Genetics of fruit yield and its traits in okra
[Abelmoschusesculentus (L.) Moench]

ABSTRACT:

A Half-diallel mating design involving nine okra genotypes was used to study the inheritance of fruit yield and its component characters in okra. Data from the F_1 generation and parents were analysed using Hayman's (1954) method of diallel analysis. The estimated component of genetic variation revealed that additive component (D) was significant for number of branches per plant and fruit girth in E_1 and fruit girth in E_3 environment. However, additive component was non-significant in all three environments for fruit yield per plant. The dominant components (H_1 and H_2) were significant for all the characters in all the environments. These results revealed the importance of both additive and non-additive component of gene action in the expression of traits under study. The relative magnitude of dominant component (H_1 and H_2) was higher than additive component for most of the traits indicating that dominance gene action involved in expression of most of the characters under studied. The average degree of dominance for fruit yield per plant and most of the traits was more than unity in all the three environments which suggested over dominance effect in expression of all the traits. The proportion of genes with positive and negative effects in parents was deviated from 0.25 in all three environments suggesting asymmetrical distribution of positive as well as negative alleles among the parents for fruit yield per plant. The ratio of dominant and recessive genes in the parents were also greater than unity in all the three environments, indicated excess of dominant genes were present in the parents for fruit yield per plant. In the presence of overdominance for yield, reciprocal recurrent selection is the best recurrent scheme to develop hybrids.

Keywords: Okra, diallel analysis, additive component, reciprocal recurrent selection

1. INTRODUCTION:

Okra [*Abelomoschusesculentus*(L.) Moench] commonly known as Bhindi belongs to the family Malvaceae. It is a warm season vegetable in the tropical and subtropical countries of the world. It is an often cross pollinated crop. The immature young seed pods are the edible part of this plant, which are consumed as cooked vegetable, mostly fresh but sometimes sun-dried. Okra is gaining importance with regard to its nutritional, medicinal, and industrial value. Apart from nutritional and health importance, It plays an important role in income generation and subsistence among rural farmers in India. Okra is commercially grown in the Indian states of Gujarat, Maharashtra, Andhra Pradesh, Karnataka and Tamil Nadu. The distinguished position of okra among Indian vegetables can be due to its easy cultivation, regular yield, wider adaptability and year round cultivation.Knowledge about the magnitude and nature of genetic variation in a specific population is prime importance for the effective prediction of most effective breeding programme. The present paper reports the gene effects controlling fruit yield and its component characters in okra.

2. MATERIALS AND METHODS

Nine okra genotypes *viz*., IC 90107, HRB 108-2, EC 169513, AOL-12-59, NOL-17-9, JOL-11-1, HRB-55, GO-2 and VRO-6 were chosen in this study to represent substantial amount of genetic diversity for different quantitative and quality traits. These were crossed in half-diallel fashion(with parents) excluding reciprocals during *Summer*, 2021. The resultant 36 F_1 hybrids along with nine parents and one check (GJOH 4) were evaluated in randomized block design with three replications at Instructional farm, Junagadh Agricultural University, Junagadh (Gujarat) with spacing of 60 x 30 cm during three seasons Early kharif 2021 (E_1), Kharif 2021 (E_2) and Late kharif 2021 (E_3). The observations were recorded on five randomly selected plants from each plot for growth and fruit yield parameters *viz.*, plant height, number of branches per plant, number of nodes per plant, intermodal length, fruit length, fruit girth, ten fruit weightand fruit yield per plant (g). The genetic components of variation from the diallel crossfor E_1, E_2 and E_3 were worked out according to method given by Hayman (1954).

3. RESULT AND DISCUSSION

Hayman (1954) derived the expectations for the statistics calculated from the diallel and also the expected values of the components of variations (D, H_1, H_2, F, h^2 and E) using the least square technique. The additional statistics needed for the genetic interpretation and the overall information derived from the genetic parameters are detailed in Table 1 and 2. The additive component (D) was significant for number of branches per plant, fruit girth in E_1 and fruit girth in E_3 environment. The additive component was non-significant in all three environments for fruit yield per plant. On the other hand, the dominant components (H_1 and H_2) were significant for all the characters in all the environments. These results revealed that importance of both additive and non-additive component of gene action in expression of traits under studied. The relative magnitude of both dominant components (H_1 and H_2) were higher than additive component (D) for most the traits indicated that dominance gene action was involved in expression of mostly characters under studied. Similar finding was also reported by Yadav et al. (2023) and Rasheed et al. (2024). The overall dominance effect (h^2) over all loci in heterozygous phase for all crosses was found non-significant for all the characters except plant height in E_2. This indicated recessive genes were more prevailed in the trait inheritance while significant value indicated involvement of dominant genes in trait inheritance. The value of F (covariance of additive and non-additive effects) was non-significant for all the traits in all environments indicated symmetrical distribution of dominant and recessive genes in parents. The significant estimate of 'E' for plant height and fruit girth in E_2 and E_3 indicated that the expression of these characters was highly affected by environmental conditions.

Table 1: Estimation of genetic components of variation in okra

S. N.	Comp.	E	Plant height			No. of branches per plant			Number of nodes per plant			Internodal length (cm)		
1	**D**	E_1	87.43	±	52.09	0.10**	±	0.03	6.42	±	4.07	0.25	±	0.20
		E_2	27.56	±	29.06	0.03	±	0.02	5.23	±	5.53	0.33	±	0.17
		E_3	19.21	±	24.93	0.03	±	0.03	2.93	±	2.22	0.34	±	0.23
2	**H_1**	E_1	410.05**	±	114.96	0.39**	±	0.06	42.76**	±	9.00	1.65**	±	0.45
		E_2	266.41**	±	64.13	0.18**	±	0.05	31.01**	±	5.58	2.04**	±	0.38
		E_3	235.84**	±	55.02	0.26**	±	0.07	19.50**	±	4.90	2.00**	±	0.51
3	**H_2**	E_1	285.96*	±	98.83	0.31**	±	0.05	31.60**	±	7.73	1.30**	±	0.39
		E_2	198.68**	±	55.13	0.17**	±	0.05	23.92**	±	4.80	1.65**	±	0.32
		E_3	163.21**	±	47.30	0.23**	±	0.06	13.69**	±	4.21	1.68**	±	0.44
4	**h^2**	E_1	115.53	±	66.21	0.02	±	0.04	0.09	±	5.18	0.03	±	0.25
		E_2	100.83*	±	36.93	0.01	±	0.03	1.90	±	3.21	-0.01	±	0.21
		E_3	2.62	±	31.69	0.01	±	0.01	-0.09	±	2.82	0.41	±	0.29
5	**F**	E_1	87.67	±	52.09	0.10	±	0.07	5.37	±	9.50	0.56	±	0.47
		E_2	7.48	±	67.78	0.03	±	0.06	3.20	±	5.90	0.68	±	0.40
		E_3	0.73	±	58.15	0.03	±	0.07	5.00	±	5.18	0.63	±	0.54
6	**E**	E_1	28.65	±	16.47	0.01	±	0.01	0.35	±	1.29	0.06	±	0.06
		E_2	23.93*	±	9.19	0.01	±	0.02	0.39	±	0.80	0.05	±	0.05
		E_3	20.84*	±	7.88	0.00	±	0.01	0.25	±	0.70	0.04	±	0.07
S. N.	**Comp.**	**E**	**Fruit length (cm)**			**Fruit girth (cm)**			**Ten fruit weight (g)**			**Fruit yield per plant (g)**		
1	**D**	E_1	0.46	±	0.48	0.02*	±	0.01	133.61	±	137.15	1117.56	±	568.59
		E_2	0.25	±	1.02	0.01	±	0.01	185.01	±	106.78	1463.34	±	832.02
		E_3	-0.07	±	0.75	0.03**	±	0.01	153.36	±	78.54	1740.90	±	780.16
2	**H_1**	E_1	8.32**	±	1.07	0.10**	±	0.02	1414.66**	±	302.72	7747.12**	±	1254.98

		E_2	8.38**	±	2.26	0.07**	±	0.01	1249.26**	±	235.69	5579.04**	±	1836.41
		E_3	6.90**	±	1.65	0.07**	±	0.02	1157.27**	±	173.36	5633.38**	±	1721.94
3	**H_2**	E_1	6.62**	±	0.92	0.09**	±	0.02	1125.99**	±	260.23	6717.52**	±	1078.82
		E_2	5.61*	±	1.94	0.07**	±	0.01	945.59**	±	202.60	4302.34**	±	1578.64
		E_3	5.15**	±	1.42	0.06**	±	0.01	953.38**	±	149.03	4512.39**	±	1480.24
4	**h^2**	E_1	0.24	±	0.61	-0.05	±	0.01	46.24	±	174.33	1031.27	±	722.72
		E_2	0.67	±	1.30	-0.01	±	0.01	-9.35	±	135.73	-14.05	±	1057.55
		E_3	1.36	±	0.95	-0.01	±	0.01	1.80	±	99.83	-34.98	±	991.63
5	**F**	E_1	-0.60	±	1.13	0.01	±	0.02	179.88	±	319.95	288.09	±	1326.41
		E_2	0.53	±	2.39	0.01	±	0.01	330.95	±	249.10	1486.83	±	1940.94
		E_3	-0.02	±	1.75	0.03	±	0.02	234.21	±	183.22	2036.22	±	1819.95
6	**E**	E_1	0.25	±	0.15	0.01*	±	0.001	32.29	±	43.31	296.72	±	179.80
		E_2	0.21	±	0.32	0.01*	±	0.004	24.33	±	33.77	148.32	±	263.11
		E_3	0.18	±	0.24	0.01*	±	0.002	17.95	±	24.84	95.56	±	246.71

The average mean degree of dominance was more than unity for all the traits under studied in all the three environments indicating presence of overdominance for these traits in respective environments. Similar finding was reported by Singh et al. (2006); Vachhani et al. (2011) and Mrinmoy et al. (2013). The $H_2/4H1$ was less than 0.25 for most of the traits in all the three environments indicated that asymmetrical distribution of positive and negative in the parental lines. The asymmetrical distribution also reported by Mrinmoy et al. (2013). The positive value of 'F' and K_D/K_Rratio more than unity (except for fruit length in E_1 and E_3) showed excess of dominant gene was present in the parents for above traits. The negative value of 'F' and K_D/K_Rratio less than unity for rest of the traits revealed that greater number of recessive gene than dominant genes in the parents for these traits. These resultswere accordance with the result of Maurya et al. (2022). Information about number of gene group which exhibit dominance and are responsible for particular characters is very important for genetic progress. In the present investigation, h^2 /$H_2$was less than unity for all the traits in all the three environments indicated not a single gene group present which control these traits. Similar findings were also reported by Singh et al. (2006) and Mrinmoy et al. (2013). According to Robinson (1966) heritability estimates in cultivated plants can be placed in following categories: low (5-10%), medium (10-30%) and high (30-60%). Low estimate of narrow sense heritability was obtained for internodal length in E_1, E_2 and E_3. Low heritability estimates indicated a major role of non-additive gene action in the inheritance of character studied and hence there is a limited scope for genetic improvement through direct selection. On the other hand, moderate narrow sense heritability was obtained for fruit yield per plant in E_3; and number of branches per plant, fruit girth, ten fruit weight and days to last picking in all three environments. Moderate heritability estimates indicated additive as well as non-additive gene action in the inheritance of characters studied and hence there is a limited scope for genetic improvement through direct selection. The high estimate of narrow sense heritability was estimated for plant height, number of nodes per plant, fruit length in all three environments; fruit yield per plant in E_1 and E_2. High heritability estimates indicated a major role of additive gene action in the inheritance of characters studied and hence there is a high scope for genetic improvement through direct selection. The results were found in agreement with Singh et al. (2006) and Mrinmoy et al. (2013).

Table 2: Estimation of genetic components of variation in okra

S. N.	ratio	Env.	Plant height	No. of branches per plant	Number of nodes per plant	Internodal length (cm)	Fruit length (cm)	Fruit girth (cm)	Ten fruit weight (g)	Fruit yiel per plant
1	$(H_1/D)^{1/2}$	E_1	2.17	1.96	2.58	2.55	4.24	2.28	3.25	2.63
		E_2	3.10	2.63	2.43	2.49	5.80	3.00	2.60	1.95
		E_3	3.50	3.03	2.58	2.43	9.75	1.52	2.75	1.80
2	$H_2/4H_1$	E_1	0.17	0.20	0.19	0.21	0.20	0.23	0.20	0.22
		E_2	0.19	0.23	0.18	0.20	0.17	0.23	0.19	0.19
		E_3	0.17	0.22	0.18	0.21	0.19	0.21	0.21	0.20

3	K_D/K_R	E_1	1.60	1.72	1.39	2.53	0.73	1.18	1.52	1.10
		E_2	1.09	1.35	1.28	2.41	1.45	1.22	2.05	1.70
		E_3	1.11	1.51	1.99	2.24	0.98	1.87	1.77	1.96
4	h^2/H_2	E_1	0.40	0.05	0.01	0.03	0.04	-0.01	0.04	0.15
		E_2	0.51	0.03	0.08	-0.01	0.12	-0.04	-0.01	-0.01
		E_3	0.02	0.02	-0.01	0.25	0.26	-0.04	0.01	-0.01
5	Heritability(ns) %	E_1	38.20	29.70	42.50	5.30	42.00	28.10	27.90	32.00
		E_2	37.40	17.30	41.70	4.10	43.70	14.40	23.20	33.90
		E_3	42.50	16.10	33.70	3.35	36.60	24.70	19.40	25.20

1. (H1 /D)½ - Average degree of dominance,
2. H_2 /4H1 – Proportion of alleles with positive and negative effects in parents,
3. K_D/K_R - Proportion of dominant and recessive alleles in parents,
4. h^2 /H_2– Number of genes controlling the character and exhibit dominance

4. CONCLUSION

The results revealed the importance of both additive and non-additive component of gene action in the expression of traits under study. The dominance gene action involved in expression of most of the characters. The ratio of dominant and recessive genes in the parents were also greater than unity in all the three environments, indicated excess of dominant genes were present in the parents for fruit yield per plant. In the presence of overdominance for yield, reciprocal recurrent selection is the best recurrent scheme to develop hybrids.

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Table 3:Genotype details with Source:

S.N.	**Name of Parents**	**Name of Source**

1	IC 90107	National Bureau of Plant Genetic Resources, New Delhi
2	HRB 108-2	Haryana Agricultural University, Hissar
3	EC 169513	National Bureau of Plant Genetic Resources, New Delhi
4	AOL-12-59	Anand Agricultural University, Anand
5	NOL-17-9	Navsari Agricultural University, Navsari
6	JOL-11-1	Junagadh Agricultural University, Junagadh
7	HRB-55	Haryana Agricultural University, Hissar
8	GO-2	Junagadh Agricultural University, Junagadh
9	VRO-6	Indian Institute of Vegetable Research, Varanasi
10	GJOH-4 (check)	Junagadh Agricultural University, Junagadh