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Studies on genetic component of variance in okra [*Abelmoschus esculentus* (L.) Moench]

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Abstract
The experiment was conducted with 120 treatments (28 F_1s, 28 F_2s, 28 B_1s and 28 B_2s Populations) developed through diallel technique excluding reciprocals along with 8 parents viz.; AB-2, AB-1, KS-312, BO-2, P-7, VRO-3, VRO-5 and PK in a randomized block design in three replication at the Research Farm of the Department of Vegetable Science, C. S. Azad University of Agriculture and Technology, Kalyanpur, Kanpur during kharif 2006. The observations were recorded for 10 quantitative traits namely days to flowering, height of plant (cm), number of branches per plant, number of first fruiting node, number of nodes per plant, length of internode (cm), length of fruit (cm), width of fruit (cm), number of fruits per plant and yield per plant (g). The study was revealed that the genetic component of variance showed both additive and dominance component of variance were significant for all the characters in both the generations except height of plant and width of fruit in F_1 generations and yield per plant in F_2 generations for additive component and width of fruit in F_1 for dominance component. Over dominance was operating for all the characters in both the generations except number of branches per plant in F_1 generation.

Keywords: Diallel technique, genetic component variance, okra, quantitative traits

Introduction
Okra is one of the important vegetable of the tropical and sub-tropical regions of the world and is native to tropical Africa. It is grown for its green tender fruits during summer and rainy season throughout India. They are eaten fresh, canned or frozen. 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 useful device for obtaining rapid overall picture of gene action involved in the inheritance of different quantitative traits. Different workers (Lal *et al.,* 1975 and Kulkarni, *et al.,* 1976) [7, 6] have studies the nature of gene action for number of biometric traits in okra. However, as the gene action differs from genetic material to material. Therefore, the present study was undertaken to elucidate the nature and magnitude of gene action involved in the inheritance of fruit yield and its components.

Materials and Methods
A set of 8 varieties/ strains of okra namely, AB-2, AB-1, KS-312, BO-2, P-7, VRO-3, VRO-5 and PK were crossed in a diallel technique excluding reciprocals. All the 28F_1s, 28F_2s, 28B_1s and 28B_2s along with parents in randomized block design in three replications at the Research Farm of the Department of Vegetable Science, Chandra Shekhar Azad University of Agriculture and Technology, Kalyanpur, Kanpur during kharif 2006. Parents were sown in single row with ten plants and F_1s, F_2s, B_1s andB_2s were sown in double row with ten plants in

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each row. The competitive plants of parents and F_1s, F_2s, B_1s and B_2s were randomly selected and observations were recorded for days to flowering, height of plant (cm), number of branches per plant, number of first fruiting node, number of nodes per plant, length of internode (cm), length of fruit (cm), width of fruit (cm), number of fruit per plant and yield per plant (g).

Results and Discussion

The analysis for the estimation of genetic components was carried out by employing diallel analysis method of Hayman (1954). The estimates of genetic parameters and their ratios for yield and its components are presented in table-1. The estimate that genetic component of variance showed significant value for additive genetic component ($\hat{D}$) for all the characters in both the generations except the height of plant and width of fruit in F_1 generation and yield per plant in F_2 generation. These estimates indicate the preponderance role of additive genetic component for controlling these characters. Similar findings were observed by Lal *et al.,* (1975), Indu Rani *et al.,* (2005) and Vacchani and Shekhat (2008), Ayesha *et al.* (2017) [7, 2, 8, 9].

The estimates of H_1 (dominance) component were also highly significant for all the characters in both the generations except width of fruit in F_1 generation. The above findings 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 in both the generation, which revealed preponderance of non-additive gene action for these characters, which could be improved by bi-parental mating or recurrent selection. Similar findings were observed by Indu rani *et al.,* (2005) [2]. Further confirmation of the preponderance of non-additive variance was available from the average degree of dominance $(\hat{H}_1/D)^{0.5}$. This estimate exhibited over dominance for all the traits in both the generation except for number of branches per plant in F_1 generation which expressed partial dominance. The dominance gene action also observed by Indu rani *et al.,* (2005) [2] and Chandra *et al.,* (1998) [3]. The values of $\hat{H}_1$ and $\hat{H}_2$ for all the characters were higher than those of $\hat{D}$ in both the generations, 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 a particular desirable trait without losing other traits of interest. In the present study, a symmetrical distribution of positive and negative gene in the parental lines was revealed from the estimates of $\hat{H}_2/4\hat{H}_1$ were less than 0.25 for all the characters except nearly symmetrical distribution for width of fruit in F_2 generation. In such a situation, the non-additive genetic variance could only be justified by either the dominance or the over dominance effect of genes in heterozygous position.

The ratio of total number of dominant to recessive alleles in the parents (KD/KR) or $(4\hat{D}\ \hat{H}_1)^{0.5} + F/(4\hat{D}\ \hat{H}_1)^{0.5}$-F indicated unequal frequency of dominant and recessive genes with more number of dominant genes in all the traits except for number of first fruiting node in both the generations and number of branches per plant, number of nodes per plant, length of internode, length of fruit, number of fruits per plant and yield per plant in F_2 generation only, in which proportion of recessive genes was more. This was also corroborated by the estimates of $F^{\wedge}$ were positive for all the characters in both the generations (Ayesha *et al.* (2017) [9] also observed same results.

The knowledge of number of gene groups responsible for a particular trait is important for the genetic progress through selection. In the present study, the ratio of $h^{\wedge 2}/H^{\wedge}_2$ was low in most of cases in both the generation except days to flowering, number of nodes per plant, length of fruit, number of fruits per plant and yield per plant in F_1 generation, indicating that a few genes or group of genes generally controlled the inheritance of a particular character. Similar results reported by Anand *et al.,* (1972) [5]. The component of variance due to dominant effects of $H^{\wedge}_2$ and $h^{\wedge 2}$ was found significant for all the characters in both the generations except $h^{\wedge 2}$ value for number of first fruiting node, length of internode and width of fruit in both the generations and number of branches per plant, number of nodes per plant and yield per plant in F_2 generation only expressed non-significant values. The correlation values between parental order of dominance and parental measurement (r) was found to be negative for most of characters except for number of fruits per plant, height of plant, number of branches per plant, length of internode in F_1 generation and yield per plant in F_2 generation. Negative value of this measurement showed that positive genes were responsible for expression of these traits and were dominant in nature. Rest of the traits in their respective generations showed negative effects of genes.

Table 1: Estimates of genetic components and related parameters for ten character in 8x8 diallel cross in F_1 and F_2 generations of okra

Characters	Generation	$\hat{D}$	$\hat{H}_1$	$\hat{H}_2$	$\hat{F}$	$\hat{h}^2$	$\hat{E}$	$(\hat{H}_1/\hat{D})^{0.5}$	$(\hat{H}_2/\hat{D})^{0.5}$	$(4D\ \hat{H}_1/\hat{D})^{0.5}$ + F/ $(4D\ \hat{H}_1/\hat{D})^{0.5}$ − F	$\hat{h}^2/\hat{H}_2$	r
Days to flowering	F_1	7.14**	18.04**	13.19**	-11.96**	29.81**	0.35	1.59	0.18	0.30	2.26	-0.67
	SE±	1.81	4.16	3.62	4.28	2.43	0.60					
	F_2	7.20**	51.11**	44.39**	-9.44	9.28**	0.29	2.66	0.22	0.61	0.20	-0.40
	SE±	1.07	9.83	8.55	5.05	1.43	0.36					
Height of plant (cm)	F_1	53.88	256.24**	182.98**	-106.49**	217.07**	4.63	2.18	0.18	0.38	1.19	0.32
	SE±	29.13	66.96	58.25	68.82	39.07	9.71					
	F_2	57.04**	759.15**	607.89**	-82.99**	79.81**	1.47	3.65	0.20	0.66	0.13	-0.21
	SE±	19.27	177.22	154.18	91.08	25.85	6.42					
Number of branches per plant	F_1	0.60**	0.35**	0.28**	-0.07	0.20**	0.04*	0.77	0.20	0.86	0.71	0.42
	SE±	0.04	0.09	0.08	0.10	0.05	0.01					
	F_2	0.58**	5.36**	4.81**	0.90	0.11	0.06	3.04	0.22	1.68	0.02	-0.41
	SE±	0.14	1.29	1.12	0.66	0.19	0.05					
Number of first fruiting node	F_1	1.11**	2.94**	2.75**	0.27	0.15	0.12	1.63	0.23	1.16	0.05	-0.59
	SE±	0.32	0.74	0.64	0.76	0.43	0.11					
	F_2	1.17**	14.43**	13.83**	1.10	0.48	0.06	3.52	0.24	1.31	0.03	-0.78
	SE±	0.26	2.39	2.08	1.23	0.35	0.09					
Number of nodes per	F_1	4.01**	7.67**	6.69**	-2.78	13.85**	1.08**	1.38	0.22	0.60	2.07	-0.43
	SE±	0.96	2.21	1.92	2.27	1.29	0.32					

Character	Gen	D	H_1	H_2	F	E	h^2	$(H_1/D)^{0.5}$	$H_2/4H_1$	KD/KR	h^2/H^2	r
plant	F_2	4.44**	61.64**	51.75**	0.89	2.48	0.65	3.73	0.21	1.06	0.05	-0.80
	SE±	1.38	12.69	11.04	6.52	1.85	0.46					
Length of internode (cm)	F_1	2.58**	4.66**	3.75**	-0.37	0.48	0.21*	1.34	0.20	0.90	0.13	0.29
	SE±	0.30	0.68	0.59	0.70	0.40	0.10					
	F_2	2.71*	44.30**	37.49**	1.19	0.85	0.08	4.04	0.21	1.11	0.02	-0.70
	SE±	1.06	9.79	8.51	5.03	1.43	0.35					
Length of fruit (cm)	F_1	1.72**	6.32**	6.06**	-0.54	19.54**	0.23*	1.92	0.24	0.85	3.22	-0.74
	SE±	0.30	0.68	0.59	0.70	0.40	0.10					
	F_2	1.85**	23.86**	20.38**	2.32	8.40**	0.11	3.59	0.21	1.42	0.41	-0.64
	SE±	0.36	3.34	2.90	1.71	0.49	0.12					
Width of fruit (cm)	F_1	0.03	0.10	0.09*	-0.03	0.02	0.01	1.81	0.22	0.57	0.22	-0.19
	SE±	0.03	0.06	0.05	0.06	0.04	0.01					
	F_2	0.02*	0.16**	0.18**	-0.01	0.00	0.02	2.67	0.28	0.84	0.00	-0.01
	SE±	0.01	0.06	0.06	0.03	0.01	0.00					
Number of fruits per plant	F_1	2.77**	6.76**	6.15**	-4.90*	18.22**	0.84*	1.56	0.23	0.28	2.96	0.72
	SE±	1.05	2.41	2.10	2.48	1.41	0.35					
	F_2	3.38*	65.78**	57.57**	4.80	5.97*	0.22	4.41	0.22	1.38	0.10	0.71
	SE±	1.61	14.76	12.84	7.59	2.15	0.54					
Yield per plant (g)	F_1	211.77*	1383.81**	1108.27**	-520.24**	2696.47**	51.18	2.56	0.20	0.35	2.43	-0.25
	SE±	100.16	230.26	200.33	236.68	134.35	33.39					
	F_2	231.91	7585.85**	6858.02**	352.69	503.09	31.04	5.72	0.22	1.31	0.08	-0.05
	SE±	227.73	2094.08	1821.85	1076.22	305.45	75.91					

*Significant at 5% level, ** Significant at 1% level.

D= Additive genetic variance, H_1= dominance variance, $H_2 = H_1 [1-(U-V)^2]$, where U and V are the proportion of positive and negative genes, respective in the parents, E= Expected environmental component of variance, F= Mean of Fr over away, where Fr is the variance of additive and dominant effects in single array, h^2= dominant effects in single $(H_1/D)^{0.5}$= Average degree of dominance, $H_2/4H$= the proportion of positive and negative effect in parents, $[(4D\hat{}H\hat{}_1)^{0.5}+F\hat{}(4D\hat{}H\hat{}_1)^{0.5}-F]$ or KD/KR = proportion of dominant and recessive genes in parents. $h\hat{}^{2}/H\hat{}_2$= number of group of genes which control the characters and exhibited dominance, r= correlation coefficient in $F_2[0.25H_1/D]$, $[0.25((4DH_1)+0.5F_1/\{0.025(0.25(4DH_1) 0.5+0.05F.\}$

Summary and conclusion

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 biparental mating followed by selection in advanced generation.

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