



Genetic analysis in okra [*Abelmoschus esculentus* (L.) Moench] through Hayman's method

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Abstract : In present investigation, 28 F₁ obtained from 8 x 8 diallel mating design excluding reciprocals for yield and its components in okra [*Abelmoschus esculentus* (L.) Moench]. The genetic study revealed that estimation of variance due to additive (D) and dominance (H) both were involved in the inheritance of most of the traits studied with preponderance of non-additive gene action for all characters. These findings were also confirmed by the values of average degree of dominance estimates (H/D)^{0.5}, which was found in the range of over dominance for all the traits except days to flowering, days to first picking and internodal length. The estimates of narrow sense heritability were low for fruit yield per plant and most of the other traits except for days to flowering, days to first picking, fruit girth and crude fiber content which had moderate heritability.

Key Words : Heterosis, Okra, Hayman's method

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INTRODUCTION

Okra [*Abelmoschus esculentus* (L.) Moench] is one of the most important vegetable crops grown extensively throughout the country during summer and rainy seasons. A good knowledge of the nature and mode of inheritance of quantitative characters of economic importance is helpful to formulate a more pragmatic breeding programme. Diallel analysis is a useful device for obtaining a rapid overall picture of gene action involved in the inheritance of different quantitative characters. Different workers have studied the nature of gene action for a number of biometric traits in okra. However, as the gene action differs from genetic material to material.

parents were raised in randomized block design with three replications at Department of Genetics and Plant Breeding, C.P. College of Agriculture, S.D. Agricultural University, Sardarkrushinagar during *Kharif*, 2009. Each entry was sown in 3.0 m long single row plot at 60 x 30 cm spacing. Observations on five randomly selected competitive plants were recorded for days to flowering, days to first picking, fruit length, fruit girth, number of nodes on main stem, internodal length, plant height, fruit yield per plant, crude protein content, crude fiber content and vitamin C content. The data were subjected to statistical analysis as per the method suggested by Panse and Sukhatme (1967).

MATERIALS AND METHODS

A set of 28 hybrids were developed using 8 parents (Gujarat Okra 2, Parbhani Kranti, Arka Bahar, Arka Abhay, Pusa Sawani, Panjab 7, AOL-03-1, and JOL-04-08) of okra through diallel mating design excluding reciprocals during Summer-2009. The trials consisting of 28 hybrids and their 8

RESULTS AND DISCUSSION

The estimates of genetic parameters and their ratios for yield and its components are presented in Table 1. The estimates of D, which measure the variance due to additive gene effects, were significant for all the traits except number of nodes on main stem, plant height and crude fiber content. The H₁, which measure the variance due to non-additive

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Table 1: Estimation of genetic component of variance and other parameters for various characters in okra

Parameters	Days to 50% flowering	Days to first picking	Days to 100% maturity	Days to 1st harvest	Days to 2nd harvest	Days to 3rd harvest	Number of nodes on main stem	Number of nodes on internode	Plant height (cm)	Fruit yield per plant (kg)	Crude fiber (%)	Crude fiber (g/100g fresh wt)	Crude fiber (g/100g dry wt)	Variance components
$\sigma^2_{(W)} / V_p$	0.25	0.31	0.67	0.79	0.77	0.77	0.7	0.77	0.19	0.91	0.11	0.11	0.11	0.99
$\sigma^2_{(D)}$	5.75**	5.75**	7.73	2.72	1.15	1.15	0.83	1.15	1.38	1.31	1.16	1.16	1.16	3.79
$\sigma^2_{(I)}$	1.17	1.36	0.81	2.23	0.73	0.73	1.96*	0.73	5.91	0.75	1.76	1.76	1.76	0.03
$\sigma^2_{(A)}$	3.72	5.07**	0.75	0.97	2.21	2.21	5.35**	2.21	9.65**	0.07	0.07	0.07	0.07	0.65
$\sigma^2_{(D)}$	9.92**	9.92**	2.94**	0.55**	0.22**	0.22**	3.78	0.22**	1.68	1.53	1.50**	1.50**	1.50**	1.94**
$\sigma^2_{(I)}$	1.07**	9.82**	7.66**	0.57**	0.24*	0.24*	1.72*	0.24*	8.96.00**	2.70.59**	3.71**	3.71**	3.71**	9.19**
$\sigma^2_{(A)}$	7.99**	7.63**	6.99**	0.50**	0.26**	0.26**	3.76*	0.26**	7.68.15**	1.82.16**	2.79**	2.79**	2.79**	7.11**
$\sigma^2_{(D)}$	9.79**	9.27**	3.72*	0.19	0.05	0.05	1.62	0.05	1.23.93	1.76.56**	1.55*	1.55*	1.55*	6.22**
$\sigma^2_{(I)}$	2.18	2.71	0.07	0.00	0.02	0.02	0.07	0.02	1.76.60	3.97.8**	0.28	0.28	0.28	0.11
$\sigma^2_{(A)}$	0.37	0.32	0.09	0.01	0.12**	0.12**	0.31	0.12**	1.67	3.77.6	0.11	0.11	0.11	0.18
$(H_1/D)^{0.5}$	1.03	1.00	1.62	1.32	1.05	1.05	1.97	1.05	2.21	1.28	1.56	1.56	1.56	1.50
H_1/H_2	0.19	0.19	0.21	0.22	0.27	0.27	0.23	0.27	0.22	0.18	0.20	0.20	0.20	0.19
KD/KR	2.86	2.78	2.29	1.56	1.25	1.25	1.27	1.25	1.38	3.40	2.25	2.25	2.25	2.93
$\sigma^2_{(W)}$	0.27	0.28	0.07	0.07	0.09	0.09	0.00	0.09	0.02	0.57	0.11	0.11	0.11	0.02
$\sigma^2_{(D)}$	0.92**	0.92**	0.50	0.65**	0.13	0.13	0.32	0.13	0.19**	0.87**	0.13	0.13	0.13	0.82**
$\sigma^2_{(I)}$	0.36	0.39	0.13	0.12	0.28	0.28	0.29	0.28	0.25	0.19	0.22	0.22	0.22	0.09

* and ** indicate significant at 5% and 1% level, respectively

effects, was significant for all the character under study. The above finding indicated that both additive and dominance components were important in the inheritance of these traits. However, additive components were lower in magnitude than corresponding dominance components for all the characters, which revealed preponderance of non-additive gene action for all the characters, which could be improved by bi-parental mating or recurrent selection. Similar finding were observed by Indu Rani *et al.* (2002b) and Rewale *et al.* (2003). Further confirmation of the preponderance of non-additive variance was available from the average degree of dominance $(H_1/D)^{0.5}$. The estimates of dominance ratio $(H_1/D)^{0.5}$ greater than unity for all the traits indicating over dominance for most of the characters except days to flowering, days to first picking and internodal length, which the dominance ratio $(H_1/D)^{0.5}$ at unity so indicating complete dominance gene action also observed by Sood *et al.* (2001), Ajmal *et al.* (1979) and Dhankar and Dhankar (2002). The values of H_1 and H_2 were significant for all the characters, which also indicated the preponderance of non-additive genetic variance to control all the traits under study.

The equal distribution of positive and negative genes in the parents helps the breeder in selecting particular desirable trait without losing any other desirable traits. In the present study, asymmetrical distribution of positive and negative genes in the parental lines was revealed from the estimates of $H_2/4H_1$ were less than 0.25 for all the characters except nearly symmetrical distribution for number of nodes on main stem and internodal length. In such a situation, the non-additive genetic variance could only be justified by either the dominance or the over dominance effects of genes in heterozygous position.

The values of component KD/KR indicated unequal frequency of dominant and recessive genes with higher frequency of dominant genes for all the characters. This was also corroborated by the estimates of F were positive for all the characters. Rao *et al.* (1996) also observed same results. The knowledge of number of genes/group of genes responsible for particular traits is important for the genetic progress through selection. The value of h^2/H_2 was low indicated at least one group of gene was operating for fruit yield per plant and most of other traits of present study. The components of variance due to dominant effect of H_2 were found significant for all the traits. The h^2 was found significant for only fruit yield per plant. Whereas, non-significant all other character under study. The estimates of narrow sense heritability were low for fruit yield per plant and most of the other traits except for days to flowering, days to first picking, fruit girth and crude fiber content which had moderate heritability. These results indicated the major role of non-additive gene action in the inheritance of most of the characters and limited scope of their improvement through straight selection.

The analysis of homogeneity (t^2) test was non-significant indicated the fulfillment of assumptions required under diallel analysis for all the characters under study except days to first picking, number of nodes on main stem, plant height and crude fiber content. Non-fulfillment of assumptions in these traits indicated the invalidity of the hypothesis of simple additive-dominance model of gene action and involvement of epistasis and/or linkage disequilibrium. The correlation between parental order of dominance ($V_r + W_r$) and parental mean (Y_i) was positive and significant for days to flowering, fruit yield per plant and vitamin C content which indicated involvement of recessive alleles for increasing the mean values. Thus, recessive genes were responsible for increase the mean for days to flowering, fruit yield per plant and vitamin C content. The regression of W_r on V_r was desirable and near unity for days to flowering, fruit length, internodal length, fruit yield per plant and vitamin C content indicating validity of simple additive-dominance hypothesis of gene action for these characters. Therefore, graphical analysis was performed for these traits only. For remaining traits, the W_r - V_r graphs were much distorted and failed to give much information.

In graphical analysis the regression line intercepted W_r axes below the origin indicated over dominance for days to flowering, fruit length, internodal length, fruit yield per plant and vitamin C content. The wide scattering of parental array points along the regression line in the W_r - V_r graph days to flowering, fruit length, internodal length, fruit yield per plant and vitamin C content indicated considerable genetic diversity among the parents for these traits. In graphical analysis, a higher proportion of dominant genes were observed in parent AOL-03-1 for affecting flowering. The parental line JOL-04-08 was found having maximum recessive gene for increasing the fruit yield per plant and early flowering. Similarly parental line

Panjab-7 had maximum recessive genes for increasing the fruit length and vitamin C content.

Thus, in the present investigation both the additive and non-additive genetic components were important in the inheritance of fruit yield and its components with preponderance of non-additive gene action. It is, therefore, suggested that improvement of fruit yield and its attributes in okra can be brought about using breeding methods like diallel selective mating or bi-parental mating followed by selection in advanced generation.

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