

Gene action and combining ability of yield and its components for late *kharif* season in okra (*Abelmoschus esculentus* (L.) Moench)

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Knowledge on the genetic system controlling the quantitative traits is important for devising an efficient selection program through the use of a suitable mating design. Forty five F₁s were generated by crossing 10 germplasm lines of okra (*Abelmoschus esculentus* (L.) Moench) namely P₁(IC282248), P₂(IC27826-A), P₃(IC29119-B), P₄(IC31398-A), P₅(IC45732), P₆(IC89819), P₇(IC89976), P₈(IC90107), P₉(IC99716), and P₁₀(IC111443) during summer 2009. Forty five F₁s along with their 10 parents were evaluated in a randomized block design with three replicates during late *kharif* (August-November) 2009 at Vegetable Research Station, Hyderabad, Andhra Pradesh, India, for studying gene action and combining ability of yield and its components. Significant general combining ability and specific combining ability variances were obtained in majority of the traits except fruit and shoot borer infestation on fruits and shoots; implying that both the additive and non-additive gene effects operated in the genetic expression of the traits. The relative magnitude of general and specific combining ability variances indicated preponderance of non-additive gene action for majority of the characters studied except number of branches per plant and fruit width. Combining ability analysis of parents revealed that the parental lines P₅(IC45732), P₆(IC89819) and P₇(IC89976) were superior general combiners for total and marketable yield per plant and other traits. The crosses C₂₃(IC29119-B × IC99716), C₁₇(IC27826-A × IC111443), C₄₂(IC89976 × IC111443) and C₄₃(IC90107 × IC111443) were superior specific combiners for total as well as marketable yield per plant with the potential of being commercially exploited for the production of F₁ hybrids. The crosses C₁₇ (IC27826-A × IC111443) and C₄₂(IC89976 × IC111443) involving one or both of the parents with positively significant general combining ability effects for marketable yield per plant could be utilized in recombination breeding.

Key words: Fruit yield, genetic analysis, genetic components, germplasm lines, half diallel crosses, hybridization, yield attributes.

INTRODUCTION

Okra, lady's finger (*Abelmoschus esculentus* (L.) Moench), is a tall, upright, fast growing, annual herb propagated by seed. It is native to the West Africa (Murdock, 1959). It is an important vegetable crop grown all over India. It is a multipurpose and multifarious crop. Okra is gaining importance with regard to its nutritional, medicinal, and industrial value. The immature young seed pods are the edible part of this plant, which are consumed as cooked vegetable, mostly fresh but sometimes sun-dried. It is commercially grown in the Indian states of Andhra Pradesh, Gujarat, Maharashtra, Karnataka, and Tamilnadu.

Being a tropical, hot weather, low land crop, susceptible to low night temperatures, it is extensively cultivated in *kharif* (June-September) and summer (February-May) seasons in Andhra Pradesh. Okra, being a warm season crop, is also sensitive to the mild winters of the state. Its cultivation in late *kharif* (August-November) has been problematic and less economic due to low productivity at low temperatures. The available open-pollinated varieties lack adaptability to late *kharif* season. Hence, there is a need to develop and identify the high yielding and highly adaptable genotypes for commercial cultivation in late *kharif*. To breed for varieties suitable for *kharif* season hybridization-based breeding strategy would be desirable.

At present, improving yield and ensuring its sustainability under adverse conditions through hybridization is the major objective of okra breeding programs. In breeding for high yielding crop plants through hybridization, the breeders often face with the problem of selecting parents and crosses. The *per se* performance of genotypes is not always a good index of their superior combining ability. Certain cross combinations nick well to provide superior hybrids where as others involving equally promising parents produce

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disappointing progeny. Hence, there is a constant need to screen germplasm to isolate potential combining lines and desirable cross combinations either to exploit heterosis or to obtain new recombinants. Thus, any method which would help in choosing desirable parents and crosses will be important for the breeders. Genetic analysis provides a guide line for the assessment of relative breeding potential of the parents or identifies best combiners in crops (Khattak et al., 2004; Weerasingh et al., 2004; Devi et al., 2005), which could be utilized either to exploit heterosis in F_1 or to accumulate fixable genes to evolve variety. The information about the relative contribution of components of variation viz., additive and non-additive, is essential for effective crop improvement program (Azhar and Ajmal, 1999). In order to apply an optimum breeding strategy for targeted quantitative traits, a genetic analysis of those traits needs to be performed (Has, 1999; Nistor et al., 2005). Diallel analysis of self and cross pollinated populations is used to study the genetic control of quantitative traits (Jinks and Hayman, 1953; Hayman, 1954; 1958) and to assess general and specific combining abilities (Griffing, 1956).

The success of a breeding program depends on the variability of the initial material. India is one of the countries with largest collection or diversity in the germplasm of okra. Genetic diversity in most of the agronomical and horticultural traits is available in the germplasm of okra (Mohapatra et al., 2007; Singh et al., 2007; Reddy, 2010). Combining ability analysis of single crosses generated from crossing elite and diverse genotypes from the germplasm of okra has been made by several researchers (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; Wammanda et al., 2010). In literature, both additive and non-additive genetic systems, controlling pod yield and yield-relating traits in okra, have been reported (Kumar et al., 2006; Jaiprakashnarayan et al., 2008b; Jindal et al., 2009; Singh et al., 2009; Wammanda et al., 2010). However, the major part of genetic variation for yield and its components was conditioned due to higher magnitude of non-additive genetic effects (Kumar et al., 2005; Jaiprakashnarayan et al., 2008b; Jindal et al., 2009; Wammanda et al., 2010).

Pod yield and several yield-contributing characters lack stability due to strong environmental influence, suggesting the need for breeding for specific environment (Ariyo, 1990). The yielding ability and response to environmental changes are the two independent attributes of a genotype and are governed by separate genetic systems. Improvement of complex characters such as pod 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. It is known that phenotypic expression of quantitative traits is highly influenced by environmental fluctuations (Allard and Bradshaw, 1964). Therefore, it is necessary to study the genetic architecture of okra genotypes in relation to the environment for which they have to be developed.

The present study involving 10×10 diallel analysis excluding reciprocals aimed to study the combining ability effects and genetic system governing yield and yield associated traits so as to determine the better general combining parents and specific combining parents for evolving productive varieties or hybrids in okra.

MATERIALS AND METHODS

Ten nearly homozygous, horticulturally superior and optimally divergent genotypes 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) selected from the germplasm were crossed in all possible combinations excluding reciprocals to generate 45 single crosses during summer 2009. Forty five half diallel progenies along with their 10 parental lines were evaluated in a randomized block design with three replicates during late *kharif* (August-November), 2009 at the Experimental Farm (17.19° N, 79.23° E, 542.6 m a.s.l.), Vegetable Research Station, Rajendranagar, India. Each entry was raised in a double-row plot. Each plot was of 3.0×1.2 m size. Inter and intra-row spacings were 60 and 30 cm, respectively. There were 10 plants per row and 20 plants per plot and entry. Standard agronomic practices were followed and plant protection measures were taken as and when required. Five randomly selected plants were used for recording observations on 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). Data on 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 (%) were recorded on whole plot basis. The mean replicated values of FSB infestation on fruits and shoots and YVMV infestation on fruits were subjected to square root transformation, while mean replicated values of YVMV infestation on plants were subjected to arc sin transformation to restore distribution to normality. Data were analyzed according to ANOVA techniques, as outlined by Panse and Sukhatme (1985), to determine the significant differences among genotypes for all the characters. The characters showing significant differences were subjected to combining ability analysis. General and specific combining ability variances and general combining ability (GCA) and

specific combining ability (SCA) effects were estimated according to Griffing's Method-II and Model-I (Griffing, 1956) as outlined by Singh and Chaudhary (1979). 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

Genetic improvement in pod yield has always been a top priority of okra breeders. Pod yield and its related parameters are quantitative traits, which are controlled by several genes thus showing a range of values in segregating generation. Genetic analysis helps in identifying traits for improvement of yield potential. Dependable biometrical techniques dealing with the genetic analysis of important characters have greatly helped plant breeder in tailoring new genotypes and ascertain the nature of gene action. Combining ability analysis is one of the powerful tools available to estimate the combining ability effects and aids in selecting the desirable parents and crosses (Subhan et al., 2003; Rashid et al., 2007). Among various techniques, genetic analysis formulated by Griffing (1956), provides a workable approach to evaluate newly developed cultivars for their parental usefulness and to assess the gene action involved in various attributes, so as to design an efficient breeding plan, for further genetic upgrading of the existing material.

ANOVA for combining ability

ANOVA of combining ability based on mean squares of different characters in okra is presented in Table 1. Significance of genotype effect ($P < 0.01$) indicated a

wide range of variability among the genotypes for all the characters. Mean squares were highly significant ($P < 0.01$) for both GCA and SCA for all the traits except FSB infestation on fruits and shoots for SCA. This indicates that both the additive and non-additive components of heritable variance are responsible for variation observed for 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. Mean squares were highly significant ($P < 0.01$) for GCA alone for FSB infestation on fruits and shoots, indicating that only additive component of heritable variance is solely responsible for the variation of these traits.

Gene action

The ratio of GCA variance to SCA variance (Table 2) was lower than unity (< 1) for majority of the traits under study except number of branches per plant (1.568) and fruit width (1.000). The magnitude of SCA variance greater than that of GCA variance suggests the predominance of the non-additive gene action for majority of the traits. However, for number of branches per plant, the greater magnitude of GCA variance than that of SCA variance suggests the preponderance of the additive gene action, while for fruit width, the equal magnitude of GCA and SCA variances suggests the equal role of the both additive and non-additive gene actions. Similar results were also

Table 1. Analysis of variance for combining ability in okra.

Character	Mean squares			
	Genotypes (54)	GCA (9)	SCA (45)	Error (108)
Plant height, cm	121.9704**	68.8543**	35.0173*	20.8017
Number of branches per plant	0.6358**	0.8611**	0.0821**	0.0381
Internodal length, cm	1.0389**	0.5412**	0.3073**	0.1711
Days to 50% flowering	1.4923**	0.6733**	0.4623**	0.2352
First flowering node	0.4134**	0.3592**	0.0935**	0.0051
First fruiting node	0.4134**	0.3592**	0.0935**	0.0051
Fruit length, cm	2.9888**	3.0901**	0.5775**	0.0089
Fruit width, cm	0.0161**	0.0220**	0.0020**	0.0001
Fruit weight, g	3.9378**	5.3425**	0.5066**	0.0293
Total number of fruits per plant	3.1098**	0.8109*	1.0817**	0.3278
Number of marketable fruits per plant	2.2584**	0.7034**	0.7627**	0.2378
Total yield per plant, g	1224.3669**	935.1122**	302.7243**	84.1695
Marketable yield per plant, g	818.6110**	633.8493**	200.6745**	60.4566
FSB infestation on fruits, %	0.0895**	0.1332**	0.0092	0.0095
FSB infestation on shoots, %	0.0926**	0.1399**	0.0091	0.0091
YVMV infestation on fruits, %	0.2081**	0.0645**	0.0703**	0.0231
YVMV infestation on plants, %	64.7156**	16.5328**	22.5797**	5.7963

GCA: General combining ability; SCA: specific combining ability; FSB: fruit and shoot borer; YVMV: *Yellow vein mosaic virus*. * $P < 0.05$; ** $P < 0.01$. 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^2 GCA	σ^2 SCA	σ^2 GCA/ σ^2 SCA
Plant height, cm	4.004	14.216	0.282
Number of branches per plant	0.069	0.044	1.568
Internodal length, cm	0.031	0.136	0.228
Days to 50% flowering	0.037	0.227	0.163
First flowering node	0.030	0.088	0.341
First fruiting node	0.030	0.088	0.341
Fruit length, cm	0.257	0.569	0.452
Fruit width, cm	0.002	0.002	1.000
Fruit weight, g	0.443	0.477	0.929
Total number of fruits per plant	0.040	0.754	0.053
Number of marketable fruits per plant	0.039	0.525	0.074
Total yield per plant, g	70.912	218.555	0.324
Marketable yield per plant, g	47.783	140.218	0.341
FSB infestation on fruits, %	0.0103	-0.0004	-25.750
FSB infestation on shoots, %	0.01090	-0.00005	-218.000
YVMV infestation on fruits, %	0.003	0.047	0.064
YVMV infestation on plants, %	0.895	16.783	0.053

σ^2 GCA: General combining ability variance; σ^2 SCA: specific combining ability variance; FSB: fruit and shoot borer; YVMV: *Yellow vein mosaic virus*.

reported for yield and its components in okra by several researchers like 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. (2008b) for days to 50% flowering and fruit weight and Jindal et al. (2009) for first flowering node. A population improvement approach in the form of diallel selective mating or mass selection with concurrent random mating could be used for the exploitation of additive and non-additive gene actions for these characters.

Combining ability

Two types of combining ability, general and specific, have been recognized in quantitative genetics. Specific combining ability is defined as the deviation in the performance of hybrids from the expected productivity based upon the average performance of lines involved in the hybrid combination, whereas general combining ability is defined as average performance of a line in a series of crosses. General combining ability is due to genes, which are largely additive in their effects and specific combining ability is due to the genes with dominance or epistatic effect.

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 10 parents and 45 crosses varied greatly from trait-to-trait. In okra, of 17 quantitative traits under study, combining ability effects are favorable in positive direction for plant height, number of branches per plant, fruit length, fruit width, fruit weight, total number of fruits per plant, number of marketable fruits per plant, total yield per plant, and marketable yield per plant except internodal length, days to 50% flowering, first flowering node, first fruiting node, FSB infestation on fruits and shoots and YVMV infestation on fruits and

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	Number of high general combiners		Number of high specific combiners	
	Positive	Negative	Positive	Negative
Plant height, cm	1	1	1	3
Number of branches per plant	2	4	5	3
Internodal length, cm	1	1	3	3
Days to 50% flowering	1	1	4	4
First flowering node	3	5	16	11
First fruiting node	3	5	16	11
Fruit length, cm	5	4	22	14
Fruit width, cm	5	3	13	18
Fruit weight, g	4	5	19	12
Total number of fruits per plant	1	1	7	5
Number of marketable fruits per plant	1	2	7	5
Total yield per plant, g	3	3	7	6
Marketable yield per plant, g	4	5	7	5
FSB infestation on fruits, %	3	2	-	-
FSB infestation on shoots, %	2	4	-	-
YVMV infestation on fruits, %	1	-	8	3
YVMV infestation on plants, %	1	-	6	5

FSB: fruit and shoot borer; YVMV: *Yellow vein mosaic virus*.

plants for which combining ability effects are favorable in negative direction. None of the parents or crosses was found to be consistently superior for all the traits. The parents and crosses displaying significant combining ability effects in favorable direction were categorized as high combiners, while the parents and crosses displaying non-significant combining ability effects in favorable direction, significant and non-significant combining ability effects in unfavorable direction were categorized as low combiners.

The high and low combining parental lines for each of 17 traits are presented in Table 4. Only one parental line P₇ was high general combiner for plant height. Parental lines P₅ and P₆ were high general combiners for number of branches per plant. Parental line P₂ was high general combiner for internodal length. Parental line P₉ was the high general combiner for days to 50% flowering. Parental lines P₁, P₃, P₄, P₅, and P₉ were the high general combiners for both first flowering and fruiting nodes. Parents P₃, P₅, P₆, P₇, and P₈ were the high general combiners for fruit length. Parental lines P₁, P₇, and P₈ were high general combiners for fruit width. Parents P₅, P₆, P₇, and P₁₀ were high general combiners for fruit weight. Parental line P₇ was high general combiner for total number of fruits per plant and number of marketable fruits per plant. Parental lines P₅, P₆, and P₇ were high general combiners for both total and marketable yield per plant. Parental lines P₂ and P₈ were high general combiners for FSB infestation on fruits, while P₂, P₄, P₇, and P₈ were high general combiners for FSB infestation on shoots. None of the parental lines was high general combiner for YVMV infestation on fruits and plants.

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

Table 4. Estimates of general combining ability effects of 10 parental lines for yield and its components in okra.

Character	Parental line									
	P ₁	P ₂	P ₃	P ₄	P ₅	P ₆	P ₇	P ₈	P ₉	P ₁₀
Plant height, cm	-0.07 ^L	-4.97 ^{**L}	-0.13 ^L	1.28 ^L	0.58 ^L	-0.21 ^L	4.52 ^{**H}	-0.73 ^L	-1.53 ^L	1.25 ^L
Number of branches per plant	-0.30 ^{**L}	0.05 ^L	-0.20 ^{**L}	-0.26 ^{**L}	0.25 ^{**H}	0.56 ^{**H}	0.07 ^L	-0.04 ^L	-0.22 ^{**L}	0.10 ^L
Internodal length, cm	-0.03 ^L	-0.51 ^{**H}	-0.06 ^L	0.13 ^L	0.06 ^L	0.17 ^L	-0.01 ^L	-0.14 ^L	0.24 ^L	0.14 ^L
Days to 50% flowering	-0.15 ^L	0.10 ^L	-0.23 ^L	0.02 ^L	-0.15 ^L	0.21 ^L	0.16 ^L	-0.01 ^L	-0.37 ^{**H}	0.43 ^{**L}
First flowering node	-0.15 ^{**H}	-0.03 ^L	-0.09 ^{**H}	-0.11 ^{**H}	-0.17 ^{**H}	0.34 ^{**L}	0.19 ^{**L}	0.03 ^L	-0.16 ^{**H}	0.13 ^{**L}
First fruiting node	-0.15 ^{**H}	-0.03 ^L	-0.09 ^{**H}	-0.11 ^{**H}	-0.17 ^{**H}	0.34 ^{**L}	0.19 ^{**L}	0.03 ^L	-0.16 ^{**H}	0.13 ^{**L}
Fruit length, cm	0.04 ^L	-0.29 ^{**L}	0.14 ^{**H}	-0.16 ^{**L}	0.71 ^{**H}	0.50 ^{**H}	0.41 ^{**H}	0.18 ^{**H}	-0.96 ^{**L}	-0.56 ^{**L}
Fruit width, cm	-0.05 ^{**H}	0.01 ^L	0.02 ^{**L}	0.05 ^{**L}	0.02 ^{**L}	-0.01 ^L	-0.03 ^{**H}	-0.08 ^{**H}	0.04 ^{**L}	0.03 ^{**L}
Fruit weight, g	0.05 ^L	-0.87 ^{**L}	-0.42 ^{**L}	-0.52 ^{**L}	1.01 ^{**H}	0.78 ^{**H}	0.59 ^{**H}	-0.08 ^{**L}	-0.19 ^{**L}	0.39 ^{**H}
Total number of fruits per plant	-0.12 ^L	0.15 ^L	0.02 ^L	0.09 ^L	0.11 ^L	-0.17 ^L	0.48 ^{**H}	-0.05 ^L	-0.53 ^{**L}	0.02 ^L
Number of marketable fruits per plant	-0.32 ^{**L}	0.17 ^L	-0.06 ^L	0.14 ^L	0.05 ^L	-0.12 ^L	0.42 ^{**H}	0.08 ^L	-0.42 ^{**L}	0.05 ^L
Total yield per plant, g	-1.36 ^L	-7.38 ^{**L}	-4.37 ^L	-4.41 ^L	12.84 ^{**H}	5.59 ^{**H}	14.03 ^{**H}	-9.63 ^{**L}	-9.96 ^{**L}	4.64 ^L
Marketable yield per plant, g	-4.29 ^L	-5.57 ^L	-4.64 ^L	-2.75 ^L	10.21 ^{**H}	5.14 ^{**H}	11.90 ^{**H}	-6.47 ^{**L}	-7.95 ^{**L}	4.43 ^{**H}
FSB infestation on fruits, %	0.15 ^{**L}	-0.05 ^{**H}	0.10 ^{**L}	-0.03 ^L	0.13 ^{**L}	-0.01 ^L	-0.03 ^L	-0.21 ^{**H}	-0.02 ^L	-0.03 ^L
FSB infestation on shoots, %	0.20 ^{**L}	-0.08 ^{**H}	0.12 ^{**L}	-0.09 ^{**H}	0.04 ^L	0.04 ^L	-0.07 ^{**H}	-0.16 ^{**H}	-0.03 ^L	0.03 ^L
YVMV infestation on fruits, %	0.19 ^{**L}	-0.02 ^L	0.03 ^L	-0.07 ^L	-0.04 ^L	-0.02 ^L	0.001 ^L	0.01 ^L	-0.04 ^L	-0.05 ^L
YVMV infestation on plants, %	2.87 ^{**L}	0.49 ^L	0.81 ^L	-1.27 ^L	-0.32 ^L	-0.16 ^L	-0.63 ^L	-0.76 ^L	-0.4 ^L	-0.63 ^L

^{*}, ^{**}Significant at 5 and 1% levels, respectively.

P₁: IC282248; P₂: IC27826-A; P₃: IC29119-B; P₄: IC31398-A; P₅: IC45732; P₆: IC89819; P₇: IC89976; P₈: IC90107; P₉: IC99716; P₁₀: IC111443.

^HDenotes significant general combining ability effect in favorable direction.

^LDenotes non-significant general combining ability effects in favorable direction, significant and non-significant general combining ability effects in unfavorable direction. FSB: fruit and shoot borer; YVMV: *Yellow vein mosaic virus*.

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 Wammanda et al. (2010), Jaiprakashnarayan et al. (2008a; 2008b), Singh et al. (2009), and Jindal et al. (2009). High GCA effects are attributed to additive or additive × additive gene effects, which represent the fixable genetic components of variance (Griffing, 1956). The parental lines with high GCA effects may be used in a multiple crossing program 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 F₁ hybrid production.

Development of precocious and prolific varieties is an important objective of okra breeding. Days to 50% flowering, first flowering node and first fruiting node are earliness attributes. The parental line P₉ was the high general combiner for all of the three earliness attributes, indicating its potential for exploiting earliness in okra. Three parental lines P₅, P₆, and P₇ out of 10 were high general combiners for total yield and marketable yield per plant. Interestingly, of the three high general combiners identified for both total and marketable yield per plant, parental line P₅ was also high general combiner for number of branches per plant, first flowering and fruiting nodes, fruit length and weight, P₆ was also high combiner for number of branches per plant, fruit length and weight and P₇ was also high combiner for plant height, fruit length, width and weight, total number of fruits per plant 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 Kumar (2001), Rewale et al. (2003), and Wammanda et al. (2010).

Significant SCA effects were observed in 45 single crosses for all the traits except FSB infestation on fruits and shoots. The top five specific combiners exhibiting significant SCA effects in desirable direction and the GCA effects of their parents for almost all the traits except FSB infestation on fruits and shoots are presented in Table 5. In general, a relatively higher magnitude of SCA effects were observed in many crosses for plant height, total number of fruits per plant and number of marketable fruits per plant, total and marketable yield per plant and YVMV infestation on plants. Of the various high specific combiners identified for each of the traits studied, the cross C₂₄(P₃×P₁₀) for plant height, C₃₆(P₆×P₇) for number of branches per plant, C₄₄(P₈×P₁₀) for internodal length, C₁₇(P₂×P₁₀) for days to 50% flowering, C₄(P₁×P₅) for first flowering and fruiting nodes, C₃₅(P₅×P₁₀) for fruit length, C₂₂(P₃×P₈) for fruit width, C₄(P₁×P₅) for fruit weight, C₂₃(P₃×P₉) for total number of fruits per plant, number of marketable fruits per plant, total yield per plant and marketable yield per plant and C₁₄(P₂×P₇) for YVMV infestation on fruits and plants were the best specific combiners.

Of the top five high specific combiners identified for total yield per plant, only one cross C₁₃(P₂×P₆) involved high × low general combiners as parents, while the remaining four crosses C₂₃(P₃×P₉), C₄₂(P₇×P₁₀), C₁₇(P₂×P₁₀), and C₄₃(P₈×P₉) involved low × low general combiners as parents. Of the top five high specific combiners identified for marketable yield per plant, one cross C₁₇(P₂×P₁₀) involved high × low general combiners as parents, one cross C₄₂(P₇×P₁₀) involved high × high general combiners as parents, while the remaining three crosses C₂₃(P₃×P₉), C₂₄(P₃×P₁₀) and C₄₃(P₈×P₉) involved

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
Plant height, cm				Fruit width, cm			
C ₂₄ (P ₃ ×P ₁₀)	11.33**	-0.13 ^L	1.25 ^L	C ₂₂ (P ₃ ×P ₈)	0.15**	0.02** ^H	-0.08** ^L
-	-	-	-	C ₄₂ (P ₇ ×P ₁₀)	0.08**	-0.03** ^L	0.03** ^H
-	-	-	-	C ₄₁ (P ₇ ×P ₉)	0.07**	-0.03** ^L	0.04** ^H
-	-	-	-	C ₂₅ (P ₄ ×P ₅)	0.07**	0.05** ^H	0.02** ^H
-	-	-	-	C ₃₇ (P ₆ ×P ₈)	0.05**	0.003 ^L	-0.08** ^L
Number of branches per plant				Fruit weight, g			
C ₃₆ (P ₆ ×P ₇)	0.69**	0.56** ^H	0.07 ^L	C ₄ (P ₁ ×P ₃)	1.17**	0.05 ^L	1.01** ^H
C ₃₁ (P ₅ ×P ₆)	0.58**	0.25** ^H	0.56** ^H	C ₃₅ (P ₅ ×P ₁₀)	1.16**	1.01** ^H	0.39** ^H
C ₆ (P ₁ ×P ₇)	0.49**	-0.30** ^L	0.07 ^L	C ₃₉ (P ₆ ×P ₁₀)	1.03**	0.78** ^H	0.39** ^H
C ₂₄ (P ₃ ×P ₁₀)	0.43*	-0.20** ^L	0.10 ^L	C ₄₂ (P ₇ ×P ₁₀)	0.96**	0.59** ^H	0.39** ^H
C ₂₉ (P ₄ ×P ₉)	0.40*	-0.26** ^L	-0.22** ^L	C ₂₁ (P ₃ ×P ₇)	0.90**	-0.42** ^L	0.59** ^H
Internodal length, cm				Total number of fruits per plant			
C ₄₄ (P ₈ ×P ₁₀)	-1.30**	-0.14 ^L	0.14 ^L	C ₂₃ (P ₃ ×P ₉)	2.50**	0.02 ^L	-0.53** ^L
-	-	-	-	C ₂₄ (P ₃ ×P ₁₀)	1.88**	0.02 ^L	0.02 ^L
-	-	-	-	C ₁₇ (P ₂ ×P ₁₀)	1.49**	0.15 ^L	0.02 ^L
-	-	-	-	C ₁₃ (P ₂ ×P ₆)	1.40**	0.15 ^L	-0.17 ^L
-	-	-	-	C ₃₆ (P ₆ ×P ₇)	1.34**	-0.17 ^L	0.48** ^H
Days to 50% flowering				Number of marketable fruits per plant			
C ₁₇ (P ₂ ×P ₁₀)	-1.36**	0.10 ^L	0.43** ^L	C ₂₃ (P ₃ ×P ₉)	2.22**	-0.06 ^L	-0.42** ^L
C ₂₅ (P ₄ ×P ₅)	-1.36	0.02 ^L	-0.15 ^L	C ₂₄ (P ₃ ×P ₁₀)	1.82**	-0.06 ^L	0.05 ^L
C ₄ (P ₁ ×P ₃)	-1.20**	-0.15 ^L	-0.15 ^H	C ₁₇ (P ₂ ×P ₁₀)	1.37**	0.17 ^L	0.05 ^L
C ₁₆ (P ₂ ×P ₉)	-0.89*	0.10 ^L	-0.37** ^L	C ₃₆ (P ₆ ×P ₇)	1.37**	-0.12 ^L	0.42** ^H
-	-	-	-	C ₄₃ (P ₈ ×P ₉)	0.96*	0.08 ^L	-0.42** ^L
First flowering node				Total yield per plant, g			
C ₄ (P ₁ ×P ₃)	-0.54**	-0.15** ^H	-0.17** ^H	C ₂₃ (P ₃ ×P ₉)	34.03**	-4.37 ^L	-9.96** ^L
C ₁₁ (P ₂ ×P ₄)	-0.48**	-0.03 ^L	-0.11** ^H	C ₄₂ (P ₇ ×P ₁₀)	32.63**	-9.63** ^L	4.64 ^L
C ₃₉ (P ₆ ×P ₁₀)	-0.40**	0.34** ^L	0.13** ^L	C ₁₇ (P ₂ ×P ₁₀)	30.61**	-7.38** ^L	4.64 ^L
C ₄₁ (P ₇ ×P ₉)	-0.39**	0.19** ^L	-0.16** ^H	C ₁₃ (P ₂ ×P ₆)	24.24**	-7.38** ^L	4.64 ^H
C ₁₅ (P ₂ ×P ₈)	-0.32**	-0.03 ^L	0.03 ^L	C ₄₃ (P ₈ ×P ₉)	24.05*	-9.63** ^L	-9.96** ^L
First fruiting node				Marketable yield per plant, g			
C ₄ (P ₁ ×P ₃)	-0.54**	-0.15** ^H	-0.17** ^H	C ₂₃ (P ₃ ×P ₉)	30.23**	-4.64 ^L	-7.95** ^L
C ₁₁ (P ₂ ×P ₄)	-0.48**	-0.03 ^L	-0.11** ^H	C ₁₇ (P ₂ ×P ₁₀)	27.57**	-5.57 ^L	4.43 ^H
C ₃₉ (P ₆ ×P ₁₀)	-0.40**	0.34** ^L	0.13** ^L	C ₂₄ (P ₃ ×P ₁₀)	21.88**	-4.64** ^L	4.43 ^L
C ₄₁ (P ₇ ×P ₉)	-0.39**	0.19** ^L	-0.16** ^H	C ₄₃ (P ₈ ×P ₉)	18.19*	-6.47** ^L	-7.95** ^L
C ₁₅ (P ₂ ×P ₈)	-0.32**	-0.03 ^L	0.03 ^L	C ₄₂ (P ₇ ×P ₁₀)	17.40*	11.90** ^H	4.43 ^H
Fruit length, cm				YVMV infestation on plants, %			
C ₃₅ (P ₅ ×P ₁₀)	1.81**	0.71** ^H	-0.56** ^L	C ₁₄ (P ₂ ×P ₇)	-8.59**	0.49 ^L	-0.63 ^L
C ₄₂ (P ₇ ×P ₁₀)	1.06**	0.41** ^H	-0.56** ^L	C ₂ (P ₁ ×P ₃)	-7.43**	2.87** ^L	0.81 ^L
C ₂₇ (P ₃ ×P ₇)	0.89**	-0.16** ^L	0.41** ^H	C ₃ (P ₁ ×P ₄)	-5.36**	2.87** ^L	-1.27 ^L
C ₃₉ (P ₆ ×P ₁₀)	0.86**	0.50** ^H	-0.56** ^L	C ₂₄ (P ₃ ×P ₁₀)	-4.90*	0.81 ^L	-0.63 ^L
C ₄ (P ₁ ×P ₃)	0.85**	0.04 ^L	0.71** ^H	C ₅ (P ₁ ×P ₆)	-4.55*	2.87** ^L	-0.16 ^L
YVMV infestation on fruits, %							
C ₁₄ (P ₂ ×P ₇)	-0.55**	-0.02 ^L	0.005 ^L				
C ₂ (P ₁ ×P ₃)	-0.37**	0.19** ^L	0.03 ^L				
C ₅ (P ₁ ×P ₆)	-0.31*	0.19** ^L	-0.02 ^L				
-	-	-	-				
-	-	-	-				

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

GCA: General combining ability; SCA: specific combining ability; YVMV: *Yellow vein mosaic virus*.

^HDenotes significant general combining ability effect in favorable direction.

^LDenotes non-significant general combining ability effects in favorable direction, significant and non-significant general combining ability effects in unfavorable direction.

low × low general combiners as parents. For other yield associated traits also, the top five crosses exhibiting significant SCA effects in desirable direction involved high × high, high × low and low × low general combiners as parents.

In general, a relatively higher magnitude of SCA effects were 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. 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. These best specific combiners having the highest magnitude of significant SCA effects in 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.

Attainment of maximum marketable yield per plant in okra is largely governed by the incidence of FSB and YVMV. Although the parental lines P₂ and P₈ were identified as high general combiners for FSB infestation on fruits and shoots and none as high general combiners for YVMV on fruits and plants, they could not be straight away utilized in further breeding programs. This is because of the fact that the screening of genotypes for reaction to FSB and YVMV was carried out in the field under natural conditions with regular plant protection measures. In such a situation, interpretation of results on FSB and YVMV would lead to exaggeration of facts. Hence, it is suggested to screen the genotypes under artificial epiphytotic conditions to get the real reaction of genotypes to both FSB and YVMV in okra.

Association between SCA effects of crosses and GCA effects of 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 × high, high × low and low × 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. High performance of these crosses may be attributed to additive × additive (high × high), additive × dominance (high × low), or dominance × dominance (low × low) epistatic interactions (Rewale et al., 2003). 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 (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.

Okra is a potentially self pollinated crop. Normally SCA effects do not contribute much to the improvement of self-pollinated crops. The crosses showing desirably high SCA along with desirably high GCA could be utilized in recombination breeding programs. Such programs would be more effective if one of the parents is a high combiner and the other one is a low combiner. In the present study, two crosses C₁₇(P₂×P₁₀) and C₄₂(P₇×P₁₀) out of top five high specific combiners for marketable yield per plant, involved at least one parent with positively significant GCA effects, therefore, are recommended for further breeding programs. These crosses will be considered for

recombination breeding with single plant selection in the passing generations to capitalize the additive gene action for isolating superior transgressive segregants to develop an okra variety with higher yield potential.

CONCLUSIONS

Since both additive and non-additive variances were found to be important in the genetic control of all 17 yield and yield related characters in the present study, the use of a population improvement method in the form of diallel selective mating or mass selection with concurrent random mating might lead to release of new varieties with higher yield in okra. From this study it is concluded that parental lines P₅(IC45732), P₆(IC89819), and P₇(IC89976) could be exploited beneficially in future okra breeding programs by adopting appropriate breeding strategy. The crosses C₂₃(IC29119-B × IC99716), C₁₇(IC27826-A × IC111443), C₄₂(IC89976 × IC111443) and C₄₃(IC90107 × IC111443) could be exploited for the production of F₁ hybrids for late *kharif* season after further testing in multiple locations in the state. The crosses C₁₇ (IC27826-A × IC111443) and C₄₂(IC89976 × IC111443) could be utilized in recombination breeding in order to evolve high yielding varieties suitable for late *kharif* season.

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