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Multivariate analysis of genetic divergence reveals an apparent separation between fruit quality and yellow vein mosaic virus response in okra (*Abelmoschus esculentus* (L.) Moench) genotypes

Aurobinda Behera[1*], Anita Mohanty[2], Pradyumna Tripathy[1], Dibya Sundar Kar[3], Subrata Sarkar[2], Akash Kumar Parida[1], Sonali Priyadarshini[1], Kirtika Mishra[1*] & Aurolipsa Panda[1]

[1]Department of Vegetable Science, College of Agriculture, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha 751 003, India

[2]All India Coordinated Research Project on Vegetable Crops, Odisha University of Agriculture and Technology, Bhubaneswar, Odisha 751 003, India

[3]Krishi Vigyan Kendra, Dhenkanal 759 013, Odisha, India

***Correspondence:** kirtikamishra.rs24@ouat.ac.in, aurobindabehera.rs24@ouat.ac.in

Abstract

Okra (*Abelmoschus esculentus* (L.) Moench) breeding is held back by yellow vein mosaic virus (YVMV) and little is known about how genetic divergence, fruit quality and virus reaction are linked. Fifty-two genotypes were grown in a randomised block design (RBD) with 3 replications at Bhubaneswar, India, during kharif 2023–24. Divergence was analysed from 18 quantitative traits by Mahalanobis D^2 with Tocher clustering, principal component analysis (PCA) and Ward clustering; fruit quality (total soluble solids [TSS], protein and total phenolic content) was summarised in a quality ideotype-distance index (QIDI); and YVMV incidence was scored visually once, at 75 days after sowing (DAS). The genotypes formed nine D^2 clusters; the widest inter-cluster distance (1107.26) separated clusters VII and IX and phenolic content (28.28 %), internodal length (20.81 %) and yield per plant (14.25 %) contributed most to divergence. Seven principal components explained 70.69 % of the variance. The YVMV incidence ranged from 26.05 % to 91.55 %. Five genotypes (BO-19-17, BO-2-4, BO-19-6, BO-2-14 and BO-19-15) had the lowest incidence (26–30 %; moderately resistant class) and incidence was negatively correlated with yield per plant (r = −0.83) but not with TSS, protein or phenolic content. None of these five ranked among the ten best by QIDI, which was led by BO-19-10 (moderately susceptible; 59.78 %). Fruit quality and YVMV reaction therefore appeared unrelated in this panel. BO-19-10 is a promising source of fruit quality, while BO-2-4 and BO-2-14 combine lower incidence with high yield; these genotypes are worth testing as parents in crosses and multi-location trials.

Keywords: cluster analysis; fruit quality; genetic divergence; okra; yellow vein mosaic virus; yield

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Introduction

Okra (*Abelmoschus esculentus* (L.) Moench), a member of the family Malvaceae, is one of the most widely grown warm-season vegetables of the tropics and subtropics (1). Its tender, mucilaginous fruits are a source of dietary fibre, vitamins A, B, C and K and minerals such as iron, calcium and potassium (2, 3). India is the world's leading okra producer and Odisha contributes approximately 662 thousand tonnes annually (4). Productivity in Odisha (approximately 10.1 t ha^{-1}) is still below the national average of approximately 12.3 t ha^{-1} (calculated from 6416 thousand tonnes on 523 thousand ha) (4). A lack of systematic multi-trait selection and a limited genetic base are commonly cited as the causes of this disparity (5).

Genetic divergence helps breeders choose parents for hybridisation, but distance alone does not guarantee good progeny, because combining ability and gene action also determine heterosis and transgressive segregation (6). Okra genotype divergence from morphological and agronomic variables is commonly measured using Mahalanobis' D^2 statistic and Tocher's clustering approach (7–9). Principal component and hierarchical cluster analyses are frequently used alongside it (10, 11). Besides yield, the market and nutritional value of okra fruit increasingly depends on biochemical quality, such as total soluble solids (TSS), protein and total phenolic content (12, 13). In South Asia, okra production is severely limited by yellow vein mosaic virus (YVMV), a begomovirus spread by the whitefly *Bemisia tabaci* (14, 15). In this study, resistance

means lower disease incidence under natural infection (field reaction) and does not imply immunity, whereas tolerance can only be assessed by comparing infected and uninfected plants.

Field screening of diverse genotypes is usually the first step in finding lower-incidence sources and studying the inheritance of resistance (16, 17). Complete resistance is rare among cultivated okra genotypes (14). The same 52-genotype panel, grown at the same site in the same season, has previously been characterised for genetic variability, heritability, correlations and path coefficients of vegetative, flowering and yield traits (18). That study did not address genetic divergence, fruit biochemical quality or YVMV reaction, nor how these relate to one another. We therefore asked whether genetically distant groups in this panel differ in fruit quality, yield and YVMV incidence and whether fruit quality and YVMV incidence are related. Using D^2/Tocher clustering, principal component analysis (PCA) and Ward clustering, the present study aimed to (i) quantify multivariate divergence among the 52 genotypes; (ii) characterise fruit quality (TSS, protein and total phenolic content) and summarise it as an ideotype-distance index; (iii) record YVMV incidence under natural infection; and (iv) examine the association of divergence groups, quality, yield and YVMV incidence and to identify genotypes worth evaluating as parents. The fruit quality and YVMV data and the divergence analyses are new to this study; means of the 15 agronomic traits shared with the earlier study (18) are given only in Supplementary Table 1 and 2, so that the multivariate analyses can be checked.

Materials and Methods

Site, soil and cropping history

The experiment took place in the eastern coastal plain agro-climatic zone, about 60 km from the Bay of Bengal, at the research farm of the All India Coordinated Research Project (AICRP) on Vegetable Crops, Odisha University of Agriculture and Technology (OUAT), Bhubaneswar, during kharif 2023–24. The exact coordinates of the location are 20°15′ N, 85°52′ E, with 25.5 m above mean sea level. Average yearly rainfall is about 1552 mm, with about 85 % falling between July and September, while relative humidity levels vary between 49–90 %. The locality experiences moderate winters and a warm, subhumid environment. The study used the following methods to analyse a composite soil sample (0–15 cm depth) that was collected before sowing: standard extraction followed by colorimetric and flame-photometric determination for available phosphorus (P) and potassium (K) (19); wet oxidation for organic carbon (20); the alkaline permanganate method for available nitrogen (N) (21); and standard procedures for pH and electrical conductivity in soil-water suspension (19). The sandy loam soil had a pH of 5.8, an electrical conductivity of 0.188 dS m^{-1}, 0.37 % organic carbon and 100 kg ha^{-1} of available N, 35.7 kg ha^{-1} of P and 413.9 kg ha^{-1} of K, respectively. For the preceding two years, the field had carried okra–cabbage/chilli (kharif–rabi) rotations, with amaranthus or ridge gourd in summer.

Plant material and experimental design

Fifty-two genetically pure okra genotypes, sourced mainly from AICRP (Vegetable Crops), OUAT, along with released checks (Pusa Sawani, Utkal Gaurav, Arka Anamika and Parbhani Kranti) obtained from Indian Agricultural Research Institute (IARI), New Delhi, the ICAR–Indian Institute of Horticultural Research (IIHR), Bangalore and College of Agriculture (COA), Parbhani, were evaluated in a randomised block design (RBD) with 3 replications (52 genotypes × 3 replications = 156 plots). Each plot measured 3 × 2.8 m, with 60 cm between rows and 45 cm between plants, five rows per plot and six plants per row (30 plants $plot^{-1}$). The crop was raised with recommended agronomic practices, including farmyard manure at 25 t ha^{-1}, a fertiliser dose of 80 : 50 : 60 kg N : P : K ha^{-1} and standard irrigation, manual weeding and plant protection measures (18).

Traits recorded

The same procedures as in the previous trial were followed to record vegetative, flowering and yield traits on three randomly selected competitive plants per genotype per replication; their genotype means are given in Supplementary Table 1 and 2 (18). Five randomly chosen tender fruits were measured for length, girth and average weight; total yield per plant was the weight of fresh marketable fruits collected throughout the harvest season; and number of fruits per plant was the mean number of fruits per plant counted at picking. These traits were recorded independently. In addition, the study recorded fruit quality traits, namely total soluble solids (TSS; °Brix, hand refractometer), protein content (g 100 g^{-1} dry weight; micro-Kjeldahl method) and total phenolic content (g 100 g^{-1} dry weight; Folin–Ciocalteu assay following Singleton and Rossi (22), with gallic acid as the standard), together with qualitative descriptors (stem, leaf, flower and fruit colour, fruit shape, number of ridges, fruit pubescence and seed colour) and YVMV incidence. Phenolic content is reported as total phenolics. Qualitative descriptors were scored visually and fruit colour was also checked against a colour chart. They were not utilised in the D^2, principal component or cluster analyses, which were based on 18 quantitative traits; they are presented only to characterise the genotypes.

Screening for yellow vein mosaic virus

Natural YVMV infection (vector: the whitefly *Bemisia tabaci*) was assessed visually once, at 75 days after sowing (DAS). Plants showing vein clearing or yellowing and leaf mosaic were scored as infected. Unlike the morphological and yield traits, YVMV was scored on all 30 plants in each plot and incidence in each plot was calculated as in Eq. 1, where I is incidence (%), n_{inf} the number of infected plants and n the number of plants observed (n = 30). The mean of the three replications was used for each genotype; for

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analysis of variance, incidence values were angular (arcsine) transformed and back-transformed means are given.

$$I = (n_{inf} / n) \times 100$$

(Eq. 1)

The incidence bands in Table 1, which adapt the 0–5 scale (23), were used to assign genotypes to reaction classes. The original scale grades the severity of symptoms on individual plants; here, the same percentage bands were applied to genotype-mean incidence, so the classes describe the relative field reaction of genotypes in this trial. Because no genotype fell in the resistant classes, only four of the six classes occurred (moderately resistant, moderately susceptible, susceptible and highly susceptible); the last two are combined in the box plot.

Statistical analysis

The plot means were subjected to analysis of variance (ANOVA) for a RBD. Treatment mean squares were compared with error mean squares at p = 0.05 and p = 0.01. Critical differences (CD) at p = 0.05 are reported for each trait. Genetic divergence among the 52 genotypes was estimated with Mahalanobis' D^2 statistic (24) from 18 quantitative traits: three quality traits (Table 2) and 15 agronomic traits (Supplementary Table 1 and 2). To calculate D^2, the study used the genotype means in conjunction with the pooled error variance-covariance matrix, which takes scale and trait correlations into account (25) and used Tocher's approach to group genotypes (6, 25). The OPSTAT and R (RStudio) statistical packages were used to conduct the analysis of variance and the D^2/Tocher analysis. Each trait's contribution to divergence was represented as the percentage of the 1326 genotype pairs (52 × 51/2) in which it contributed most to D^2 (6). The average intra- and inter-cluster D^2 values and cluster means were then calculated. These percentages do not reflect the agronomic significance of the traits, but rather their contribution to the multivariate distance.

To cross-check the D^2-based grouping, the genotype means of the same 18 traits were standardised (mean 0, variance 1) and subjected to PCA on the correlation matrix (26); components with eigenvalues ≥ 1 were retained (Kaiser criterion) and a PC1–PC2 biplot was drawn to visualise the main trait gradients. For agglomerative hierarchical clustering, Ward's minimum-variance approach on Euclidean distances was applied using the same standardised matrix (27). Rather than using a statistical stopping criterion, the dendrogram was divided into nine groups to facilitate direct comparison with the nine Tocher clusters. Neither the D^2 nor the PCA nor the Ward analyses included the YVMV incidence nor the quality index (shown below) among their 18 variables.

The quality ideotype-distance index (QIDI) was developed by combining three fruit quality traits: total phenolic content, total soluble solids (TSS) and protein. It is a simplified form of the ideotype-distance concept of the multi-trait genotype–ideotype distance index (28). Higher values are desirable for all three traits. Each trait was rescaled across the 52 genotypes as in Eq. 2, where X_{ij} is the value of trait j in genotype i and R_{ij} the rescaled value, so that the lowest observed value of each trait is mapped to 10 and the highest to 100.

$$R_{ij} = 10 + 90 \times (X_{ij} - X_{j,min}) / (X_{j,max} - X_{j,min})$$

(Eq. 2)

The ideotype was defined as the best (highest) observed value of every trait, that is, R = 100 for all three traits and QIDI was computed as the Euclidean distance from the ideotype (Eq. 3), so that lower values indicate closer similarity to the ideotype.

$$QIDI_i = \sqrt{[\ \Sigma_{j=1}^{3} (100 - R_{ij})^2]}$$

(Eq. 3)

Because all traits share the same rescaled range, the choice of lower bound (10, 0 or any other value) only multiplies all QIDI values by a constant and does not change the ranking; unlike the original index, no factor analysis is involved. The three traits were given equal weight. To assess the impact of this choice, QIDI was recalculated with the weight of each trait in turn halved or doubled and with z-score standardisation instead of rescaling. QIDI describes quality only; its association with yield and YVMV incidence was examined separately by Pearson correlation of genotype means (n = 52). A descriptive cut-off is presented for the ten genotypes with the lowest QIDI, which accounts for around 20 % of the panel. The box-and-whisker plots (Fig. 1 and 2) summarised the distributions of the quality attributes and YVMV incidence by reaction class. The PCA, Ward clustering, QIDI and correlations were run in Python 3.12.3 with NumPy 2.4.4, pandas 3.0.2, SciPy 1.17.1 (scipy.cluster.hierarchy.linkage with method = 'ward'; scipy.stats.pearsonr) and scikit-learn 1.8.0 (PCA, StandardScaler); figures were drawn with Matplotlib 3.10.8.

Results and Discussion

Variation among genotypes

Genotypes differed significantly (p < 0.01) for TSS (F = 21.62), protein (F = 8.18) and total phenolic content (F = 61.06) in the analysis of variance reported for this trial (18). Coefficients of variation for the quality traits were low (5.00–5.56 %; Table 2). Broad-sense heritability estimated for the same trial was high for TSS (87.30 %), protein (70.55 %), total phenolic content (95.24 %) and total yield per plant (91.13 %) (18), so most of the phenotypic variation among these genotypes was genetic in origin.

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Table 1. Reaction classes used to describe genotype-mean yellow vein mosaic virus (YVMV) incidence (%), adapted from the 0–5 rating scale and the number of genotypes in each class

Severity grade	Reaction class	YVMV incidence band (%)	No. of genotypes
0	Highly resistant (HR)	0 (no infected plants)	0
1	Resistant (R)	> 0–25	0
2	Moderately resistant (MR)	> 25–50	5
3	Moderately susceptible (MS)	> 50–75	39
4	Susceptible (S)	> 75–90	7
5	Highly susceptible (HS)	> 90–100	1

The bands were applied to genotype means of the percentage of infected plants per plot (30 plants per plot; three replications). The original scale grades the proportion of leaves with symptoms on individual plants. Classes are descriptive of relative field reaction in this trial.

Table 2. Mean performance of 52 okra genotypes for fruit quality traits and quality ideotype-distance index (QIDI)

Sl. No.	Genotype	TSS (°Brix)	Protein (g 100 g^{-1} DW)	Total phenolic content (g 100 g^{-1} DW)	QIDI	QIDI rank
1	BO-18-40	6.83	8.46	0.96	89.18	23
2	BO-18-57	8.80	7.90	1.05	67.36	6
3	BO-18-37	5.80	6.83	0.82	127.60	52
4	BO-18-38	9.70	7.90	0.95	66.29	5
5	BO-18-7	6.10	7.20	0.86	117.38	50
6	BO-18-47	7.90	7.20	0.84	96.69	30
7	BO-18-8	7.53	7.23	0.55	116.56	47
8	BO-18-5	8.30	8.83	0.74	79.61	16
9	BO-18-9	7.50	8.10	0.74	95.19	27
10	BO-18-6	7.10	8.43	0.62	104.42	36
11	BO-19-7	6.56	8.20	0.75	105.57	39
12	BO-19-1	6.50	7.50	1.20	97.99	32
13	BO-19-3	7.63	7.66	0.51	113.41	44
14	BO-19-4	6.20	7.46	0.86	112.94	43
15	BO-19-5	6.30	6.96	0.81	119.77	51
16	BO-19-2	9.56	8.16	0.84	70.06	9
17	BO-19-6	6.30	8.44	0.70	109.92	42
18	BO-19-22	8.16	7.46	0.43	116.86	49
19	BO-18-17	8.50	8.36	1.04	64.06	3
20	BO-2-14	8.00	7.70	0.58	104.83	37
21	BO-19-8	8.60	8.16	0.93	71.47	10
22	BO-2-4	7.40	7.43	0.53	116.77	48
23	Pusa Sawani	8.80	8.33	0.98	64.41	4

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Sl. No.	Genotype	TSS (°Brix)	Protein (g 100 g^{-1} DW)	Total phenolic content (g 100 g^{-1} DW)	QIDI	QIDI rank
24	Utkal Gaurav	7.46	8.03	0.66	101.33	33
25	BO-19-20	6.93	7.50	0.65	113.58	45
26	BO-19-21	7.10	8.13	0.92	90.35	24
27	BO-19-13	6.40	7.90	0.95	101.60	34
28	BO-19-14	9.16	8.23	0.84	71.48	11
29	BO-19-15	6.80	8.46	1.07	85.52	21
30	BO-19-16	8.76	7.43	0.50	108.10	41
31	BO-19-17	8.20	7.33	0.49	113.76	46
32	BO-19-9	9.83	6.06	1.10	94.70	26
33	BO-19-10	9.66	10.20	1.38	16.09	1
34	BO-19-11	8.40	7.86	0.97	75.59	13
35	BO-19-12	8.56	8.46	0.92	68.63	8
36	BO-2-19	10.50	8.26	0.96	57.98	2
37	BO-1	6.70	8.30	0.96	92.65	25
38	BO-20-2	9.33	7.26	0.82	86.03	22
39	BO-21-2	7.70	8.40	0.64	96.54	29
40	BO-12-2	9.36	7.83	0.55	96.51	28
41	BO-2-13	9.53	7.43	0.85	80.57	17
42	Arka Anamika	8.26	7.66	0.89	83.93	19
43	BO-2-3	7.83	7.96	0.94	81.99	18
44	Parbhani Kranti	7.46	7.50	0.73	103.08	35
45	BO-2-5	9.43	8.46	0.61	84.69	20
46	BO-2-6	9.76	7.93	0.90	68.58	7
47	BO-2-7	9.73	6.53	0.67	105.39	38
48	BO-2-9	7.73	8.10	0.99	79.14	15
49	BO-4-6	7.60	8.40	0.64	97.62	31
50	BO-5-6	9.10	7.70	0.90	75.76	14
51	BO-8-3	6.70	8.46	0.67	106.07	40
52	BO-10-2	7.70	8.70	0.96	74.31	12
	Grand mean	8.00	7.90	0.82		
	SE(m)±	0.25	0.22	0.02		
	CD (0.05)	0.72	0.64	0.07		
	CV (%)	5.56	5.00	5.35		

TSS: total soluble solids; DW: dry weight; SE(m): standard error of the mean; CD: critical difference at $p = 0.05$; CV: coefficient of variation. Means of three replications. The values of protein and phenolic content are those given as mg 100 g^{-1} in (18); the unit is corrected here to g 100 g^{-1} dry weight.

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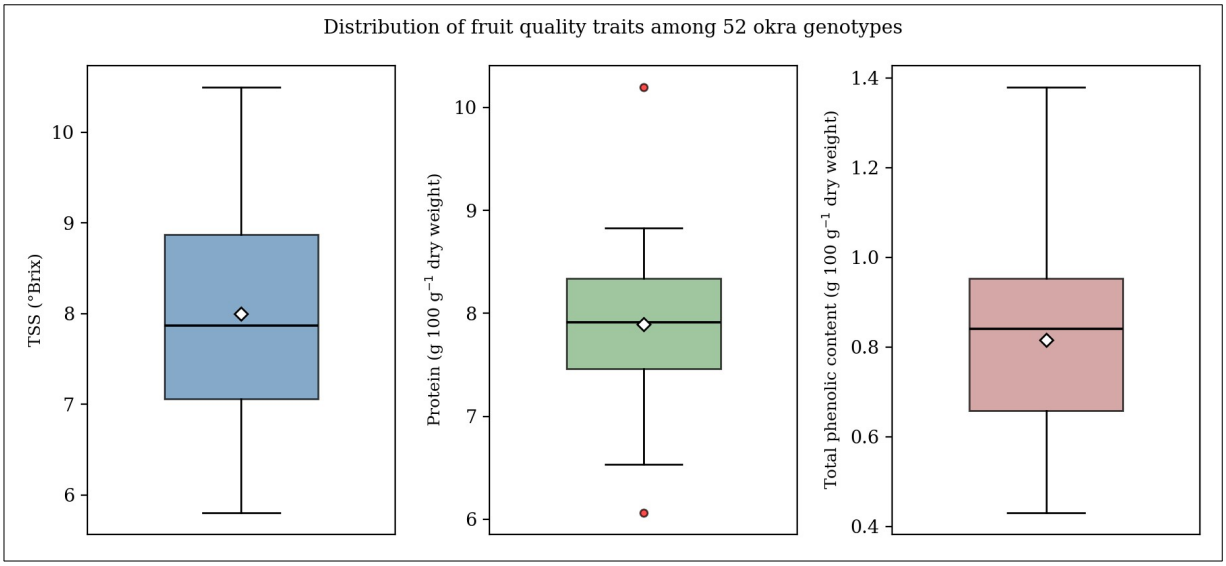


Fig. 1. Box-and-whisker plots of total soluble solids (TSS), protein and total phenolic content (left to right) of 52 okra genotypes. The diamond marks the mean, the line the median, the box the interquartile range, the whiskers 1.5 × the interquartile range and red points outlying genotypes.

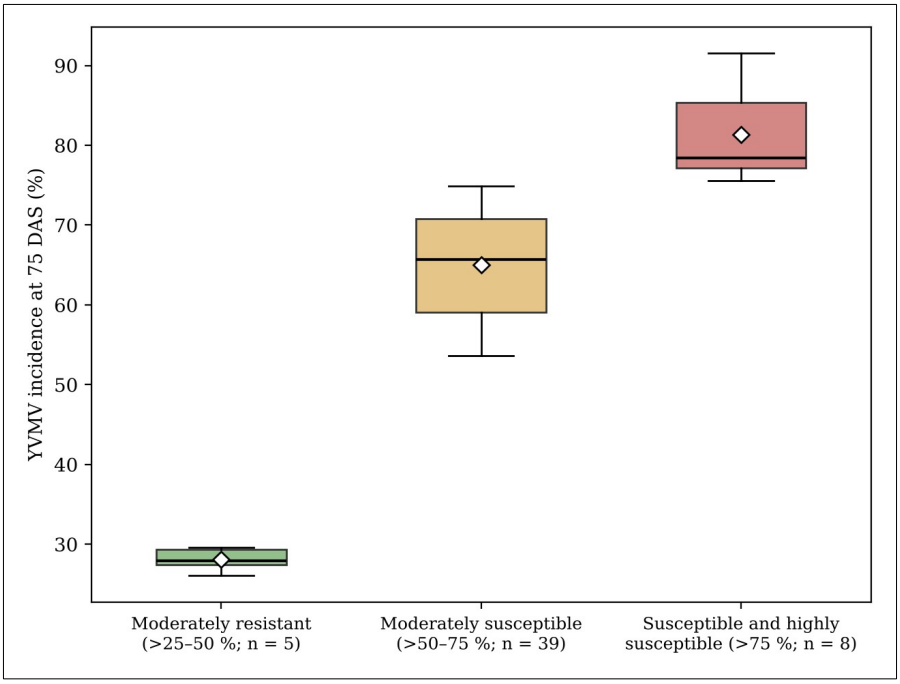


Fig. 2. Box-and-whisker plot of yellow vein mosaic virus (YVMV) incidence (%) at 75 days after sowing (DAS) by reaction class (Table 1) among 52 okra genotypes; susceptible and highly susceptible genotypes are combined. Symbols as in Fig. 1.

Fruit quality attributes

The TSS ranged from 5.80 °Brix (BO-18-37) to 10.50 °Brix (BO-2-19), with a mean of 8.00 °Brix; BO-2-6 (9.76), BO-2-7 (9.73), BO-2-13 (9.53) and BO-2-5 (9.43) were next highest, but all differed significantly from the top genotype (CD at p = 0.05 = 0.72). Protein content ranged from 6.06 to 10.20 g 100 g^{-1} dry weight (mean 7.90), with the highest value in BO-19-10. Total phenolic content ranged from 0.43 g 100 g^{-1} (BO-19-22) to 1.38 g 100 g^{-1} (BO-19-10), with BO-19-17 (0.49) and BO-19-16 (0.50) next lowest (Table 2). The box plots (Fig. 1) show that TSS and phenolic content were distributed fairly symmetrically without outliers, whereas two genotypes lay outside the whiskers for protein content: BO-19-10 (10.20 g 100 g^{-1}) at the upper end and BO-19-9 (6.06 g 100 g^{-1}) at the lower end. The three quality traits were weakly correlated with one another (TSS–protein r = 0.05, TSS–phenolic content r = 0.12, protein–phenolic content r = 0.29; only the last was significant, p = 0.04), so they were combined into a single index. These ranges agree with earlier reports of wide biochemical variability among okra genotypes (12, 13).

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Qualitative traits

The 52 genotypes differed for several qualitative descriptors (Table 3). Two genotypes (3.85 %) were short (<100 cm), 3 (5.77 %) medium (100–130 cm) and 47 (90.38 %) tall (>130 cm). Eighteen genotypes (34.62 %) had reddish-green and 34 (65.38 %) green stems; 5 (9.62 %) had light-green and 47 (90.38 %) dark-green leaves. Flowers were creamy yellow in 5 genotypes (9.62 %) and golden yellow in 47 (90.38 %). Fruits were pale green in 7 genotypes (13.46 %), deep green in 6 (11.54 %) and green in 39 (75.00 %); 16 genotypes (30.77 %) had oblique and 36 (69.23 %) cylindrical fruits; 4 (7.69 %) had six ridges and 48 (92.31 %) five ridges. Fruit pubescence was present in all genotypes. Seed colour was black in 48 genotypes (92.31 %) and grayish-black in 4 (7.69 %). These descriptors are useful for cultivar identification (29, 30); photographs of representative fruits of this panel are given in the earlier report (18).

Reaction to yellow vein mosaic virus

The YVMV incidence at 75 DAS ranged from 26.05 % (BO-19-17) to 91.55 % (BO-19-3), with a mean of 63.97 %; the critical difference at $p = 0.05$ was 7.65 % (Table 4). No genotype was free of symptoms or fell in the resistant classes (≤ 25 %). Five genotypes (BO-19-17, BO-2-4, BO-19-6, BO-2-14 and BO-19-15; 26.05–29.62 %) were in the moderately resistant class, 39 genotypes (75.0 %) were moderately susceptible (> 50–75 %), seven were susceptible (> 75–90 %) and one (BO-19-3, 91.55 %) was highly susceptible (Fig. 2; susceptible and highly susceptible genotypes are combined for display). The five lowest-incidence genotypes were separated from the next lowest genotype, BO-19-8 (53.67 %), by more than 24 percentage points. The absence of fully resistant genotypes agrees with reports that complete resistance is rare in cultivated okra (14, 15). Incidence was strongly and negatively correlated with total yield per plant ($r = −0.83$, $p < 0.001$) and, more weakly, with number of nodes ($r = −0.53$, $p < 0.001$) and number of fruits per plant ($r = −0.37$, $p = 0.008$), but not with TSS ($r = 0.10$), protein ($r = −0.14$) or total phenolic content ($r = 0.20$) ($p \geq 0.15$ for all three). In other words, genotypes with less disease generally yielded more.

Genetic divergence

The D^2/Tocher analysis grouped the 52 genotypes into nine clusters (Table 5). Cluster I contained 30 genotypes, including checks from different institutions (Pusa Sawani, Arka Anamika and Parbhani Kranti) together with OUAT breeding lines, so grouping did not follow the source of the genotypes, as reported earlier for other okra panels (9). Clusters II to VIII contained 7, 3, 2, 3, 2, 2 and 2 genotypes, respectively and cluster IX was monotypic (BO-19-10). A single large cluster with several small ones is typical of Tocher's method and was also seen in a recent study of 25 okra genotypes (clusters of 11, 11, 2 and 1 genotypes) (31).

Average intra-cluster D^2 was highest in cluster VII (252.36), whereas cluster IX had zero intra-cluster distance, as expected for a monotypic cluster (Table 6). Inter-cluster D^2 ranged from 223.49 (clusters II–III) to 1107.26 (clusters VII–IX), followed by 999.57 (clusters VII–VIII). The widest separation was thus between the monotypic cluster IX (BO-19-10) and cluster VII (BO-2-14 and BO-2-4). Previous researchers found a similar pattern, with the largest inter-cluster distance involving small clusters; their maximum inter-cluster D^2 (124.88) was between a two-genotype and a one-genotype cluster, with intra-cluster values of 0 to 30.43 (31). Absolute D^2 values are not comparable among studies because they depend on the number and units of traits, the number of genotypes and the error covariance used; the larger values here (223–1107) may partly reflect the 18 traits and 52 genotypes analysed. Because D^2 measures phenotypic distance, crosses between distant clusters may widen the scope for recombination, although heterosis, combining ability and transgressive segregation can only be confirmed through progeny testing (6). BO-2-4, BO-2-14 and BO-19-10 are therefore candidate parents for such tests.

Cluster means differed widely (Table 7). Cluster VII (BO-2-14, BO-2-4) had the widest plant spread (58.70 cm north–south (N–S); 65.27 cm east–west (E–W)), the most nodes (21.91), the earliest flowering (35.99 and 42.66 days to first and 50 % flowering) and the highest number of fruits per plant (20.49) and total yield per plant (259.65 g). Cluster IX (BO-19-10) showed the opposite phenology, with the latest flowering and fruiting (39.66, 45.33 and 47.66 days) and the longest internodes (12.36 cm) and had the highest TSS (9.66 °Brix), protein (10.20 g 100 g^{-1}) and total phenolic content (1.38 g 100 g^{-1}). Cluster I had the highest fruit girth (6.35 cm) and average fruit weight (84.10 g), cluster II the tallest plants (151.42 cm), cluster III the longest fruits (14.11 cm) and earliest fruiting (44.44 days), cluster IV the longest pedicels (3.08 cm) and cluster VIII the largest leaf area (560.84 cm^2); clusters V and VI did not have the highest (or, for phenology, earliest) mean for any trait. Cluster IX, which had the best quality values and cluster VII, which had the highest yield, were also the two most distant clusters (Table 6) and differed in the direction of vigour, earliness and yield versus quality traits. This contrast should be read as descriptive, because cluster VII contains only two genotypes and cluster IX only one.

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Table 3. Distribution of qualitative morphological traits among 52 okra genotypes

Trait	Class	No. of genotypes	Percentage (%)
Plant height	Short (< 100 cm)	2	3.85
	Medium (100–130 cm)	3	5.77
	Tall (> 130 cm)	47	90.38
Stem color	Reddish-green	18	34.62
	Green	34	65.38
Leaf color	Light green	5	9.62
	Dark green	47	90.38
Flower color	Creamy yellow	5	9.62
	Golden yellow	47	90.38
Fruit color	Pale green	7	13.46
	Deep green	6	11.54
	Green	39	75.00
Fruit shape	Oblique	16	30.77
	Cylindrical	36	69.23
No. of ridges	6 ridges	4	7.69
	5 ridges	48	92.31
Seed color	Greyish-black	4	7.69
	Black	48	92.31

Descriptors were classified visually (fruit color additionally compared with a color scale) and were not used in the multivariate analyses.

Table 4. Mean yellow vein mosaic virus (YVMV) incidence (%) at 75 days after sowing (DAS) among 52 okra genotypes, with reaction class

Sl. No.	Genotype	YVMV incidence (%)	Class	Sl. No.	Genotype	YVMV incidence (%)	Class
1	BO-18-40	58.66 (49.99)	MS	29	BO-19-15	29.62 (32.97)	MR
2	BO-18-57	54.22 (47.42)	MS	30	BO-19-16	61.66 (51.74)	MS
3	BO-18-37	71.44 (57.70)	MS	31	BO-19-17	26.05 (30.69)	MR
4	BO-18-38	73.56 (59.06)	MS	32	BO-19-9	89.53 (71.12)	S
5	BO-18-7	84.00 (66.42)	S	33	BO-19-10	59.78 (50.64)	MS
6	BO-18-47	61.00 (51.35)	MS	34	BO-19-11	72.44 (58.33)	MS
7	BO-18-8	76.11 (60.74)	S	35	BO-19-12	65.67 (54.13)	MS
8	BO-18-5	69.44 (56.44)	MS	36	BO-2-19	70.44 (57.06)	MS
9	BO-18-9	67.57 (55.29)	MS	37	BO-1	74.89 (59.93)	MS
10	BO-18-6	58.89 (50.12)	MS	38	BO-20-2	77.56 (61.72)	S
11	BO-19-7	62.44 (52.20)	MS	39	BO-21-2	70.67 (57.21)	MS
12	BO-19-1	73.22 (58.84)	MS	40	BO-12-2	59.11 (50.25)	MS
13	BO-19-3	91.55 (73.10)	HS	41	BO-2-13	63.11 (52.60)	MS
14	BO-19-4	58.44 (49.86)	MS	42	Arka Anamika	58.33 (49.80)	MS
15	BO-19-5	72.89 (58.62)	MS	43	BO-2-3	66.22 (54.46)	MS
16	BO-19-2	67.11 (55.01)	MS	44	Parbhani Kranti	59.11 (50.25)	MS
17	BO-19-6	27.92 (31.90)	MR	45	BO-2-5	74.78 (59.85)	MS
18	BO-19-22	61.78 (51.81)	MS	46	BO-2-6	69.00 (56.17)	MS
19	BO-18-17	55.11 (47.93)	MS	47	BO-2-7	62.56 (52.27)	MS
20	BO-2-14	29.35 (32.80)	MR	48	BO-2-9	77.55 (61.72)	S

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Sl. No.	Genotype	YVMV incidence (%)	Class	Sl. No.	Genotype	YVMV incidence (%)	Class
21	BO-19-8	53.67 (47.10)	MS	49	BO-4-6	61.22 (51.48)	MS
22	BO-2-4	27.39 (31.56)	MR	50	BO-5-6	59.00 (50.18)	MS
23	Pusa Sawani	79.22 (62.88)	S	51	BO-8-3	73.77 (59.19)	MS
24	Utkal Gaurav	55.11 (47.93)	MS	52	BO-10-2	71.00 (57.42)	MS
25	BO-19-20	75.55 (60.37)	S		Grand mean	63.97 (53.25)	
26	BO-19-21	72.11 (58.12)	MS		SE(m)±	2.53 (1.78)	
27	BO-19-13	69.67 (56.58)	MS		CD (0.05)	7.65 (5.37)	
28	BO-19-14	66.00 (54.33)	MS				

Values in parentheses represent angular (arcsine-transformed) values. MR: moderately resistant; MS: moderately susceptible; S: susceptible; HS: highly susceptible (Table 1). SE(m): standard error of the mean; CD: critical difference at $p = 0.05$ (7.65 % on the original scale).

Table 5. Clustering pattern of 52 okra genotypes based on Tocher's method

Cluster	No. of genotypes	Genotypes included
I	30	BO-18-40, BO-18-57, BO-18-37, BO-18-38, BO-18-7, BO-18-8, BO-18-5, BO-18-9, BO-18-6, BO-19-7, BO-18-17, BO-19-8, Pusa Sawani, BO-19-20, BO-19-21, BO-19-13, Parbhani Kranti, Arka Anamika, BO-19-14, BO-19-15, BO-19-11, BO-2-19, BO-20-2, BO-21-2, BO-2-13, BO-2-3, BO-2-9, BO-4-6, BO-5-6, BO-10-2
II	7	BO-19-16, BO-19-17, BO-12-2, BO-2-5, BO-2-6, BO-2-7, BO-8-3
III	3	BO-18-47, BO-19-5, Utkal Gaurav
IV	2	BO-19-3, BO-1
V	3	BO-19-4, BO-19-6, BO-19-22
VI	2	BO-19-9, BO-19-12
VII	2	BO-2-14, BO-2-4
VIII	2	BO-19-1, BO-19-2
IX	1	BO-19-10

Clusters were formed from Mahalanobis' D^2 among the 18 quantitative traits.

Table 6. Average intra-cluster (diagonal) and inter-cluster (D^2) distances among nine clusters of okra genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	178.97	237.87	257.00	330.80	308.71	249.14	500.38	332.78	436.67
II		162.19	223.49	286.86	384.80	322.01	380.89	509.90	746.78
III			142.25	251.67	446.64	273.77	642.52	379.24	721.61
IV				243.29	605.04	413.19	828.98	482.86	703.41
V					182.66	514.24	473.09	637.83	577.49
VI						136.92	714.27	310.87	508.73
VII							252.36	999.57	1107.26
VIII								125.69	332.99
IX									0

Diagonal values are average intra-cluster distances; a value of 0 for cluster IX reflects a single genotype.

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Table 7. Cluster means for the traits in which a cluster had the highest mean (or, where stated, the earliest or latest mean)

Cluster	Trait(s)	Mean value
I	Fruit girth (cm) / Average fruit weight (g)	6.35 / 84.10
II	Plant height (cm)	151.42
III	Fruit length (cm) / Days to 1st fruiting (earliest)	14.11 / 44.44
IV	Pedicel length (cm)	3.08
V	None (no highest or earliest mean)	-
VI	None (no highest or earliest mean)	-
VII	Plant spread N–S / E–W (cm) / No. of nodes / Days to 1st and 50 % flowering (earliest) / Fruits per plant / Total yield per plant (g)	58.70 / 65.27 / 21.91 / 35.99 and 42.66 / 20.49 / 259.65
VIII	Leaf area (cm^2)	560.84
IX	Internodal length (cm) / Days to 1st flowering, 50 % flowering and 1st fruiting (latest) / TSS (°Brix) / Protein (g 100 g^{-1}) / Total phenolic content (g 100 g^{-1})	12.36 / 39.66, 45.33 and 47.66 / 9.66 / 10.20 / 1.38

TSS: total soluble solids. Cluster VII comprises BO-2-14 and BO-2-4 and cluster IX comprises BO-19-10 only; means of such small clusters are descriptive. Means are of genotype means (Table 2 and Supplementary Table 1 & 2).

Phenolic content contributed most to divergence (28.28 %), followed by internodal length (20.81 %), total yield per plant (14.25 %), plant spread E–W (4.98 %), average fruit weight (4.68 %) and number of fruits per plant (4.60 %) (Table 8); each remaining trait contributed 4.22 % or less. Yield or yield components also ranked high in previous reports (9), in which yield per plot (36.45 %), plant height (26.27 %) and seeds per plant (16.83 %) contributed most among the traits studied in 46 genotypes; another study (11) likewise included quality traits in a D^2 analysis of okra. Because contributions depend on the traits and units analysed, such comparisons are only approximate.

Principal component analysis

Seven principal components had eigenvalues ≥ 1 and together explained 70.69 % of the variance (Supplementary Fig. 1, Table 9). PC1 and PC2 explained 19.49 % and 13.05 %, respectively (32.54 % jointly); the biplot (Fig. 3) was used to visualise the main trait gradients.

PC1 loaded mainly on number of nodes and plant spread (E–W and N–S) and, in the opposite direction, on days to flowering (a vigour–earliness gradient). PC2 loaded on fruit girth, average fruit weight, fruit length and days to first flowering and first fruiting (a fruit-size gradient). PC3 loaded on protein content, days to first fruiting, total yield per plant and leaf area. The flowering-time vectors pointed away from the plant-spread and node vectors, as expected from the negative correlations of flowering time with vigour traits reported for this panel (18). BO-2-4, BO-2-14 and BO-19-17 lay at the positive end of PC1, in the direction of high node number and plant spread; the first two belong to Tocher cluster VII and the third to cluster II. The PCA did not include YVMV incidence and QIDI.

Table 8. Percentage contribution of individual characters to total genetic divergence (D^2) among 52 okra genotypes

Character	Times ranked 1st	% contribution
Plant height (cm)	6	0.45
Plant spread (N-S) (cm)	40	3.02
Plant spread (E-W) (cm)	66	4.98
No. of nodes	41	3.09
Internodal length (cm)	276	20.81
Leaf area (cm^2)	56	4.22
Days to 1st flowering	8	0.60
Days to 50 % flowering	9	0.68
Days to 1st fruiting	11	0.83
Pedicel length (cm)	14	1.06
Fruit length (cm)	6	0.45
Fruit girth (cm)	7	0.53
Average fruit weight (g)	62	4.68

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Character	Times ranked 1st	% contribution
No. of fruits per plant	61	4.60
TSS (°Brix)	56	4.22
Protein (g 100 g^{-1})	43	3.24
Total phenolic content (g 100 g^{-1})	375	28.28
Total yield per plant (g)	189	14.25
Total	**1326**	100.00

TSS: total soluble solids. 'Times ranked 1st, is the number of the 1326 genotype pairs (52 × 51/2) in which the trait contributed most to D^2. Percentages describe contribution to the multivariate distance only.

Hierarchical clustering

Ward clustering of the same standardised traits was cut at nine groups for comparison with the Tocher solution (Fig. 4); group sizes were 2, 2, 3, 5, 5, 6, 6, 10 and 13. The two methods agreed in part. BO-19-10, the monotypic Tocher cluster IX, was placed in a 10-member Ward group, while BO-2-4 and BO-2-14, whi ch comprise Tocher cluster VII, were placed in the same group as BO-19-6, BO-19-15 and BO-19-17. Since D^2 takes into account the error covariance of characteristics while Ward clustering of standardised means assumes that traits are uncorrelated, as well as the fact that the two algorithms utilise different definitions of groups, it is not surprising that there may be some disagreement. Even though YVMV incidence was not one of the 18 clustering variables, the five genotypes that had the lowest incidence also belonged to the same Ward group. Although this does not prove a common resistance mechanism, it does show that they have a similar agronomic profile (more nodes and higher yield per plant than the panel mean; Supplementary Table 1 and 2) and fits the negative correlation between incidence and vigour and yield attributes that was mentioned before.

Quality ideotype-distance index

Total soluable solids, protein and total phenolic content were not strongly correlated and the genotype with the highest TSS (BO-2-19) was not the highest for protein or phenolic content; hence, the three traits were combined in the QIDI (Table 2). QIDI ranged from 16.09 (BO-19-10) to 127.60 (BO-18-37). BO-19-10 was closest to the ideotype by a wide margin because it combined the highest protein and phenolic content with above-average TSS. The ten genotypes with the lowest QIDI were BO-19-10, BO-2-19, BO-18-17, Pusa Sawani, BO-18-38, BO-18-57, BO-2-6, BO-19-12, BO-19-2 and BO-19-8 (Supplementary Fig. 2); this list overlaps only partly with the best genotypes for individual traits.

The ideotype is a relative goal within this panel that was defined using the best observed value of each characteristic. When the weight of any one trait was halved or doubled, or z-scores were used instead of rescaled values, QIDI ranks remained highly correlated with the baseline ranks (Spearman ρ = 0.94–0.98). In every instance, BO-19-10 ranked first and none of the five genotypes with the lowest YVMV incidence made it into the top 10 (their best rank was 13). The index ranks quality traits only; yield and YVMV incidence were examined separately.

Apparent separation of fruit quality and yellow vein mosaic virus reaction

None of the five genotypes with the lowest YVMV incidence (BO-19-17, BO-2-4, BO-19-6, BO-2-14 and BO-19-15) ranked among the ten best by QIDI; their ranks were 21, 37, 42, 46 and 48 of 52 (Table 2). Conversely, BO-19-10, the genotype closest to the quality ideotype, had 59.78 % incidence and belongs to the moderately susceptible class. BO-19-6 had TSS (6.30 °Brix) and total phenolic content (0.70 g 100 g^{-1}) below the panel means (8.00 and 0.82), whereas BO-19-15 combined low incidence (29.62 %) with above-average phenolic content (1.07 g 100 g^{-1}) but below-average TSS. In line with this, YVMV incidence was not significantly correlated with TSS, protein or total phenolic content ($|r| \leq 0.20$, $p \geq 0.15$) and the quality traits were not significantly correlated with total yield per plant ($|r| \leq 0.10$, $p \geq 0.49$).

Taken together, these genotype-mean associations point to an apparent separation between fruit quality and YVMV reaction in this panel. In practical terms, selecting for lower YVMV incidence alone would not improve fruit quality and the reverse also holds. The divergence analysis points the same way: BO-19-10 (cluster IX) and BO-2-4 and BO-2-14 (cluster VII), the latter two having low incidence (27.39 % and 29.35 %) and high yields (270.80 and 248.50 g $plant^{-1}$), belong to the most distant pair of clusters (D^2 = 1107.26). Crosses between these groups, with evaluation of progeny for quality, yield and YVMV reaction, would show whether the two can be combined. The high heritability estimates reported for this trial indicate that most of the observed variation in the quality traits and yield is genotypic, which justifies further work with these genotypes (18).

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Table 9. Eigenvalues and per cent variance explained by the first eight principal components (18 standardised traits)

Component	Eigenvalue	% Variance	Cumulative %
PC1	3.509	19.49	19.49
PC2	2.349	13.05	32.54
PC3	1.704	9.47	42.01
PC4	1.461	8.12	50.13
PC5	1.356	7.53	57.66
PC6	1.211	6.73	64.39
PC7	1.133	6.30	70.69
PC8	0.952	5.29	75.98

The 18 eigenvalues sum to 18.0, the number of standardised traits. Components 1–7 have eigenvalues ≥ 1.

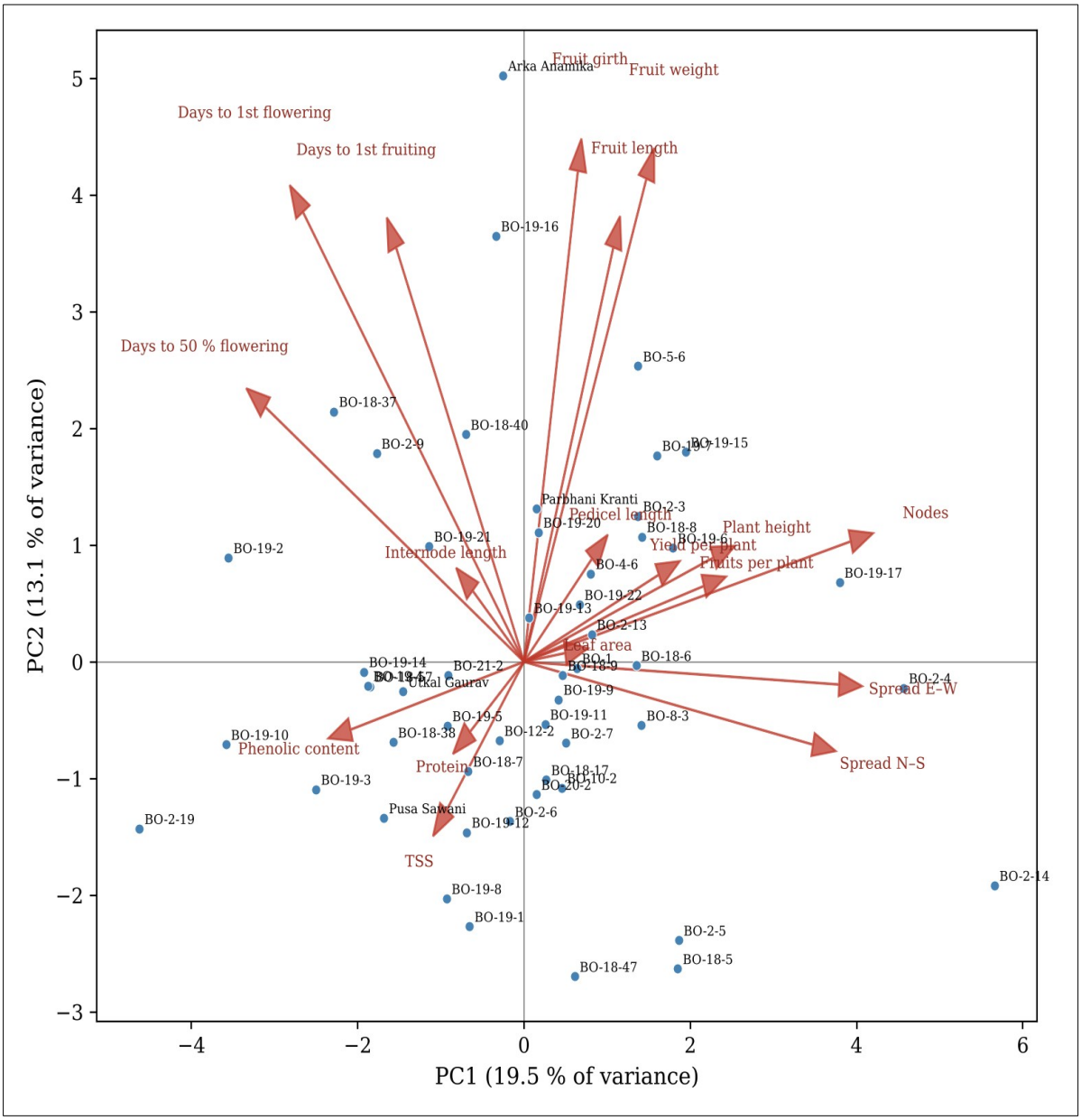


Fig. 3. Principal component biplot (PC1 vs PC2) of 52 okra genotypes based on 18 quantitative traits. Arrows show scaled trait loadings; points show genotype scores. PC1 and PC2 together explain 32.54 % of the variance.

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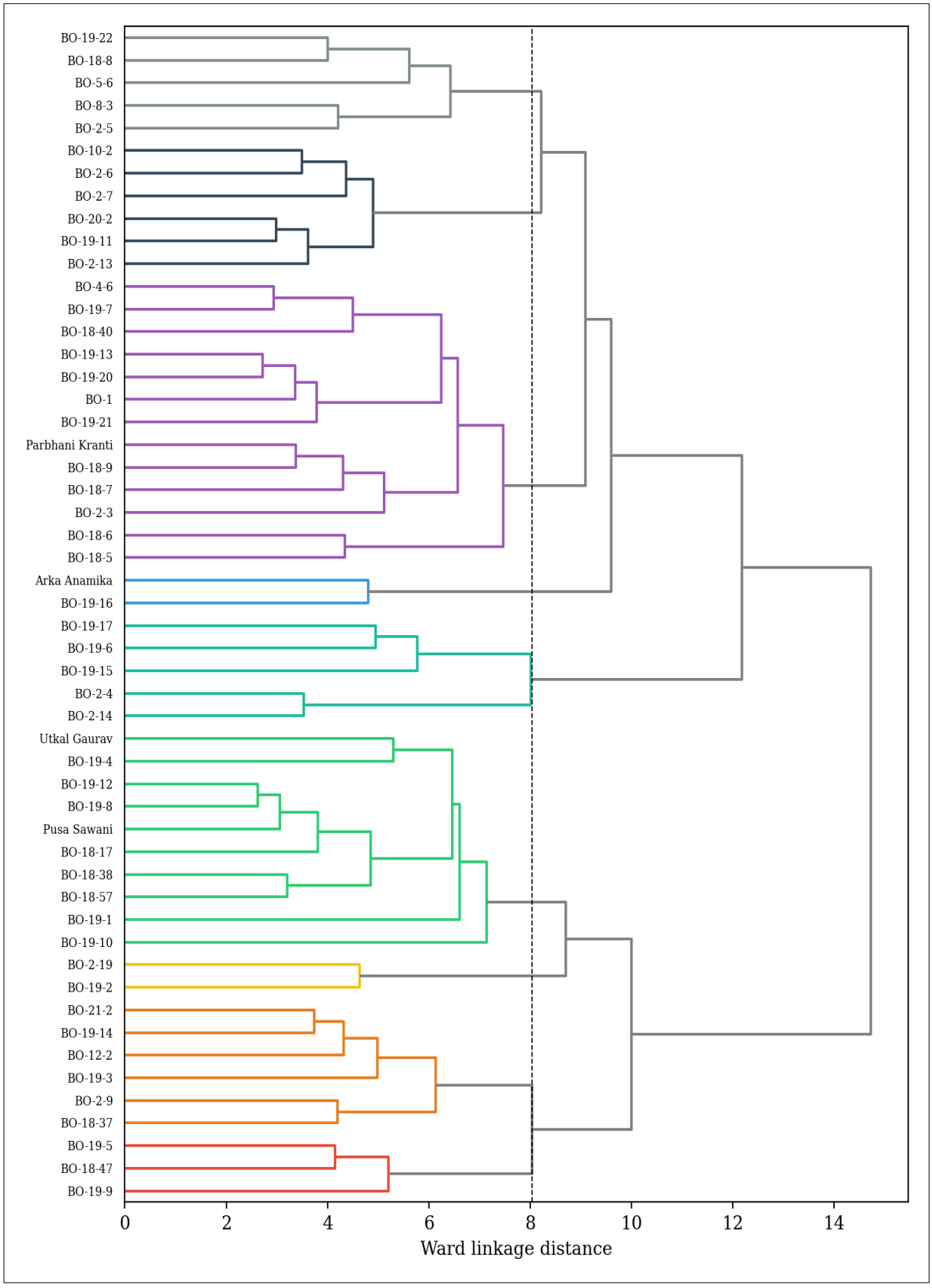


Fig. 4. Dendrogram of 52 okra genotypes from Ward's hierarchical clustering (Euclidean distance; standardised means of 18 quantitative traits). Colors mark the nine-group cut (dashed line), chosen for comparability with the Tocher clusters.

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Conclusion

Fifty-two okra genotypes separated into nine D^2 clusters, with the greatest divergence between cluster VII (BO-2-4, BO-2-14) and the monotypic cluster IX (BO-19-10); PCA and Ward clustering gave partly concordant groupings. There was no correlation between incidence and total soluble solids (TSS), protein, or phenolic content, but there was a substantial and negative relationship between incidence and yield. The five genotypes with the lowest incidence (26–30 %) ranked 21st to 48th for quality, while BO-19-10 had the best fruit quality index but was moderately susceptible to YVMV (59.78 %). Thus, BO-19-10 is a candidate source of fruit quality, while BO-2-4 and BO-2-14 are candidates for lower YVMV incidence with high yield. The next step is to cross these groups and evaluate the progeny over several environments for combining ability, heterosis, quality inheritance and YVMV reaction.

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Authors' contributions

AB conceived and conducted the field study, recorded and analysed the data and drafted the manuscript. AM and SS coordinated the AICRP trial and supervised field operations. PT and KM contributed to trait recording, data compilation and manuscript revision. DSK provided elite genotypes used in the study. AKP, SP and AP assisted with trait recording and manuscript revision. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest

Authors do not have any conflict of interests to declare.

Ethical issues

None

References

1. De Candolle A. Origin of cultivated plants. 2nd ed. London: Kegan Paul, Trench & Co; 1886. https://doi.org/10.5962/bhl.title.55127
2. Tindall HD. Vegetables in the tropics. London: Macmillan; 1983. https://doi.org/10.1007/978-1-349-17223-8
3. Berry SK, Kalra CL, Sehgal RC. Quality characteristics of seeds of five okra (*Abelmoschus esculentus* (L.) Moench) cultivars. J Food Sci Technol. 1988;25(5):303–5.
4. National Horticulture Board. Horticultural statistics at a glance 2021–22. Gurugram: NHB; 2022. https://www.nhb.gov.in/annual_report.aspx
5. Ranga AD, Darvhankar MS. Diversity analysis of phenotypic traits in okra (*Abelmoschus esculentus* (L.) Moench). J Hortic Sci. 2022;17(1):63–72. https://doi.org/10.24154/jhs.v17i1.1214
6. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. New Delhi: Kalyani Publishers; 1977.
7. Munshi R, Acharyya P, Chattopadhyay A, Mishra P, Sahoo B, Chakraborty L. Diversity analysis in okra [*Abelmoschus esculentus* (L.) Moench] genotypes under saline situation. Biol Forum Int J. 2023;15(6):385–94.
8. Samiksha RS, Patel VK, Prakash S, Maurya SK, Kumar S. Genetic divergence in okra [*Abelmoschus esculentus* (L.) Moench]. Ind J Pure Appl Biosci. 2020;8(4):635–8.
9. Nanthakumar S, Kuralarasu C, Gopikrishnan A. D2 analysis for assessing genetic diversity in okra (*Abelmoschus esculentus* (L.) Moench). Electron J Plant Breed. 2021;12(4):1249–53. https://doi.org/10.37992/2021.1204.171
10. Mohammed J, Mohammed W, Shiferaw E. Phenotypic diversity assessment of okra (*Abelmoschus esculentus* (L.) Moench) genotypes in Ethiopia using multivariate analysis. Scientifica (Cairo). 2022;2022:3306793. https://doi.org/10.1155/2022/3306793
11. Neeraja S, Srinivas J, Joshi V, Nikhil B, Sathish G. Genetic divergence studies for yield, yield attributes and quality traits in okra [*Abelmoschus esculentus* (L.)]. Int J Bio-Resour Stress Manag. 2025;16(1):1–9. https://doi.org/10.23910/1.2025.5695
12. Noopur K, Samnotra RK, Kumar S. Influence of okra (*Abelmoschus esculentus*) genotypes on growth, yield and biochemical traits. Indian J Agric Sci. 2023;93(1):57–61. https://doi.org/10.56093/ijas.v93i1.122668
13. Al-Dabbas MM, Moumneh M, Hamad HJ, Abughoush M, Abuawad B, Al-Nawasrah BA, et al. Impact of processing and preservation methods and storage on total phenolics, flavonoids and antioxidant activities of okra (*Abelmoschus esculentus* L.). Foods. 2023;12(19):3711. https://doi.org/10.3390/foods12193711
14. Jamir I, Mandal AK, Devi AP, Bhattacharjee T, Maurya PK, Dutta S, et al. Screening of genotypes against viral diseases and assessment of yield loss due to yellow vein mosaic virus in okra grown in the eastern part of India. Indian Phytopathol. 2020;73:125–33. https://doi.org/10.1007/s42360-019-00183-0
15. Santhiya S, Yadav RK, Lata S, Sharma BB, Talukdar A, Ghosh A, et al. Screening of wild okra (*Abelmoschus esculentus*) against yellow vein mosaic and enation leaf curl diseases. Indian J Agric Sci. 2022;92(10):1268–73. https://doi.org/10.56093/ijas.v92i10.125710
16. Venkataravanappa V, Lakshminarayana Reddy CN, Krishna Reddy M. Begomovirus characterization and development of

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https://doi.org/10.14719/pst.18012

phenotypic and DNA-based diagnostics for screening of okra genotype resistance against Bhendi yellow vein mosaic virus. 3 Biotech. 2013;3(6):461–9. https://doi.org/10.1007/s13205-012-0107-z

17. Khade YP, Kumar R, Yadav RK. Genetic control of yellow vein mosaic virus resistance in okra (*Abelmoschus esculentus*). Indian J Agric Sci. 2020;90(3):606–9.
18. Behera A, Mohanty A, Tripathy P, Sarkar S, Dhar S, Parida AK, et al. Assessment of genetic variability and trait association in okra (*Abelmoschus esculentus* (L.) Moench). J Adv Biol Biotechnol. 2025;28(6):431–47. https://doi.org/10.9734/jabb/2025/v28i62409
19. Jackson ML. Soil chemical analysis. New Delhi: Prentice Hall of India; 1973.
20. Walkley A, Black IA. An examination of the Degtjareff method for determining soil organic matter and a proposed modification of the chromic acid titration method. Soil Sci. 1934;37(1):29–38.
21. Subbiah BV, Asija GL. A rapid procedure for the estimation of available nitrogen in soils. Curr Sci. 1956;25:259–60.
22. Singleton VL, Rossi JA Jr. Colorimetry of total phenolics with phosphomolybdic-phosphotungstic acid reagents. Am J Enol Vitic. 1965;16(3):144–58.
23. Ali S, Khan MA, Habib A, Rasheed S, Iftikhar Y. Management of yellow vein mosaic disease of okra through pesticide/biopesticide and suitable cultivars. Int J Agric Biol. 2005;7(1):145–7.
24. Mahalanobis PC. On the generalised distance in statistics. Proc Natl Inst Sci India. 1936;2:49–55.
25. Rao CR. Advanced statistical methods in biometric research. New York: John Wiley & Sons; 1952.
26. Jolliffe IT, Cadima J. Principal component analysis: a review and recent developments. Philos Trans R Soc A. 2016;374(2065):20150202. https://doi.org/10.1098/rsta.2015.0202
27. Ward JH. Hierarchical grouping to optimize an objective function. J Am Stat Assoc. 1963;58(301):236–44. https://doi.org/10.1080/01621459.1963.10500845
28. Olivoto T, Nardino M. MGIDI: toward an effective multivariate selection in biological experiments. Bioinformatics. 2021;37(10):1383–9. https://doi.org/10.1093/bioinformatics/btaa981
29. Temam N, Mohamed W, Aklilu S. Agro-morphological characterization and evaluation of okra [*Abelmoschus esculentus* (L.) Moench] genotypes for yield and other variability components at Melkassa, Central Ethiopia. MOJ Eco Environ Sci. 2020;5(2):80–7.
30. Kenaw U, Mohammed W, Woldetsadik K. Morpho-agronomic variability of okra [*Abelmoschus esculentus* (L.) Moench] genotypes in Dire Dawa, eastern Ethiopia. PLoS One. 2023;18(7):e0288534. https://doi.org/10.1371/journal.pone.0288534
31. Pathania R, Singh A, Mehta DK, Kaplex A, Kaushal A, Singh K. Genetic variability, divergence, correlation and path analysis in okra (*Abelmoschus esculentus*) for yield improvement. Indian J Agric Sci. 2026;96(5):637–45. https://doi.org/10.56093/ijas.v96i5.172164

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