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Genetic variability, combining ability, and stability analysis studies on traditional okra genotypes and their hybrids (*Abelmoschus esculentus* (L.) Moench) using line × tester design

Abstract. Improving fruit yield in traditional okra varieties is vital for food security, sustainable agriculture, and the conservation of landrace diversity. Evaluating their genetic potential and stability with modern testers is key to achieving higher yields and advancing crop improvement.

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The study aimed to assess the genetic variability, combining ability, gene action, and stability of traditional okra genotypes and their hybrids using a line × tester design to identify high-yielding, stable hybrids with specific environmental adaptability and enhanced fruit yield. A line × tester analysis was conducted during the period 2022-2024 at Annamalai University, Chidambaram (India), using seven lines and three testers to investigate combining ability, gene action, and heterosis in traditional okra genotypes (*Abelmoschus esculentus* (L.) Moench). The parents were selected from a diverse group of 32 traditional landraces. The study evaluated ten economically important traits, including days to 50% flowering, plant architecture, and yield components. Combining ability analysis indicated the predominance of nonadditive gene action for all traits studied. Among the parents, Heirloom White, Anchita Local (lines), and Arka Anamika (tester) exhibited superior general combining ability for multiple traits, including fruit yield. The crosses Green Long Okra × Arka Anamika and Anchita Local × Arka Anamika emerged as superior hybrids, demonstrating significant specific combining ability effects and desirable standard heterosis for fruit yield and its component traits. AMMI analysis confirmed these hybrids' environmental adaptability, with Anchita Local × Arka Anamika showing particular stability across environments. Strong correlations were observed between yield components, notably between fruit dimensions and yield per plant. The high heritability combined with the prevalence of nonadditive gene action suggests that hybrid breeding would be more effective than pure line selection for crop improvement. These findings provide valuable insights for okra breeding programmes aimed at developing high-yielding, stable hybrids with specific adaptation

Keywords: okra breeding; environmental adaptability; hybrid performance; gene action; AMMI analysis; heterosis

INTRODUCTION

Okra (*Abelmoschus esculentus*), commonly known as lady's fingers, is an annual plant of significant agronomic and nutritional importance. As a mallow family (*Malvaceae*) member, okra is cultivated globally, particularly in tropical and subtropical regions, for its edible pods, which are rich in dietary fibre, vitamins, and antioxidants. It is an allopolyploid species with a chromosome number ranging from 2n = 72 to 2n = 130, a characteristic that underpins its genetic complexity and potential for breeding. Despite its wide cultivation, enhancing okra's productivity, disease resistance, and adaptability to diverse growing conditions remains a key challenge for breeders. The relevance of this research lies in addressing the increasing demand for high-yielding and disease-resistant okra varieties to ensure food security and sustainable agriculture.

Okra production substantially contributes to the income of smallholder farmers and helps ensure nutritional security in these regions (Kshash & Oda, 2022). Developing high-yielding and stable okra varieties faces several challenges, including environmental stressors and disease pressure, particularly from the yellow vein mosaic virus (Rahman, 2020). A comprehensive study by A. Das *et al.* (2022b) examined okra's population structure and genetic diversity, revealing significant variation between cultivated and wild germplasm. This variation indicates potential for genetic improvement through systematic breeding strategies. Their research, utilising microsatellite markers, identified distinct genetic clusters that could be utilised in heterotic breeding programmes. The value of traditional germplasm in okra improvement has garnered renewed attention. Genetic variability studies by M. Reddy *et al.* (2016) and C. Alake (2020) on okra landraces showed significant diversity in agro-morphological traits and mineral content, highlighting their potential utility in breeding programmes. This research underscored the importance of characterising and preserving traditional varieties for future breeding efforts.

Recent advancements in molecular breeding have enhanced the understanding of disease resistance mechanisms. According to G. Singh *et* *al.* (2023), significant progress in identifying SSR markers associated with YVMV resistance using bulk segregant analysis illustrates how resistance genes are inherited from parents to offspring. This breakthrough provides valuable resources for marker-assisted selection in breeding initiatives. Environmental stability is crucial for developing new varieties. S. Sanwal *et al.* (2021) evaluated genotype × environment interactions for fruit yield across various alkaline environments, emphasising the significance of stability analysis in variety development. Their use of AMMI analysis (Additive Main Effects and Multiplicative Interaction) established a framework for identifying stable, high-performing genotypes across diverse conditions.

Exploiting heterosis in okra has shown promising outcomes for enhancing both yield and quality traits. Research by A. Das *et al.* (2022a) on heterotic potential for antioxidant and nutritional traits revealed significant positive heterosis for quality parameters. These findings suggest the potential to develop superior hybrids with enhanced nutritional value. Recent metabolic profiling research by A. Elshafy *et al.* (2024) further demonstrated the potential for enhancing phytochemical content through hybrid breeding. A comprehensive review by B. Singh *et al.* (2023) stressed the need to integrate traditional breeding methods with modern genomic tools to improve okra. They highlighted the importance of systematically evaluating combining ability and stability in developing superior varieties, especially in the context of changing climatic conditions.

Given these recent advances and ongoing challenges, systematic evaluation of genetic variability, combining ability, and stability in okra improvement programmes remains essential. This line × tester mating design, combined with stability analysis, offers a robust framework for identifying superior hybrid combinations while accounting for genotype × environment interactions. This research aimed to assess the genetic variability, combining ability, heterotic potential, and stability of traditional okra genotypes and their hybrids, providing valuable insights for future breeding programmes.

MATERIALS AND METHODS

The present line × tester study was carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Chidambaram, India, during the period from December 2022 to August 2024. A total of 21 hybrids were developed using a line × tester mating design, with lines serving as females and testers as males (pollen source). Ten parents were selected from a pool of 32 traditional genotypes. The seeds of mostly selected traditional okra genotypes were obtained from the Rangamalai Seed Bank Community, Karur, India. The list of the 10 selected parents used in the hybridisation programme is provided in Table 1. These parents were evaluated for yield and yield-related component traits alongside the 32 traditional genotypes. The evaluation of F_1 hybrids was conducted using a Randomised Complete Block Design (RCBD) with three replications per location.

Table 1. List of hybrids used in the programme

No.	Lines	Sl. No	Testers
1	L_1 - Salkeerthi	1	T_1 - Arka Anamika
2	L_2 - Red Long Okra	2	T_2 - Pusa A4
3	L_3 - Green Round Okra	3	T_3 - Kashi Chaman
4	L_4 - Anchita Local	**Arka Anamika – standard check**	
5	L_5 - Sri Lankan Candle Okra		
6	L_6 - Heirloom White		
7	L_7 - Green Long Okra		

Source: compiled by the authors

A multi-location trial was conducted to evaluate the stability and performance of F_1 hybrids using AMMI stability analysis during 2023 and 2024. Fifty per cent of the F_1 hybrid seeds from 21 crosses, developed through a line × tester mating design described by O. Kempthorne (1957), were sown in the multi-location fields along with their parental lines. The trial was conducted across three environments to assess the performance of the 21 hybrids and 10 parents included in this line × tester study. The environments were ENV-1 (Malliakarai, Attur, India), ENV2 (Salem, India), and ENV-3 (Chidambaram, India), with further details provided in Table 2.

Table 2. Environment details of experimental sites

Code	Location	Sowing date	Season	Latitude	Longitude	Year
ENV-1	Malliakarai, Attur, India	24.04.2023	Summer	11°34'35.3"N	78°29'29.4"E	2023
ENV-2	Kannankurichi, Salem, India	18.07.2023	Kharif	11.697412"N	78.176074"E	2023
ENV-3	Chidambaram, India	07.03.2024	Summer	11.385494"N	79.722557"E	2024

Source: compiled by the authors

All the parents and hybrids were evaluated, and the observed data were analysed to assess combining ability, heterosis, and stability parameters. Ten quantitative traits were examined from five randomly selected plants of each parent and F_1 generation *viz*. DFF – days to 50% flowering; NPB – number of primary branches per plant; PHT – plant height at maturity (cm): IL – internode length (cm), FG – fruit girth (cm); FL – fruit length (cm); SFW – single fruit weight (g); NFP – number of fruits per plant; FYP – fruit yield per plant; NSPP – number of seeds per pod. One of the parents, Arka Anamika, was chosen as the standard check variety. The performance of the F_1 hybrids was evaluated for heterosis compared to both the superior parent and the standard check, using the method described by S. Fonseca & F. Patterson (1968). To calculate heterosis, the percentage increase or decrease in the F_1 hybrid's performance was determined relative to the superior parent and the standard check.

AMMI analysis was performed for 31 okra genotypes, comprising G_{1-21} hybrids and G_{21-31} parents. The study of okra yield across different genotypes and environments was conducted using AMMI biplots. Two types of biplots, AMMI1 and AMMI2, provided insights into genotype performance, stability, and adaptability across varying environmental conditions. The AMMI model fit was achieved using two components: the main effect, representing the additive part of the model, was analysed using ordinary analysis of variance (ANOVA), while the non-additive residual (the genotype × environment interaction, the multiplicative part of the model) was analysed using principal component analysis (PCA). The main effect of a genotype × environment combination was calculated by adding the genotype mean to the environment mean and subtracting the grand mean. The interaction effect was determined by multiplying the genotype's PCA scores by the environment's PCA scores.

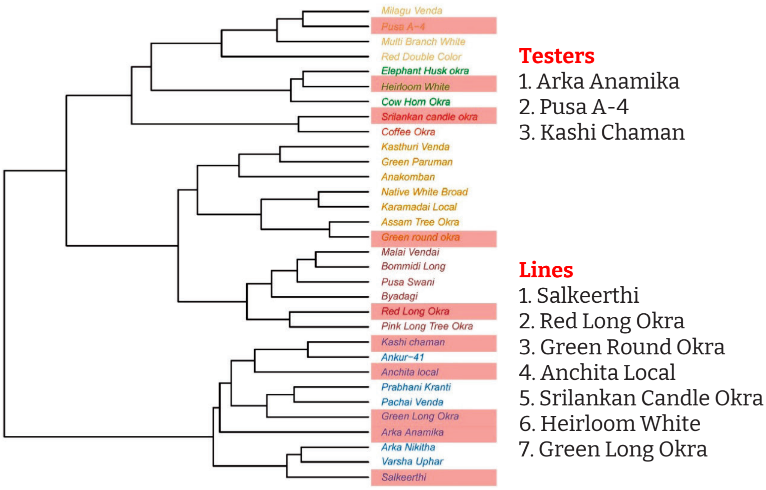
The experimental research conducted in this study adhered to institutional, national, and international guidelines for plant research. The collection of traditional okra genotypes, including seeds obtained from the Rangamalai Seed Bank Community, Karur, India, was carried out in compliance with the principles outlined in the Convention on Biological Diversity (CBD) (1992) and the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) (1973). No endangered or protected plant species were involved in this study.

RESULTS AND DISCUSSION

Diversity analysis for traditional genotypes – dendrogram

The diverse selection from various clusters indicates that these lines likely exhibit distinct morphological and yield-related traits among the 32 traditional landraces, focusing on selecting those with high fruit yield potential. Such genetic divergence among parents is crucial for a line × tester breeding programme as it can lead to higher heterosis (hybrid vigour) in the resulting crosses. Based on the phylogenetic tree diagram, the selection of okra lines for the line × tester breeding programme appears to be strategically chosen to maximise genetic diversity and capture a broad range of desirable yield characteristics. Based on Ward's cluster analysis method, six clusters have been formed using the Euclidean distance (Caliński

& Harabasz, 1974). The selected lines represent distinct genetic clusters from different branches of the dendrogram, which suggests good genetic divergence among the chosen parents. Specifically, Salkeerthi, Green Long Okra, Kashi Chaman, and Arka Anamika are from the bottom cluster (high-yield clusters), while Red Long Okra comes from a separate middle cluster (long fruit length). Green Round Okra (short internode and plant height) and Anchita Local represent different intermediate branches. Sri Lankan Candle Okra and Heirloom White are selected from the upper portion of the tree (moderate fruit yield), while Pusa A-4 is distributed across a different cluster. All lines possessed a significant degree of phenotypic variation, with most of them being traditional okra genotypes (Fig. 1).



Diversity Analysis for 32 different Okra genotypes for Cluster based Analysis

Figure 1. Diversity analysis for 32 traditional genotypes
Source: compiled by the authors

The wide genetic base also increases the probability of obtaining superior recombinants in segregating generations. Additionally, selecting representatives from different clusters helps maintain genetic diversity while pursuing yield improvement objectives in the breeding programme.

Correlation studies on traditional genotypes

The correlation analysis of various traits in okra genotypes reveals significant genotypic and phenotypic relationships that are valuable for breeding. Days to 50% flowering (DFF) has a strong positive genotypic correlation with plant height (PHT), fruit length (FL), and number of fruits per plant (NFPP), suggesting that selecting for early flowering could be associated with increased plant height and fruit size genetically. Phenotypically, DFF exhibits negative correlations with the number of seeds per pod (NSPP), indicating a possible trade-off between early flowering and seed number (Table 3). Similarly, the number of primary branches (NPB) is positively correlated with plant height and fruit length at the genotypic level, indicating that plants with more branches could also grow taller and produce longer fruits. Traits such as plant height (PHT) and internode length (IL) show strong genotypic correlations with fruit length, suggesting that taller plants with longer internodes may have larger fruits. However, phenotypic correlations are weaker, hinting at environmental influences. Positive genotypic correlations between fruit girth (FG), fruit length (FL), and the number of fruits per plant (NFPP) suggest that selecting for larger fruits could also increase fruit yield. Furthermore, fruit width (FW) shows a positive genotypic correlation with the number of fruits per plant, suggesting that wider fruits may accompany higher yields (Fig. 2).

Table 3. Correlation results: Genotypic correlations are presented in the upper diagonal, while phenotypic correlations are shown in the lower diagonal for the 32 traditional genotypes

	DFF	NPB	PHT	IL	FG	FL	FW	NFPP	FYP	NSPP
DFF		0.00074	0.018	-0.43*	0.15	-0.03	0.2	-0.23	-0.16	-0.46*
NPB	0.004		0.331	-0.16	-0.04	0.07	0.35	-0.33	-0.18	0.09
PHT	0.02	0.32*		-0.11	0.032	-0.18	-0.08	-0.22	-0.34	0.09
IL	-0.4**	-0.16	-0.11		-0.13	-0.35	-0.4	0.074	-0.2	0.23
FG	0.13	-0.03	0.031	-0.13		0.12	0.25	-0.01	0.14	0.09
FL	-0.03	0.06	-0.17	-0.34**	0.11		0.09	0.371	0.54*	-0.46*
FW	0.16	0.34**	-0.06	-0.38**	0.23	0.08		-0.61**	-0.05	0.12
NFPP	-0.2	-0.32**	-0.22	0.07	-0.01	0.35**	-0.61**		0.82**	-0.14
FYP	-0.15	-0.17	-0.33**	-0.19	0.14	0.518**	-0.05	0.81**		-0.07
NSPP	-0.43**	0.08	0.09	0.23	0.09	-0.45**	0.11	-0.14	-0.07	

Note: DFF – days to 50% flowering; NPB – number of primary branches per plant; PHT – plant height at maturity (cm); IL – internode length (cm); FG: fruit girth (cm); FL – fruit length (cm); SFW – single fruit weight (g); NFP – number of fruits per plant; FYP – fruit yield per plant; NSPP – number of seeds per pod; * – significant at the 5% level; ** – significant at the 1% level

Source: compiled by the authors

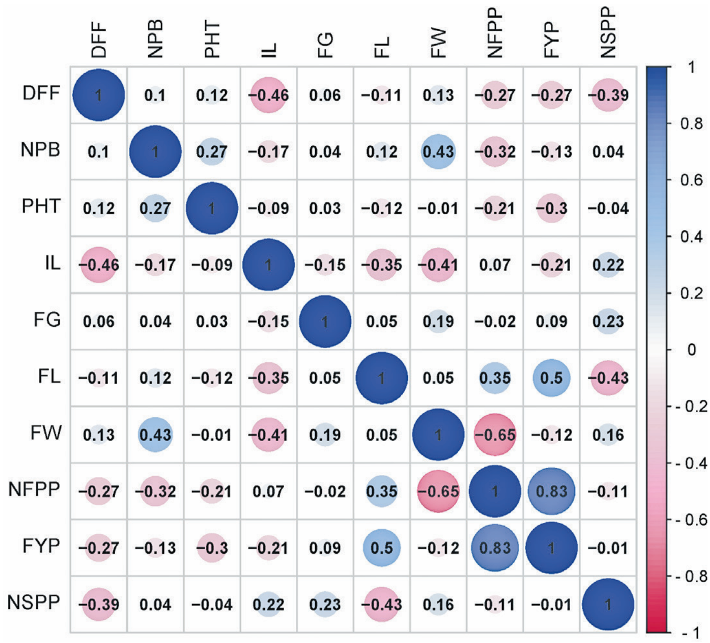


Figure 2. Correlation results

Source: compiled by the authors

However, the number of seeds per pod (NSPP) tends to have negative correlations with several traits, indicating a trade-off between seed quantity and fruit size or number.

Variability parameters for 32 traditional genotypes

The analysis of variability parameters for various traits in okra demonstrated substantial genetic diversity among the 32 traditional genotypes studied (Table 4). The phenotypic expression showed considerable variation, with plant height ranging from 92.60 cm to 144.60 cm, fruit yield per plant varying from 331.90 g to 484.80 g, and the number of seeds per pod ranging from 42.67 to 59.33. High broad-sense heritability estimates (>0.90) were observed for most traits, with values ranging from 0.88 to 0.99, indicating strong genetic control over trait expression and minimal environmental influence on phenotypic manifestation. Days to 50% flowering (DFF) exhibited a relatively high genotypic variance (1.12) and phenotypic variance (1.28), indicating a significant influence of genetic factors on this trait. High heritability (0.88) and moderate genetic advance as a percentage of the mean (4.97%) suggest that selection could effectively improve early flowering in okra. Similarly, the number of primary branches (NPB) exhibited high heritability (0.98) and genetic advance (25.61%), implying strong genetic control and potential for improvement through selection. Plant height (PHT) displayed high genotypic (142.47) and phenotypic variance (145.36), with very high heritability (0.98), indicating that height is largely genetically determined and can be effectively selected for breeding programmes. Traits such as fruit girth (FG) and fruit length (FL) also demonstrated high heritability (0.98 and 0.96, respectively) with considerable genetic advance as a percentage of the mean (27.31% for FG and 17.28% for FL), suggesting that selection for larger fruit size could yield significant improvements in yield. The yield-related trait, fruit yield per plant (FYP), showed extremely high genotypic and phenotypic variance coupled with high heritability (0.98) and genetic advance (21.90%), highlighting its genetic control and responsiveness to selection. The number of fruits per plant (NFPP) also displayed high genetic variance and heritability, supporting the potential for yield improvement through selection for fruit number.

Table 4. Variability parameters for 32 traditional genotypes

Sl. No.	Variability parameters	DFF	NPB	PHT	IL	FG	FL	FW	NFPP	FYP	NSPP
1	Maximum mean	51.45	3.45	194.60	7.49	6.41	24.74	26.53	27.25	539.80	59.33
2	Minimum mean	42.16	2.17	92.60	4.76	3.56	14.87	15.29	16.52	211.90	42.67
3	Grand mean	41.16	2.82	123.89	6.27	4.75	17.80	18.28	21.97	399.36	49.03
4	Standard error of the mean (SEm)	0.23	0.03	0.98	0.04	0.05	0.17	0.22	0.33	3.81	0.02
5	Critical difference (CD) at 5%	0.65	0.09	2.81	0.10	0.14	0.48	0.63	0.96	10.88	0.01
6	Critical difference (CD) at 1%	0.87	0.12	3.76	0.14	0.19	0.65	0.85	1.28	14.56	0.01
7	Environmental variance	0.16	0.00	2.89	0.01	0.01	0.09	0.15	0.34	43.46	0.01
8	Genotypic variance	1.12	0.13	142.47	0.54	0.40	2.31	1.61	8.58	1,844.54	22.43
9	Phenotypic variance	1.28	0.13	145.36	0.54	0.41	2.40	1.75	8.92	1,888.0	22.43
10	Environmental coefficient of variance	0.96	2.00	1.37	1.01	1.80	1.65	2.10	2.64	1.65	0.01
11	Genotypic coefficient of variance (GCV)	2.57	12.59	9.63	11.68	13.38	8.54	6.93	13.33	10.75	9.66
12	Phenotypic coefficient of variance (PCV)	2.75	12.75	9.73	11.73	13.50	8.70	7.24	13.59	10.88	9.66
13	Heritability (Broad sense)	0.88	0.98	0.98	0.99	0.98	0.96	0.92	0.96	0.98	0.99
14	Genetic advance (GA)	2.04	0.72	24.34	1.50	1.30	3.07	2.50	5.92	87.45	9.76
15	Genetic advance as a percentage of the mean	4.97	25.61	19.65	23.98	27.31	17.28	13.67	26.94	21.90	19.90

Note: DFF – days to 50% flowering; NPB – number of primary branches per plant; PHT – plant height at maturity (cm); IL – internode length (cm); FG: fruit girth (cm); FL – fruit length (cm); SFW – single fruit weight (g); NFP – number of fruits per plant; FYP – fruit yield per plant; NSPP – number of seeds per pod
Source: compiled by the authors

The genotypic coefficient of variation (GCV) demonstrated substantial genetic variability, with the highest magnitude recorded for the number of fruits per plant (13.33%) and fruit girth (13.38%). The relatively small difference between the phenotypic coefficient of variation (PCV) and GCV for most traits further confirmed the limited environmental influence on trait expression. This conclusion is substantiated by the low environmental coefficient of variance and the considerably smaller environmental variance compared to genotypic variance, suggesting that phenotypic expression is predominantly under genetic control. Similar results were reported by O. AdeOluwa & O. Kehinde (2011). The genetic advance (GA) as a percentage of the mean showed promising values for several traits, notably the number of primary branches (25.61%), fruit girth (27.31%), and the number of fruits per plant (26.94%).

ANOVA for L × T, combining ability analysis, *per se* performance of L × T parents and hybrids

The ANOVA results for parents and hybrids across ten traits, as shown in Table 5, indicated significant differences among lines, testers, and hybrids for all traits. Both lines and testers exhibited significant variance for each of the ten traits.

Table 5. ANOVA for L × T and combining ability analysis in okra

Source of variation	Df	MSS									
		DFF	NPB	PHT	IL	FG	FL	SFW	NFF	NSPP	FYP
Replication	2	0.154	0.055	2.796	0.003	0.013	0.067	0.197	0.459	7.311	9.991
Hybrid	20	3.7**	0.4**	430.3**	1.6**	1.2**	7.4**	5.0**	26.1**	232.3**	5577.1**
Lines	6	6.3**	0.6**	650.8**	2.0**	1.9**	8.1**	6.2**	41.7**	615.4**	6099.7**
Tester	2	9.2**	0.1**	342.1**	0.5**	5.6**	40.5**	2.4**	31.3**	297.6**	12642.1**
L × T	12	1.4**	0.3**	334.7**	1.6**	0.1**	1.6**	4.8**	17.4**	29.8**	4138.3**
Error	60	0.137	0.018	3.009	0.007	0.008	0.061	0.109	0.246	2.956	30.199

Note: DFF – days to 50% flowering; NPB – number of primary branches per plant; PHT – plant height at maturity (cm); IL – internode length (cm); FG – fruit girth (cm); FL – fruit length (cm); SFW – single fruit weight (g); NFP – number of fruits per plant; FYP – fruit yield per plant; NSPP – number of seeds per pod; * – significant at the 5% level; ** – significant at the 1% level
Source: compiled by the authors

The importance of high *per se* performance, according to V. Singh *et al.* (1983), in breeding programmes was emphasised. In this study, parental lines Anchita, Red Long Okra, Salkeerthi, and Green Long Okra, along with testers Kashi Chaman and Arka Anamika, exhibited maximum fruit yield per plant. Anchita showed remarkable performance in traits such as primary branches, plant height, internode length, fruit length, girth, single fruit weight, and fruit count. Green Long Okra also excelled in fruit yield, with notable performance in days to 50% flowering, fruit girth, length, fruit count, and seeds per pod. Salkeerthi and Red Long Okra performed well in both fruit yield and fruit number. Among the testers, Arka Anamika displayed excellent performance in fruit yield and traits like days to 50% flowering, plant height, fruit length, single fruit weight, and fruit count, while Kashi Chaman demonstrated favourable traits including days to 50% flowering, primary branches, internode length, fruit count, and seeds per pod. These results show the genetic potential of the parents used for hybridisation programmes.

The hybrids like Green Long Okra × Arka Anamika, Anchita Local × Arka Anamika, Heirloom White × Arka Anamika, Heirloom White × Pusa A-4, Heirloom White × Kashi Chaman, and Salkeerthi × Pusa A-4 demonstrated higher fruit yield per plant. Anchita Local × Arka Anamika showed high yield along with favourable traits such as days to 50% flowering, primary branches, internode length, fruit length, girth, single fruit weight, and fruit count. Green Long Okra ×

Arka Anamika also excelled in fruit yield, days to 50% flowering, internode length, fruit length, seeds per pod, and fruit count. Salkeerthi × Pusa A-4 exhibited desirable traits like primary branches, internode length, fruit girth, and single fruit weight. Overall, Anchita Local × Arka Anamika and Green Long Okra × Arka Anamika hybrids demonstrated superior performance in fruit yield and most traits under study, while Heirloom White × Arka Anamika and Salkeerthi × Pusa A-4 also performed favourably across several traits.

General combining ability effect of parents

The parent lines Heirloom White, Salkeerthi, and the tester Arka Anamika showed strong positive effects for general combining ability (GCA) regarding fruit yield per plant (Table 6). This suggests that they could be valuable in breeding new varieties aimed at increasing yield.

Table 6. GCA effect of parents

L/T	Parental Genotypes	DFF	NYB	PHT	IL	FG	FL	FW	NFF	NSPP	FYP
L1	Salkeerthi	0.94**	0.06**	3.60**	-0.22**	0.29**	0.14	-0.41**	1.65**	7.64**	19.52**
L2	Red Long Okra	-0.67**	0.01	3.27**	0.77**	-0.29**	-0.50**	-0.89**	1.72**	5.9**	9.41**
L3	Green Round Okra	0.40**	-0.31**	-14.28**	0.59**	-0.23**	-1.15**	0.24	-0.57**	8.95**	-3.61
L4	Anchita Local	0.08	0.29**	-3.43**	-0.20**	-0.20**	1.61**	1.38**	-2.15**	-11.73**	-8.74**
L5	Srilankan Candle Okra	0.95**	0.02	7.82**	-0.30**	0.83**	-0.92**	0.73**	-3.44**	1.13*	-47.73**
L6	Heirloom White	-0.45**	-0.38**	-6.51**	-0.45**	0.17**	0.40**	-0.30*	2.23**	-2.25**	34.87**
L7	Green Long Okra	-1.26**	0.32**	9.53**	-0.19**	-0.56**	0.41**	-0.76**	0.56**	-9.64**	-3.71
T1	Arka Anamika	-0.33**	0.001	-4.15**	0.11**	0.53**	1.35**	0.13	0.95**	1.17**	28.17**
T2	Pusa A-4	0.76**	-0.08**	0.25	-0.19**	-0.50**	0.08	-0.38**	-0.74**	3.04**	-16.71**
T3	Kashi Chaman	-0.43**	0.08**	3.91**	0.07**	-0.03	-1.43**	0.26**	-0.21	-4.21**	-11.46**

Note: DFF – days to 50% flowering; NPB – number of primary branches per plant; PHT – plant height at maturity (cm); IL – internode length (cm); FG – fruit girth (cm); FL – fruit length (cm); SFW – single fruit weight (g); NFP – number of fruits per plant; FYP – fruit yield per plant; NSPP – number of seeds per pod; * – significant at the 5% level; ** – significant at the 1% level
Source: compiled by the authors

Heirloom White also showed positive GCA for multiple traits, including days to 50% flowering, plant height, internode length, fruit length, number of fruits, and seeds per pod. Green Long Okra demonstrated desirable GCA effects for six traits, including days to 50% flowering, primary branches, fruit girth, and fruit length. Anchita Local ranked second in positive GCA for traits like primary branches, plant height, and fruit length but had negative GCA for fruit yield per plant. Among testers, Arka Anamika was portrayed as a good general combiner for most traits, while Kashi Chaman showed desirable GCA effects for flowering, primary branches, and single fruit weight but was negative for fruit yield. Based on the GCA scores, Arka Anamika and Pusa A-4 were average combiners, while Kashi Chaman was a poor combiner.

Specific combining ability effect of hybrids

Specific combining ability (SCA) represents the deviation from expected performance based on GCA and is influenced by non-additive gene action (Sprague & Tatum, 1942). Significant positive SCA effects for fruit yield per plant were perceived in cross combinations such as Anchita Local × Arka Anamika, Green Long Okra × Arka Anamika, Heirloom White × Pusa A-4, and others, making them ideal candidates for heterosis breeding to enhance fruit yield. Each of these crosses included at least one strong parent contributing desirable traits.

The hybrid Anchita Local × Arka Anamika ranked as the top performer, showing strong SCA effects for traits such as fruit length, primary branches, and single fruit weight, despite negative SCA effects for some traits such as days to 50% flowering and plant height. Heirloom White × Pusa A-4 also performed well, with superior SCA effects for traits such as days to 50% flowering, internode length, fruit length, and fruit yield. Green Round Okra × Kashi Chaman and other hybrids, including Sri Lankan Candle Okra × Kashi Chaman, exhibited desirable SCA effects for traits such as fruit girth, fruit number, and yield. Based on SCA scores, hybrids such as Heirloom White × Pusa A-4, Green Round Okra × Kashi Chaman, Salkeerthi × Kashi Chaman, and Anchita Local × Arka Anamika showed the highest SCA effects, indicating their strong potential as specific combiners. Similar results were reported by V. Bendalel *et al.* (2004) and A. Shwetha *et al.* (2018). Overall, the results highlight the superior performance of Anchita Local and Arka Anamika in various hybrid combinations, contributing to enhanced fruit yield and trait improvement across multiple hybrids (Table 7).

Table 7. SCA effect of hybrids

Hybrids	DFF	NYB	PHT	IL	FG	FL	FW	NFF	NSPP	FYP
$L_1 \times T_1$	0.13	0.10**	-1.24	1.00**	0.01	-0.57**	-2.23**	1.73**	2.60**	-25.77**
$L_1 \times T_2$	0.35*	0.28**	5.40**	-0.32**	-0.04	-0.01	1.96**	-1.55**	2.39*	20.36**
$L_1 \times T_3$	-0.48**	-0.38**	-4.16**	-0.67**	0.03	0.58**	0.27	-0.18	-4.99**	5.4
$L_2 \times T_1$	-0.08	0.27**	-7.77**	-0.24**	0.10*	-0.51**	1.05**	-2.59**	3.40**	-19.78**
$L_2 \times T_2$	0.75**	-0.22**	-3.57**	0.53**	-0.20**	-0.08	-1.66**	3.67**	-1.9	22.57**
$L_2 \times T_3$	-0.67**	-0.04	11.34**	-0.29**	0.1	0.59**	0.61**	-1.08**	-1.5	-2.79
$L_3 \times T_1$	-0.01	-0.17**	5.43**	-0.04	-0.02	0.3	-0.08	-1.18**	0.48	-25.33**
$L_3 \times T_2$	-0.64**	-0.20**	13.92**	0.16**	0.13*	-0.1	-0.50*	-0.04	2.01*	-8.60*
$L_3 \times T_3$	0.65**	0.37**	-19.35**	-0.12**	-0.10*	-0.2	0.57*	1.22**	-2.49*	33.93**
$L_4 \times T_1$	-0.97**	0.12**	-3.24**	-1.33**	-0.07	1.36**	0.62**	2.27**	-2.27*	59.65**
$L_4 \times T_2$	0.42*	-0.35**	-12.23**	0.58**	-0.10*	-0.32*	-0.57*	-0.54	-1.63	-19.80**
$L_4 \times T_3$	0.55**	0.23**	15.47**	0.75**	0.17**	-1.04**	0.06	-1.73**	3.90**	-39.86**
$L_5 \times T_1$	0.2	-0.08*	0.08	0.24**	0.22**	-0.56**	-0.58*	-0.90**	-3.12**	-27.27**
$L_5 \times T_2$	0.29	0.40**	3.34**	-0.77**	0.03	-0.22	1.25**	1.48**	1.09	-3.02
$L_5 \times T_3$	-0.48**	-0.32**	-3.42**	0.52**	-0.25**	0.78**	-0.67**	2.39**	2.03*	30.29**
$L_6 \times T_1$	0.86**	-0.04	1.44	0.63**	-0.40**	-0.31	0.92**	-2.24**	0.47	-18.49**
$L_6 \times T_2$	-0.79**	-0.12**	-0.72	-0.40**	0.23**	0.39*	-0.91**	2.07**	-2.69**	15.19**
$L_6 \times T_3$	-0.07	0.17**	-0.72	-0.23**	0.17**	-0.08	-0.01	0.17	2.22*	3.3
$L_7 \times T_1$	-0.13	-0.20**	5.30**	-0.26**	0.16**	0.29	0.29	2.91**	-1.57	56.99**
$L_7 \times T_2$	-0.38*	0.21**	-6.13**	0.22**	-0.04	0.33*	0.42	-2.12**	0.74	-26.71**
$L_7 \times T_3$	0.50**	-0.01	0.84	0.03	-0.12*	-0.62**	-0.71	-0.79*	0.82	-30.28**

Note: DFF – days to 50% flowering; NPB – number of primary branches per plant; PHT – plant height at maturity (cm); IL – internode length (cm); FG – fruit girth (cm); FL – fruit length (cm); SFW – single fruit weight (g); NFP – number of fruits per plant; FYP – fruit yield per plant; NSPP – number of seeds per pod; * – significant at the 5% level; ** – significant at the 1% level
Source: compiled by the authors

The analysis of variance components for combining ability demonstrated that SCA variance exceeded GCA variance across all evaluated traits (Table 8).

Table 8. Estimation of combining ability variance

VARIANCE	DFF	NYB	PHT	IL	FG	FL	FW	NFF	NSPP	FYP
GCA variance	0.06	0.002	2.48	0.05	0.03	0.15	0.00	0.22	37.46	5.27
SCA variance	0.45	0.09	110.6	0.53	0.04	0.49	1.55	5.69	1,364.93	9.03
GCA/SCA variance	0.13	0.02	0.02	0.094	0.67	0.31	0.00	0.04	0.03	0.58

Note: DFF – days to 50% flowering; NPB – number of primary branches per plant; PHT – plant height at maturity (cm); IL – internode length (cm); FG – fruit girth (cm); FL – fruit length (cm); SFW – single fruit weight (g); NFP – number of fruits per plant; FYP – fruit yield per plant; NSPP – number of seeds per pod
Source: compiled by the authors

This observation suggests that non-additive gene action plays a significant role in the inheritance of these traits, highlighting the complexity and adaptive potential of the genetic mechanisms involved.

Estimation of heterosis concerning fruit yield

The top five hybrids based on heterobeltiosis for fruit yield per plant were Heirloom White × Pusa A4 (48.31%), Green Long Okra × Arka Anamika (22.32%), Heirloom White × Arka Anamika (19.11%), Sri Lankan Candle Okra × Pusa A-4 (9.57%), and Green Round Okra × Arka Anamika (6.94%) (Fig. 3). These hybrids also exhibited desirable heterobeltiosis for traits such as days to 50% flowering, plant height, internode length, fruit length, and fruit number. For standard heterosis, the top five hybrids were Green Long Okra × Arka Anamika (29.00%), Anchita Local × Arka Anamika (28.37%), Heirloom White × Arka Anamika (19.11%), Heirloom White × Pusa A-4 (16.1%), and Heirloom White × Kashi Chaman (14.32%). These crosses also recorded significant standard heterosis for traits such as fruit number, primary branches, internode length, and seed number per pod. Hybrids like Green Long Okra × Arka Anamika, Heirloom White × Pusa A-4, and Heirloom White × Arka Anamika showed high heterosis for both heterobeltiosis and standard heterosis, making them promising candidates for fruit yield improvement. According to S. Rynjah *et al.* (2020), the F_1 hybrids with high heterosis for fruit yield also exhibited favourable heterosis in other traits, supporting their use for okra yield enhancement.

The findings have significant implications for okra breeding programmes. The combination of high heritability and substantial genetic advance indicates the effectiveness of selection breeding, while the predominance of non-additive gene action supports the adoption of hybrid breeding approaches. The minimal environmental effects suggest stable expression of traits across environments, which is favourable for breeding programmes. The SCA variances were higher than the GCA variance for all ten characters, *viz.* days to 50% flowering, plant height at maturity, number of primary branches per plant, internode length, fruit length, fruit girth, single fruit weight, number of fruits per plant and fruit yield per plant. The ratio of GCA/SCA was less than unity, indicating the pre-dominance of nonadditive gene action. For traits such as plant height at maturity and fruit yield per plant, high SCA variance suggests the influence of non-additive gene effects or dominant gene action, indicating that hybridisation could be effective in improving these traits. Selecting hybrids for heterosis breeding based on *per se* performance, specific combining ability (SCA) effects and standard heterosis is highly effective. Among the 21 hybrids evaluated, Anchita Local × Arka Anamika and Heirloom White × Pusa A-4 emerged as superior hybrids based on all three criteria. Anchita Local × Arka Anamika excelled across nine out of ten traits, making it the top-performing hybrid. Heirloom White × Pusa A4 also demonstrated desirable performance for most traits, making it a strong candidate for hybrid breeding.

Figure 3. Relative, heterobeltiosis, and standard heterosis in per cent (%)
Source: compiled by the authors

Additionally, the hybrids Green Long Okra × Arka Anamika and Salkeerthi × Pusa A-4 showed notable fruit yield per plant. The strong correlation observed between *per se* performance, SCA effects, and standard heterosis suggests that SCA effects can serve as a useful biometrical marker for hybrid breeding in okra. This study highlights the significance of non-additive gene action for fruit yield and its related traits, indicating that developing hybrid varieties is the best approach to capitalise on the genetic gain in F_1 generations. While recurrent selection, as proposed by C. Andrus (1963), can produce high-performing pure lines and hybrids, it is time-consuming. Combining pedigree breeding with recurrent selection may offer a more efficient strategy for developing high-yielding segregants and maximising hybrid potential.

Diallel selective mating design, according to N. Jensen (1970), can also be adopted to encourage recombination. The hybrid Heirloom White × Arka Anamika showed high combining ability with positive, non-significant SCA effects for plant height and negative, non-significant values for fruit length. Similarly, the hybrid Green Long Okra × Kashi Chaman had non-significant SCA effects for seeds per pod and negative values for primary branches. These crosses suggest additive genes contributing to traits such as plant height and earliness in later generations. Green Long Okra × Arka Anamika and Heirloom White × Arka Anamika were selected for recombination breeding due to their superior fruit yield and component traits. Therefore, crosses involving Arka Anamika, Heirloom white, and Green long okra are expected to yield superior segregants for fruit yield improvement.

The results of AMMI analysis of hybrids

The AMMI1 biplot shows yield (YLD) on the x-axis and the first principal component (PC1) on the yaxis. This visualisation facilitates the assessment of the yield performance and stability of 31 different okra genotypes across multiple environments (ENV-1, ENV-2, and ENV-3). Genotypes positioned further along the x-axis towards higher yield values indicate superior performance in terms of yield (Patel *et al.*, 2023). For example, hybrids Red Long Okra × Arka Anamika, Anchita Local × Arka Anamika, and the tester Arka Anamika exhibit relatively high yields, making them potential candidates for yield-focused breeding programmes. Stability, in this context, refers to a genotype's consistency across different environmental conditions. Genotypes located near the origin, such as Heirloom White × Pusa A-4, display low interaction effects, indicating stable performance across environments. In contrast, genotypes farther from the origin, such as Red Long Okra and Heirloom White × Kashi Chaman, exhibit higher interaction effects, suggesting variability in yield depending on the environment. Thus, while Heirloom White × Pusa A-4 is stable across conditions, Red Long Okra and Heirloom White × Kashi Chaman may be better suited to specific environments rather than being broadly adapted. The AMMI2 biplot displays genotype × environment interactions by plotting the first principal component (PC1) on the x-axis and the second principal component (PC2) on the y-axis. In this biplot, the proximity of genotypes to specific environments reveals patterns of adaptability. For instance, Red Long Okra aligned closely with ENV-2, indicating a particular suitability for that environment, while the hybrid Heirloom White × Kashi Chaman showed a similar alignment with ENV-3. Stability and specific adaptation were also apparent in this biplot. Genotypes positioned near the origin, such as Anchita Local × Arka Anamika and Heirloom White × Pusa A-4, showed low interaction effects, indicating stable performance across environments. Similar genotype × environment interaction techniques were reported by C. Alake & O. Ariyo (2012) (Fig. 4). In contrast, genotypes positioned farther from the origin, such as Heirloom White × Kashi Chaman and Red Long Okra, demonstrated specific adaptability to certain environments (ENV-3 and ENV-2, respectively).

Environmental influence is represented by the direction and length of the arrows from the origin toward each environment (ENV-1, ENV-2, and ENV-3). Longer arrows, such as the one for ENV-2, indicate a stronger interaction effect on the genotypes aligned along that vector, emphasising the environment's impact on yield performance in that direction. ENV-1 exhibits greater stability as it is positioned closer to the origin in both the AMMI biplot for yield and the AMMI1 biplot. This proximity indicates minimal interaction effects with genotypes, making ENV-1 a reliable environment for consistent performance across a wide range of genotypes. In contrast, ENV-2 and ENV-3 are located farther from the origin, reflecting stronger interaction effects. These environments are more suitable for specific adaptation, as they may favour certain genotypes and potentially lead to higher yield performance. In terms of variance explained, the contributions of PC1 (73.6%) and PC2 (26.4%) account for the full variance of the genotype × environment interactions in the AMMI2 biplot (16). Genotypes near the origin, such as Heirloom White × Pusa A-4 and Anchita Local × Arka Anamika, emerge as ideal candidates due to their stability across environments. Meanwhile, high-yielding genotypes like Red Long Okra × Arka Anamika and Arka Anamika show promise for breeding programmes aimed at yield improvement and multi-location trials to confirm broad adaptability and yield consistency across environments.

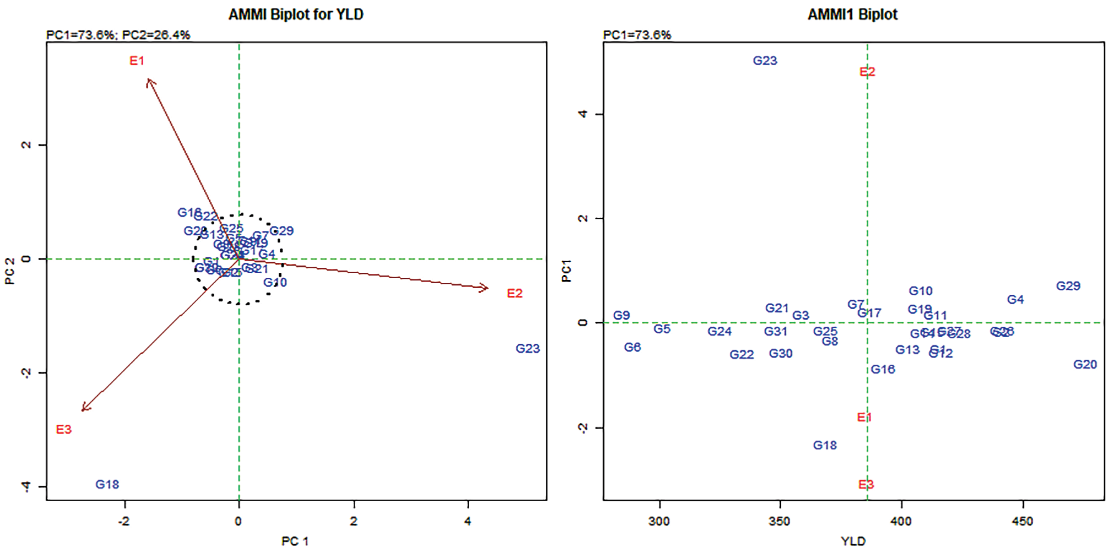


Figure 4. AMMI analysis biplot

Source: compiled by the authors

The study demonstrated that improving traits and fruit yield per plant through standard pedigree selection may be challenging. Correlation analysis revealed that days to 50% flowering (DFF) is negatively correlates with internode length (IL) and number of seeds per pod (NSPP), suggesting that early-flowering plants may have shorter internodes and fewer seeds. The number of primary branches (NPB) is positively correlated with plant height (PHT) and fruit width (FW), while fruit girth (FG) and fruit length (FL) are positively correlated with the number of fruits per plant (NFPP) and fruit yield per plant (FYP). However, wider fruits were negatively correlated with NFPP, indicating potential tradeoffs. The genetic parameters indicated that most traits are under genetic control, with high heritability (0.88-0.99) and narrow gaps between genotypic and phenotypic variances. Days to 50% flowering exhibited high heritability (0.88) and moderate genetic advance (4.97%), making it a promising trait for developing early-maturing varieties (Reddy *et al.*, 2012; Patel *et al.*, 2023). Traits such as plant height and primary branches demonstrated high heritability (0.98) and genetic advance (19.65% and 25.61%, respectively), highlighting additive gene action and their amenability to selection. Fruit-related traits, including fruit girth and the number of fruits per plant, displayed high genetic variability and heritability, supporting their effectiveness for selection, consistent with findings from P. Sharma *et al.* (2016). Fruit yield per plant showed high heritability (0.98) and genetic advance (21.90%), confirming the potential for yield improvement via selection (Basir, 2020). Stable genetic expression across traits supports reliable phenotypic selection, although multi-location trials remain necessary to confirm superior genotypes (Hill & Mulder, 2010). The predominance of specific combining ability (SCA) over general combining ability (GCA) for most traits underscores the significance of non-additive gene action, suggesting hybrid breeding is more effective than pure-line selection for crop improvement, as mentioned by V. Verma *et al.* (2018) and M. Srivastava *et al.* (2023).

Green Long Okra demonstrated desirable GCA effects for traits like primary branches and fruit girth, while Anchita Local showed positive GCA effects for plant height and primary branches but was less favourable for yield. Among testers, Arka Anamika emerged as the best general combiner for multiple traits, while Kashi Chaman showed favourable GCA effects for flowering and fruit weight but not for yield. For SCA, high-performing hybrids such as Anchita Local × Arka Anamika and Heirloom White × Pusa A-4 displayed strong potential, particularly for fruit yield and key traits like fruit length and primary branches. These crosses benefited from at least one high-GCA parent, underscoring their suitability for yield-oriented breeding. Top hybrids for heterosis included Heirloom White × Pusa A-4 (48.31%) and Green Long Okra × Arka Anamika (22.32%), which showed desirable performance in days to 50% flowering, plant height, and fruit number. Overall, hybrids like Green Long Okra × Arka Anamika and Anchita Local × Arka Anamika displayed promising heterosis. The hybrid Heirloom White × Arka Anamika exhibited high combining ability with positive, non-significant SCA effects for plant height at maturity and negative, non-significant values for fruit length. The hybrid Green Long Okra × Kashi Chaman showed high combining ability with non-significant SCA effects for the number of seeds per pod and negative, non-significant values for the number of primary branches. This indicated that these crosses possessed additive genes from the parents which are likely to produce desirable recombinants for traits like plant height, internode length, and earliness in later segregating generations. The hybrids selected for recombination breeding were Green Long Okra × Arka Anamika and Heirloom White × Arka Anamika, as they excelled in fruit yield per plant and most of their component traits. Therefore, the crosses involving the parents *viz*. Arka Anamika, Heirloom White, and Green Long Okra were also expected to throw superior segregants for pedigree breeding with favourable genes for improving fruit yield and its component traits.

The AMMI analysis identified hybrids such as Anchita Local × Arka Anamika, Green Long Okra × Arka Anamika, and Heirloom White × Pusa A-4 as high-yielding genotypes with strong adaptability to specific environments. This aligns with the combining ability analysis, which highlighted these hybrids for their superior specific combining ability (SCA) and high heterosis for fruit yield per plant and related traits. The dominance of SCA variance over general combining ability (GCA) variance, as observed in traits like fruit yield, days to flowering, and fruit size, supports the AMMI results. This indicates that non-additive gene action plays a major role in determining these traits. This non-additive genetic control aligns with the variability observed across environments. This captured by AMMI biplots, where specific genotypes excelled in particular environments, suggests strong genotype × environment interactions and highlights the need for multi-location trials to confirm broad adaptability and yield consistency across environments.

In both analyses, the hybrids Anchita Local × Arka Anamika and Green Long Okra × Arka Anamika emerged as high performers for key traits, including fruit yield per plant, fruit length, and reduced days to flowering. In the AMMI biplots, these hybrids displayed high yield and specific adaptability to certain environments, while in the combining ability analysis, they demonstrated significant SCA effects and heterosis. These findings indicate that these hybrids are not only highyielding but also capable of thriving under specific environmental conditions, which is beneficial for region-specific cultivation. The AMMI analysis highlighted Anchita Local × Arka Anamika as stable across different environments, which correlates well with its high SCA effects and superior performance across multiple traits in the combining ability study, positioning it as an ideal candidate for stable yield improvement (Komolafe *et al.*, 2022). Instead, fruit yield improvement may be achieved by delaying selection to later generations and using intermating of segregants followed by recurrent selection. Okra breeders have the choice between lines and hybrids. Single crosses can be justified at the beginning, while lines can be prioritised later if all heterosis is fixable.

CONCLUSIONS

The authors concluded that the high heritability and genetic variance observed in these traits indicated the potential for effective yield improvement through selective breeding. The parental genotypes, such as Anchita Local, Green Long Okra, and Arka Anamika, were identified as superior combiners for key traits like fruit yield and plant height in the combining ability analysis. The AMMI biplots further highlighted the adaptability and stability of these genotypes, particularly in specific hybrid combinations, across different environments. Heirloom White stood out for its high general combining ability (GCA) effects on yield-related traits, signifying its potential to enhance overall yield in hybrids. This high GCA effect aligned with its performance in the AMMI analysis, where hybrids like Heirloom White × Pusa A-4 demonstrated strong adaptability and high yield potential. The integration of AMMI results with combining ability analysis confirmed that most hybrids were stable across all three environments, exhibited high specific combining ability (SCA), and adapted well to diverse climatic conditions, minimising environmental influences on quality. Hybrids such as Anchita Local × Arka Anamika and Green Long Okra × Arka Anamika displayed both strong genetic potential and environmental adaptability, making them promising candidates for breeding programmes aimed at improving yield stability and performance.

In the near future, okra breeding should focus on integrating molecular techniques with traditional breeding approaches to enhance selection accuracy and efficiency. Using genomic selection, marker-assisted breeding, and transcriptomics can help understand the genetic factors behind important traits such as fruit yield, earliness, and adaptability to different environments. Multi-location trials are also important to study how different genotypes interact with their environments, helping identify hybrids that can adapt broadly as well as specifically. Exploring underutilised genetic resources and the wild relatives of okra can provide new genes for trait improvement. Breeding programmes should aim to develop hybrids and lines that can withstand climate challenges and perform well under stress, ensuring sustainable production and resilience against pests and environmental stressors. Integrating biochemical trait analysis into breeding programmes can reveal new genetic variations and improve the selection process for superior genotypes, aligning future breeding efforts with market demands.

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CONFLICT OF INTEREST

All authors declare that they have no conflict of interest.

REFERENCES

[1] AdeOluwa, O.O., & Kehinde, O.B. (2011). Genetic variability studies in West African okra (*Abelmoschus caillei*). *Agriculture and Biology Journal of North America*, 2(10), 1326-1335. doi: 10.5251/abjna.2011.2.10.1326-1335.

[2] Alake, C.O. (2020). Genetic variability and diversity in okra landraces using agromorphological traits and seed elemental minerals. *International Journal of Vegetable Science*, 26(2), 127-49. doi: 10.1080/19315260.2019.1610926.

[3] Alake, C.O., & Ariyo, O.J. (2012). Comparative analysis of genotype x environment interaction techniques in West African Okra (*Abelmoschus caillei*, A. Chev Stevels). *Journal of Agricultural Science*, 4(4), 135-150. doi: 10.5539/jas.v4n4p135.

[4] Andrus, C.F. (1963). Plant breeding systems. *Euphytica*, 12, 205-228. doi: 10.1007/BF00022357.

[5] Basir, A. (2020). Assessment of genetic variability for YVM resistance in okra (*Abelmoschus esculentus* (L.) Moench). (Doctoral dissertation, Department of Plant Breeding and Genetics, College of Horticulture, Vellanikkara, India).

[6] Bendalel, V.W., Madav, R.R., Thave, S.G., & Pethe, U.B. (2004). Heterosis and combining ability of okra (*Abelmoschus esculentus* (L.) Moench) cultivars. *Journal of Soils and Crops*, 14(2), 269-272.

[7] Caliński, T., & Harabasz, J. (1974). A dendrite method for cluster analysis. *Communications in Statistics*, 3(1), 1-27. doi: 10.1080/03610927408827101.

[8] Convention on Biological Diversity (CBD). (1992, May). Retrieved from https://surl.li/ziertr.

[9] Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES). (1973, March). Retrieved from https://cites.org/eng/disc/text.php.

[10] Das, A., Yadav, R.K., Bhardwaj, R., Choudhary, H., & Khade, Y.P. (2022a). Study of heterotic potential for important antioxidant and nutritional traits in okra (*Abelmoschus esculentus*). *Indian Journal of Agricultural Sciences*, 92(8), 986-990. doi: 10.56093/ijas.v92i8.110389.

[11] Das, A., Yadav, R.K., Choudhary, H., Lata, S., Singh, S., Kumar, C., Kumari, S., Boopalakrishnan, G., Bhardwaj, R., & Talukdar, A. (2022b). Population structure, gene flow and genetic diversity analyses based on agro-morphological traits and microsatellite markers within cultivated and wild germplasms of okra (*Abelmoschus esculentus* (L.) Moench). *Genetic Resources and Crop Evolution*, 69(2), 771-91. doi: 10.1007/s10722-021-01263-9.

[12] Elshafy, A.A., Abou-Ellail, M., & El-Sayed, M. (2024). Metabolic profiling of bioactive phytochemicals of two okra genotypes and their F1 and backcrosses. *International Journal of Vegetable Science*, 30(2), 198-224. doi: 10.1080/19315260.2024.2354773.

[13] Fonseca, S., & Patterson, F.L. (1968). Hybrid vigor in a seven-parent diallel cross in common winter wheat (*Triticum aestivum* L.). *Crop Science*, 8(1), 85-88. doi: 10.2135/cropsci1968.0011183X000800010025x.

[14] Hill, W.G., & Mulder, H.A. (2010). Genetic analysis of environmental variation. *Genetics Research*, 92(5-6), 381-395. doi: 10.1017/s0016672310000546.

[15] Jensen, N.F. (1970). A diallel selective mating system for cereal breeding. *Crop Science*, 10(6), 629-635. doi: 10.2135/cropsci1970.0011183X001000060006x.

[16] Kempthorne, O. (1957). *An introduction to genetic statistics*. New York: John Wiley and Sons.

[17] Komolafe, R.J., Ariyo, O.J., & Alake, O.C. (2022). The yield performance and stability analysis of okra (*Abelmoschus esculentus* L. Moench) accessions using AMMI and GGE biplots. *Journal of Agricultural Sciences*, 67(4), 335-354. doi: 10.2298/JAS2204335K.

[18] Kshash, B.H., & Oda, H. (2022). Economics of okra production. *Euphrates Journal of Agriculture Science*, 14(2), 12-18.

[19] Patel, A.A., Vekariya, R.D., Patel, R., & Patel, A. (2023). Selection of elite genotypes deploying AMMI, GGE and MTSI in okra (*Abelmoschus esculentus* (L.) Moench). *South African Journal of Botany*, 163, 457-467. doi: 10.1016/j.sajb.2023.10.060.

[20] Rahman, K.Z. (2020). *Screening, characterization and improvement of nutrient rich okra variety for resistance to yellow vein mosaic virus*. (Doctoral dissertation, University of Rajshahi, Rajshahi, Bangladesh).

[21] Reddy, M.T., Haribabu, K., Ganesh, M., Reddy, K.C., Begum, H., Subbararama, R., Reddy, K., & Dilip Babu, J. (2012). Genetic analysis for yield and its components in okra (*Abelmoschus esculentus* (L.) Moench). *Songklanakarin Journal of Science and Technology*, 34(2), 133-141. doi: 10.4067/S0718-58392012000300003.

[22] Reddy, M.T., Pandravada, S.R., Sivaraj, N., & Sunil, N. (2016). Characterization of Indian landrace germplasm and morphological traits desirable for designing a customer-driven variety in okra (*Abelmoschus esculentus* L. Moench). *Journal of Global Agriculture and Ecology*, 6(1), 7-34.

[23] Rynjah, S., Arumugam, T., Mohankumar, S., & Kamala Kannan, A. (2020). Exploitation of heterosis for yield and yield related traits in okra (*Abelmoschus esculentus* (L.) Moench). *International Journal of Chemical Studies*, 8(4), 886-893. doi: 10.22271/chemi.2020.v8.i4f.9715.

[24] Sanwal, S.K., Mann, A., Kesh, H., Kaur, G., Kumar, R., & Rai, A.K. (2021). Genotype environment interaction analysis for fruit yield in okra (*Abelmoschus esculentus* L.) under alkaline environments. *Indian Journal of Genetics and Plant Breeding*, 81(1), 101-110. doi: 10.31742/IJGPB.81.1.11.

[25] Sharma, P.K., Mishra, D.P., & Pandey, A. (2016). Genetic variability studies for yield and its contributing traits in okra (*Abelmoschus esculentus* (L.) Moench). *Journal of Applied and Natural Science*, 8(3), 1634-1637. doi: 10.31018/jans.v8i3.1014.

[26] Shwetha, A., Mulge, R., Evoor, S., Kantharaju, V., & Masuti, D.A. (2018). Diallel analysis for combining ability studies in okra (*Abelmoschus esculentus* (L.) Moench) for yield and quality parameters. *International Journal of Current Microbiology and Applied Sciences*, 7(9), 2114-2121. doi: 10.20546/ijcmas.2018.709.258.

[27] Singh, B., Karmakar, P., Singh, P., Maurya, B.K., Singh, H., Sagar, V., Mishra, G.P., & Sanwal, S.K. (2023). Okra: Breeding and genomics. *Vegetable Science*, 50(2), 261-273. doi: 10.61180/vegsci.2023.v50.i2.01.

[28] Singh, G., Pathak, M., Pathak, D., & Sarao, N.K. (2023). Identification of SSR markers through bulk segregant analysis and inheritance of resistance to yellow vein mosaic disease in okra (*Abelmoschus esculentus* L. Moench). *VirusDisease*, 34, 498-503. doi: 10.1007/s13337-023-00844-9.

[29] Singh, V.K., Singh, H.G., & Chauhan, Y.S. (1983). Combining ability in sesame. *Indian Journal of Agricultural Sciences*, 53(5), 305-310.

[30] Sprague, G.F., & Tatum, L.A. (1942). General vs. specific combining ability in single crosses of corn. *Agronomy Journal*, 34(10), 923-932. doi: 10.2134/agronj1942.00021962003400100008x.

[31] Srivastava, M., Kathayat, K., & Mashkey, V.K. (2023). Performance of okra genotypes for different quality parameters. *Journal of Food Chemistry and Nanotechnology*, 9(S1), 285-290. doi: 10.17756/jfcn.2023-s1-037.

[32] Verma, V., Singh, B., Singh, M.K., & Singh, S.K. (2018). Studies on genetic variability, heritability and genetic advance in okra (*Abelmoschus esculentus* (L.) Moench). *Journal of Pharmacognosy and Phytochemistry*, 7(4), 1114-1115.

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Генетична варіативність, комбінаційна здатність та аналіз стабільності традиційних генотипів бамії та їх гібридів (*Abelmoschus esculentus* (L.) Moench) із використанням схеми «лінія × тестер»

Анотація. Покращення врожайності традиційних сортів бамії має важливе значення для забезпечення продовольчої безпеки, сталого сільського господарства та збереження генетичного різноманіття сортів. Оцінка їх генетичного потенціалу та стабільності за допомогою сучасних тестерів є ключовим фактором для досягнення вищої врожайності та вдосконалення культури. Дослідження мало на меті оцінити генетичну варіативність, комбінаційну здатність, дію генів та стабільність традиційних генотипів бамії та їх гібридів за допомогою схеми «лінія × тестер» для визначення високоврожайних, стабільних гібридів зі специфічною адаптацією до умов середовища. Аналіз за схемою «лінія × тестер» було проведено у 2022-2024 роках в Університеті Аннамалай, Чидамбарам (Індія), із використанням семи ліній і трьох тестерів для вивчення комбінаційної здатності, генетичних дій та гетерозису у традиційних генотипах бамії (*Abelmoschus esculentus* (L.) Moench). Батьківські лінії були обрані з групи 32 місцевих сортів. У дослідженні оцінювали 10 економічно важливих ознак, включаючи кількість днів до 50 % цвітіння, архітектуру рослини та компоненти врожайності. Аналіз комбінаційної здатності показав перевагу неадитивної дії генів для всіх досліджуваних ознак. Серед батьківських рослин Heirloom White, Anchita Local (лінії) та Arka Anamika (тестер) продемонстрували вищу загальну комбінаційну здатність за кількома ознаками, включаючи врожайність плодів. Гібриди Green Long Okra × Arka Anamika та Anchita Local × Arka Anamika виявилися кращими, демонструючи значні ефекти специфічної комбінаційної здатності та бажаний стандартний гетерозис за врожайністю та її складовими ознаками. Аналіз AMMI підтвердив екологічну адаптивність цих гібридів, при цьому Anchita Local × Arka Anamika відзначився особливою стабільністю в різних умовах. Висока спадковість у поєднанні з перевагою неадитивної дії генів свідчить про те, що гібридизація є ефективнішим підходом для вдосконалення культури, ніж селекція чистих ліній. Отримані результати дають цінну інформацію для реалізації програм із селекціонування бамії, спрямованих на створення високоврожайних, стабільних гібридів зі специфічною адаптацією

Ключові слова: селекція бамії; адаптивність до навколишнього середовища; продуктивність гібридів; дія генів; аналіз AMMI; гетерозис