89976) were high general combiners for total and marketable yield per plant and other yield associated traits. The crosses C_{23}(IC29119-B × IC99716), C_{17}(IC27826-A × IC111443), C_{42}(IC89976 × IC111443) and C_{43}(IC90107 × IC111443) were superior specific combiners for total and marketable yield/plant and other yield-related traits, which could be exploited for the production of F_1 hybrids. The cross C_{42}(IC89976 × IC111443), having one of the parents with significantly positive general combining ability effect for total and marketable yield/plant, could be utilized in recombination breeding.

Keywords: additive gene action, combining ability, general combining ability, non-additive gene action, specific combining ability

Abbreviations: FSB, fruit and shoot borer; **GCA**, general combining ability; **IC**, indigenous collection; **P**, parent; **SCA**, specific combining ability; **YVMV**, *Yellow vein mosaic virus*

INTRODUCTION

Okra (*Abelmoschus esculentus* (L.) Moench) belongs to the Malvaceae family. It is native to West Africa (Murdock 1959). It is especially valued for its fresh, thin, luxuriant green and tender fruits, which are used as a vegetable in different parts of the world. It is rich in valuable nutrients, low in calories, fat-free and provides a valuable supplementary nutrition in human diet in developing countries where there is often a great alimentary imbalance (Kumar and Sreeparvathy 2010). Okra has good medicinal value with its antispasmodic, demulcent, diaphoretic, diuretic, emollient, stimulant and vulnerary properties (Mehta 1959; Nadkarni 1972). Okra's potential as an industrial crop also has been tested in the developed world (Camciuc *et al.* 1998). It is an annual vegetable grown extensively in tropical, subtropical and Mediterranean climatic zones of the world (Hammon and Van Sloten 1989). Okra is the most popular and widely cultivated in an Indian state of Andhra Pradesh, which is one of the leading okra producing states of India with an area of 0.029 million ha and production of 0.439 million t/year (NHB 2010). The productivity of okra (NHB 2010) in Andhra Pradesh is higher (15.00 t/ha) than national average productivity (10.50 t/ha), but lower than that of Egypt (15.70 t/ha). This is because of the fact that okra is widely cultivated by the resource-poor small and marginal farmers, who still grow pure line varieties as a result of unavailability of high yielding and *Yellow vein mosaic virus* (YVMV) and fruit and shoot borer (FSB) resistant/tolerant cultivars or hybrids. The proportion of total yield to be sold as marketable yield is largely dependent on the incidence of FSB and YVMV, which are the important yield detriments in okra. Of these, YVMV is the most serious viral disease with an incidence of 3.2 to 97.8% (Sharma *et al.* 1987) causing yield loss of 10 to 90% (Jam-bale and Nerkar 1986). Hence, it is of practical importance to develop a high yielding variety or hybrid coupled with reistance/tolerance to YVMV.

The ultimate goal of any okra breeding programme is the maximization of marketable yield. There is no separate gene system for yield *per se* and yield is an end product of the multiplication interaction between the yield components (Grafius 1959). Griffing (1956) has suggested the possibility of working with yield components which are likely to be more simply inherited than is by itself. In okra, all growth, earliness and yield associated characters of economic importance are quantitatively inherited. Therefore, the improvement in yield through yield contributing traits depends on the nature and magnitude of heritable variation. Such characters are controlled by polygenes and are much influenced by environmental fluctuations. A breeder, therefore, should have information on the mode of inheritance and genetic architecture for yield and its component characters. This will enable breeder to decide suitable breeding methodology for the crop improvement programme. The major components of marketable yield in okra were plant height, number of branches/plant, first flowering and fruiting node, fruit length and weight, total number of fruits/plant, number

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of marketable fruits/plant and fruit and shoot bore infestation on fruits (Medagam *et al*. 2011).

Okra is an allopolyploid (Joshi and Hardas 1956) and an often-cross pollinated crop, which account for considerable variation in fruit yield and its associated traits. Considerable magnitude of genetic variability has been reported for yield and yield attributes of okra by several researchers (Dhall *et al*. 2003; Dakahe *et al*. 2007; Mohapatra *et al*. 2007; Reddy 2010). To develop varieties or hybrids, genetic variability is prerequisite, which can be created through either hybridization or hybridization, followed by selection in segregating generations. Hybridization is the most potent technique for breaking yield barriers and evolving varieties having high yielding potential. Selection of suitable parents is one of the most important steps in hybridization programme. 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. Therefore, selection of potential parents, based on genetic information and knowledge of their combining ability is very important.

Combining ability analysis is increasingly important in plant breeding. The concept of general combining ability (GCA) and specific combining ability (SCA) was introduced by Sprague and Tatum (1942) and its mathematical modeling was set about by Griffing (1956) in conjunction with the diallel crosses. Griffing (1956) made the best use of diallel mating design for the choice of better parents to be used in hybridization programme. A set of crosses produced by involving '*n*' lines in all possible combinations is designated as diallel cross and the analysis is known as diallel analysis. Diallel analysis has been identified as an important statistical tool for evaluating combining ability and genetic components underlying inheritance of biometric characters (Kehinde and Adeniji 2004). Diallel analysis provides a systematic approach for the detection of appropriate parents and crosses superior in terms of the investigated traits and also helps plant breeders to choose the most efficient selection method by allowing them to estimate several genetic parameters (Verhalen and Murray 1967). Among various diallel forms, the half-diallel technique that includes one set of single cross progeny and the parents have certain advantages over others, giving maximum information about genetic architecture of a trait, parents and allelic frequency (Kearsey 1965). Analysis of diallel data is usually conducted according to the methods of Griffing (1956) which partition the total variation of diallel data into GCA of the parents and SCA of the crosses (Yan and Hunt 2002).

Several researchers have made combining ability analysis of single crosses generated from 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 general and specific combining ability 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; Wammada *et al*. 2010). 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*. 2008a; Jindal *et al*. 2009; Singh *et al*. 2009; Wammada *et al*. 2010).

Hence, the present study was undertaken with the following objectives in mind: (1) To estimate the GCA and SCA variances in the okra population; this would indicate the nature of gene action governing the different characters under study and (2) To determine the GCA and SCA of parents and crosses respectively, that will identify superior parents and cross combinations.

MATERIALS AND METHODS

The material for the present study comprised of a set of 55 entries involving 10 horticulturally superior, genetically divergent and nearly homozygous parental lines of okra *viz*., IC282248(P_1), IC27826-A(P_2), IC29119-B(P_3), IC31398-A(P_4), IC45732(P_5), IC89819(P_6), IC89976(P_7), IC90107(P_8), IC99716(P_9) and IC111443(P_{10}) and their 45 half-diallel progenies. The experiment was conducted in a randomized block design with three replications during early *kharif* (1st June to 30th September), 2009 at the Vegetable Research Station, Rajendranagar, Andhra Pradesh, India. Each entry was raised in a double-row plot of 3.0 m length and 1.2 m width. A row-to-row and plant-to-plant distance of 60 and 30 cm, respectively was maintained to accommodate 10 plants/row and 20 plants/plot and entry. Recommended cultural practices were followed to raise the crop. Regular plant protection measures were carried out to safeguard the crop from major insect pests and diseases. Quantitative data were recorded on 17 characters. In each entry and in each replication, observations on plant height (cm), number of branches/plant, internode length (cm), first flowering node, first fruiting node, fruit length (cm), fruit width (cm) and fruit weight (g) were recorded on five randomly selected competitive plants, but observations on days to 50% flowering, total number of fruits/plant, number of marketable fruits/plant, total yield/plant (g), marketable yield/plant (g), FSB infestation on fruits and shoots (%) and YVMV infestation on fruits and plants (%) were recorded on whole plot basis. The replication mean values of FSB infestation on fruits and shoots (%) and YVMV infestation on fruits (%) were subjected to square root transformation while YVMV infestation on plants (%) were subjected to arcsine transformation to restore distribution to normality. The data were analysed according to analysis of variance (ANOVA) (Panse and Sukhatme 1985) to determine the significance of differences among the genotypes for all the characters. 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 ANOVA 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).

RESULTS AND DISCUSSION

The rapidly increasing vegetarian population of the world necessitates intensifying breeding programmes in vegetable crops for increasing vegetable yield potential. There is a need to develop vegetable genotypes having better yield potential per unit area. This could be achieved only by exploring maximum genetic potential from available germplasm of vegetable crops.

One of the major problems in okra cultivation in India is lack of location specific high-yielding varieties coupled with resistance to YVMV. The increase in yield per unit area of the crop is a prime concern of okra breeding programmes. In often cross-pollinated crops like okra, improvement in the past was based on selection in locally adapted populations. During recent past, exploitation of hybrid vigour and selection of parents on the basis of combining ability effects have opened a new line of approach in crop improvement. The productivity of okra should be increased by improving the genetic architecture through hybridization.

In earlier days, breeders used to select the parents for hybridization either on the basis of their *per se* performance or sometimes arbitrarily. The common approach of selecting the parents on the basis of *per se* performance does not necessarily lead to fruitful results (Allard 1960). Combining ability analysis is one of the potential tools for identifying prospective parents for hybridization and shifting productive hybrids from a set of crosses in F_1 generation (Griffing 1956). According to Jensen (1970), diallel mating offers advantages like broad use of germplasm, simultaneous input of parents, creation of dynamic gene-pools and fostering genetic recombination. There is an opportunity, therefore, for gene exchange and recombination through crossing and introgression from many varieties (Clarke and MacRae 1985). Diallel analysis provides comprehensive and useful genetic information about the material under investigation

Table 1 Analysis of variance for combining ability in okra.

Character	Mean sum of squares		
	GCA (9)	SCA (45)	Error (108)
Plant height (cm)	190.4602*	96.2894	80.4337
Number of branches/plant	1.0413**	0.0864*	0.0518
Internodal length (cm)	0.6307**	0.3096*	0.1797
Days to 50% flowering	1.2617**	0.3800*	0.2290
First flowering node	0.3609**	0.0831**	0.0033
First fruiting node	0.3609**	0.0831**	0.0033
Fruit length (cm)	3.2546**	0.5752**	0.0167
Fruit width (cm)	0.0220**	0.0020**	0.0001
Fruit weight (g)	5.4086**	0.5301**	0.0421
Total number of fruits/plant	2.634**	3.528**	0.831
Number of marketable fruits/plant	2.4610**	2.5620**	0.6439
Total yield/plant (g)	3071.3242**	1066.4996**	196.2407
Marketable yield/plant (g)	2093.6121**	719.3147**	153.8157
FSB infestation on fruits (%)	0.1595**	0.0080	0.0107
FSB infestation on shoots (%)	0.1515**	0.0086	0.0093
YVMV infestation on fruits (%)	0.0822**	0.0869**	0.0249
YVMV infestation on plants (%)	32.0592**	33.4480**	8.8313

*, ** 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)	9.169	15.856	0.578
Number of branches/plant	0.082	0.035	2.343
Internodal length (cm)	0.038	0.130	0.292
Days to 50% flowering	0.086	0.151	0.570
First flowering node	0.030	0.080	0.375
First fruiting node	0.030	0.080	0.375
Fruit length (cm)	0.270	0.558	0.484
Fruit width (cm)	0.002	0.002	1.000
Fruit weight (g)	0.447	0.488	0.916
Total number of fruits/plant	0.150	2.698	0.056
Number of marketable fruits/plant	0.151	1.918	0.079
Total yield/plant (g)	239.590	870.259	0.275
Marketable yield/plant (g)	161.650	565.499	0.286
FSB infestation on fruits (%)	0.012	-0.003	-4.000
FSB infestation on shoots (%)	0.012	-0.001	-12.000
YVMV infestation on fruits (%)	0.005	0.062	0.081
YVMV infestation on plants (%)	1.936	24.617	0.079

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

and thus has great practical utility in the improvement of crop species. Such an analysis provides information on (i) the nature and magnitude of genetic parameters and (ii) general and specific combining ability of parents and their crosses, respectively.

Analysis of variance for combining ability

The results of the analysis of variance of combining ability are summarized in **Table 1**. Analysis of variance of combining ability revealed significance of mean squares due to GCA for all the characters and significance of mean squares due to SCA for majority of the characters except plant height, FSB infestation on fruits and FSB infestation on shoots. Significance of the variances due to both GCA and SCA (**Table 1**) implies that both the additive and non-additive components of heritable variance are responsible for variation observed for number of branches/plant, internode length, days to 50% flowering, first flowering node, first fruiting node, fruit length, fruit width, fruit weight, total number of fruits/plant, number of marketable fruits/plant, total yield/plant, marketable yield/plant, YVMV infestation on fruits and YVMV infestation on plants. Significance ($P = 0.05$) of the variances due to GCA alone for plant height, FSB infestation on fruits and FSB infestation on shoots suggests that only the additive component of heritable variance is responsible for variation of these attributes. These findings are in line with those of Ahmed *et al.* (1997), Sundhari *et al.* (1992), and Wammada *et al.* (2010), who also indicated the importance of both additive and non-additive components of heritable variances conditioning these characters in okra.

Gene action

It is well recognized that knowledge and understanding of the genetic basis of economic traits is important to enhance the progress in breeding new varieties of a crop. Diallel crosses have been widely used in genetic research to investigate the inheritance of important traits among a set of genotypes. The GCA and SCA variances are related to the type of gene action involved. Variance for GCA includes additive portion while that of SCA includes non-additive portion of total variance arising largely from dominance and epistatic deviations (Rojas and Sprague 1952).

In okra, most of the economic characters are polygenically controlled and are, therefore, greatly influenced by the environment in which it is grown. Hence, it is essential to partition the overall variability into heritable and non-heritable components. Further, it is also essential to partition heritable variation into additive (fixable) and non-additive (non-fixable) components. The partitioning of heritable variation into its components is useful to provide information on the inheritance of quantitative characters. According to Adeniji and Kehinde (2003), estimates of gene effects have a direct bearing on the breeding methods that could be adopted in crop improvement programme. In order to develop pure line varieties in okra, estimates of additive effects are very useful. In order to develop hybrid varieties in okra, estimates of non-additive effects are very useful. Also, understanding the mechanism of gene action in the inheritance of yield and yield associated characters in okra will aid the development of appropriate breeding strategies for the improvement of okra for yield and yield components in a given environment.

However, since additive gene effect is the genetic expression of a mid-parent value, and is expressed in both homozygotes and heterozygotes, it can be selected for in each generation. Thus, the additive portion of genetic variation is more important in self-pollinated crops and it is of use to the breeder if he wants to release a true breeding variety. The dominance gene effect is only found in heterozygotes and will disappear with each generation of selfing after a cross and hence delays selection in early generations (Strickberger 1990). According to Baker (1978), when crossing for quantitative traits, populations that reveal high GCA estimates for a character could serve as good parents for a diallel (or half-diallel) cross.

In the present study, Model-I was involved in the estimation of variance components, which were subsequently used to estimate the GCA variance (σ^2GCA) and SCA variance (σ^2GCA) ratios. The ratio of GCA variance to SCA variance (**Table 2**) was lower than unity (<1) for plant height (0.578), internode length (0.292), days to 50% flowering (0.570), first flowering node (0.375), first fruiting node (0.375), fruit length (0.484), fruit weight (0.916), total number of fruits/plant (0.056), number of marketable fruits/plant (0.079), total yield/plant (0.275), marketable yield/plant (0.286), FSB infestation on fruits (-4.000), FSB infestation on shoots (-12.000), YVMV infestation on fruits (0.081) and YVMV infestation on plants (0.079). The greater magnitude of SCA variance than that of GCA suggests the predominance of the non-additive gene action involved in the inheritance of these traits. The ratio of GCA variance to SCA variance (**Table 2**) is more than unity (>1) for number of branches/plant (2.343). For this character, the greater magnitude of GCA variance than that of SCA suggests the predominance of the additive gene action. The ratio of GCA variance to SCA variance (**Table 2**) 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.

Growth attributes like plant height and internode length were under the preponderance of non-additive gene action, while number of branches per plant was under the preponderance of additive gene action. Similar gene action was also reported by Kumar *et al.* (2005), Bhalekar *et al.* (2006), Dahake and Bangar (2006), Singh *et al.* (2006), Kumar *et al.* (2006), Jindal *et al.* (2009) and Wammada *et al.* (2010) for plant height, Patil *et al.* (1996), Ahmed *et al.* (1997), Kumar *et al.* (2005), Bhalekar *et al.* (2006), Singh *et al.* (2006), Jaiprakashnarayan *et al.* (2008b), Jindal *et al.* (2009), Khanpara *et al.* (2009) and Wammada *et al.* (2010) for internode length and by Partap and Dhankar (1980) and Singh *et al.* (2009) for number of branches/plant in okra.

All earliness attributes *viz.*, days to 50% flowering, first flowering node and first fruiting node were under the preponderance of non-additive gene action. The present results are in conformity with earlier reports of Patil *et al.* (1996), Dahake and Bangar (2006), Singh *et al.* (2006), Jaiprakashnarayan *et al.* (2008a) and Wammada *et al.* (2010) for days to 50% flowering, Singh *et al.* (2006) and Jindal *et al.* (2009) for first flowering node and Kumar *et al.* (2005) and Bhalekar *et al.* (2006) for first fruiting node in okra.

Fruit traits like fruit length and weight were under the preponderance of non-additive gene action. Similar type of gene action was also reported by Patil *et al.* (1996), Kumar *et al.* (2005), Dahake and Bangar (2006), Singh *et al.* (2006), Kumar *et al.* (2006) and Wammada *et al.* (2010) for fruit length and Singh *et al.* (2006), Kumar *et al.* (2006) and Jaiprakashnarayan *et al.* (2008a) for fruit weight. However, both additive and non-additive gene actions were equally important for fruit width. These findings differ to the findings of Sundhari *et al.* (1992), Kumar *et al.* (2005), Singh *et al.* (2006) and Wammada *et al.* (2010), who reported the preponderance of non-additive gene action.

There was a predominant role of non-additive gene action for total number of fruits and number of marketable fruits/plant. These results are in accordance with the earlier findings of Patil *et al.* (1996), Kumar *et al.* (2005), Dahake and Bangar (2006), Singh *et al.* (2006), Kumar *et al.* (2006), Jaiprakashnarayan *et al.* (2008a) and Wammada *et al.* (2010) for total number of fruits and Patil *et al.* (1996) for number of marketable fruits/plant in okra.

Total and marketable yield/plant were also under the preponderance of non-additive gene action. These results agree with the earlier findings of Kumar *et al.* (2005), Dahake and Bangar (2006), Singh *et al.* (2006), Kumar *et al.* (2006), Jaiprakashnarayan *et al.* (2008a) and Wammada *et al.* (2010) for total yield/plant and Pathak *et al.* (1998) and Rewale *et al.* (2003) for marketable yield/plant in okra.

FSB and YVMV are the most important detriments to yield in okra. YVMV infestation was under the preponderance of non-additive gene action. These results agree with the findings of Nerkar and Jambhale (1985) and Rattan and Arvind (2000) who also reported the preponderance of non-additive gene action governing YVMV infestation in okra. The ratio of GCA variance to SCA variance of less than unity (<1) for FSB infestation on fruits and shoots indicated the preponderance of non-additive gene action involved in the inheritance of these traits. These findings agree with those of Patil *et al.* (1996) for FSB infestation on fruits. Since additive gene action is responsible for the inheritance of number of branches/plant and FSB infestation on fruits and shoots, direct selection by pure line selection or mass selection or, progeny selection or hybridization and, selection with pedigree method could be employed to improve these traits. Therefore, it is recommended to undertake either direct selection or hybridization among the promising parents for genetic improvement of these characters in okra.

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. It was apparent that the non-additive gene action was discovered to be more important than the additive gene effect as majority of the ratios were less than unity. Similar results were also reported for yield and its components in okra by several researchers (Bhalekar *et al.* 2006; Jindal *et al.* 2009; Singh *et al.* 2009). The reason for such a result was due to the fact that the parental lines used for this study were selected for divergence for most of the traits. A breeding procedure that would take cognizance of the two types of gene effects simultaneously would be most desirable. In view of the above, it is suggested that a breeding approach which can mop up the fixable additive gene action and at the same time maintain considerable heterozygosity for exploiting the non-additive gene action may prove most beneficial in improving this vegetable crop. 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.

Combining ability

The degree and direction of combining ability effects varied greatly among different traits and genotypes. Some of the parents and crosses exhibited significant or non-significant combining ability in desirable and undesirable direction (data not shown). Number of parents and crosses with significantly positive and negative GCA and SCA effects are presented in **Table 3**.

Table 3 Number of parental lines and cross combinations with significantly positive and 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	-	-
Number of branches/plant	2	4	6	2
Internodal length (cm)	1	1	3	3
Days to 50% flowering	2	3	4	1
First flowering node	4	6	17	12
First fruiting node	4	6	17	12
Fruit length (cm)	5	4	20	13
Fruit width (cm)	5	3	13	18
Fruit weight (g)	4	5	16	9
Total number of fruits/plant	1	1	10	6
Number of marketable fruits/plant	2	2	7	4
Total yield/plant (g)	3	4	11	7
Marketable yield/plant (g)	3	5	11	6
FSB infestation on fruits (%)	3	3	-	-
FSB infestation on shoots (%)	3	5	-	-
YVMV infestation on fruits (%)	1	-	9	4
YVMV infestation on plants (%)	1	1	9	4

GCA= General combining ability; SCA= Specific combining ability

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

Parental lines									
P_1	**P_2**	**P_3**	**P_4**	**P_5**	**P_6**	**P_7**	**P_8**	**P_9**	**P_{10}**
Plant height (cm)									
-1.50^{L}	-8.38^{**L}	0.06^{L}	2.74^{L}	1.36^{L}	-0.21^{L}	7.62^{**H}	-0.68^{L}	-1.49^{L}	0.49^{L}
Number of branches/plant									
-0.29^{**L}	0.03^{L}	-0.28^{**L}	-0.30^{**L}	0.29^{**H}	0.60^{**H}	0.10^{L}	-0.02^{L}	-0.25^{**L}	0.12^{L}
Internodal length (cm)									
-0.08^{L}	-0.55^{**H}	-0.06^{L}	0.14^{L}	0.07^{L}	0.18^{L}	0.01^{L}	-0.12^{L}	0.25^{*L}	0.15^{L}
Days to 50% flowering									
-0.27^{*H}	0.12^{L}	-0.18^{L}	0.21^{L}	-0.35^{**H}	0.40^{**L}	0.04^{L}	0.01^{L}	-0.49^{**H}	0.51^{**L}
First flowering node									
-0.13^{**H}	-0.06^{**H}	-0.10^{**H}	-0.12^{**H}	-0.16^{**H}	0.35^{**L}	0.18^{**L}	0.04^{**L}	-0.16^{**H}	0.14^{**L}
First fruiting node									
-0.13^{**H}	-0.06^{**H}	-0.10^{**H}	-0.12^{**H}	-0.16^{**H}	0.35^{**L}	0.18^{**L}	0.04^{**L}	-0.16^{**H}	0.14^{**L}
Fruit length (cm)									
0.03^{L}	-0.33^{**L}	0.10^{**H}	-0.19^{**L}	0.75^{**H}	0.55^{**H}	0.39^{**H}	0.22^{**H}	-0.96^{**L}	-0.56^{**L}
Fruit width (cm)									
-0.05^{**L}	0.001^{L}	0.02^{**H}	0.05^{**H}	0.02^{**H}	-0.002^{L}	-0.03^{**L}	-0.08^{**L}	0.04^{**H}	0.03^{**H}
Fruit weight (g)									
0.04^{L}	-0.83^{**L}	-0.43^{**L}	-0.53^{**L}	1.01^{**H}	0.82^{**H}	0.57^{**H}	-0.82^{**L}	-0.21^{**L}	0.40^{**H}
Total number of fruits/plant									
-0.38^{L}	0.4^{L}	0.1^{L}	0.21^{L}	0.24^{L}	-0.32^{L}	0.83^{**H}	-0.04^{L}	-0.85^{**L}	-0.19^{L}
Number of marketable fruits/plant									
-0.71^{**L}	0.45^{*H}	-0.1^{L}	0.32^{L}	0.16^{L}	-0.29^{L}	0.72^{**H}	0.17^{L}	-0.60^{**L}	-0.13^{L}
Total yield/plant (g)									
-5.07^{L}	-11.62^{**L}	-7.46^{L}	-7.62^{*L}	24.96^{**H}	11.26^{**H}	25.04^{**H}	-17.88^{**L}	-17.31^{**L}	5.7^{L}
Marketable yield/plant (g)									
-10.14^{**L}	-8.20^{*L}	-8.88^{*L}	-4.33^{L}	20.54^{**H}	9.47^{**H}	21.27^{**H}	-12.23^{**L}	-12.72^{**L}	5.22^{L}
FSB infestation on fruits (%)									
0.12^{**L}	-0.10^{**H}	0.17^{**L}	-0.03^{L}	0.11^{**L}	0.04^{L}	-0.03^{L}	-0.21^{**H}	-0.07^{*H}	-0.01^{L}
FSB infestation on shoots (%)									
0.20^{**L}	-0.08^{**H}	0.12^{**L}	-0.10^{**H}	0.05^{L}	0.04^{L}	-0.06^{*H}	-0.15^{**H}	-0.08^{**H}	0.05^{*L}
YVMV infestation on fruits (%)									
0.21^{**L}	0.002^{L}	0.002^{L}	-0.09^{L}	-0.07^{L}	-0.01^{L}	0.01^{L}	0.02^{L}	-0.04^{L}	-0.04^{L}
YVMV infestation on plants (%)									
4.20^{**L}	0.08^{L}	-0.19^{L}	-1.66^{*H}	-1.4^{L}	-0.36^{L}	0.37^{L}	0.46^{L}	-0.85^{L}	-0.65^{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 ability effects in unfavorable direction

Of the 17 characters, plant height, number of branches/plant and internode length largely determine the fruit-bearing surface thus considered as growth attributes. Okra bears pods at almost all nodes on the main stem and primary branches. The higher the plant height with more branches on the main stem, the higher the number of fruits/plant because of more nodes for a given internode length. Shorter internode distance results in more nodes leading to higher fruit number hence, fruit production. Thus, positive combining ability effect is desirable for plant height and number of branches, while negative combining ability effect is desirable for internode length to accommodate more nodes for higher fruit yield.

The most important breeding objective in okra is to breed for earliness. Days to 50% flowering, first flowering node and first fruiting node are the indicators of earliness. Early flowering not only gives early pickings and better returns but also widens fruiting period of the plant. Flowering and fruiting at lower nodes contributes in increasing the number of fruits/plant and early harvest. Negative combining ability effect is highly desirable for all these three attributes of earliness.

Total number of fruits/plant and, fruit length, width and weight are considered to be associated directly with total yield/plant, for which positive combining ability effect is desirable. Positive combining ability effect is desirable for both total and marketable yield/plant. For yield detriments such as FSB infestation on fruits and shoots and YVMV infestation on fruits and plants, negative combining ability effect is desirable.

General combining ability of parents

Significance of mean squares for GCA suggests significant differences among the GCA effects of 10 parental lines for all the 17 traits under study. The GCA effects of the parents revealed that none of the parents were found to be a good general combiner for all the characters studied. A wide range of variability of GCA effects was observed among the parents. The parental lines with significant general combining ability effects in desirable direction are categorized as high general combiners, while the lines with non-significant general combining ability effects in desirable direction, significant and non-significant general combining ability effects in undesirable direction are categorized as low general combiners (**Table 4**). 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 and marketable yield/plant and YVMV infestation on plants. High GCA effects for some or all of these characters in okra were also reported by Jaiprakashnarayan *et al.* (2008a, 2008b), Jindal *et al.* (2009) and Singh *et al.* (2009). High GCA effects are related to additive gene effects or additive × additive effects, which represent the fixable genetic components of variance, as also pointed out by Griffing (1956). The high magnitude of GCA effects observed for different attributes of economic importance may be useful for sorting outstanding parents with favorable alleles for different attributes of pod yield.

Study of general combining abilities resulted in the identification of a good number of high general combiners in okra. Parental line P_7 was the high general combiner for plant height. Parental lines P_5 and P_6 were the high general combiners for number of branches/plant. For internode length, P_2 was the high general combiner. For days to 50% flowering, P_1, P_5 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 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/plant. For number of marketable fruits/plant, parental lines P_2 and P_7 were the high general combiners. Parental lines P_5, P_6 and P_7 were the high general combiners for both total and marketable yield/plant. Parental lines P_2, P_8 and P_9 were the high general combiners for FSB infestation on fruits, while P_2, P_4, P_7, P_8 and P_9 were the high general combiners for FSB infestation on shoots. None of the parental lines was the high general combiner for YVMV infestation on fruits, while parental line P_4 was the high general combiner for YVMV infestation on plants.

From the results of general combining ability effects on growth attributes, it is evident that none of the 10 parents was found to be consistently superior for all or few of the growth attributes under study. The parental lines P_1(IC282248), P_5(IC45732) and P_9(IC99716) were found to be high general combiners for all of the three earliness attributes under study *viz*., days to 50% flowering, first flowering node and first fruiting node. These parental lines indicate their role in breeding of varieties for earliness.

Parental lines P_2, P_8 and P_9 were found to be high general combiners for FSB infestation on fruits as well as on shoots, while parental line P_4 was found to be superior general combiner for YVMV infestation on plants. 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 an 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 high general combiners for yield and its components identified in this study will produce useful transgressive segregants for selection when crossed together. The high general combiners identified for different traits are thus recommended for use in breeding programmes to generate genetic variability in desirable direction for effective selection to improve a specific trait. The parental lines with high GCA 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. Ariyo (1993) reported that the parental varieties that showed good general combining ability may be used in a multiple crossing programme for isolating high yielding varieties in West African okra (*Abelmoschus caillei* Stevels).

Specific combining ability of crosses

SCA, which represents the predominance of non-additive gene action, is a major component that may be utilized in heterosis breeding. SCA effects are generally useful to identify the best cross-combinations for hybrid production. Significant SCA effects were observed in 45 single crosses for all the traits except plant height and FSB infestation on fruits and shoots (**Table 2**). None of the cross combinations was observed to be a good cross combination for all the traits studied (data not shown). In general, a relatively higher magnitude of SCA effects were observed in many crosses for plant height, total number and number of marketable fruits, total and marketable yield/plant, and YVMV infestation on plants (data not shown), which may probably be due to the formation of superior gene recombinations, as also pointed out by Singh *et al.* (1989) in okra. 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 in okra.

Study of SCA resulted in the identification of a good number of high specific combiners for each of the traits studied in the okra population. Of the various high combiners identified for each of the traits (**Table 5**), the cross combination $C_{31}(P_5xP_6)$ for number of branches/plant, $C_{44}(P_8\times P_{10})$ for internodal length, $C_{17}(P_2\times P_{10})$ for days to 50% flowering, $C_{11}(P_2xP_4)$ 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, $C_{35}(P_5\times P_{10})$ for fruit weight, $C_{23}(P_3\times P_9)$ for total number of fruits/plant, number of marketable fruits/plant and marketable yield/plant, $C_{42}(P_7\times P_{10})$ for total yield/plant and $C_{14}(P_2\times P_7)$ for YVMV infestation on fruits and plants were the best specific combiners. The top two crosses displaying negatively significant SCA effects for days to 50% flowering were $C_{17}(P_2\times P_{10})$ and $C_4(P_1\times P_5)$ and top five crosses showing negatively significant SCA effects for first flowering and fruiting nodes were $C_{11}(P_2\times P_4)$, $C_4(P_1\times P_5)$, $C_{39}(P_6\times P_{10})$, $C_{41}(P_7\times P_9)$ and $C_{45}(P_9\times P_{10})$. The cross combination $C_4(P_1\times P_5)$ being the high specific combiner for all the three indicators of earliness could offer good scope for exploiting earliness in okra. These best specific combiners having the highest magnitude of significant specific combining ability effects in favorable direction are recommended for heterosis breeding. The intercrossing of these materials could, therefore, generate a population with a large gene pool, where genetic linkages and genetic blocks could be broken. The top five high specific combiners identified for pod yield (**Table 5**) were also found to be high specific combiners for most of the yield contributing traits.

Superior combiners for yield and yield-associated traits

Improvement of complex characters such as yield may be accomplished through the component approach of breeding. This method in general assumes strong associations of yield with a number of characters making up yield and simpler inheritance for these component characters (Edwards *et al.* 1976). Using yield components as a quantification and selection criterion is superior to using yield alone. Combining ability study finds out the good general combiners for yield and its components, promising cross combinations, nature and magnitude of gene action governing the expression of yield and yield components which in turn helps in identification of proper breeding methodology. Correlation coefficient analysis revealed that plant height, number of branches/plant, first flowering and fruiting node, fruit length and weight, total number of fruits/plant, number of marketable fruits/plant and fruit and shoot bore infestation on fruits were the major components of marketable yield in okra (Medagam *et al.* 2011).

Parental lines P_5, P_6 and P_7 were high general combiners for total yield and marketable yield/plant. Interestingly, of the three high combiners identified for both total and marketable yield/plant (P_5, P_6 and P_7), P_5 was also the high general combiner for number of branches/plant, first flowering node, first fruiting node, fruit length, width and weight, P_6 was also high combiner for number of branches/plant, fruit length and weigh and P_7 was also high combiner for plant height, fruit length, fruit weight, total number of fruits/plant, number of marketable fruits/plant and FSB infestation on shoots. From these results, it is evident that parental lines showing high GCA effects for total yield/plant and marketable yield/plant might be due to their high GCA effects for some of the yield-contributing characters that agrees with the earlier findings of Wammada *et al.* (2010) who identified Mothol-AE2 as the overall best general combiner, while Gerio-AE1 and Mothol-AE3 as the second and third best general combiners, respectively. Mothol-AE2 not only showed significant GCA effect for yield per plant but also for other yield associated traits like days to plant height, 50% flowering, fruit length and fruit diameter in desirable direction. Hence, lines P_5, P_6 and P_7 are recommended for use in breeding programmes to develop preco-

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 its parents		Character/ Cross	SCA effect	GCA effect of its parents	
		Female	Male			Female	Male
No. of branches/plant				**Fruit weight (g)**			
$C_{31}(P_5xP_6)$	0.65^{**}	0.29^{**H}	0.60^{**H}	$C_{35}(P_5xP_{10})$	1.14^{**}	1.01^{**H}	0.40^{**H}
$C_{36}(P_6xP_7)$	0.63^{**}	0.60^{**H}	0.10^{L}	$C_4(P_1xP_5)$	1.10^{**}	0.04^{L}	1.01^{**H}
$C_{24}(P_3xP_{10})$	0.56^{**}	-0.28^{**L}	0.12^{L}	$C_{39}(P_6xP_{10})$	1.07^{**}	0.82^{**H}	0.40^{**H}
$C_{29}(P_4xP_9)$	0.47^{*}	-0.30^{**L}	-0.25^{**L}	$C_{42}(P_7xP_{10})$	1.05^{**}	0.57^{**H}	0.40^{**H}
$C_6(P_1xP_7)$	0.45^{*}	-0.29^{**L}	0.10^{L}	$C_{21}(P_3xP_7)$	0.87^{**}	-0.43^{**L}	0.57^{**H}
Internodal length (cm)				**Total no. of fruits/plant**			
$C_{44}(P_8xP_{10})$	-1.32^{**}	-0.12^{L}	0.15^{L}	$C_{23}(P_3xP_9)$	4.63^{**}	0.10^{L}	-0.19^{L}
$C_2(P_1xP_3)$	-0.79^{*}	-0.08^{L}	-0.06^{L}	$C_{36}(P_6xP_7)$	3.17^{**}	-0.32^{L}	0.83^{**H}
$C_{30}(P_4xP_{10})$	-0.78^{*}	0.14^{L}	0.15^{L}	$C_{24}(P_3xP_{10})$	3.10^{**}	0.10^{L}	-0.19^{L}
-	-	-	-	$C_{42}(P_7xP_{10})$	2.37^{**}	0.83^{**H}	-0.19^{L}
-	-	-	-	$C_{17}(P_2xP_{10})$	2.20^{**}	0.40^{L}	-0.19^{L}
Days to 50% flowering				**No. of marketable fruits/plant**			
$C_{17}(P_2xP_{10})$	-0.92^{**}	0.12^{L}	0.51^{**L}	$C_{23}(P_3xP_9)$	4.31^{**}	-0.10^{L}	-0.60^{**L}
$C_4(P_1xP_5)$	-0.49^{**}	-0.27^{*H}	-0.35^{**H}	$C_{36}(P_6xP_7)$	3.13^{**}	-0.29^{L}	0.72^{**H}
-	-	-	-	$C_{24}(P_3xP_{10})$	2.83^{**}	-0.10^{L}	-0.13^{L}
-	-	-	-	$C_{28}(P_4xP_8)$	1.87^{**}	0.32^{L}	0.17^{L}
-	-	-	-	$C_{17}(P_2xP_{10})$	1.81^{**}	0.45^{*H}	-0.13^{L}
First flowering node				**Total yield/plant (g)**			
$C_{11}(P_2xP_4)$	-0.50^{**}	-0.06^{**H}	-0.12^{**H}	$C_{42}(P_7xP_{10})$	63.81^{**}	25.04^{**H}	5.70^{L}
$C_4(P_1xP_5)$	-0.49^{**}	-0.13^{**H}	-0.16^{**H}	$C_{23}(P_3xP_9)$	62.82^{**}	-7.46^{L}	-17.31^{**L}
$C_{39}(P_6xP_{10})$	-0.36^{**}	0.35^{**L}	0.14^{*L}	$C_{17}(P_2xP_{10})$	46.66^{**}	-11.62^{**L}	-5.70^{L}
$C_{41}(P_7xP_9)$	-0.30^{**}	0.18^{**L}	-0.16^{**H}	$C_{43}(P_8xP_9)$	42.91^{**}	-17.88^{**L}	-17.31^{**L}
$C_{45}(P_9xP_{10})$	-0.26^{**}	-0.16^{**H}	0.14^{**L}	$C_{13}(P_2xP_6)$	40.83^{**}	-11.62^{**L}	11.26^{**H}
First fruiting node				**Marketable yield/plant (g)**			
$C_{11}(P_2xP_4)$	-0.50^{**}	-0.06^{**H}	-0.12^{**H}	$C_{23}(P_3xP_9)$	58.71^{**}	-8.88^{*L}	-12.72^{**L}
$C_4(P_1xP_5)$	-0.49^{**}	-0.13^{**H}	-0.16^{**H}	$C_{17}(P_2xP_{10})$	39.01^{**}	-8.20^{*L}	5.22^{L}
$C_{39}(P_6xP_{10})$	-0.36^{**}	0.35^{**H}	0.14^{*L}	$C_{24}(P_3xP_{10})$	36.25^{**}	-8.88^{*L}	5.22^{L}
$C_{41}(P_7xP_9)$	-0.30^{**}	0.18^{**H}	-0.16^{**H}	$C_{42}(P_7xP_{10})$	33.10^{**}	21.27^{**H}	5.22^{L}
$C_{45}(P_9xP_{10})$	-0.26^{**}	-0.16^{**H}	0.14^{**L}	$C_{43}(P_8xP_9)$	31.55^{**}	-12.23^{**L}	-12.72^{**L}
Fruit length (cm)				**YVMV infestation on fruits (%)**			
$C_{35}(P_5xP_{10})$	1.83^{**}	$0.75^{**\ H}$	-0.56^{**L}	$C_{14}(P_2xP_7)$	-0.67^{**}	0.001^{L}	0.01^{L}
$C_{42}(P_7xP_{10})$	1.19^{**}	$0.39^{**\ H}$	-0.56^{**L}	$C_2(P_1xP_3)$	-0.43^{**}	0.21^{L}	0.001^{L}
$C_4(P_1xP_5)$	1.00^{**}	0.03^{L}	0.75^{**H}	$C_{30}(P_4xP_{10})$	-0.34^{*}	-0.09^{L}	-0.04^{L}
$C_{27}(P_4xP_7)$	0.89^{**}	-0.19^{**L}	0.39^{**H}	$C_5(P_1xP_6)$	-0.31^{*}	0.21^{L}	-0.01^{L}
$C_{39}(P_6xP_{10})$	0.86^{**}	0.55^{**H}	-0.56^{**L}	-	-	-	-
Fruit width cm)				**YVMV infestation on plants (%)**			
$C_{22}(P_3xP_8)$	0.15^{**}	0.02^{**H}	-0.08^{**L}	$C_{14}(P_2xP_7)$	-12.22^{**}	0.08^{L}	0.37^{L}
$C_{42}(P_7xP_{10})$	0.08^{**}	-0.03^{**L}	0.03^{**H}	$C_2(P_1xP_3)$	-8.33^{**}	4.20^{L}	-0.10^{L}
$C_{41}(P_7xP_9)$	0.07^{**}	-0.03^{**L}	0.04^{**H}	$C_5(P_1xP_6)$	-6.23^{*}	4.20^{L}	-0.36^{L}
$C_{25}(P_4xP_5)$	0.07^{**}	0.05^{**H}	0.02^{**H}	$C_{30}(P_4xP_{10})$	-6.10^{*}	-1.66^{L}	-0.65^{L}
$C_{37}(P_6xP_8)$	0.05^{**}	0.003^{L}	-0.08^{**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

cious and prolific varieties of okra.

Association between SCA of crosses and GCA of parents

The parental lines of the various cross combinations displayed very critical trends in their GCA effects for different characters (**Table 5**). Of the top two cross combinations showing negatively significant SCA effects for days to 50% flowering, the cross $C_{17}(P_2 \times P_{10})$ had low (L) × low (L) general combiners as parental lines, while $C_4(P_1 \times P_5)$ had high × low general combiners as parental lines. Of the top five cross combinations showing negatively significant SCA effects for first flowering and fruiting nodes, the crosses $C_{11}(P_2 \times P_4)$ and $C_4(P_1 \times P_5)$ had high × high general combiners as parental lines, the crosses $C_{41}(P_7 \times P_9)$ and $C_{45}(P_9 \times P_{10})$ had high × low general combiners as parental lines and the crosses $C_{39}(P_6 \times P_{10})$ had low × low general combiners as parental lines. 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 × low general combiners as parental lines, 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 × low general combiners as parental lines. Similarly, of the top five crosses showing significantly positive SCA effects for marketable yield/plant, only one cross $C_{42}(P_7 \times P_{10})$ involved high × low general combiners as parental lines, while the remaining crosses $C_{23}(P_3 \times P_9)$, $C_{17}(P_2 \times P_{10})$, $C_{24}(P_3 \times P_{10})$ and $C_{43}(P_8 \times P_9)$ involved low × low general combiners as parental lines. For other yield-associated traits also, the top five cross combinations exhibiting significant SCA effects in desirable direction involved high × high, high × low and low × low general combiners as parental lines. From the perusal of the GCA status of the high specific combiners for various traits, it is evident that the high specific combiners involved high × high, high × low and × low general combiners as parents, indicating that high specific combiners are not only obtained from the combination of high × high general combiners but also obtained from the combination of high × low and low × 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. Patil *et al.* (1996) and Rewale *et al.* (2003) also noticed the involvement of all combinations of high × high, high × low and low × low general combiners in the high specific combiners in okra and concluded that it cannot be generalized that the parents with high GCA effects could only generate crosses with high SCA effects. High performance of these crosses may be attributed to additive × additive (high × high), additive × dominance (high × low) or, dominance × dominance (low × low) epistatic interactions.

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. However, the present results varies with the findings of Sivakumar *et al.* (1995) and Rani *et al.* (2002), who found high specific combiners emanating from low × low general combiners in okra. Superiority of the cross combinations involving high × low or, low × 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 as also pointed out by Shukla and Gautam (1990) and Kumar *et al.* (2006). Of the top five promising specific combiners identified for total yield *viz.*, C_{42}, C_{23}, C_{17}, C_{43} and C_{13}, the crosses $C_{42}(P_7 \times P_{10})$ and $C_{13}(P_2 \times P_6)$ having one of the parents with high GCA effect, 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 yield/plant. Similarly, of the top five promising specific combiners identified for marketable yield *viz.*, C_{23}, C_{17}, C_{24}, C_{42} and C_{43}, the cross $C_{42}(P_7 \times P_{10})$ having one of the parents with high GCA effect, 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 marketable yield/plant. These crosses involved high × low combiners, and such combinations may yield desirable transgressive segregants and may be exploited for varietal improvement. Due to non-additive genetic mechanism governing most of the yield-relating traits, selection of the superior plants would have to be practiced with great care while handling the plant-material in segregating generations. Ahmed *et al.* (1997) 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 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.

CONCLUSIONS

From the analysis of variance for combining ability, it is evident that the mean squares due to GCA and SCA were significant suggesting involvement of both additive and non-additive components of heritable variance in the inheritance of all the traits except plant height, FSB infestation on fruits and shoots for which only additive variance is involved. The overall study reveals the importance of both additive and non-additive genetic variability which suggests the use of integrated breeding strategies which can efficiently utilize the additive as well as non-additive genetic variability. The combining ability analysis revealed that the parental lines P_5, P_6 and P_7 exhibiting outstanding GCA effects for both total and marketable yield/plant and a few yield related characters were the superior general combiners, could be exploited for developing pure line varieties, while the crosses C_{23}(IC29119-B × IC99716), C_{17}(IC27826-A × IC111443), C_{42}(IC89976 × IC111443) and C_{43}(IC90107 × IC111443) exhibiting outstanding SCA effects for both total and marketable yield/plant and a few yield related characters were the superior specific combiners, could be commercially exploited for the production of F_1 hybrids. However, the cross C_{42} ($P_7 \times P_{10}$) having one of the parents with positively significant GCA effect could be utilized in recombination breeding with single plant selection in the passing generations to utilize additive gene action to develop lines or varieties with higher total and marketable yields/plant. These best parents and cross combinations could be effectively utilized in okra breeding for the improvement of yield components and thus their incorporation in further breeding program is suggested. Thus, use of diallel mating with recurrent selection could provide better conditions for recombination and accumulation of desirable genes and is recommended for such a type of study.

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