



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
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NAAS Rating (2025): 5.20
www.agronomyjournals.com
2025; 8(12): 385-390
Received: 16-09-2025
Accepted: 24-10-2025

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Genetic variability and line $\times$ tester analysis of agronomic and nutritional traits in okra (*Abelmoschus esculentus* L.)

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DOI: <https://www.doi.org/10.33545/2618060X.2025.v8.i12f.4395>

Abstract

Genetic variability and heritability estimates are essential for identifying promising genotypes and designing effective breeding programs in okra (*Abelmoschus esculentus* L. Moench). The present study was conducted to evaluate the extent of genetic variability, heritability, genetic advance, and the nature of gene action governing agronomic and nutritional traits using a line $\times$ tester mating design. Ten lines and five testers were crossed to generate fifty F_1 hybrids, which were evaluated along with their parents under four environments at the Department of Genetics and Plant Breeding, AKS University, Satna (M.P.). Analysis of variance revealed highly significant differences among parents and crosses for all traits, indicating substantial genetic variability in the experimental material. High genotypic and phenotypic coefficients of variation were observed for fruit yield per plant (12509.48 & 2535.96), total number of fruit per plant (38.48 & 38.95), and Plant height (34.20 & 34.80), suggesting ample scope for selection. High heritability combined with high genetic advance as percent of mean was recorded for Number of Branches per plant (97.69 & 25.10), Internodal length (99.42 & 24.00) and Fruit Girth (99.33 & 42.82), implying predominance of additive gene action. Line $\times$ tester analysis revealed significant general and specific combining ability effects, indicating the importance of both additive and non-additive gene effects in the inheritance of yield and nutritional components. The study demonstrates the existence of substantial genetic variability and useful heterosis that can be utilized for developing high-yielding and nutrient-rich okra hybrids. Overall, the results provide insights into trait interrelationships and the genetic basis for simultaneous improvement of yield and nutritional quality in okra breeding programs.

Keywords: Okra (*Abelmoschus esculentus*), genetic variability, heritability, genetic advance, line $\times$ tester analysis, nutritional traits and yield components

Introduction

Okra (*Abelmoschus esculentus* L. Moench), commonly known as lady's finger, is an important vegetable crop grown for its immature green fruits that serve as a rich source of vitamins, minerals, and dietary fiber (Reddy *et al.*, 2013; Mehta *et al.*, 2006) ^[17, 22]. India is one of the largest producers and consumers of okra, accounting for nearly 70% of global production (FAO, 2022). Despite its economic importance, okra productivity remains constrained by limited genetic diversity, susceptibility to biotic and abiotic stresses, and the complex inheritance of yield and quality traits (Bhatnagar *et al.*, 2019) ^[4]. Understanding the nature and magnitude of genetic variability for yield and its component traits is therefore crucial for developing superior okra cultivars through conventional and molecular breeding approaches.

Quantitative traits such as fruit yield, pod length, and nutrient composition are polygenically controlled and strongly influenced by the environment (Panse & Sukhatme, 1985; Singh & Chaudhary, 2014) ^[18, 28]. Estimation of genotypic variance, heritability, and genetic advance helps determine the relative contribution of genetic and environmental factors to phenotypic expression of traits (Johnson *et al.*, 1955) ^[13]. High heritability accompanied by high genetic advance indicates predominant additive gene action and effectiveness of simple selection, whereas moderate heritability with low genetic advance suggests the involvement of dominance and epistasis (Kumar *et al.*, 2018) ^[16].

The line $\times$ tester mating design (Kempthorne, 1957) ^[14] is one of the most effective methods for

evaluating the combining ability of parental lines and for dissecting the genetic basis of quantitative traits (Singh *et al.*, 2016) [26]. This approach provides information on both general combining ability (GCA) — an indicator of additive effects — and specific combining ability (SCA) — reflecting non-additive gene effects (Griffing, 1956) [11]. By analyzing the GCA and SCA variances, breeders can identify superior parents and cross combinations for developing hybrids with enhanced yield and nutritional attributes (Ramya *et al.*, 2020; Sankar *et al.*, 2021) [20, 23].

Previous studies on okra have reported considerable variability in fruit yield and quality traits (Ramesh *et al.*, 2018; Sharma & Singh, 2020) [19, 24]. However, few investigations have simultaneously addressed agronomic and nutritional traits using a multi-environment evaluation. Hence, the present study was undertaken to quantify genetic variability, heritability, and genetic advance for important traits and to assess the general and specific combining ability effects of parental lines and their crosses under three different environments in okra. The results aim to facilitate the selection of potential parental combinations for developing high-yielding and nutrient-rich okra hybrids suitable for diverse growing conditions.

Materials and Methods

Experimental Site and Environment

The present investigation was conducted during Kharif 2024 to 2025 at the Experimental Farm, Department of Genetics and Plant Breeding, Faculty of Agricultural Science and Technology, AKS University, Satna (M.P.), situated at 24°34' N latitude and 80°48' E longitude. The region falls under the sub-tropical climate characterized by hot summers, moderate rainfall, and mild winters. The mean annual rainfall is approximately 100 mm, most of which is received between June and September. To study environmental interactions, the material was evaluated under four distinct environments on the basis of different date of sowing.

The soil at the experimental site was a sandy loam, slightly alkaline in reaction (pH 7.5-7.8) with moderate fertility. Recommended packages of practices were followed to raise a healthy crop in all environments (Singh & Chaudhary, 2014) [28].

Experimental Material and Breeding Design

The experimental material comprised ten lines (female parents) and five testers (male parents) selected from diverse genetic backgrounds on the basis of variability for yield, earliness, and fruit quality attributes. Crosses were made following the line × tester mating design (Kempthorne, 1957) [14] during Kharif 2024-Summer 2025 to obtain 50 F₁ hybrids. Along with the parents and with two standard check variety, these 67 entries (10 lines + 5 testers + 50 crosses + 2 check) were evaluated in a randomized block design (RBD) with three replications at each environment. Each genotype was sown in two rows of 5 m length with spacing of 60 cm × 30 cm. Standard agronomic practices and plant-protection measures were followed uniformly across environments to ensure good crop stand and minimize experimental error (Panse & Sukhatme, 1985) [18]. Observations were recorded on five randomly selected plants from each replication for the following 14 agronomic and nutritional traits: days to 50% flowering, days to first picking, number of branches per plant, internodal length, plant height, fruit length and girth, total number of fruits per plant, total number of seeds per fruit, days to last picking, crude protein content, crude fiber content, vitamin C content, and fruit yield per plant.

Physiological maturity was determined when pods turned light green and showed the first sign of lignification. Nutritional parameters (vitamin C, protein, and TSS) were analyzed from fresh fruit samples using standard biochemical protocols (AOAC, 2019) [2]. Analysis of Variance Pooled data across environments were subjected to analysis of variance (ANOVA) as per the model described by Panse and Sukhatme (1985) [18] to partition the total variation into components due to genotypes, environments, and genotype × environment interaction. The line × tester analysis was performed following Kempthorne (1957) [14] to estimate: General Combining Ability (GCA) effects for lines and testers, and Specific Combining Ability (SCA) effects for crosses. The mean squares were tested for significance using the F-test at 5% and 1% probability levels.

Estimation of Genetic Parameters

Phenotypic (σ_p^2) and genotypic (σ_g^2) variances were estimated from mean squares, and coefficients of variation were computed according to Burton and DeVane (1953) [5]. Heritability (h^2_b) in the broad sense and genetic advance (GA) were calculated using standard formulae (Johnson *et al.*, 1955) [13].

$$h_b^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100, GA = k \times \sigma_p \times h_b^2$$

where k = selection intensity (2.06 for 5% selection).

Genetic advance as percent of mean (GAM) was derived to categorize the nature of gene action: High heritability + high GAM → predominance of additive genes, Moderate heritability + moderate GAM → both additive and non-additive genes, and Low heritability + low GAM → non-additive gene action (Falconer & Mackay, 1989) [8].

Correlation and Path-Coefficient Analysis

Phenotypic and genotypic correlation coefficients among traits were computed following Al-Jibouri *et al.* (1958) [12]. Direct and indirect effects of yield-contributing characters were determined using path-coefficient analysis (Dewey & Lu, 1959) [7] to identify major yield-determining components.

Software Utilized all statistical computations were performed using INDOSTAT Ver. 9.3 and cross-checked with R (Version 4.3.1). Graphs and figure placeholders were created using Microsoft Excel 2021.

Environmental Index and Stability Assessment

To assess genotype × environment interaction for yield and related traits, the environmental index was computed for each environment as the deviation of environmental mean from the grand mean (Finlay & Wilkinson, 1963). The stability of genotypes was analyzed following the regression approach to identify stable and high-performing crosses across variable environments.

Results

1. Analysis of variance (pooled L×T)

Pooled L×T ANOVA revealed substantial sources of variation across the trial. Location and the Parents vs Hybrids source contributed very large sums-of-squares for many characters (for example, for fruit yield per plant the Location and Par vs Hybrid sources have very large variance terms), showing that environment and hybrid status strongly influenced expression of agronomic and nutritional traits. Genotype-related variance

(Parents, Females, Males, Hybrids) and their interactions with locations (PAR×LOC, HYBRIDS×LOC) were also appreciable for most traits, indicating both genetic variation among entries and genotype × environment interaction (Table 1). The residual (error) mean squares are generally small compared with treatment sums for most traits, suggesting adequate precision in the experiment.

Location effects for fruit yield per plant and many agronomic traits are very large (e.g., Location SS for fruit yield = 327505.10 in the uploaded ANOVA), and PAR VS HYB shows very high variance for fruit yield and other traits, indicating strong hybrid vigor / difference between parents and hybrids at the trial level.

2. Genetic variability — descriptive statistics and variance components (pooled and year-wise)

The genetic variability table gives means, ranges, genetic (σ^2_g) and phenotypic (σ^2_p) variances, heritability (broad-sense, as reported), genetic advance (GA) and GA% of mean, plus GCV and PCV for four years (E1-E4) and pooled (P). Summary of major traits (pooled values unless otherwise stated) presented table-2.

- **Days to 50% flowering:** Pooled mean = 44.92 days; σ^2_g = 2.21, σ^2_p = 2.29; high broad-sense heritability (96.34%); GA% (6.69) low GCV (3.31%) and PCV (3.37%). This indicates limited variability but very high heritability — the trait is largely genetically controlled and will respond to selection though GA% is modest.
- **Days to first picking:** Pooled mean = 55.74 days; σ^2_g = 1.91, σ^2_p = 1.99; high heritability (96.30%); low GCV (2.48%). Similar to flowering time genetically stable with limited variability.
- **Number of branches per plant:** Pooled mean = 3.35; σ^2_g = 0.17, σ^2_p = 0.17; very high heritability (97.69%); moderate GA% (25.10) and moderate GCV (12.33%). Shows moderate potential for selection despite small absolute variance due to low trait mean.
- **Internodal length:** Pooled mean 6.76 cm; σ^2_g = 0.62, σ^2_p = 0.63; heritability (99.42%), relatively high GA% (24.00) and GCV (11.68%) > good selection prospects.
- **Plant height:** Pooled mean=111.66 cm; σ^2_g = 34.20, σ^2_p = 34.80; high heritability (98.29%); GA% = 10.70; moderate GCV (5.24%). Genetic control is strong; selection expected to be effective for plant height.
- **Fruit length and girth:** Both show high heritability (>99% for fruit length pooled, 99.33% for girth pooled), GCV and PCV moderate (fruit length GCV 7.14%, PCV 7.16%). These quality traits are under strong genetic control and amenable to selection.
- **Total number of fruits per plant:** Pooled mean = 74.81; σ^2_g = 38.48, σ^2_p = 38.95; heritability 98.79%; GA% 16.98% and GCV 8.29%. This suggests good genetic variability and high expected response to selection.
- **Total number of seeds per fruit:** Pooled mean = 43.37; σ^2_g = 3.39, σ^2_p = 3.56; heritability 95.36%; GA% 8.54%; moderate GCV (4.25%).
- **Crude protein:** Pooled mean = 15.67%; σ^2_g = 1.05, σ^2_p = 1.06; heritability = 99.18%; GA% = 13.39%; GCV = 6.53% promising genetic control for nutritional quality.
- **Crude fiber (%):** Pooled mean = 13.28%; σ^2_g = 4.15, σ^2_p = 4.16; very high heritability (99.70%); very high GA% (31.55%) and large GCV (15.34%) high scope for improvement by selection.

- **Vitamin C:** Pooled mean = 20.44 mg/100g (units assumed as per dataset); σ^2_g = 1.07, σ^2_p = 1.11; heritability = 96.73%; GA% = 10.26%; moderate GCV (5.07%).
- **Fruit yield per plant (g):** Pooled mean = 844.97 g; σ^2_g = 2509.48, σ^2_p = 2535.96; heritability = 98.96% (reported); GA% = 12.15%; pooled GCV 5.93%, PCV 5.96%. Although heritability is high, GCV is moderate — indicating that while yield is largely genetically determined here, the relative genetic variability (as CV) is moderate and gains per selection cycle will be modest-to-moderate.

Discussion

1. Genetic control and selection prospects

Across traits, broad-sense heritability is uniformly high (mostly >95% pooled) indicating that a large proportion of total phenotypic variation observed in this material is genetic rather than environmental. High heritability combined with moderate-to-high genetic advance (GA% of mean) is usually interpreted as additive genetic control and predictable response to selection. Traits such as crude fiber, internodal length, total number of fruits per plant, crude protein and fruit length/girth show particularly favorable combinations of high heritability and moderate-high GA% — these are excellent targets for direct selection in an appropriate breeding scheme. For **fruit yield**, although heritability is reported very high (99%), the GCV is moderate (5.9% pooled) and GA% = 12.15%. That pattern suggests yield differences among genotypes are genetically controlled in this trial (and selection should work), but the relative variability is not as large as for some component traits (e.g., crude fiber, number of fruits). Practically, this means breeders can expect improvement in yield via selection, but faster gains may be achieved by indirect selection on high-GCV, high-heritability yield components (e.g., total number of fruits per plant, internodal length where appropriate) or by exploiting specific hybrid combinations. (Bambhaniya *et al.* 2024) [3] reported high heritability and moderate-to-high genetic advance for traits like internodal length and fruit girth, suggesting additive genetic effects and promising selection response. (Chandramouli *et al.* 2016) [6] emphasized that while fruit yield had very high heritability (99%), its moderate GCV and GA% pointed to better gains through indirect selection on component traits.

2. Trait-specific breeding implications

Phenology (days to 50% flowering / first picking / last picking): Very high heritability and low GCV indicate these are stable, genetically governed traits. If early or late maturity is a breeding objective, selection would be effective but genetic variation is limited-gain per cycle may be small and may need broadening of parental base to increase variability. Yield components (total fruits, fruit size, seeds/plant): These show substantial genetic variance and high heritability with appreciable GA% (e.g., total number of fruits GA% = 16.98). Given the moderate-to-high GCV, selection for these traits is promising and should result in correlated yield gains. As a strategy, selection for number of fruits per plant and fruit size (length/girth) can produce rapid improvements in marketable yield. Nutritional traits (crude protein, crude fiber, vitamin C): High heritability and meaningful GA% (crude protein GA% = 13.39; crude fiber GA% = 31.55) indicate strong potential to breed for improved nutritional quality. Crude fiber shows especially large GA% careful interpretation needed (improvement direction depends on breeding objective: reduce or increase fiber). (Goudara *et al.* 2024) [10] reported very high heritability for phenological traits

like days to 50% flowering and first picking, with low GCV, indicating genetic stability. Yield components such as number of fruits per plant and fruit length showed high heritability and GA%, supporting direct selection.

3. Environment and G×E considerations

Large Location effects and non-negligible genotype × location interaction terms (PAR×LOC, HYBRIDS×LOC, etc.) in the pooled ANOVA show the environment and G×E are important for many traits. The presence of sizeable HYBRIDS×LOC and PAR×LOC components implies that some genotypes (parents or hybrids) perform inconsistently across locations. Therefore: Multi-location evaluation and selection should be used to identify stable high-yielding genotypes or those with specific adaptation. Where G×E is large for yield, selection indices or stability analysis (AMMI/GGE) are recommended to identify broadly adapted entries. The present ANOVA supports a strategy that combines mean performance with stability parameters to choose advanced lines/hybrids. Ranga & Darvhanekar, (2022) ^[21]. Demonstrating significant genotype × environment interactions in okra across multiple seasons. Using Eberhart and Russell's model to assess stability across three

environments. Highlighting the need for multi-location trials to identify stable genotypes.

4. Applied breeding recommendations

Direct selection: For traits showing both high heritability and high GA% (e.g., crude fiber, internodal length, total fruits), direct selection in early segregating generations should be effective. **Indirect selection for yield:** Given moderate GCV for yield, consider indirect selection through high-heritability, high-GA yield components (total fruits, fruit size) to maximize realized gain. **Hybrid exploitation:** The very large PAR VS HYB variance for several traits (notably fruit yield) suggests heterosis/hybrid advantage exists in the material. If hybrid seed production is feasible, targeted exploitation of specific crosses (after GCA/SCA analysis) could accelerate yield gains. (Note: GCA/SCA tables and heterosis estimates—if available—should be examined to identify specific crosses and parental lines.) **Multi-environment testing:** Because of notable location and G×E effects, candidate genotypes (both lines and hybrids) should be advanced through multi-location trials to evaluate stability and adaptation prior to release. Combine mean performance with stability indices.

Table 1: Anova for Pooled LxT analysis

Source of variation	DF	Day to 50% flowering	Day to first picking	No. Branches per plant	Internodal length cm	Plant height cm	Fruit length cm	Fruit Girth cm	Total no of fruit per plant	Total no seed per fruit	Day to last picking	Crude protein content	Crude fiber content%	Vitamin C	Fruit yield per plant g
Repl/Loc	8	1.56	2.16	0.08	0.04	13.50	0.18	0.02	23.34	8.45	7.67	0.27	0.14	0.42	1307.57
Locations	3	299.07	398.16	7.76	145.79	84184.20	59.69	6.05	13155.06	342.29	2661.65	136.34	5110.50	184.50	327505.10
Parents	14	19.54	22.67	1.23	1.81	156.36	11.33	0.40	266.18	25.00	98.05	11.26	8.30	11.30	20656.19
Females	9	16.13	18.07	1.32	1.60	213.99	15.93	0.55	166.13	15.49	117.06	9.20	7.66	13.86	21040.00
Males	4	31.87	17.91	0.59	2.56	50.73	2.79	0.15	506.96	51.85	56.32	17.76	10.80	7.33	23438.67
Female vs Males	1	0.93	83.09	2.98	0.69	60.19	4.12	0.04	203.44	3.15	93.78	3.71	4.02	4.15	6072.00
Hybrids	49	17.19	18.19	2.29	7.74	255.98	7.22	0.40	399.88	47.63	57.03	8.82	24.87	10.53	28430.15
Par Vs Hyb	1	571.13	140.88	6.23	6.79	11351.12	27.25	1.55	2758.56	3.09	6229.50	156.45	1684.36	66.83	276936.00
Parxloc	42	24.43	9.51	1.18	1.62	164.46	6.09	0.61	101.01	22.52	70.83	12.11	7.15	13.74	12036.48
Femalexloc	27	26.74	8.96	1.28	1.96	184.12	7.76	0.60	125.23	26.41	62.53	15.79	7.63	13.67	11602.21
Malexloc	12	23.99	5.89	1.06	1.00	120.96	3.11	0.69	61.26	15.67	45.47	6.56	6.96	12.10	14888.36
(Fvsm)Xloc	3	5.33	28.99	0.69	1.12	161.44	2.95	0.42	42.11	14.93	246.99	1.22	3.61	20.89	4537.31
Hybridsxloc	147	27.81	13.56	1.60	5.63	172.14	7.65	0.42	348.02	59.10	82.60	16.68	18.67	9.25	16379.31
(Par vs Hyb)Xloc	3	86.39	200.80	8.82	126.67	7052.09	115.19	6.86	6708.76	780.26	2235.02	151.04	959.79	48.43	83094.94
Error	512	0.36	0.29	0.01	0.01	2.00	0.02	0.00	1.88	0.64	2.46	0.04	0.05	0.13	81.50
Repl/Loc	8	1.56	2.16	0.08	0.04	13.50	0.18	0.02	23.34	8.45	7.67	0.27	0.14	0.42	1307.57

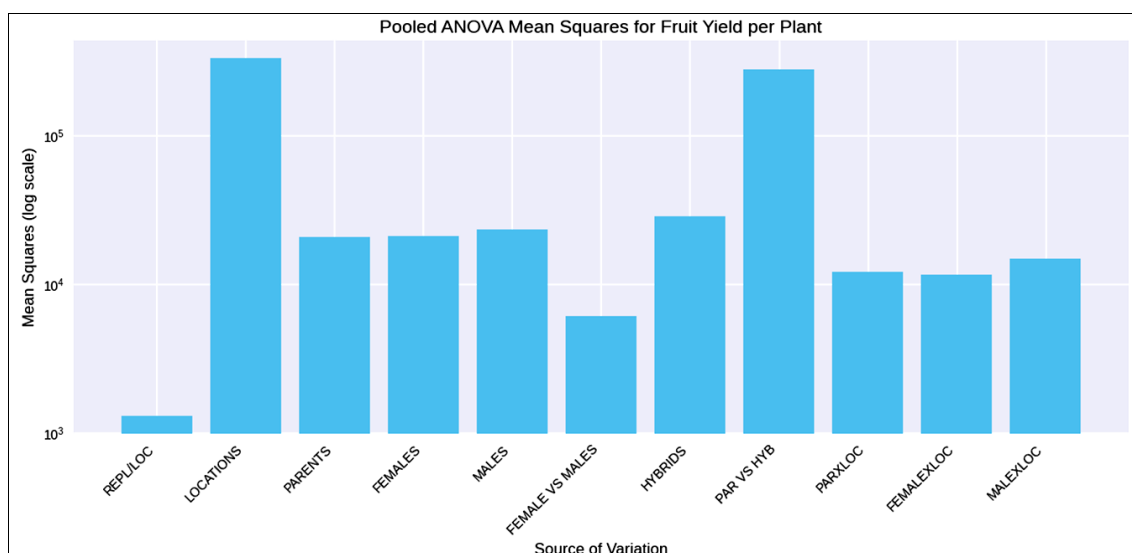


Table 2: Genetic variability of quantitative traits for across environment

Characters		Mean	Min	Max	var (g)	var (p)	Heritability (%)	GA	GA% mean	GCV (%)	PCV (%)
Day to 50% flowering	Y1	45.41	41.00	53.00	8.04	8.68	92.56	5.62	12.37	6.24	6.49
	Y2	45.60	38.40	54.20	10.38	10.52	98.61	6.59	14.45	7.06	7.11
	Y3	43.13	38.07	49.27	9.95	10.07	98.87	6.46	14.98	7.31	7.36
	Y4	45.52	39.00	51.27	7.57	8.12	93.20	5.47	12.02	6.04	6.26
	P	44.92	41.42	48.49	2.21	2.29	96.34	3.01	6.69	3.31	3.37
Day to first picking	Y1	56.83	51.03	59.67	3.79	4.52	83.99	3.68	6.47	3.43	3.74
	Y2	56.80	50.80	60.47	5.07	5.15	98.46	4.60	8.10	3.96	3.99
	Y3	53.93	48.93	59.93	7.21	7.43	97.08	5.45	10.11	4.98	5.05
	Y4	55.41	51.20	59.65	6.70	6.84	97.90	5.27	9.52	4.67	4.72
	P	55.74	52.03	58.50	1.91	1.99	96.30	2.80	5.01	2.48	2.53
No. Branches per plant	Y1	3.37	2.06	4.80	0.47	0.48	96.59	1.39	41.08	20.29	20.65
	Y2	3.31	1.60	5.80	0.87	0.88	98.00	1.90	57.38	28.14	28.42
	Y3	3.59	2.47	4.80	0.47	0.48	97.82	1.40	38.87	19.08	19.29
	Y4	3.12	1.96	4.60	0.45	0.46	97.18	1.36	43.51	21.43	21.74
	P	3.35	2.57	4.45	0.17	0.17	97.69	0.84	25.10	12.33	12.47
Internodal length cm	Y1	6.60	4.40	9.23	0.91	0.92	98.99	1.95	29.59	14.44	14.51
	Y2	6.03	3.20	9.11	1.74	1.75	99.50	2.71	45.01	21.91	21.96
	Y3	6.43	4.90	7.93	0.72	0.74	97.28	1.72	26.73	13.16	13.34
	Y4	7.97	4.24	12.10	5.62	5.63	99.79	4.88	61.22	29.75	29.78
	P	6.76	4.80	8.41	0.62	0.63	99.42	1.62	24.00	11.68	11.72
Plant height cm	Y1	135.69	113.43	146.33	45.45	47.30	96.09	13.61	10.03	4.97	5.07
	Y2	116.74	85.47	138.13	192.91	196.10	98.38	28.38	24.31	11.90	12.00
	Y3	87.46	69.93	121.50	61.87	62.56	98.90	16.11	18.42	8.99	9.04
	Y4	106.76	83.07	135.87	149.33	151.68	98.45	24.98	23.40	11.45	11.54
	P	111.66	98.20	122.13	34.20	34.80	98.29	11.94	10.70	5.24	5.28
Fruit length cm	Y1	13.21	9.67	18.07	2.51	2.53	99.45	3.26	24.66	12.00	12.04
	Y2	13.53	8.70	19.10	4.39	4.43	99.11	4.30	31.76	15.49	15.56
	Y3	13.35	9.60	20.03	3.53	3.57	98.80	3.84	28.79	14.06	14.15
	Y4	12.34	9.63	16.47	1.84	1.84	99.80	2.79	22.62	10.99	11.00
	P	13.11	10.93	16.04	0.88	0.88	99.31	1.92	14.65	7.14	7.16
Fruit Girth cm	Y1	2.31	1.70	4.30	0.18	0.19	97.67	0.87	37.78	18.56	18.78
	Y2	1.99	1.25	4.30	0.23	0.23	97.94	0.98	49.24	24.15	24.40
	Y3	2.08	1.18	4.40	0.59	0.60	99.30	1.58	75.94	36.99	37.13
	Y4	1.93	1.10	4.43	0.30	0.30	98.55	1.11	57.72	28.23	28.44
	P	2.08	1.69	4.36	0.19	0.19	99.33	0.89	42.82	20.86	20.92
Total no of fruit per plant	Y1	80.63	66.00	98.00	70.93	73.75	96.17	17.01	21.10	10.45	10.65
	Y2	78.76	50.67	109.33	220.39	223.60	98.57	30.36	38.55	18.85	18.99
	Y3	63.16	36.20	94.33	134.14	134.39	99.82	23.84	37.74	18.34	18.35
	Y4	76.70	56.80	97.17	118.62	120.21	98.67	22.29	29.06	14.20	14.29
	P	74.81	63.00	89.99	38.48	38.95	98.79	12.70	16.98	8.29	8.34
Total no seed per fruit	Y1	44.20	38.33	52.00	12.38	12.94	95.67	7.09	16.04	7.96	8.14
	Y2	43.40	34.93	53.20	26.03	27.15	95.89	10.29	23.71	11.76	12.01
	Y3	44.30	34.87	54.00	20.49	21.03	97.41	9.20	20.78	10.22	10.35
	Y4	41.57	33.87	49.23	15.06	15.36	98.04	7.92	19.04	9.34	9.43
	P	43.37	39.47	46.73	3.39	3.56	95.36	3.70	8.54	4.25	4.35
Day to last picking	Y1	91.43	73.67	103.40	44.55	47.42	93.95	13.33	14.58	7.30	7.53
	Y2	87.57	70.80	98.33	44.21	48.24	91.66	13.11	14.98	7.59	7.93
	Y3	85.76	79.00	95.47	15.80	16.07	98.32	8.12	9.47	4.63	4.67
	Y4	93.58	78.50	109.67	58.21	60.64	96.00	15.40	16.46	8.15	8.32
	P	89.59	78.66	96.18	13.21	13.89	95.13	7.30	8.15	4.06	4.16
Crude protein content	Y1	16.25	12.90	19.23	2.28	2.32	98.40	3.09	19.01	9.30	9.38
	Y2	15.06	11.00	19.03	3.39	3.44	98.37	3.76	24.97	12.22	12.32
	Y3	16.47	10.97	23.28	12.37	12.41	99.68	7.23	43.90	21.35	21.38
	Y4	14.90	12.40	18.87	3.47	3.50	99.29	3.83	25.67	12.51	12.55
	P	15.67	13.50	18.26	1.05	1.06	99.18	2.10	13.39	6.53	6.55
Crude fiber Content%	Y1	10.51	5.60	19.63	16.49	16.54	99.68	8.35	79.49	38.65	38.71
	Y2	11.60	7.61	17.07	5.83	5.89	99.08	4.95	42.69	20.82	20.92
	Y3	20.69	11.13	29.53	19.25	19.31	99.68	9.02	43.62	21.21	21.24
	Y4	10.34	7.23	17.43	7.18	7.20	99.73	5.51	53.34	25.93	25.96
	P	13.28	9.49	16.96	4.15	4.16	99.70	4.19	31.55	15.34	15.36
Vitamin C	Y1	20.08	15.97	25.27	4.05	4.15	97.54	4.09	20.39	10.02	10.15
	Y2	21.69	15.79	26.00	5.20	5.53	94.13	4.56	21.02	10.52	10.84
	Y3	20.52	18.37	23.70	1.66	1.68	98.53	2.63	12.84	6.28	6.32
	Y4	19.45	15.90	24.10	3.96	4.00	98.85	4.07	20.95	10.23	10.29
	P	20.44	18.31	23.23	1.07	1.11	96.73	2.10	10.26	5.07	5.15

Fruit yield per plant g	Y1	865.70	713.33	1083.33	8414.25	8592.51	97.93	186.99	21.60	10.60	10.71
	Y2	893.98	715.67	1035.00	5274.89	5376.84	98.10	148.19	16.58	8.12	8.20
	Y3	809.00	687.33	977.57	6664.83	6684.45	99.71	167.93	20.76	10.09	10.11
	Y4	811.20	703.00	1122.33	5997.51	6063.60	98.91	158.66	19.56	9.55	9.60
	P	844.97	736.33	965.50	2509.48	2535.96	98.96	102.66	12.15	5.93	5.96

Conclusion

The material used in L×T trial exhibits ample genetic variability and high broad-sense heritability for most agronomic and nutritional traits, indicating good prospects for genetic improvement. Traits such as crude fiber, internodal length, total number of fruits per plant, crude protein and fruit size are especially promising targets for direct selection. Fruit yield shows high heritability but moderate relative genetic variability; thus, improvement is expected but may be faster when achieved indirectly via component traits or by exploiting specific hybrid combinations. Significant location effects and G×E require multi-location evaluation and stability analysis before final selections are recommended.

Acknowledgments

The authors express their sincere gratitude to AKS University, Satna (M.P.), for providing the necessary facilities and academic support to conduct this experiment as part of the Ph.D. research work.

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