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EVALUATION OF GENETIC VARIABILITY, CHARACTER ASSOCIATION AND MULTIVARIATE ANALYSIS IN OKRA (*Abelmoschus esculentus* L. MOENCH)

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ABSTRACT

The purpose of the field experiment was to evaluate 27 different genotypes of okra (*Abelmoschus esculentus* (L.) Moench) using a Randomized Block Design with three replications. “The experiment took place during kharif 2021-22 at the All India Coordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha. The variables of interest included genetic variability, character association, path coefficient, and genetic divergence. There is plenty of room for selection and crop improvement based on the high genetic diversity for 16 quantitative variables observed in 27 okra genotypes. The widest range of variation was observed for number of branches (0.55–5.22), followed by north-south spread (21.77–77.89 cm), plant height (52.55–183.77 cm) and fruit yield per plant (108.81–292.42 g). Higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) was observed for all traits, suggesting environmental influence on trait expression. High PCV and GCV estimates were recorded for number of branches (55.55% and 50.77%), There was a 37.02% east-west spread, a 35.65% north-south spread, a 33.89% fruit yield, a 25.71% fruit number, and a 20.82% fruit number per plant. In terms of plant height, branch count, node count, fruit length, average fruit weight, fruit output, and number of fruits per plant, there was a significant degree of heritability and genetic advancement relative to the mean, indicating predominance of additive gene action and effectiveness of direct selection. Correlation analysis revealed significant positive association of fruit yield with plant height, number of nodes, fruit length, number of fruits per plant and average fruit weight, whereas days to flowering and harvesting traits exhibited significant negative association with yield. Path coefficient analysis identified number of fruits per plant (0.744) and average fruit weight (0.742) as the major contributors to yield through strong positive direct effects. Mahalanobis D² analysis grouped the genotypes into seven clusters, with maximum inter-cluster distance observed between clusters V and VI (24.74), suggesting greater genetic divergence and their potential utility in hybridization programmes for exploiting heterosis and developing superior okra genotypes indicating greater potential utility in future hybridization and crop improvement programmes.

Key words : Okra, Genetic variability, Character association, Multivariate analysis, Divergence, Yield attributing traits.

Introduction

The Malvaceae family includes the okra, or lady’s finger, as stated by Kishor *et al.* (2016). The vegetable crop, which is known to be susceptible to cross-pollination,

is thought to have originated in Tropical Africa and then expanded to many regions around the globe, including Asia, America, and Southern Europe (Temam *et al.*, 2020). The chromosomal variety within the genus

Abelmoschus is rather large, spanning from $2n = 56$ to 130. *Abelmoschus angulosus* possesses the lowest chromosome number ($2n = 56$), whereas *Abelmoschus manihot* var. *caillei* has chromosome numbers approaching 200 (Ford, 1938; Singh and Bhatnagar, 1975; Siemonsma, 1982a; Siemonsma, 1982b). The crop bears yellow flowers with crimson pigmentation at the petal base and produces capsule-type fruits with 5–9 lobed stigma. Okra is an annual, day-neutral crop cultivated throughout the year for its tender green pods known as capsules (Dhar *et al.*, 2025) and is widely grown in tropical, subtropical and warm temperate regions (Balai *et al.*, 2015).

The nutritional and therapeutic qualities of okra makes it highly prized beyond its culinary uses alone. According to many studies (Zhang *et al.*, 2020; Adetuyi *et al.*, 2021; Olawuyi and Lee, 2021), various components of plants, including their leaves, seeds, stems and roots, have various medical and industrial applications. There are several ways to enjoy tender pods, one of which is in soups, salads, stews and fried dishes (Gemedé *et al.*, 2015). The fruits are rich in digestible fibre, vitamins and minerals, while being low in fat and calories (Vennila *et al.*, 2026). The mucilaginous nature of okra makes it useful as a natural thickening agent in soups and curries (Araújo *et al.*, 2020). The fruits contain 7.0% carbohydrates, 2.0% protein, 3.0% fibre and 0.2% fat (USDA Food Data, 2024; Elshout, 2021). Medicinally, okra has been reported to be beneficial against fever, genito-urinary disorders, gonorrhoea and chronic dysentery (Singh and Nigam, 2023).

India is the leading producer of okra, contributing nearly 67% of global production. The crop occupies about 523 thousand hectares with an annual production of 6416 thousand metric tonnes (NHB Database, 2022). Major okra growing states include Gujarat, West Bengal, Bihar, Madhya Pradesh and Odisha. With a production of 662 thousand metric tons, Odisha is one of the major states that produce okra (NHB Database, 2022). The use of unimproved cultivars, limited acceptance of improved hybrids, and significant prevalence of biotic stressors, notably yellow vein mosaic disease, contribute to relatively low yield in India, despite its economic significance.

Genetic improvement in okra largely depends on the extent of variability present in the available germplasm. Evaluation of genetic diversity and association among yield-contributing traits is therefore essential for effective crop improvement (Swetha *et al.*, 2022; Sravanthi *et al.*, 2022). Estimation of parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance helps in distinguishing heritable variation from environmental influence and provides valuable

information for selection (Tudu *et al.*, 2021; Prakash *et al.*, 2022).

Several component features impact yield, making it a complicated attribute. Thus, for indirect selection and yield enhancement, it is crucial to understand the link among these features via correlation research. In order to find desired qualities associated with yield, breeders use correlation analysis, which assesses the strength and direction of relationship between attributes. Vinod and Gaibriyal (2023) and Juboori (2021) both point out that correlation is not a sufficient criterion to draw firm conclusions about the relative importance of directly and indirectly contributing features.

Path coefficient analysis partitions correlation coefficients into direct and indirect effects and identifies the traits exerting maximum influence on yield (Vinod and Gaibriyal, 2023; Awasthi *et al.*, 2022). This technique helps in understanding the cause-and-effect relationship among characters and facilitates the selection of superior traits for breeding high-yielding okra genotypes.

Materials and Methods

The experiment was conducted at the All-India Co-ordinated Research Project (AICRP) on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha, India during 2021-22 to study the nature and extent of genetic variability, correlation and path analysis of 27 genotypes of Okra in Randomised Block Design (RBD) with 3 replications during *khari*f season. The experiment details and layout given below on Table 1 along with source of genotypes in Table 2. From randomly selected 5 plants per plot observations were recorded for 18 parameters that included 6 vegetative growth parameters like plant height, plant spread (N-S), plant spread (E-W), number of primary branches, number of nodes and 1st node at which fruit appears; 2 flowering parameters like days to 1st flowering

Table 1 : Experimental details.

Design of layout	Randomized Block Design (RBD)
Number of genotypes	27
Number of replications	3
Total number of plots	81
Plot size	3 m × 2.8 m
Spacing	60 cm × 30 cm
Number of rows per plot	2
Number of plants per row	9
Number of plants per plot	18

Table 2 : Source of okra genotypes.

Genotypes	Variety	Name	Sources
1.	V1	2019/OKYVRES-1	AICRP, VC, OUAT
2.	V2	2019/OKYVRES-2	AICRP, VC, OUAT
3.	V3	2019/OKYVRES-3	AICRP, VC, OUAT
4.	V4	2019/OKYVRES-5	AICRP, VC, OUAT
5.	V5	2019/OKYVRES-6	AICRP, VC, OUAT
6.	V6	2019/OKYVRES-7	AICRP, VC, OUAT
7.	V7	2019/OKYVRES-8	AICRP, VC, OUAT
8.	V8	2019/OKYVRES-9	AICRP, VC, OUAT
9.	V9	2019/OKYVRES-10	AICRP, VC, OUAT
10.	V10	2019/OKYVRES-11	AICRP, VC, OUAT
11.	V11	2019/OKYVRES-12	AICRP, VC, OUAT
12.	V12	BO-1	AICRP, VC, OUAT
13.	V13	BO-2 Utkal Gaurav	AICRP, VC, OUAT
14.	V14	BO-2-1	AICRP, VC, OUAT
15.	V15	BO-2-2	AICRP, VC, OUAT
16.	V16	BO-2-1-1	AICRP, VC, OUAT
17.	V17	BO-2-9	AICRP, VC, OUAT
18.	V18	BO-2-10	AICRP, VC, OUAT
19.	V19	BO-2-3	AICRP, VC, OUAT
20.	V20	BO-2-4	AICRP, VC, OUAT
21.	V21	BO-2-5	AICRP, VC, OUAT
22.	V22	BO-2-6	AICRP, VC, OUAT
23.	V23	BO-2-7	AICRP, VC, OUAT
24.	V24	BO-2-8	AICRP, VC, OUAT
25.	V25	BO-2-4-6	AICRP, VC, OUAT
26.	V26	BO-2-5-6	AICRP, VC, OUAT
27.	V27	BO-2-3-5	AICRP, VC, OUAT

and days to 50% flowering; 7 fruit yield attributing parameters like fruit girth, fruit length, number of fruits per plant, average fruit weight, number of ridges, days to 1st fruiting, days to 1st harvest and 3 fruit yield parameters like fruit yield per plant(g), fruit yield per plot (kg), fruit yield per hectare. The data were statistically analysed for computation of genetic variability, character association and path coefficient analysis. Mahalanobis (1928) generalized distance, D² statistic was used for computing genetic divergence as described by Rao (1952). The original measurements were transformed to standardize uncorrelated variables by pivotal condensation (Rao, 1952). The divergence between any two varieties was obtained as the sum of squares of the difference in the

values of the corresponding transformed values (V_{ij})

$$D^2_{jk} = \sum n_i = 1 Y_{ij} - Y_{ik}$$

Gives the D² between jth and kth genotypes for 'n' characters. The all possible pairs of D² were calculated from the 27 genotypes of okra using the formula $n(n-1)/2$.

The genotypes were clustered according to Rao's (1952) description of Tocher's approach. The D² value between any two genotypes in the same cluster should be less than the D² value between genotypes in different clusters; this was the criteria for grouping. We calculated and displayed inter- and intra-cluster distances.

Results and Discussion

Per se performance of 27 Genotypes of Okra

The analysis of variance (ANOVA) revealed the presence of substantial variability among the 27 okra genotypes for all the 18 traits studied, except days to first flowering and days to first fruiting, which were found to be non-significant (Table 3). The presence of highly significant differences among genotypes for most traits indicated adequate genetic variability in the experimental material, so there's plenty of room for efficient selection and bettering crops. Swetha *et al.* (2022), Nayak *et al.* (2022), Jemal *et al.* (2022) and Reddy *et al.* (2022) all demonstrated similar results, suggesting a great deal of variation across okra genotypes.

Additional evidence of the high degree of genetic variability was provided by the ranges and averages of the various characteristics. With so much diversity in growth, blooming, and yield characteristics, there is a chance to find better genotypes that work better for certain breeding goals. The coefficient of variation remained below 10 per cent for all the traits except number of branches per plant, indicating high experimental precision and reliability of the data. The coefficient of variation below 20 per cent for all the characters suggested that the experiment was conducted with acceptable precision and minimum environmental error.

Mean performance

Vegetative Growth parameters

Significant variations in okra genotypes were recorded for vegetative growth parameters (Table 4) viz., plant height from 52.557 cm(2019/OKYVRES-1) to 183.777 cm(2019/OKYVRES-8), north- south spread from 21.777 cm(BO-2-1) to 77.890 cm(BO-2-3), east-west spread from 21.223 cm(BO-2-1) to 67.223 cm(BO-2-3), primary branches per plant from 0.557(BO-2-3) to 5.223 (2019/OKYVRES-9), number of nodes from 12.667

Table 3 : Analysis of variance for 18 characters of 27 okra genotypes.

S. no.	Characters	DF	SS	MSS (Genotype)	Calculated F	Tabulated F
1.	Plant height	26	49865.64	1917.90	24.77**	1.709
2.	North-south spread	26	16112.48	619.71	62.09**	1.709
3.	East-west spread	26	18881.75	726.22	39.33**	1.709
4.	Nos. of branches	26	113.98	4.38	42.58**	1.709
5.	Nos. of nodes	26	538.19	20.70	13.24**	1.709
6.	1st node at which fruit appears	26	103.67	3.98	29.42**	1.709
7.	Fruit girth	26	8.97	0.34	2.97*	1.709
8.	Fruit length	26	165.06	6.34	5.15**	1.709
9.	Nos. of fruits/plant	26	481.94	18.53	15.44**	1.709
10.	Fruit weight	26	725.53	27.90	21.33**	1.709
11.	Nos. of ridges	26	17.91	0.68	3.18*	1.709
12.	Days to 1 st flowering	26	144.00	5.53	0.94	1.709
13.	Days to 1 st fruiting	26	144.89	5.57	0.86	1.709
14.	Days to 50% flowering	26	155.33	5.97	5.44**	1.709
15.	Days to 1 st harvest	26	161.95	6.22	3.55*	1.709
16.	Yield/plant(g)	26	161068.74	6194.95	53.09**	1.709
17.	Yield/plot(kg)	26	421.21	16.20	59.26**	1.709
18.	Yield/ha(q/ha)	26	64203.16	2469.35	82.11**	1.709

Table 4 : Mean performance for 18 characters in 27 genotypes of okra.

S. no.	Genotypes	Plant height	North-south spread	East-west spread	No. of branches	No. of nodes	1st node at which fruit appears	Fruit girth	Fruit length	No. of fruits/plant
1.	2019/OKYVRES-1	97.33	42.78	58.55	0.77	12.66	3.66	5.23	11.10	8.00
2.	2019/OKYVRES-2	124.44	30.11	37.22	1.33	13.00	3.33	4.63	14.23	9.66
3.	2019/OKYVRES-3	124.44	42.77	35.66	0.77	13.11	3.00	5.43	12.20	10.66
4.	2019/OKYVRES-5	156.66	32.55	21.22	1.78	15.44	5.89	5.22	13.02	10.33
5.	2019/OKYVRES-6	145.55	51.77	38.00	3.33	21.55	5.11	5.05	14.22	13.67
6.	2019/OKYVRES-7	158.00	34.77	27.78	3.00	19.77	5.89	5.48	15.22	11.33
7.	2019/OKYVRES-8	183.77	38.77	43.77	1.11	20.44	4.66	5.48	15.23	16.55
8.	2019/OKYVRES-9	174.33	33.55	36.78	5.22	21.22	7.00	5.25	13.43	13.89
9.	2019/OKYVRES-10	153.44	36.78	28.33	3.89	20.33	4.66	5.26	15.66	14.00
10.	2019/OKYVRES-11	163.22	33.78	32.11	3.00	18.89	5.55	5.01	15.01	10.66
11.	2019/OKYVRES-12	137.11	34.33	31.89	2.78	17.44	4.78	5.01	16.03	16.00
12.	BO-1	52.55	34.22	37.66	3.89	15.00	3.00	5.26	11.45	9.66
13.	BO-2 Utkal Gaurav	140.89	30.33	24.00	2.11	18.33	4.33	5.14	9.22	14.00
14.	BO-2-1	120.33	21.77	23.67	1.22	16.44	3.44	5.74	13.50	8.89
15.	BO-2-2	120.11	33.55	30.67	1.55	17.55	3.89	4.69	13.10	15.22
16.	BO-2-1-1	136.33	24.22	32.33	2.55	19.55	5.44	4.67	14.37	12.44
17.	BO-2-9	122.00	21.89	23.22	2.44	20.33	5.00	4.56	13.55	12.66
18.	BO-2-10	133.77	66.89	59.66	3.55	17.55	4.44	4.73	13.74	15.22

Table 4 continued...

Table 4 continued...

19.	BO-2-3	161.66	77.89	67.22	0.55	16.55	2.00	5.43	13.74	14.89
20.	BO-2-4	151.11	55.88	53.55	3.44	17.77	3.67	4.48	14.13	14.00
21.	BO-2-5	147.22	54.88	45.00	3.89	16.89	5.77	5.42	13.34	9.33
22.	BO-2-6	135.00	47.89	62.44	1.77	18.33	3.11	4.85	14.14	10.20
23.	BO-2-7	148.55	45.78	65.78	0.89	18.33	3.00	5.44	14.04	12.00
24.	BO-2-8	147.22	65.11	58.00	2.44	17.33	4.66	5.26	13.02	10.00
25.	BO-2-4-6	150.00	58.77	63.66	2.44	17.66	3.66	4.85	13.03	13.22
26.	BO-2-5-6	127.44	56.89	58.11	1.89	16.33	4.33	5.04	15.03	11.11
27.	BO-2-3-5	133.22	46.66	66.66	0.77	11.67	3.55	5.53	13.49	8.00
Mean		138.73	42.76	43.07	2.31	17.39	4.32	5.12	13.64	12.06
CV		6.34	7.38	9.97	13.87	7.18	8.50	6.64	8.13	9.08
SE (±m)		5.08	1.82	2.48	0.18	0.722	0.21	0.19	0.64	0.63
CD at 5 %		14.45	5.19	7.06	0.52	2.05	0.60	0.55	1.82	1.80

Table 4 continued...

S. no.	Genotypes	Fruit weight	No. of ridges	Days to 1 st flowering	Days to 1 st fruiting	Days to 50 % flowering	Days to 1 st harvest	Yield/ plant (g)	Yield/ plot(kg)	Yield/ha (q/ha)
1.	2019/OKYVRES-1	16.06	5.33	40.33	49.33	45.66	51.33	122.46	6.00	74.08
2.	2019/OKYVRES-2	16.33	4.66	40.33	49.33	46.33	51.66	146.00	6.71	82.91
3.	2019/OKYVRES-3	14.00	5.00	39.33	48.33	46.00	50.66	145.66	7.14	88.11
4.	2019/OKYVRES-5	16.86	5.00	38.33	47.33	45.00	49.33	167.40	8.87	109.53
5.	2019/OKYVRES-6	20.42	5.00	36.33	45.33	42.66	47.66	268.56	13.43	165.78
6.	2019/OKYVRES-7	18.40	5.00	39.33	48.33	46.00	50.33	200.15	9.20	113.67
7.	2019/OKYVRES-8	18.15	5.00	36.33	45.33	42.00	47.66	292.42	14.62	180.51
8.	2019/OKYVRES-9	12.91	5.00	38.33	47.33	44.66	49.66	176.42	8.64	106.72
9.	2019/OKYVRES-10	14.60	5.00	37.33	46.33	44.00	48.00	190.74	9.92	122.45
10.	2019/OKYVRES-11	10.22	5.00	40.33	49.33	45.00	51.33	108.81	5.44	67.17
11.	2019/OKYVRES-12	11.68	5.00	37.33	46.33	43.00	48.33	185.34	9.64	118.97
12.	BO-1	16.20	7.44	38.33	47.33	45.00	49.33	150.42	7.82	96.56
13.	BO-2 Utkal Gaurav	9.09	5.00	39.33	48.33	45.00	50.66	128.17	6.53	80.70
14.	BO-2-1	16.91	5.00	40.33	49.33	46.00	51.66	143.44	6.59	81.46
15.	BO-2-2	11.00	5.00	40.33	49.33	46.00	52.00	166.44	7.66	94.52
16.	BO-2-1-1	16.38	5.00	37.33	46.33	43.33	48.66	197.41	10.07	124.30
17.	BO-2-9	14.97	5.00	37.33	46.33	43.33	48.33	184.76	9.42	116.33
18.	BO-2-10	16.57	5.00	36.33	45.33	42.00	47.66	245.75	12.04	148.67
19.	BO-2-3	12.71	5.00	39.33	48.33	44.66	50.33	186.53	8.58	105.93
20.	BO-2-4	15.71	5.00	37.33	46.33	43.00	49.66	214.23	10.71	132.24
21.	BO-2-5	14.09	5.00	40.33	49.33	46.66	51.66	127.35	5.98	73.90
22.	BO-2-6	17.11	5.00	39.33	48.33	45.33	51.00	167.77	6.87	84.92
23.	BO-2-7	15.02	5.00	38.33	47.33	44.00	50.00	175.25	8.58	106.07

Table 4 continued...

24.	BO-2-8	12.15	5.00	40.33	49.33	46.00	51.3	119.43	5.61	69.30
25.	BO-2-4-6	12.86	5.00	39.33	48.33	46.00	51.33	167.23	8.02	99.10
26.	BO-2-5-6	22.09	5.00	38.33	47.33	43.00	49.33	233.32	10.73	132.51
27.	BO-2-3-5	18.49	5.00	38.33	48.33	43.33	51.00	139.40	6.97	86.05
Mean		15.22	5.09	38.66	47.70	44.55	50.00	175.96	8.59	106.02
CV		7.51	9.13	6.27	5.32	2.35	2.64	6.13	6.08	5.17
SE(±m)		0.66	0.26	1.40	1.46	0.60	0.76	6.23	0.30	3.16
CD at 5%		1.87	0.76	1.62	1.79	1.72	2.17	17.74	0.85	9.01

(2019/OKYVRES-1) to 21.557(2019/OKYVRES-9), 1st node at which fruit appears from 2.000 (BO-2-3) to 7.000(2019/OKYVRES-9) (Awasthi *et al.*, 2022; Reddy *et al.*, 2022; Kenaw *et al.*, 2023).

Flowering parameters

In the okra development program, earliest maturity is regarded as a key trait that eventually affects fruit yield (Table 4). For days to 1st flowering, significant differences were observed among the genotypes ranging from 36.333 days to 40.333 days. Significantly earliest time for appearance of 1st flower (days) was recorded in 2019/OKYVRES-6 (36.333 days), 2019/OKYVRES-8 (36.333 days) and BO-2-10 (36.333 days). Similarly, the results revealed significant variations for the flowering trait days to 50% flowering ranging from 42.000 days (2019/OKYVRES-8 and BO-2-10) to 46.667 days (BO-2-5). Significantly earliest time for appearance of 50% flower was recorded in 2019/OKYVRES-8 (42.000 days) and BO-2-10 (42.000 days) and showed statistical parity with 2019/OKYVRES-6, 2019/OKYVRES-12, BO-2-1-1, BO-2-9 and BO-2-4 (Awasthi *et al.*, 2022; Reddy *et al.*, 2022; Kenaw *et al.*, 2023; Kumar *et al.*, 2021).

Fruit yield and yield attributing parameters

Significant variation was observed among the okra genotypes for fruit yield and related traits (Table 4). Fruit girth ranged from 4.480 cm (BO-2-4) to 5.743 cm (BO-2-1), with BO-2-1 remaining statistically at par with several genotypes. Fruit length varied between 9.223 cm in BO-2 Utkal Gaurav and 16.033 cm in 2019/OKYVRES-12, which was statistically comparable with 2019/OKYVRES-2, 6, 7, 8, 10, 11, BO-2-1-1 and BO-2-5-6. Number of fruits per plant ranged from 8.000 to 16.557, with the highest value recorded in 2019/OKYVRES-8, statistically at par with 2019/OKYVRES-12, BO-2-2, BO-2-8 and BO-2-3. Average fruit weight varied significantly from 9.090 g (BO-2 Utkal Gaurav) to 22.090 g (BO-2-5-6). Earliness traits showed that 2019/

OKYVRES-6, 2019/OKYVRES-8 and BO-2-10 recorded earliest fruiting (45.333 days), while 2019/OKYVRES-6 exhibited earliest harvest (47.667 days). Total fruit yield per plant ranged from 108.817 g in 2019/OKYVRES-11 to 292.427 g in 2019/OKYVRES-8, which remained statistically at par with several high-yielding genotypes, indicating their superior adaptability (Temam *et al.*, 2020; Awasthi *et al.*, 2022; Reddy *et al.*, 2022; Kenaw *et al.*, 2023; Kumar *et al.*, 2021).

Genetic variability

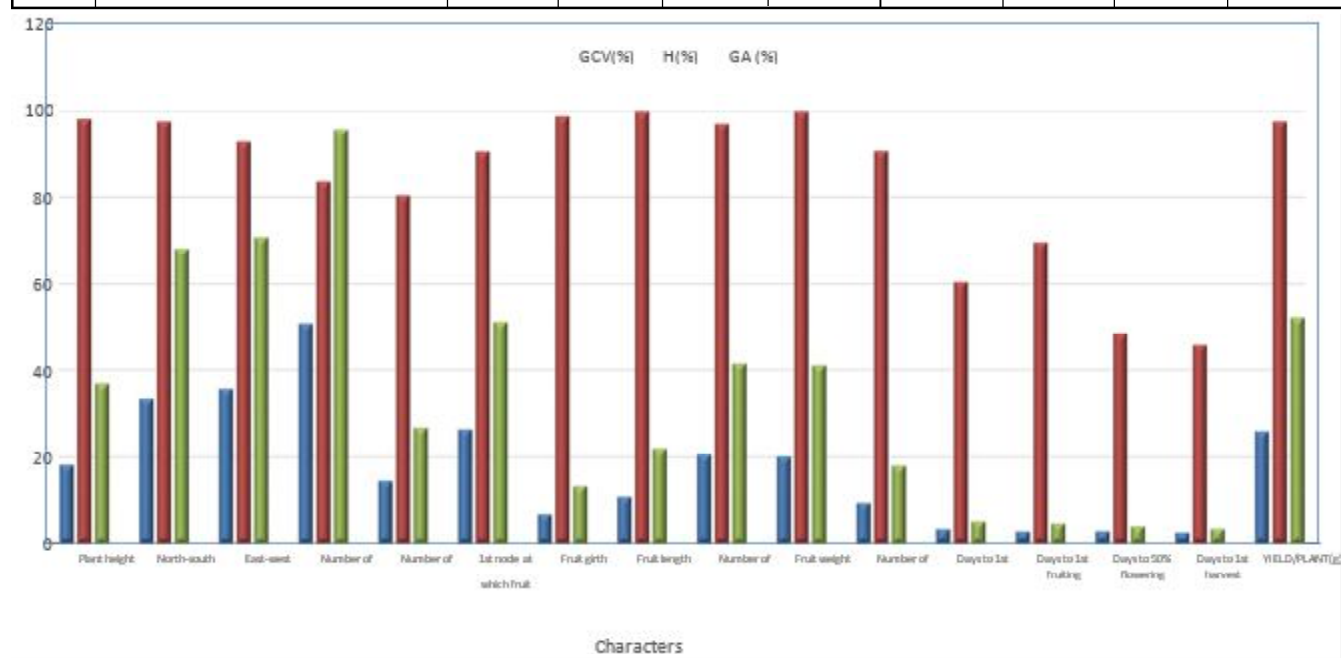
There was a lot of room for improvement in crop quality and selection efficiency since all sixteen quantitative parameters examined showed a high degree of genetic diversity across the 27 okra genotypes (Table 5). The most variable variable was total fruit output per plant, which ranged from 108.817 to 292.427 g. whereas minimum variation was observed for fruit girth (4.480–5.743 cm). The ratio between maximum and minimum values ranged from 1.08 times for days to first fruiting to 9.37 times for number of branches, suggesting substantial variability among the genotypes (Behera *et al.*, 2025).

Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits, indicating environmental influence on trait expression (Fig. 1). High GCV and PCV values (>20%) were recorded for number of branches, east-west spread, north-south spread, first node bearing fruit, number of fruits per plant and fruit yield per plant, reflecting greater scope for selection (Ashraf *et al.*, 2020; Setu, 2023).

Table 5 shows that the heritability estimates varied from 45.74 percent for the days to first harvest to 99.71 percent for the length of the fruit and the average weight of the fruit. Branches per plant, average fruit weight, plant height, average fruit length, average fruit output, and average fruit weight all showed substantial heritability and genetic advancement relative to the mean, indicating predominance of additive gene action and effectiveness of direct phenotypic selection (Swetha *et al.*, 2022;

Table 5 : Estimation of Mean, range, component of variance, GCV, PCV, heritability, Genetic advance as % of mean (GA%).

S. no.	Characters	Mean	Range		GCV (%)	PCV (%)	H (%)	GA	GA(%) of mean
			Min	Max					
1.	Plant height	138.73	52.55	183.77	18.16	18.34	98.08	51.41	37.06
2.	North-south spread	42.76	21.77	77.89	33.46	33.89	97.47	29.16	68.06
3.	East-west spread	43.07	21.22	67.22	35.65	37.02	92.74	30.47	70.74
4.	Number of branches	2.31	0.55	5.22	50.77	55.55	83.52	2.21	95.59
5.	Number of nodes	17.391	12.66	21.57	14.52	16.20	80.32	4.66	26.81
6.	1st node at which fruit appears	4.32	2.00	7.00	26.17	27.51	90.45	2.22	51.27
7.	Fruit girth	5.12	4.48	5.74	6.60	6.65	98.67	0.69	13.52
8.	Fruit length	13.64	9.22	16.03	10.65	10.673	99.71	2.99	21.92
9.	Number of fruits/plants	12.06	8.00	16.55	20.50	20.82	96.89	5.01	41.56
10.	Fruit weight	15.22	9.09	20.42	20.02	20.05	99.71	6.27	41.19
11.	Number of ridges	5.09	4.66	7.44	9.25	9.72	90.56	0.92	18.14
12.	Days to 1 st flowering	38.67	36.33	40.33	3.18	4.09	60.42	1.97	5.08
13.	Days to 1 st fruiting	47.70	45.33	49.33	2.66	3.20	69.51	2.18	4.58
14.	Days to 50% flowering	44.55	42.00	46.66	2.72	3.91	48.42	1.73	3.90
15.	Days to 1 st harvest	50.00	47.66	52.00	2.38	3.53	45.74	1.66	3.32
16.	Yield/Plant (g)	175.96	108.81	292.42	25.71	26.04	97.47	92.02	52.29

**Fig. 1 :** Estimation of GCV, heritability, Genetic advance as % of mean (GA%).

Kenaw *et al.*, 2023; Khajuria *et al.*, 2016; Sood *et al.*, 2018; Melaku *et al.*, 2020; Ranga *et al.*, 2021).

Genetic advance (GA) showed wide variation among the traits, ranging from 0.69 for fruit girth to 92.02 for fruit yield per plant, while GA as per cent of mean varied from 3.32% for days to first harvest to 95.59% for number

of branches. Higher GA as per cent of mean (>20%) was observed for number of branches (95.59%), east-west spread (70.74%), north-south spread (68.06%), fruit yield per plant (52.29%), first node at which fruit appears (51.27%), number of fruits per plant (41.56%), average fruit weight (41.19%), plant height (37.06%), number of

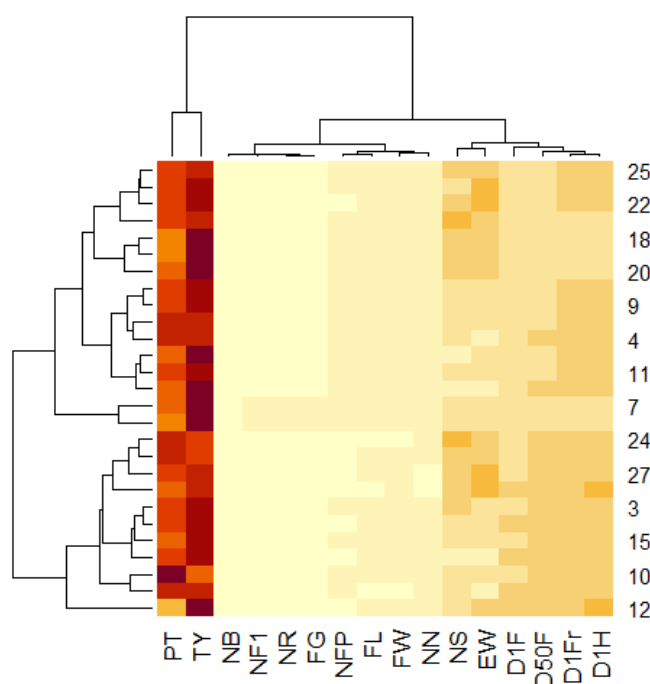


Fig. 2 : Co-relation clustered Heatmap for 16 characters among 27 genotypes of okra.

nodes (26.81%) and fruit length (21.92%), indicating the predominance of additive gene action and greater effectiveness of direct selection for these traits (Table 5) (Khajuria *et al.*, 2016; Ranga *et al.*, 2021; Sravanthi *et al.*, 2021).

Correlation coefficient

Correlation analysis revealed that genotypic correlation coefficients were generally higher than phenotypic correlation coefficients, indicating strong inherent genetic association among the characters, though environmental factors reduced their phenotypic expression and having high significance as observed under the correlation heatmap (Fig. 2).

Correlation analysis revealed that genotypic correlation coefficients were generally higher than phenotypic correlation coefficients for all the characters studied, indicating strong inherent genetic association among the traits with comparatively lesser environmental influence. Fruit yield per plant exhibited significant positive correlation with plant height (0.312 and 0.320), number of nodes (0.483 and 0.522), fruit length (0.495 and 0.502), number of fruits per plant (0.648 and 0.641) and average fruit weight (0.553 and 0.559) at phenotypic and genotypic levels, respectively. In contrast, days to first flowering (-0.699 and -0.898), days to 50% flowering (-0.609 and -0.887) and days to first harvest (-0.614 and -0.933) showed significant negative association with yield, suggesting the importance of earliness for yield improvement (Tables 6 and 7) (Umrao *et al.*, 2015;

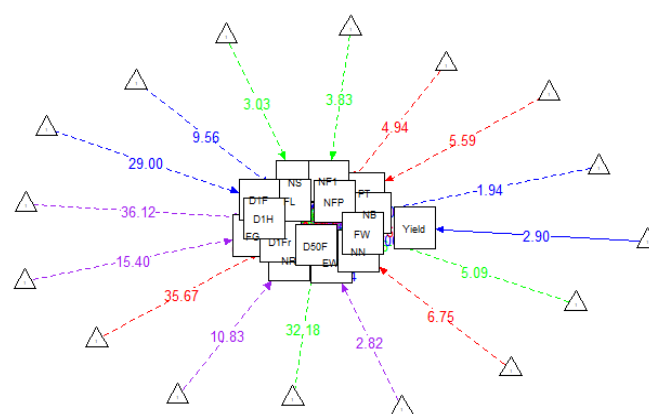


Fig. 3 : Path coefficient diagram depicting direct and indirect effects of different traits on yield.

Pachiyappan and Saravannan, 2016; Chandramouli *et al.*, 2019; Sujata *et al.*, 2019; Alam *et al.*, 2020; Bagadia *et al.*, 2022; Abdallah *et al.*, 2025).

Plant height showed significant positive association with number of nodes (0.489 and 0.552), fruit length (0.452 and 0.457), number of fruits per plant (0.433 and 0.452) and fruit yield per plant, indicating that taller plants with higher node number contributed towards increased fruit production. Fruit length also maintained positive correlation with average fruit weight (0.325 and 0.326), number of fruits per plant (0.282 and 0.287) and yield per plant, whereas negative association was observed with days to flowering and harvesting traits (Tables 6 and 7) (Ranga *et al.*, 2021).

Number of fruits per plant and average fruit weight emerged as the most important yield contributing characters due to their strong positive association with fruit yield per plant. The promising genotypes 2019/OKYVRES-8, 2019/OKYVRES-6 and BO-2-5-6 exhibited superior performance for these traits along with higher fruit yield, indicating their potential utility in future breeding programmes (Umrao *et al.*, 2015; Pachiyappan and Saravannan, 2016; Chandramouli *et al.*, 2019; Sujata *et al.*, 2019; Alam *et al.*, 2020; Bagadia *et al.*, 2022; Abdallah *et al.*, 2025).

Path analysis

Correlation alone does not provide complete information regarding direct and indirect contribution of component traits towards yield. Therefore, path coefficient analysis was carried out to partition the correlation coefficients into direct and indirect effects (Table 8) well supported with the Path analysis diagram depicting causal relationships among yield-contributing characters (Fig. 3).

Path coefficient analysis revealed that number of fruits per plant (0.744) exerted the highest positive direct

Table 6 : Correlation coefficient among 16 characters in 27 genotypes of okra at genotypic level.

	PH	NS	EW	NB	NN	NF1	FG	FL	NFP	FW	NR	D1F	D1Fr	D50F	D1H	TY
PH	1.000															
NS	0.203	1.000														
EW	0.038	0.821**	1.000													
NB	0.101	-0.047	-0.287**	1.000												
NN	0.552**	-0.122	-0.310**	0.557**	1.000											
NF1	0.447**	-0.330**	-0.514**	0.664**	0.568**	1.000										
FG	0.116	0.041	0.034	-0.244*	-0.185	-0.055	1.000									
FL	0.457**	0.037	0.012	0.161	0.398**	0.247*	-0.093	1.000								
NFP	0.452**	0.128	-0.102	0.239*	0.643**	0.132	-0.309**	0.287**	1.000							
FW	-0.128	0.073	0.190	-0.110	-0.087	-0.015	0.102	0.326**	-0.263*	1.000						
NR	-0.711**	-0.096	-0.035	0.255*	-0.182	-0.224*	0.135	-0.359**	-0.207 ^{NS}	0.061	1.000					
D1F	-0.203	-0.040	0.050	-0.317***	-0.504**	-0.213	0.241*	-0.404**	-0.639**	-0.440**	-0.059	1.000				
D1Fr	-0.203	-0.027	0.064	-0.363**	-0.566**	-0.219*	0.266*	-0.394**	-0.671**	-0.393**	-0.071	0.219*	1.000			
D50F	-0.222*	-0.138	-0.177	-0.160	-0.427**	-0.127	0.264*	-0.462**	-0.629**	-0.443**	0.060	0.326**	0.074	1.000		
D1H	-0.166	0.021	0.195	-0.440**	-0.611**	-0.334**	0.189	-0.450**	-0.692**	-0.419**	-0.129	0.210*	0.216*	0.065	1.000	
TY	0.320**	0.195	0.072	0.140	0.522**	0.135	-0.178	0.502**	0.641**	0.559**	-0.123	-0.898**	-0.897**	-0.887**	-0.933**	1.000

PH=Plant height, NS= North-South Spread, EW= East-West Plant, NB= Number of branches, NN= Number of Nodes, NF1= First node at which fruit appears, FG= Fruit girth, FL= Fruit length, NFP= Number of fruits per plant, FW= Fruit weight, NR= Number of ridges, D1F= Days to first flowering, D1Fr= Days to first fruiting, D50F= Days to 50% flowering, D1H= Days to first harvest, TY= Total yield per plant (*Significant @5% level and **significant @1% level).

Table 7 : Correlation coefficient among 16 characters in 27 genotypes of okra at phenotypic level.

	PH	NS	EW	NB	NN	NF1	FG	FL	NFP	FW	NR	D1F	D1Fr	D50F	D1H	TY
PH	1.000															
NS	0.202	1.000														
EW	0.032	0.771**	1.000													
NB	0.094	-0.039	-0.242*	1.000												
NN	0.489**	-0.102	-0.246*	0.517**	1.000											
NF1	0.432**	-0.307**	-0.462**	0.582**	0.489**	1.000										
FG	0.118	0.042	0.038	-0.218	-0.161	-0.045	1.000									
FL	0.452**	0.035	0.012	0.145	0.356**	0.235*	-0.092	1.000								
NFP	0.433**	0.121	-0.093	0.219*	0.584**	0.117	-0.298**	0.282*	1.000							
FW	-0.127	0.073	0.184	-0.102	-0.077	-0.015	0.100	0.325**	-0.257*	1.000						
NR	-0.671**	-0.087	-0.024	0.221*	-0.182	-0.208	0.127	-0.340**	-0.207	0.060	1.000					

Table 7 continued...

Table 7 continued...

D1F	-0.160	-0.021	-0.023	-0.276*	-0.377**	-0.192	0.181	-0.310**	-0.493**	-0.342**	-0.033	1.000				
D1Fr	-0.170	-0.020	0.062	-0.291**	-0.427**	-0.228*	0.224*	-0.324**	-0.545**	-0.327**	-0.025	1.000				
D50F	-0.174	-0.086	-0.086	-0.094	-0.266*	-0.096	0.185	-0.322**	-0.429**	-0.303**	0.036	1.000				
D1H	-0.150	0.035	0.122	-0.240*	-0.388**	-0.237*	0.126	-0.305**	-0.438**	-0.286**	-0.063	1.000				
TY	0.312**	0.186	0.073	0.137	0.483**	0.126	-0.169	0.495**	0.648**	0.553**	-0.126	-0.699**	-0.614**	1.000		

PH=Plant height, NS= North-South Spread, EW= East-West Plant, NB= Number of branches, NN= Number of Nodes, NF1= First node at which fruit appears, FG= Fruit girth, FL= Fruit length, NFP= Number of fruits per plant, FW=Fruit weight, NR= Number of ridges, D1F= Days to first flowering, D1Fr= Days to first fruiting, D50F= Days to 50% flowering, D1H= Days to first harvest, TY= Total yield per plant (*Significant @5% level and **significant @1% level).

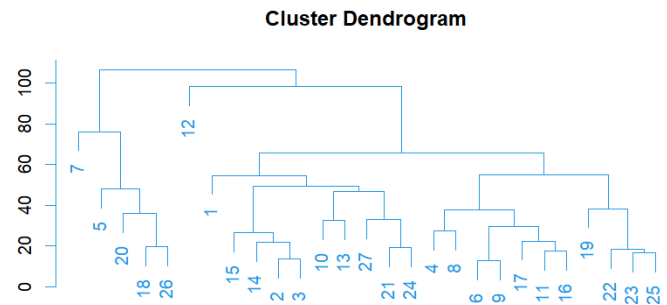


Fig. 4: Hierarchical cluster dendrogram showing genetic divergence among 27 okra genotypes based on quantitative traits.

effect on fruit yield per plant followed by average fruit weight (0.742), indicating their major contribution towards yield improvement in okra. Moderate positive direct effects were also observed for plant height (0.077), number of nodes (0.071), north-south spread (0.064) and number of ridges (0.064), whereas days to first flowering (-0.077), number of branches (-0.043), fruit girth (-0.030) and days to first fruiting (-0.023) exhibited negative direct effects on yield (Ranga *et al.*, 2021; Bagadia *et al.*, 2022; Dwivedi and Sharma, 2017; Rynjah *et al.*, 2020; Pundir *et al.*, 2022).

The positive direct effect of number of fruits per plant was mainly contributed through favourable indirect effects via plant height (0.033), number of nodes (0.041) and days to first fruiting (0.013), whereas average fruit weight exhibited positive indirect contribution through north-south spread (0.005), number of branches (0.004) and number of ridges (0.004). The high yielding genotypes 2019/OKYVRES-8, 2019/OKYVRES-6 and BO-2-5-6 possessed higher number of fruits per plant and average fruit weight, confirming the importance of these traits as reliable selection indices for yield improvement (Ranga *et al.*, 2021; Alam *et al.*, 2020; Abdallah *et al.*, 2025).

The present findings clearly indicated that direct selection based on number of fruits per plant, average fruit weight, plant height and number of nodes would be highly effective for enhancing fruit yield in okra breeding programmes due to their positive correlation and substantial direct contribution towards yield.

Multivariate analysis

The data presented in Table 9. represents the cluster formation derived using Tocher's method. The 27 genotypes of okra used in the study were grouped on basis of genetic closeness or divergence in D^2 into seven clusters (Fig. 4). Cluster I was found to be largest with 6 genotypes. It included the genotypes like 2019/OKYVRES-1, 2019/OKYVRES-2, 2019/OKYVRES-3, 2019/OKYVRES- 6, BO-2-1-1 and BO-2-9 indicating lack of significant genetic differences among them i.e.,

Table 8 : Direct and indirect effects of component traits on yield in 27 genotypes of okra at phenotypic level for 16 characters.

	PH	NS	EW	NB	NN	NF1	FG	FL	NFP	FW	NR	D1F	D1Fr	D50F	D1H
PH	0.077	0.013	-0.001	-0.004	0.035	0.009	-0.003	-0.006	0.322	-0.095	-0.043	0.004	0.004	-0.001	0.002
NS	0.016	0.064	-0.018	0.002	-0.007	-0.006	-0.001	0.000	0.090	0.054	-0.006	0.001	0.000	-0.001	0.000
EW	0.002	0.049	-0.024	0.010	-0.017	-0.009	-0.001	0.000	-0.069	0.136	-0.002	0.001	-0.001	0.000	-0.001
NB	0.007	-0.003	0.006	-0.043	0.037	0.012	0.006	-0.002	0.163	-0.076	0.014	0.007	0.007	-0.001	0.002
NN	0.038	-0.007	0.006	-0.022	0.071	0.010	0.005	-0.005	0.434	-0.057	-0.012	0.009	0.010	-0.002	0.004
NF1	0.033	-0.020	0.011	-0.025	0.035	0.020	0.001	-0.003	0.087	-0.011	-0.013	0.004	0.005	-0.001	0.002
FG	0.009	0.003	-0.001	0.009	-0.011	-0.001	-0.030	0.001	-0.221	0.074	0.008	-0.004	-0.005	0.001	-0.001
FL	0.035	0.002	0.000	-0.006	0.025	0.005	0.003	-0.013	0.209	0.241	-0.022	0.007	0.007	-0.002	0.003
NFP	0.033	0.008	0.002	-0.009	0.041	0.002	0.009	-0.004	0.744	-0.191	-0.013	0.011	0.013	-0.003	0.005
FW	-0.010	0.005	-0.004	0.004	-0.005	0.000	-0.003	-0.004	-0.191	0.742	0.004	0.008	0.007	-0.002	0.003
NR	-0.052	-0.006	0.001	-0.009	-0.013	-0.004	-0.004	0.004	-0.154	0.044	0.064	0.001	0.001	0.000	0.001
D1F	-0.012	-0.001	0.001	0.012	-0.026	-0.003	-0.005	0.004	-0.336	-0.232	-0.002	-0.077	-0.019	0.004	-0.006
D1Fr	-0.013	-0.001	-0.002	0.013	-0.031	-0.004	-0.007	0.004	-0.408	-0.242	-0.002	-0.020	-0.023	0.004	-0.007
D50F	-0.014	-0.005	0.002	0.004	-0.020	-0.010	-0.009	0.004	-0.325	-0.205	0.002	-0.016	-0.015	0.006	-0.008
D1H	-0.011	0.002	-0.003	0.010	-0.026	-0.005	-0.004	0.004	-0.314	-0.204	-0.004	-0.015	-0.038	0.004	-0.011

PH=Plant height, NS= North-South Spread, EW= East-West Plant, NB= Number of branches, NN= Number of Nodes, NF1= First node at which fruit appears, FG= Fruit girth, FL= Fruit length, NFP= Number of fruits per plant, FW=Fruit weight, NR= Number of ridges, D1F= Days to first flowering, D1Fr= Days to first fruiting, D50F= Days to 50% flowering, D1H= Days to first harvest, TY= Total yield per plant. *Significant @5% level and **significant @1% level.

Table 9 : Composition of D² based on clusters.

Cluster No.	Number of genotypes (s)	Name of the genotypes
1	6	2019/OKYVRES-1, 2019/OKYVRES-2, 2019/OKYVRES-3, 2019/OKYVRES-5, BO-2-1-1, BO-2-9
2	5	2019/OKYVRES-7, 2019/OKYVRES-8, 2019/OKYVRES-9, BO-2-6, BO-2-7
3	4	2019/OKYVRES-10, 2019/OKYVRES-11, 2019/OKYVRES-12, BO-2 Utkal Gaurav
4	2	BO-2-8, BO-2-4-6
5	2	BO-2-10, BO-2-4
6	4	BO-1, BO-2 Utkal Gaurav, BO-2-1, BO-2-2
7	4	BO-2-3, BO-2-5, BO-2-5-6, BO-2-3-5

geographically they may be from different sources but genotypically they are similar. Similarly, cluster II consists of 5 genotypes which includes 2019/OKYVRES-7, 2019/OKYVRES-8, 2019/OKYVRES-9, BO-2-6 and BO-2-7. Cluster III includes 4 genotypes that are 2019/OKYVRES-10, 2019/OKYVRES-11, 2019/OKYVRES-12 and BO-1. Cluster IV has the following 2 genotypes that are BO-2-8 and BO-2-4-6. Cluster V has also 2 genotypes which includes BO-2-10 and BO-2-4. Cluster VI includes 4 genotypes that consists of BO-1, BO-2 Utkal Gaurav, BO-2-1 and BO-2-2. Similarly, cluster VII has 4 genotypes that includes BO-2-3, BO-2-5, BO-2-5-6 and BO-2-3-5.

Results on intra cluster distances showed minimum intra-cluster D² value of 6.400 (cluster IV), whereas, maximum intra-cluster D² value of 17.085 (cluster VII) indicated that genotypes included in this cluster are very

diverse and to both natural and artificial selection forces among the genotypes.

Similarly, results on inter cluster distances ranged from 12.907 (between cluster IV and V) to 24.747 (between cluster V and VI). Minimum inter-cluster D² value indicated close relationship among the genotypes included in these clusters. Highest intercluster distance was present between cluster IV and V. Therefore, crossing the parents of these two divergent groups can result in promising hybrid derivatives, possibly as a result of the complimentary interaction of divergent gene parents (Sraavanthi *et al.*, 2022; Farooqkhan *et al.*, 2023; Alam *et al.*, 2024).

There was a wide range in the size of the cluster means for all of the traits when looking at the 27 genotypes in Table 11. Cluster II genotypes outperformed in terms of average fruit weight (17.823) and number of nodes

Table 10 : Average intra cluster (diagonal) and inter cluster distance (D^2 value) of 27 genotypes of okra.

Cluster distances							
	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	12.045	16.176	14.627	16.869	19.996	14.121	19.710
Cluster II		15.147	17.901	16.571	14.932	21.135	17.182
Cluster III			10.797	17.415	19.800	16.232	22.020
Cluster IV				6.400	12.907	20.685	13.342
Cluster V					7.079	24.747	14.180
Cluster VI						14.671	24.584
Cluster VII							17.085

Table 11 : Cluster mean of 27 genotypes of okra for 16 characters.

S. no.	Particulars	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
1.	Plant height	126.869	154.177	157.027	148.613	142.445	108.473	142.390
2.	North-south spread	32.389	43.800	34.612	61.943	61.388	29.972	59.083
3.	East-west spread	34.704	47.556	32.278	60.833	56.612	29.003	59.251
4.	Nos. of branches	1.611	2.023	3.723	2.443	3.500	2.223	1.778
5.	Nos. of nodes	15.685	19.689	19.473	17.500	17.667	16.833	15.364
6.	1st node at which fruit appears	4.389	4.355	5.501	4.167	4.057	3.667	3.917
7.	Fruit girth	4.960	5.265	5.136	5.060	4.607	5.211	5.357
8.	Fruit length	13.083	14.573	15.036	13.027	13.938	11.825	13.903
9.	No. of fruits/plant	10.629	12.756	13.639	11.610	14.610	11.944	10.833
10.	Fruit weight	15.771	17.823	12.355	12.510	16.145	13.301	16.846
11.	No. of ridges	5.000	5.000	5.000	5.000	5.000	5.611	5.000
12.	Days to 1 st flowering	38.833	37.933	38.333	39.833	36.833	39.583	39.083
13.	Days to 1 st fruiting	47.833	46.933	47.333	48.833	45.833	48.583	48.333
14.	Days to 50% flowering	44.889	44.000	44.167	46.000	42.500	45.500	44.417
15.	Days to 1 st harvest	50.000	49.333	49.333	51.667	48.667	50.917	50.583
16.	Yield/plant(g)	160.619	220.833	165.331	143.337	229.995	147.117	171.654

Table 12 : Relative contribution of each character towards total genetic divergence in 27 genotypes of okra.

Character	No. of first rank	% contribution
Plant height	7	1.99
North -south spread	10	2.84
East -west spread	5	1.42
No. of branches	34	9.68
No. of nodes	5	1.42
1st node at which fruit appears	34	9.68
Fruit girth	12	3.41
Fruit length	3	0.85
No. of fruits/plant	6	1.70
Fruit weight	26	7.40
No. of ridges	15	4.27
Days to 1 st flowering	5	1.42
Days to 1 st fruiting	9	2.56
Days to 50% flowering	7	1.99
Days to 1 st harvest	7	1.99
Yield/plant(g)	166	47.29
Total	351	100

(19.689). Traits such as plant height (157.027), number of branches (3.723), and fruit length (15.036) were determined to be better in genotypes from Cluster III. North-south spread (61.943) and east-west spread (60.833) was maximum in Genotypes in Cluster IV. Genotypes in Cluster V was found to be superior for number of fruits plant⁻¹ (14.610), days to 1st flowering (36.833), days to 1st fruiting (45.833), days to 50% flowering (42.500), days to 1st harvest (48.667) and yield plant⁻¹ (229.995). Cluster mean of cluster VI was found to be highest for 1st node at which fruit appears (3.667) and number of ridges (5.611). In the same way cluster mean of cluster VII was highest for fruit girth (5.357) (Sravanthi *et al.*, 2022; Farooqkhan *et al.*, 2023; Alam *et al.*, 2024). They reported that the clustering pattern could be utilized in choosing parents for cross combinations likely to generate the highest possible variability for various economic characters.

Results on percentage contribution of 16 yield attributing traits towards divergence indicated maximum

contribution by yield plant⁻¹ (47.29%) followed by number of branches (9.6866%). The traits contributing more (>5.00%) towards divergence viz., 1st node at which fruit appears (9.6866%) and average fruit weight (7.4074%). So, selection of parents differing in these quantitative traits proved useful for heterosis breeding programme in okra. (Sravanthi *et al.*, 2022; Joshi *et al.*, 2026). Table 12 shows that the genotypes of highly divergent clusters may be used in heterosis breeding programs to create F₁ hybrids with better yield and quality traits, as well as in breeding programs to create high yielding varieties with desired attributes.

Conclusion

The present investigation revealed substantial genetic variability among the evaluated okra genotypes for yield and its associated traits. High genotypic and phenotypic coefficients of variation, coupled with high heritability and genetic advance as percent of mean, were observed for plant height, number of branches per plant, number of nodes per plant, number of fruits per plant, average fruit weight and fruit yield per plant. These findings indicate the predominance of additive gene action and comparatively lower environmental influence on the expression of these traits, suggesting that simple and effective selection strategies can be employed for their improvement.

The most important factors influencing fruit output were determined using path coefficient and correlation studies to be plant height, average fruit weight, number of nodes per plant, and number of fruits per plant. Thus, these characteristics may be used as solid selection criteria to create okra genotypes with increased yields.

Mahalanobis D² analysis revealed considerable genetic divergence among the genotypes, with the maximum inter-cluster distances observed between clusters III and VII and between clusters VI and VII. Hybridization among genotypes belonging to these divergent clusters may generate desirable recombinants and transgressive segregants for future breeding programmes.

Among the genotypes evaluated, 2019/OKYVRES-8 and 2019/OKYVRES-6 exhibited superior fruit yield per plant and showed considerable promise for commercial cultivation and utilization in breeding programmes. However, their performance should be further validated through multilocation trials and larger plot evaluations across different agro-climatic regions of Odisha before large-scale recommendation.

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