



Genetic Component Analysis in Fruit Yield and Quality Traits in Okra [*Abelmoschus esculentus* (L.) Moench]

Limbani Harsiddhi ^{a++*}, Bhagyashree Acharya ^{b++}
and Mehta DR ^{a#}

^a Department of GPB, Junagadh Agricultural University, Junagadh, India.
^b Department of GPB, Institute of Agricultural Science, BHU, Varanasi, India.

Authors' contributions

This work was carried out in collaboration among all authors. Author LH designed the study, performed the statistical analysis and wrote the final manuscript. Author BA managed the literature searches and Author MDR guided throughout the research work. All authors read and approved the final manuscript.

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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 F₁ 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 E₁, and for the number of fruits per plant in environments E₂ and E₃, but non-significant across all environments for fruit yield per plant. The dominant components (H₁ and H₂) were found significant for all traits studied under all

⁺⁺ Ph.D. Scholar;

[#] Professor and Head;

^{*}Corresponding author: E-mail: limbani.hari111@gmail.com;

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environmental condition. This revealed 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 effects on expression of those 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 the presence of overdominance for yield, reciprocal technique is the most effective recurrent breeding scheme for producing improved hybrids.

Keywords: Fruit yield; genotypes; okra; breeding.

1. INTRODUCTION

Okra, scientifically named *Abelmoschus esculentus* (L.) Moench and commonly referred 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 [1-3]. 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 [4] based on the diallel cross data for E_1 , E_2 , and E_3 .

3. RESULTS AND DISCUSSION

Hayman [4] established the expectations for the statistics derived from diallel crosses, including the anticipated values of variation components (D, H_1 , H_2 , F, h^2 , 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 E_1 , the number of fruits per plant in E_2 , and the number of fruits per plant in E_3 . However, the additive component did not show significance for fruit yield per plant across all three environments. In contrast, the dominant components (H_1 and H_2) 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 (H_1 and H_2) were more prominent than the additive component (D), suggesting that dominance gene action was primarily involved. Similar findings were reported by Vachhani et al. [5] and Mrinmoy et al. [6]. The overall dominance effect (h^2) 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 E_1 and E_2 , and the number of pickings in E_2 and E_3 . 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

Table 2. 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	Number of pickings	Number of fruits per plant	Fruit yield per plant(g)
1	$(H_1/D)^{1/2}$	E ₁	4.91	5.32	2.03	3.55	2.34	2.63
		E ₂	3.69	2.70	2.36	1.89	1.53	1.95
		E ₃	5.74	10.05	2.09	2.61	1.48	1.80
2	$H_2/4H_1$	E ₁	0.21	0.20	0.21	0.23	0.18	0.22
		E ₂	0.22	0.18	0.22	0.16	0.19	0.19
		E ₃	0.18	0.18	0.21	0.23	0.18	0.20
3	K_D/K_R	E ₁	2.44	3.23	2.00	1.28	1.60	1.10
		E 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

pickings in E₃) 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. [6]. 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 E₂ and E₃), indicating the absence of a distinct gene group controlling these traits. Similar observations were made by Singh et al. [7] and Mrinmoy et al. [6]. Low narrow-sense heritability estimates were found for days to first picking in E₁ and E₃, and for days to first flowering and number of pickings in E₁, 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 E₂; number of fruits per plant in E₂ and E₃; number of pickings in E₁ and E₂; fruit yield per plant in E₃; 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 E₁ and fruit yield per plant in E₁ and E₂, 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. [7] and Mrinmoy et al. [6-10].

4. CONCLUSION

For most of the traits studied, the dominant components (H_1 and H_2) 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 the overdominance was observed for yield, while, reciprocal recurrent selection is the most effective approach for developing hybrids.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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