

Genetic component analysis in fruit yield and quality traits in okra (*Abelmoschus esculentus* (L.) Moench)

ABSTRACT:

A half-diallel cross involving nine okra genotypes was utilized to investigate the inheritance of fruit yield and its component traits. Data from the F_1 generation and the parent genotypes were analysed using Hayman's (1954) diallel method. The additive genetic component (D) was found to be significant for the traits like days to last picking in environment E_1 , and for the number of fruits per plant in environments E_2 and E_3 , but non-significant across all environments for fruit yield per plant. The dominant components (H_1 and H_2) were found significant for all traits studied under in all environmental condition. This revealed indicates that both additive and non-additive gene actions play a vital role in the expression of the traits studied. The dominant component's (H_1 and H_2) relative magnitude was greater than the additive component for most of the traits, suggesting the importance of dominance effect on expression of those are important for these traits. The average degree of dominance showed an overdominance effect for the traits studied. The ratio of dominant to recessive genes indicated that the parents had an excess of dominant genes for fruit yield per plant. Thus stated Given the presence of overdominance for yield, reciprocal technique is the most effective recurrent breeding scheme for producing improved hybrids.

1. INTRODUCTION

Okra, scientifically named *Abelmoschus esculentus* (L.) Moench and commonly referred to as lady's finger, is a member of the Malvaceae family. This vegetable thrives best in warm climates and is cultivated in tropical and subtropical regions worldwide. It is an allopolyploid with a commonly observed chromosome number of $2n=8x=130$ and is frequently cross-pollinated. The okra fruit comprises 90% water, 3% dietary fiber, 7% carbohydrates, 2% protein, and is rich in minerals, vitamins C and A, as well as moderate levels of thiamin, folate, and magnesium. Okra holds a prominent place among Indian vegetables due to its ease of cultivation, consistent yield, adaptability, and ability to be grown throughout the year. Understanding the genetic mechanisms governing fruit traits is crucial for any significant improvement efforts in okra. This knowledge is essential for designing effective breeding programs. This paper discusses the genetic effects influencing fruit yield and related characteristics in okra.

2. MATERIALS AND METHODS

In this study, nine okra genotypes—IC 90107, HRB 108-2, EC 169513, AOL-12-59, NOL-17-9, JOL-11-1, HRB-55, GO-2, and VRO-6—were selected to represent a broad range of genetic diversity across various quantitative and quality traits. These genotypes were crossed in a half diallel pattern, excluding reciprocal crosses, during the summer of 2021. The resulting 36 F_1 hybrids, together with the nine parental lines and one control, were evaluated using a randomized block design with three replications at the Instructional Farm, Junagadh Agricultural University, Junagadh (Gujarat). The experimental layout included spacing of 60 x 30 cm and was evaluated over three seasons: Early Kharif 2021 (E_1), Kharif 2021 (E_2), and Late Kharif 2021 (E_3). Data were collected from five randomly chosen plants per plot on growth and fruit yield parameters, including days to first flowering, days to first picking, days to last picking, number of pickings, number of fruits per plant, and fruit yield per plant (g). The genetic components of variation were analysed using the method described by Hayman (1954) based on the diallel cross data for E_1 , E_2 , and E_3 .

3. RESULT AND DISCUSSION

Hayman (1954) established the expectations for the statistics derived from diallel crosses, including the anticipated values of variation components (D, H₁, H₂, F, h², and E) using the least squares method. Additional statistics required for genetic interpretation and the comprehensive information from these genetic parameters are outlined in Table 1. The additive component (D) was significant for days to last picking in E₁, the number of fruits per plant in E₂, and the number of fruits per plant in E₃. However, the additive component did not show significance for fruit yield per plant across all three environments. In contrast, the dominant components (H₁ and H₂) were significant for all traits in every environment. This indicates that both additive and non-additive gene actions play a prominent role in the expression of the studied traits. For most traits, the dominant components (H₁ and H₂) were more prominent than the additive component (D), suggesting that dominance gene action was primarily involved. Similar findings were reported by Vachhani *et al.* (2011) and Mrinmoy *et al.* (2013). The overall dominance effect (h²) across all loci in the heterozygous phase for all crosses was non-significant for all traits, except for the number of fruits per plant in E₁ and E₂, and the number of pickings in E₂ and E₃. This suggests that recessive genes were more prevalent in the inheritance of these traits. The value of F (covariance between additive and non-additive effects) was non-significant for all traits in all environments, except for the number of fruits per plant in E₃, indicating a symmetrical distribution of dominant and recessive genes among the parents. Significant estimates of 'E' for days to first flowering, days to first picking, number of fruits per plant in E₁, and number of pickings in E₁ and E₂ suggest that environmental conditions had a substantial impact on these traits.

Table 1: Estimation of genetic components of variation in okra

S. N.	Components/ ratio	Env.	Days to first flowering			Days to first picking			Days to last picking		
				±			±			±	
1	D	E ₁	2.72	±	5.35	2.09	±	5.54	144.77*	±	52.06
		E ₂	-0.97	±	1.03	-1.35	±	0.99	44.45	±	39.65
		E ₃	1.03	±	3.70	-0.30	±	3.53	17.05	±	8.33
2	H₁	E ₁	65.71**	±	11.80	59.20**	±	12.92	596.60**	±	114.98
		E ₂	13.20**	±	2.28	9.89**	±	2.19	247.33**	±	87.52
		E ₃	34.09**	±	8.17	30.32**	±	7.80	74.26**	±	18.39
3	H₂	E ₁	53.78**	±	10.14	46.30**	±	10.50	491.52**	±	98.84
		E ₂	11.37**	±	1.96	7.09**	±	1.88	217.93**	±	75.24
		E ₃	24.94**	±	7.02	21.71**	±	6.71	62.07**	±	15.80
4	h²	E ₁	1.60	±	6.80	0.59	±	7.04	-2.37	±	66.22
		E ₂	-0.74	±	1.32	-0.78	±	1.26	33.50	±	50.40
		E ₃	6.04	±	4.70	5.79	±	4.49	3.96	±	10.59
5	F	E ₁	11.20	±	12.47	11.73	±	12.92	196.91	±	121.53
		E ₂	-0.80	±	2.41	-1.42	±	2.31	43.54	±	92.50
		E ₃	7.99	±	8.63	6.49	±	8.24	19.93	±	19.43
6	E	E ₁	1.89	±	1.69	2.48	±	1.75	12.06	±	16.47
		E ₂	2.30**	±	0.33	3.01**	±	0.31	9.10	±	12.54
		E ₃	2.72*	±	1.17	4.24**	±	1.12	5.41	±	2.63
S. N.	Components/ ratio	Env.	Number of pickings			Number of fruits per plant			Fruit yield per plant (g)		
1	D	E ₁	0.27	±	0.33	2.60	±	1.54	1117.56	±	568.59
		E ₂	0.52	±	0.25	8.04**	±	1.99	1463.34	±	832.02
		E ₃	0.25	±	0.19	12.37**	±	2.46	1740.90	±	780.16
2	H₁	E ₁	3.37**	±	0.73	14.21**	±	3.40	7747.12**	±	1254.98
		E ₂	1.86**	±	0.55	18.83**	±	4.39	5579.04**	±	1836.41
		E ₃	1.69**	±	0.41	27.06**	±	5.43	5633.38**	±	1721.94
3	H₂	E ₁	3.15**	±	0.63	10.33**	±	2.92	6717.52**	±	1078.82

		E ₂	1.20*	±	0.47	14.10**	±	3.77	4302.34**	±	1578.64
		E ₃	1.56**	±	0.35	19.15**	±	4.67	4512.39**	±	1480.24
4	h²	E ₁	0.11	±	0.42	5.13*	±	1.96	1031.27	±	722.72
		E ₂	4.06**	±	0.32	-0.10**	±	2.53	-14.05	±	1057.55
		E ₃	2.41**	±	0.24	0.02	±	3.13	-34.98	±	991.63
5	F	E ₁	0.23	±	0.78	2.81	±	3.59	288.09	±	1326.41
		E ₂	0.93	±	0.58	9.49	±	4.64	1486.83	±	1940.94
		E ₃	-0.10	±	0.43	17.92*	±	5.74	2036.22	±	1819.95
6	E	E ₁	0.39**	±	0.11	1.40*	±	0.49	296.72	±	179.80
		E ₂	0.26*	±	0.08	1.00	±	0.63	148.32	±	263.11
		E ₃	0.09	±	0.06	0.86	±	0.78	95.56	±	246.71

D = Additive genetic variance of the parents, *H*₁ = Dominance of genetic variance, *H*₂ = Adjusted dominance variance according to gene distribution, *h*² = Overall dominance effects, *F* = Relative frequencies of dominant and recessive alleles in parents, *E* = Environmental effects

(what does * & ** indicating in the table 1: whether the results are significant @ 1% or 5 % level of Significance....? Please mention level of significance which is missing.....)

The average degree of dominance exceeded one for all traits across the three environments, suggesting the presence of overdominance for these traits. This finding aligns with the results reported by Singh *et al.*(2006), Vachhani *et al.*(2011), and Mrinmoy *et al.*(2013). The ratio of *H*₂ to 4*H*₁ was below 0.25 for most traits in all environments, indicating an asymmetrical distribution of positive and negative traits among the parental lines. Mrinmoy *et al.*(2013) also observed this asymmetry. Positive values for 'F' and *K*_D/*K*_R ratios greater than one (except for days to first flowering in *E*₂, days to first picking in *E*₂ and *E*₃, and number of pickings in *E*₃) suggest an excess of dominant genes in the parents for these traits. Conversely, negative values for 'F' and *K*_D/*K*_R ratios less than one for the remaining traits indicate a predominance of recessive genes in the parents. These results are consistent with those of Mrinmoy *et al.*(2013). The ratio of *h*² to *H*₂ was below one for all traits in the three environments (except for the number of pickings in *E*₂ and *E*₃), indicating the absence of a distinct gene group controlling these traits. Similar observations were made by Singh *et al.*(2006) and Mrinmoy *et al.*(2013). Low narrow-sense heritability estimates were found for days to first picking in *E*₁ and *E*₃, and for days to first flowering and number of pickings in *E*₁, suggesting that non-additive gene action plays a major role in these traits, limiting the potential for genetic improvement through direct selection. Moderate narrow-sense heritability was observed for days to first flowering and days to first picking in *E*₂; number of fruits per plant in *E*₂ and *E*₃; number of pickings in *E*₁ and *E*₂; fruit yield per plant in *E*₃; and days to last picking across all environments, indicating a mix of additive and non-additive gene actions, which also limits genetic improvement through direct selection. High narrow-sense heritability was noted for the number of fruits per plant in *E*₁ and fruit yield per plant in *E*₁ and *E*₂, pointing to a significant role of additive gene action and a greater potential for genetic improvement through direct selection. These results are in agreement with findings by Singh *et al.*(2006) and Mrinmoy *et al.*(2013).

Table 2: Estimation of genetic components of variation in okra

S. N.	Components/ ratio	Env.	Days to first flowerin g	Days to first picking	Days to last picking	Number of pickings	Number of fruits per plant	Fruit yield per plant(g)
1	(<i>H</i> ₁ / <i>D</i>) ^{1/2}	<i>E</i> ₁	4.91	5.32	2.03	3.55	2.34	2.63
		<i>E</i> ₂	3.69	2.70	2.36	1.89	1.53	1.95
		<i>E</i> ₃	5.74	10.05	2.09	2.61	1.48	1.80
2	<i>H</i> ₂ /4 <i>H</i> ₁	<i>E</i> ₁	0.21	0.20	0.21	0.23	0.18	0.22
		<i>E</i> ₂	0.22	0.18	0.22	0.16	0.19	0.19
		<i>E</i> ₃	0.18	0.18	0.21	0.23	0.18	0.20
3	<i>K</i> _D / <i>K</i> _R	<i>E</i> ₁	2.44	3.23	2.00	1.28	1.60	1.10
		<i>E</i> ₂	0.80	0.68	1.52	2.78	2.26	1.70

		E ₃	5.11	0.59	1.78	0.86	2.92	1.96
4	h ² /H ₂	E ₁	0.03	0.01	-0.01	0.03	0.50	0.15
		E ₂	-0.07	-0.11	0.15	3.39	-0.01	-0.01
		E ₃	0.24	0.27	0.06	1.54	0.01	-0.01
5	Heritability(ns)%	E ₁	10.10	10.40	16.40	9.90	31.60	32.00
		E ₂	13.90	23.00	19.20	18.50	26.50	33.90
		E ₃	10.90	8.60	18.20	33.30	17.30	25.20

1. $(H_1/D)^{1/2}$ - Average degree of dominance,
2. $H_2/4H_1$ - 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

For most of the traits studied, the dominant components (H₁ and H₂) were more pronounced than the additive component, indicating that dominance gene action plays a significant role in the traits under investigation. The average degree of dominance further suggests the presence of overdominance in these traits. The ratio of dominant to recessive genes points to an excess of dominant genes in the parents for fruit yield per plant. Stated Given the overdominance was observed for yield, while, reciprocal recurrent selection is the most effective approach for developing hybrids.

REFERENCES

1. Hayman, B. I. (1954). The analysis of variance of diallel tables. *Biometrics*, 10(2): 235-244.
2. Vachhani, J.H., Shekhat, H.G., Kachhadia, V.H., Jivani, L.L. and Padhar, P.R. (2011). Heterosis and inbreeding depression in okra (*Abelmoschus esculentus* L. Moench.). *Res. on Crops.*, 12 (2): 556- 560
3. Mrinmoy, D., Asif, M., Venkatesha, K.T. and Vijaya Kumar, K.V. (2013). Nature of gene action in okra through diallel analysis. *Asian J. Bio Sci.*, 8(1): 145-146.
4. Singh, S., B. Singh and A.K. Pal (2006). Line x tester analysis of combining ability in okra. *Indian J. Hort.* 63 (4): 397-401