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Research Article

Deciphering multivariate patterns and diversity analysis of yield and associate traits in okra (*Abelmoschus esculentus* (L.) Moench) accessions of northwestern India

Sai Keerthana
Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara (Punjab), India
Hardeep Singh
Punjab state rural livelihood mission, Jalandhar (Punjab), India
N. Dubey*
Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara (Punjab), India
I. R. Delvadiya
Department of Genetics and Plant Breeding, Junagadh Agricultural University, Junagadh (Gujarat), India
H. Avinashe
Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara (Punjab), India

*Corresponding authors. Emails: drnidhi355@gmail.com

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Abstract

Okra is a valuable crop cultivated worldwide for its edible fruits. Understanding genetic variability and the relationship among key traits is essential for improving yield and other agronomic characteristics. This study focused on evaluating 27 okra (*Abelmoschus esculentus* (L.) Moench) genotypes at research farm of Lovely Professional University, Phagwara, Punjab to explore their genetic diversity and yield-contributing traits. The genetic variability of okra genotype assessed the relationships between yield-contributing traits and identified the traits with the most significant direct and indirect effects on the yield of okra. A Randomized Complete Block Design (RCBD) with three replications was used for traits such as plant height, fruit production, seed weight and other characteristics. Variance analysis, heritability estimation, correlation analysis, path coefficient analysis and cluster analysis were conducted to identify significant relationships and genetic diversity among genotypes. The highest coefficient of variation was observed for fruit weight per plant, the number of main branches and seed weight per plant. Path analysis showed that seed weight per plant had the largest direct positive effect on fruit production per plant (0.878) and total number of main branches (0.845). Negative influences were seen from days to first flowering (-0.164). Cluster analysis revealed the highest genetic distance between cluster II and V ($D^2 = 356.76$). Plant height (23.93%) and biological yield (22.22%) contributed most to genetic divergence. This study identified key traits such as seed weight and fruit production with the highest genetic potential for yield improvement in okra. The findings can be applied in breeding programs to develop high-yielding okra varieties through targeted selection.

Keywords: Cluster analysis, Correlation, Genetic variation, Okra, Path analysis

INTRODUCTION

Okra, scientifically known as (*Abelmoschus esculentus* (L.) Moench) stands out as a frequently employed species within the Malvaceae family. It is native to the areas that it originated in, which include Sudan and Ethiopia. Around the world, warm, tropical, and subtropical areas are where it is grown as a vegetable crop (Abhilash *et al.*, 2023). It is a crop of great importance in most developing nations, accounting for about 4% of all vegetable consumption, and ranking higher than other vegetable crops such as lettuce, cabbage, and amaranths. It has a large potential for foreign exchange earnings and accounts for more than 60% of fresh vegetable exports (Dholariya *et al*., 2018).

The primary reason okra is grown is for its immature fruits, which can be eaten raw, cooked, as a snack, or added to salads, soups, and stews. It is an excellent source of fat, iron, thiamine, nicotinamide, calcium, magnesium, potassium, protein, dietary fiber, iron, and vitamins A and C. Okra seed has a balanced protein content that is similar to soybeans, with high levels of tryptophan and lysine amino acids (Shiri *et al*., 2024).

It is also a rich source of phenolic compounds and zinc. Once roasted, the dried seeds can be added to coffee or used as a substitute for making vegetable curds. These characteristics increase the significance of fruits, seeds, and okra in humans' diets. Okra is a plant with several uses. Its young fruits are utilized as vegetables, its roots and stem are used to clarify sugar cane juice, and its high fiber-containing stem is used in the paper industry. Another source of edible oils is extracts from okra seeds. Edible oil has a greenish-yellow colour and a pleasant smell and is rich in unsaturated fats, such as linolic and oleic acids. The seeds have a significant oil content of approximately 40%. India's principal states that produce ladies' fingers include Bihar, Orissa, Uttar Pradesh, Andhra Pradesh, Karnataka, and West Bengal as stated by (Pattan *et al*., 2023; Veeresh *et al*., 2024).

Okra is an excellent choice for sustainable farming since it grows, yields, and is of high quality, making it appealing to growers as well as consumers. In okra germplasm, a notably large genetic variability has been observed to be linked to yield, early development, and characteristics (Kumar *et al*., 2012). The yellow vein mosaic virus lowers okra yield nationwide and is the main obstacle to okra cultivation. By means of hybridization, selection, and introduction, numerous new types are being created. Enhancement within any agricultural species is predominantly contingent upon the extent of genetic diversity in the crop species. Detailed comprehension of the variation found in the breeding material of a crop species for a particular trait helps the breeder choose which genotype has the greatest potential (Chavan *et al*., 2019).

The present research evaluates the genetic variability among 27 okra genotypes and assesses the relationships between key yield-contributing traits through correlation and path coefficient analysis. The study seeks to identify traits with significant direct and indirect effects on yield, which can be targeted for selection in breeding programs to improve okra productivity and overall performance.

MATERIALS AND METHODS

Experimental material

The study comprised 27 okra crop genotypes acquired from the National Bureau of Plant Genetic Resources (NBPGR) located in New Delhi. In a field experiment, three replications and a randomized complete block design were used to assess the genotypes. At Department of Genetics and Plant Breeding, Lovely Professional University (LPU) in Phagwara, Punjab. The location of the farm is at an elevation of 243 MSL and has coordinates of 31º 19º 32″ North, 75º 34º 45″ East during the *Kharif* 2020. Each entry was planted with rows and plants were spaced 45 cm apart, with row lengths of three meters. For every genotype, four rows were sown. The entire area of the field was 650 square meters. All recommended protocols were followed to raise a healthy crop. In accordance with the package and practices recommended by Punjab Agricultural University (PAU), For successful okra cultivation, sow on well-drained loam soils, applying 100 kg Nitrogen, 50 kg Phosphorus, and 50 kg Potassium per hectare. Irrigate every 7-10 days (less during monsoon), and manage pests using IPM strategies, including insecticides and biological control. Weed manually or use herbicides like Pendimethalin, and harvest pods 45-60 days after sowing. Regular harvesting ensures a yield of 10-15 tons/ha.

The following quantitative characteristics were noted: Plant height (cm, PH), Total Number of main branches (NPB), Stem diameter (SD), Internode length (IL), Days to first harvest (DFH), Fruit weight (FW), Fruit diameter (FD), Fruit length (cm, FL), Fruits production per plant (NFPP), Weight of 10 green fruit (WGF), Fruit weight per plant (WFPP), Number of seed per fruit (NSPF), Weight of each fruit seed (WSPF), Weight of seed per plant (g, WSPP), 100 Seed weight (SW), Average fruit weight (g, AFW), Harvest index (HI) and Biological yield (g, BY).

As recommended by Panse and Sukatme (1967), five randomly selected plants means were used for the statistical analysis (ANOVA). Calculations were made for heritability, the phenotypic and genotypic coefficients of variation, and genetic advancement expressed as a percentage of the mean using R software. The D2 analysis, the route coefficient of Dewey and Lu (1959), and the formula of Karl Pearson *et al*. (1902) were used to calculate the correlation coefficient.

RESULTS AND DISCUSSION

Variance analysis (ANOVA)

Table 1 represents every trait under study. The analysis of variance showed a significant genetic variance among genotypes, suggesting that there is adequate variation among the genotypes.

Estimation of genetic variability

The estimates of genetic advance (GA), genetic advance over mean (GAM), mean, heritability (h2), and phenotypic and genotypic co-efficient of variance (PCV

Table 1. Variance analysis of eighteen characters in okra

Characters	Replication (df-2)	Treatment (df-26)	Error (df-52)	CV%
DFF	1.44	28.67**	0.77	1.49
DFH	2.70	32.21**	0.71	1.23
PH	20.07	2646.50**	6.42	2.10
NPB	0.29	6.66**	0.09	6.68
SD	0.00	0.054**	0.00	3.00
IL	0.04	6.57**	0.06	3.74
FL	0.11	9.22**	0.13	2.66
FD	0.00	0.09**	0.00	1.90
NFPP	0.10	6.97**	0.13	7.97
AFW	1.78	17.16**	0.64	3.98
WFPP	10.91	3028.05**	74.50	9.20
WGF	203.09	1614.70**	104.99	5.10
NSPF	4.25	195.26**	1.45	2.10
WSPP	0.05	3.78**	0.01	1.76
WSPF	6.06	261.10**	9.09	9.22
SW	0.06	17.09**	0.12	2.83
BY	182.95	17004.04**	70.43	2.86
HI	0.83	25.80**	1.25	9.73

*, ** Significant at 5% and 1% level

Table 2. Estimation of genetic variability parameters for eighteen okra characteristics

Characters	GCV%	PCV%	HERITABILITY %	GA	GA%
DFF	5.14	5.35	92.3	7.73	13.04
DFH	4.70	4.86	93.6	8.27	12.02
PH	24.57	24.66	99.3	78.03	64.63
NPB	32.07	32.76	95.8	3.82	82.91
SD	9.71	10.19	90.9	0.33	24.46
IL	21.91	22.23	97.2	3.83	57.03
FL	12.80	13.08	95.9	4.49	33.10
FD	9.00	9.208	95.7	0.44	23.27
NFPP	32.39	33.36	94.3	3.87	83.04
AFW	11.60	12.27	89.5	5.85	28.98
WFPP	33.45	34.69	93.0	79.86	85.15
WGF	11.15	12.26	82.7	53.87	26.78
NSPF	16.69	16.87	97.8	20.98	43.57
WSPF	15.44	15.54	98.7	2.94	40.50
WSPP	28.03	29.50	90.2	22.98	70.29
SW	18.87	19.08	97.8	6.19	49.27
BY	25.62	25.78	98.8	197.11	67.24
HI	24.90	26.74	86.7	7.03	61.24

and GCV) for different aspects are represented in Table 2. The WFPP had a phenotypic coefficient of variation of (34.6) and the DFH had a coefficient of variation of (4.86). The genotypic coefficient of variation varied from (33.4) for WFPP and (4.70) for DFH to have low GCV and PCV, but WSPP, BY, HI. WFPP, NFPP, and the NPB all showed high PCV and GCV values. IL, FD, SD, DFH, and DFF were determined having intermediate GCV and PCV. Based on these features, selection might be successful, and phenotypic expression of these qualities would provide a reliable indicator of genotypic potential. (Syfullah *et al*., 2018; Kumar *et al*., 2013; Thulasiram *et al*., 2017). High heritability, especially when paired with high genetic advance, indicates that these traits can be reliably selected for breeding programs. The high genetic advance as a percentage of the mean (GAM) for these traits confirms their potential for improvement through simple selection, suggesting that additive genetic factors play a major role in their inheritance. This contrasts traits such as DFF and DFH, which showed lower genetic advances despite having high heritability. This suggests the presence of non-additive gene action which complicates the breeding process and may require alternative strategies, such as hybridization or heterosis exploitation.

The level of additive genetic variation for associated traits that exists in the genetic material is the primary determinant of a breeding plan's success. Of the 18 traits, the heritability estimates were the greatest

Table 3. Estimation of the correlation coefficient of 18 okra traits at different phenotypic levels

Traits	DFF	DFH	PH	NPB	SD	IL	FL	FD	NFPP	AFW	WFPP	WGF	NSPF	WSPF	SW	BY	HI	WSPP
DFF	1.000	0.979**	0.405**	-0.147	0.011	0.340**	0.203	-0.454**	-0.136	0.211	-0.054	0.179	-0.168	-0.072	-0.061	0.159	-0.351**	-0.164
DFH		1.000	0.483**	-0.093	0.110	0.371**	0.228*	-0.491**	-0.065	0.254*	0.019	0.219*	-0.217	-0.049	0.000	0.261*	-0.365**	-0.087
PH			1.000	0.135	0.610**	0.745**	0.431**	-0.061	0.222*	0.465**	0.314**	0.374**	-0.302**	0.172	0.363**	0.534**	-0.134	0.330**
NPB				1.000	0.334**	-0.115	-0.085	0.457**	0.960**	-0.010	0.877**	0.042	-0.286**	-0.329**	-0.023	0.587**	0.390**	0.845**
SD					1.000	0.326**	0.422**	0.276*	0.365**	0.652**	0.508**	0.617**	-0.062	0.254*	0.498**	0.722**	-0.060	0.501**
IL						1.000	0.620**	-0.080	-0.059	0.406**	0.048	0.356**	-0.062	0.498**	0.417**	0.228*	-0.006	0.196
FL							1.000	-0.067	-0.001	0.681**	0.215	0.680**	0.299**	0.577**	0.300**	0.153	0.315**	0.335**
FD								1.000	0.458**	0.085	0.455**	0.153	-0.087	-0.077	0.091	0.201	0.337**	0.411**
FPP									1.000	0.086	0.943**	0.132	-0.353**	-0.364**	-0.002	0.608**	0.410**	0.878**
AFW										1.000	0.403**	1.001**	0.400**	0.602**	0.302**	0.372**	0.140	0.407**
FWPP											1.000	0.459**	-0.191	-0.141	0.063	0.640**	0.458**	0.935**
WGF												1.000	0.401**	0.582**	0.281*	0.350**	0.204	0.447**
NSPF													1.000	0.627**	-0.137	-0.318**	0.198	-0.093
WFS														1.000	0.409**	-0.083	0.207	0.089
SW															1.000	0.522**	-0.261*	0.225*
BY																1.000	-0.302**	0.593**
HI																	1.000	0.572**

** Significant at p =0.01; *Significant at p =0.05

(>60%). The following metrics were measured: plant height (99.3%), biological yield (98.8%), weight of each fruit seed per fruit (98.7%), number of seeds per fruit (97.8%), length of the internode (97.2%), fruit length (95.9%), total number of main branches (95.8%), fruit diameter (95.7%), fruits production per plant (94.3%), days to first harvest (93.6%), fruit weight per plant (93.0%), days to first flowering (92.3%), stem diameter (90.9%), weight of 100 seed (90.2%), average fruit weight (89.5%), harvest index (86.7%), plant height (99.3%) in okra exhibited a high heritability indicating that most of the observed variations were due to genetic factors rather than environmental variations (Nanditha *et al*., 2023).

The WFPP (85.1), NFPP (83.1), NPB (82.9), WSPP (70.2), BY (67.2), PH (64.6), HI (61.2), IL (57.0), 100 SW (49.2), NSPF (43.5), WSPF (40.5), FL (33.1), WGF (26.7), and SD (24.4) were, as a percentage of mean, the regions with the greatest genetic advancement. On the other hand, days to first harvest (12.2) and days to first flowering (14.0) showed a significant genetic gain (<20% to 10%).Most of the studied characters showed high heritability coupled with high GAM, at the exception of DFF and DFH, which showed large heritability but low GAM, suggesting the influence of additives genes to regulat their expression of these features and, consequently, was determined to be presenting greater possibilities for reliable and efficient selection for these characters. The results of (Mihretu *et al*., 2014; Nwangburuka *et al.*, 2012; Kumar *et al.*, 2011) were in conformity with these results. DFH and DFF were recorded as a percentage of mean, indicating moderate heritability with moderate to low genetic progress showing that these variables have varying additive and/or nonadditive genes. Because nonadditive gene expressions are more prominent, there was minimal genetic progress and modest heritability. This implies that while there is some heritability, improving these traits may require more sophisticated breeding strategies, such as hybridization or heterosis, rather than simple selection (Raval *et al*., 2018).

Genotypic and phenotypic correlation

The estimated 18 traits genotypic and phenotypic correlation coefficients are shown in Table 3. The outcome showed that, regardless of environmental effect, compared to the phenotypic correlation coefficients, the genotypic correlation coefficient was higher, indicating a natural relationship among different features (Fig. 1). The NFPP (0.878), the NPB (0.845), the HI (0.572), the BY (0.5930), and the SD (0.501) all exhibited a positive and a strong relationship with the WSPP; comparable outcomes were discovered in okra by Abhilash *et al.* (2024). DFF (-0.164), NSPF (-0.093), and DFH (-0.087) at the phenotypic and genotypic levels all indicated a negative and non-significant connection that revealed results that were largely consistent comparable results

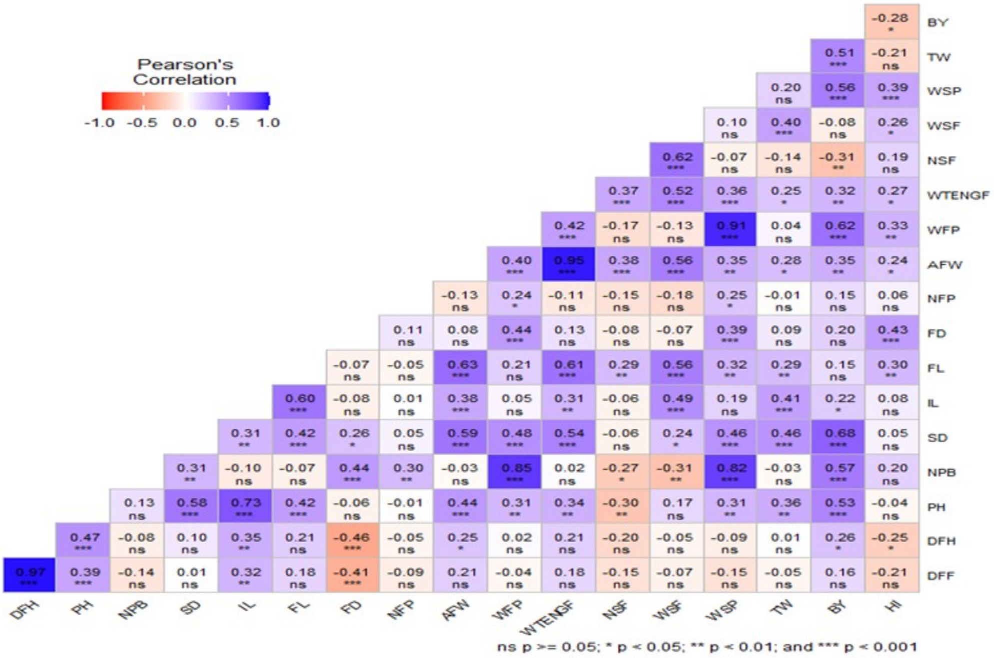

Fig. 1. *Pearson's Correlation table for phenotypical levels among eighteen traits in okra*

provided by earlier workers in garden pea, okra, brinjal (Sharma *et al*., 1998; Chattopadhyay *et al*., 2011; Mohammad *et al*., 2017; Chavan *et al*., 2019). This illustrates how the different characters are connected. For every character combination under investigation, the genotypic correlation coefficients are generally higher than the phenotypic correlations, suggesting that there was an innate relationship between the different characters and that the environment had little effect on the phenotypic expression of the correlation. Understanding the correlation between the traits, having a high positive significant correlation towards the weight of seed per plant breeders can combine these traits in breeding programs.

Path analysis

The primary goal of the breeder is to decrease the potential for yield production while exhibiting particular problems. While some have a direct impact on yield through their significance, others have an indirect effect through their influence on the development and behaviour of other features. It is consequently better to recognize how other factors directly and indirectly influence yield. The Path analysis was utilised to determine each feature's relative worth and set limitations on the overall number of characteristics utilized in selection programs. Study of the routes analysis at the genotypic level and the indirect and direct impact on genotypic features on yield can provide insight into how plant elements coordinate to produce yield. The estimated characteristics genotypic and phenotypic path coefficient analyses are shown in Table 4 and Fig. 2. WFPP (0.935), NFPP (0.878), NPB (0.845), HI (0.593), BY (0.572), and WGF (0.4478) all showed a strong positive direct influence towards WSPP. DFF (-0.164), NSPF (-0.093), and DFH (-0.087) all showed a great but negative direct influence on the production of fruits per plant, indicating that selection of these traits hasdirect effect on fruit yield per plant, thus highlighting their importance for selection in okra breeding programs. Similar results have been reported earlier in okra crop (Magar *et al*., 2009; Prakash *et al*., 2010; Sateesh *et al*., 2011; Ranga *et al*., 2022; Nanditha *et al*., 2023).

Genetic divergence

The mean value of clusters for all 18 features under investigation varied in magnitude, according to the cluster mean of the twenty-seven variants shown in Table 5. The biological yield (357.21), weight of 10 green fruit (201.48), and number of seeds per fruit (163.14) showed the highest mean values in Cluster III, while the number of seeds per fruit (505.40), weight of 10 green fruit (186.20), and fruit weight per plant (179.94) showed the highest cluster mean values in Cluster V. Similar genetic divergence results were earlier recorded for fruit weight per plant by Dhankhar *et al*. (2002) among 40 genotypes in okra, Magar *et al*. (2009) observed 14 genotypes of okra reported for weight of 10 green fruit, Chauhan *et al*. (2016) observed 26 genotypes of okra reported for the number of seeds per fruit, Ullangula *et al*. (2022) observed 32 genotypes of okra reported for plant height, Abilash *et al*. (2024) observed 55 okra genotypes reported for biological yield exhibited comparable findings to the present study . Cluster IV contains the highest mean values for biological yield (289.87), weight of 10 green fruits (237.87). Cluster I

Table 4. Path coefficient analysis shows both direct and indirect impacts of 18 traits on okra

Traits	DFF	DFH	PH	NPB	SD	IL	FL	FD	NFPP	AFW	WFPP	WGF	NSPF	WSPF	SW	BY	HI	WSPP
DFF	-1.220	1.135	-0.007	-0.091	-0.003	0.134	-0.063	0.015	0.185	0.037	-0.015	0.020	-0.052	0.056	-0.015	0.182	-0.462	-0.164
DFH	-1.195	1.159	-0.009	-0.057	-0.030	0.147	-0.071	0.016	0.089	0.045	0.005	0.024	-0.067	0.038	0.000	0.299	-0.480	-0.087
PH	-0.493	0.559	-0.018	0.083	-0.164	0.294	-0.134	0.002	-0.301	0.081	0.085	0.041	-0.093	-0.135	0.087	0.612	-0.176	0.330**
NPB	0.179	-0.108	-0.003	0.616	-0.090	-0.045	0.026	-0.015	-1.302	-0.002	0.237	0.005	-0.088	0.257	-0.006	0.672	0.512	0.845**
SD	-0.014	0.127	-0.011	0.206	-0.269	0.129	-0.131	-0.009	-0.495	0.114	0.137	0.068	-0.019	-0.198	0.120	0.827	-0.079	0.501**
IL	-0.415	0.430	-0.014	-0.071	-0.088	0.395	-0.193	0.003	0.080	0.071	0.013	0.039	-0.019	-0.388	0.100	0.261	-0.008	0.196
FL	-0.248	0.264	-0.008	-0.052	-0.114	0.245	-0.311	0.002	0.001	0.119	0.058	0.075	0.092	-0.450	0.072	0.175	0.414	0.335**
FD	0.553	-0.569	0.001	0.281	-0.074	-0.032	0.021	-0.033	-0.622	0.015	0.123	0.017	-0.027	0.060	0.022	0.231	0.443	0.411**
NFPP	0.166	-0.076	-0.004	0.591	-0.098	-0.023	0.000	-0.015	-1.357	0.015	0.255	0.015	-0.109	0.284	-0.001	0.697	0.539	0.878**
AFW	-0.257	0.295	-0.009	-0.006	-0.175	0.160	-0.212	-0.003	-0.116	0.175	0.109	0.110	0.123	-0.470	0.073	0.426	0.184	0.407**
WFPP	0.066	0.022	-0.006	0.540	-0.137	0.019	-0.067	-0.015	-1.280	0.071	0.270	0.051	-0.059	0.110	0.015	0.732	0.602	0.935**
WGF	-0.219	0.254	-0.007	0.026	-0.166	0.140	-0.212	-0.005	-0.180	0.175	0.124	0.110	0.124	-0.454	0.068	0.401	0.269	0.447**
NSPF	0.205	-0.251	0.006	-0.176	0.017	-0.024	-0.093	0.003	0.478	0.070	-0.052	0.044	0.308	-0.490	-0.033	-0.364	0.260	-0.093
WSPF	0.088	-0.057	-0.003	-0.203	-0.068	0.196	-0.180	0.003	0.494	0.105	-0.038	0.064	0.193	-0.781	0.098	-0.096	0.272	0.089
SW	0.074	0.000	-0.007	-0.014	-0.134	0.165	-0.093	-0.003	0.003	0.053	0.017	0.031	-0.042	-0.319	0.241	0.598	-0.344	0.225*
BY	-0.194	0.302	-0.010	0.361	-0.194	0.090	-0.048	-0.007	-0.826	0.065	0.173	0.039	-0.098	0.065	0.126	1.145	-0.397	0.593**
HI	0.429	-0.423	0.003	0.240	0.016	-0.002	-0.098	-0.011	-0.556	0.025	0.124	0.023	0.061	-0.162	-0.063	-0.345	1.314	0.572**

Residual effect = 0.0065 indicating that only 0.65% of the variation in the observed data was left unaccounted for by the model

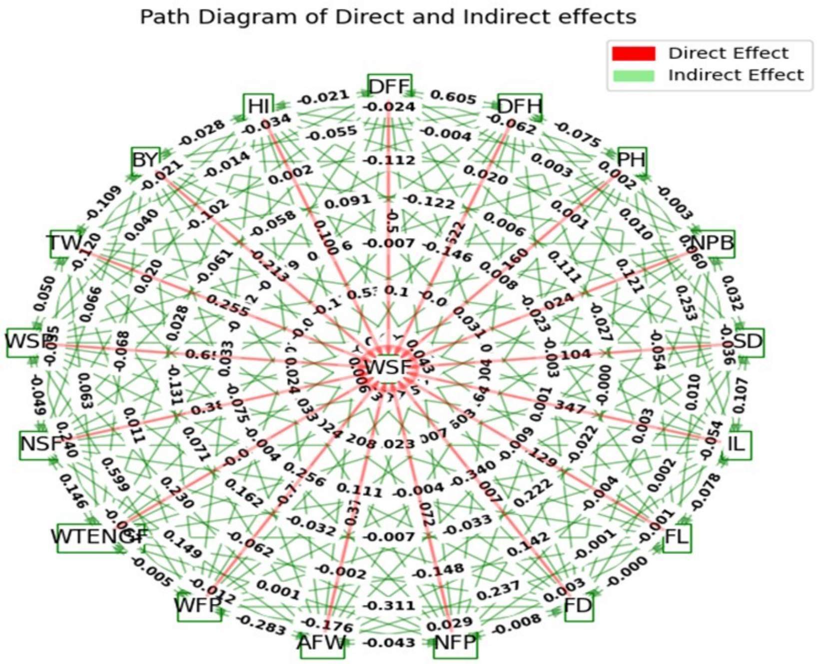

Fig. 2. *Diagram of the path analysis shows the indirect and direct impacts*

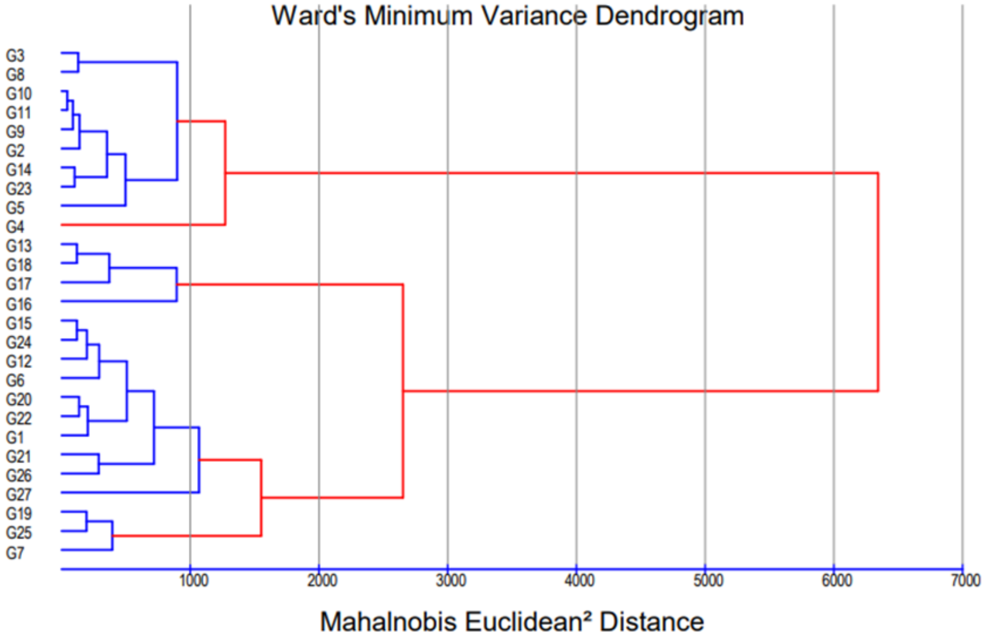

Fig. 3. *Dendrogram using ward's minimum variance for twenty - seven genotypes in okra*

contained the highest mean values for biological yield (283.14), weight of 10 green fruits (205.44), plant height (119.14) and Cluster II contained height mean values for biological yield (198.07) and weight of 10 green fruits (167.24). Lower mean values were observed for stem diameter, internode length and fruit diameter. Evidence suggests that genotypes from distinct clusters have more substantial similarities when genetic distance values are lower. In breeding activities, choosing parents from genetically distinct clusters can be a considered method to maximize heterosis.

The percentage contributions of the various important traits to the genetic divergence represented in (Fig. 4) showed that, all the characters, plant height made the largest contribution (23.93%), followed by biological yield (22.22%), weight of seed per fruit (19.94%), number of seed per fruit (9.4%), and 100 seed weight (10.54%). Thus, focusing on the traits that significantly influenced divergence could encourage crop improvement diversification going forward.

The degree of genetic diversity between clusters can be determined via statistical distance. Multivariate analysis results showed that 27 genotypes were distributed into 5 clusters (Fig. 3). Out of the five clusters, Cluster

Table 5. Cluster mean for eighteen characters of okra

Characters	I	II	III	IV	V
DFF	59.15	59.22	61.08	57.00	57.33
DFH	68.63	67.78	71.00	67.00	68.33
PH	119.14	73.61	163.14	95.97	146.07
NPB	4.66	3.81	4.05	3.20	9.73
SD	1.35	1.16	1.49	1.57	1.55
IL	6.97	4.38	7.66	6.48	5.72
FL	14.12	10.26	14.12	15.00	10.52
FD	1.92	1.89	1.81	1.89	2.25
NFPP	4.75	3.38	4.37	3.07	9.73
AFW	20.58	16.43	20.87	23.82	18.66
WFPP	97.85	55.88	87.61	73.18	179.94
WGF	205.44	167.24	201.48	237.87	186.20
NSPF	49.24	46.91	41.29	70.53	37.47
WSPF	7.50	5.98	7.06	9.43	5.43
SW	12.68	9.62	14.06	13.23	12.77
BY	283.14	198.07	357.21	289.87	505.40
HI	12.55	9.67	8.72	9.93	10.46
WSPP	34.55	18.76	30.46	28.15	52.84

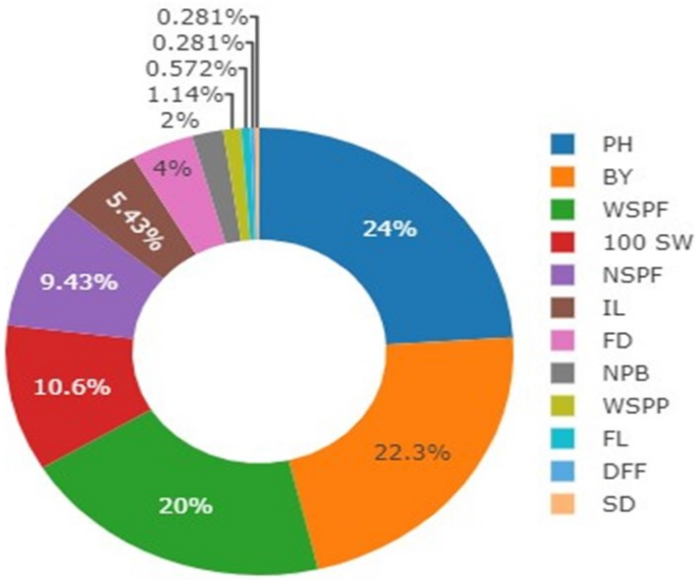

Fig. 4. *Contribution of individual characters towards divergence*

III, with the smallest intra-cluster distance, indicates that the genotypes within this group are genetically similar, suggesting limited variability and potentially fewer options for selecting highly divergent traits. In contrast, Cluster IV, which exhibited the largest intra-cluster distance, implies greater genetic variability, offering better prospects for selecting diverse traits and improving breeding outcomes. The maximum inter-cluster distance was observed between Cluster V and the other clusters, particularly Cluster III, signifying that genotypes in Cluster V are genetically distant from the rest. This large genetic distance indicates that these genotypes could serve as excellent parents for hybridization programs, as crossing genetically distant genotypes often leads to hybrid vigor. The clustering results, therefore, provide valuable insights for selecting parent genotypes to improve desirable traits in future breeding programs.

Conclusion

In the present study, 18 traits were studied, and the genetic diversity analysis of 27 okra (Abelmoschus esculentus (L.) Monech) germplasm varieties was evaluated. The germplasm beneath cluster IV possessed the most diversity, as illustrated by the highest intra-cluster distance observed in this cluster . The greatest inter-cluster distance was identified among clusters V and II. Because of their greater diversity, these two cluster genotypes might benefit crossing programs. More divergence was seen in the biological yield, weight of 10 green fruits, days to first flowering, and plant height. It was determined in correlation and path analysis that selection for characteristics including fruit production per plant, total number of main branches, harvest index, and biological yield affected seed weight per plant. Hence, selecting these features as a priority would aid in increasing the weight of seed produced per plant.

Conflict of interest

The authors declare that they have no conflict of interest.

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