

Revealing genetic diversity of okra (*Abelmoschus esculentus* L. Moench) for yield improvement

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ABSTRACT

Fifteen Okra (*Abelmoschus esculentus* L. Moench) accessions were evaluated for 10 yield component traits during spring season of 2019. Assessment of genotypes is very essential and the information about the variation present in accessible breeding materials helps in successful selection of parents for further use in crop improvement. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) occurred for seven traits viz., plant height, first flowering node, fruit length, number of fruits per plant, number of seeds per fruit, 100 seed weight and yield per plant and narrow differences between GCV and PCV indicated the influence of environment was negligible. High estimates of heritability, coupled with moderate to high genetic advance as a percent over mean, were recorded for all traits. First flowering node, fruit diameter and number of seed per fruit had a significant and positive correlation with yield per plant. First flowering node and number of seed per fruit had the highest direct positive effect on yield per plant. The principal component analysis indicated the first 3 principal components (PC I, II and III) contributed 69.371% of total variation among traits describing accessions. Cluster analysis indicated hybridization of accessions among inter-cluster I and II could be used to develop stable, uniform varieties in diverse climatic conditions. IC 014600 and IARI Selection 2 are distantly placed and can be used for further crop breeding.

Keywords: Cluster analysis, GCV, Heritability, Okra, PCV, Principal component Analysis, Yield

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is known globally and one of the most used species of the Malvaceae family. Its origin is believed to be at Ethiopia (Africa). The crop is cultivated around the world in tropical, sub-tropical and warm regions. Improvements for better quality okra, will initiate higher export potential not only in India but also African and South Eastern nations when compared to other field crops. Okra has high nutritive content as well as high anti-oxidant value (Elkhalifa *et al.*, 2021). Edible okra pods are constitutes a high source of protein, carbohydrate, iron, fibre, mineral matter, calcium, fat, phosphorous and high calorific values (Petropoulos *et al.*, 2018). Dried seeds are used as substitute or as an additive to coffee. Characterization of genotypes is prominent for current and future genetic improvement programs of the crop. Plant morphological characterisation has been advised as the initial step before doing extensive molecular research and biochemical studies (Temam *et al.*, 2020). It can produce a

permanent gain in the mean performance of plant, while high heritability of the traits gives a better opportunity to select precisely for the traits of interest. Since, yield potential is a restricting factor because of poor yielding cultivars and the incidence of different pests and diseases, therefore, knowledge of genetic diversity is a pre-requisite to develop hybrids/varieties or to identify parental lines to use in heterosis breeding. Crop improvement in okra focuses on plant height, higher yield, early flowering, fruit length and disease and pest resistance (Ranga *et al.*, 2019). The aim of current investigation was to evaluate the nature and magnitude of genetic divergence for fruit yield and its association traits using multivariate analysis.

MATERIALS AND METHODS

The field experiment was conducted at the Experimental Farm of Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab, India, during February – May 2019. Experimental Farm is situated at

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31°14'31.0"N latitude and 75°41'50.2"E longitude with an altitude of 234 meters above the sea level. The soil of experimental site was loamy in origin and poor in organic matter. The climate of the area represents tropical condition with semi-arid, hot and subtropical monsoon type.

Fifteen accessions were repatriated from Indian Council of Agricultural Research – National Bureau of Plant Genetic Resources, New Delhi, India and their details are represented in Table 1. These accessions were grown in three replications of 5 meter length with

a spacing of 60 cm between lines and 30 cm between plants in a Randomised Complete Block Design. Before sowing, farm yard manure (25 t/ha) and half dose nitrogen and full dose of P and K were applied and remaining N was given as top dressing in a ratio of 125:75:63 kg/ha as suggested by Package of Practices for Vegetable Crops by Dr YS Parmar University of Horticulture and Forestry, Nauni, Solan, HP. The recommended package of practices and plant protection measures to raise a good crop were timely and uniformly applied.

Table 1: Fifteen Okra (*Abelmoschus esculentus* L. Moench) accessions are patriated from ICAR-NBPGR used in the study

Sr. No.	Genotype	Country	Acquired On	Cultivar Name
1.	EC305615	BANGLADESH	28/05/90	T/B-78/-
2.	EC305740	ITALY	29/05/90	ORS-773/-
3.	EC305768	ITALY	29/05/90	ORS-202/-
4.	EC306696	SINGAPORE	08/06/90	ORS-1106/ESC
5.	EC359637	-	-	-
6.	IC003769	India	-	-
7.	IC010265	Gujarat, India	09/01/63	-
8.	IC013356	India	-	-
9.	IC013664	Tamil Nadu, India	14/09/67	-
10.	IC014018	India	-	-
11.	IC014026	India	-	-
12.	IC014600	Himachal Pradesh, India	31/08/70	-
13.	Akola bahar	Maharashtra, India	-	-
14.	IARI Selection 2	Delhi, India	-	-
15.	AKO107	Maharashtra, India	-	-

Where, EC: Exotic collection, IC: Indigenous collection and IARI: Indian Agricultural Research Institute

Data were collected during plant development stages and upon harvesting for phenology traits viz., days to 50% flowering, days to 80% maturity, plant height (cm), first flowering node, fruit diameter (cm), fruit length (cm), number of fruit per plant, number of seed per fruit, 100 seed weight (g) and yield per plant (g) from five representative plants of each accession. These were recorded according to the ICAR-NBPGR descriptor list developed for okra. Yield per plant was taken as dependent variable whereas all other traits were considered as independent variables. Data collected were subjected to ANOVA (Analysis of Variance) to evaluate the presence of statistically significant differences among accessions for the traits studied (Panse and Sukhatme, 1954). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated as

per the formula suggested by Burton (1952). GCV and PCV values were categorized as low (<10%), moderate (10-20%) and high (>20%) as indicated by Deshmukh *et al.* (1986). Genetic advance and heritability were calculated by using the formula of Allard (1960). Heritability of less than 30% is considered as low, moderate (31% to 60%) and high (>60%). Genetic advance lesser than 10% is considered as low, moderate (11% to 20%) and high (>20%).

Genotypic and phenotypic correlation coefficient was calculated using OP-STAT (Sheoran *et al.*, 1998) to determine the relation of one trait with another. Genotypic correlation coefficients plot was created using PAST (Hammer *et al.*, 2001). Genotypic path analysis was calculated using OP-STAT (Sheoran *et al.*, 1998) to determine the direct and indirect effects of traits in correlation to dependent trait.

Principal component analysis (PCA) was calculated to estimate traits which accounted more for total variation using OP-STAT (Sheoran *et al.*, 1998). Scree plot and biplot were created using PAST (Paleontological Statistics) (Hammer *et al.*, 2001). Accessions were analysed for distance matrix and construction of dendrogram was done by Ward's method (Ward, 1963) using PAST (Hammer *et al.*, 2001).

RESULTS AND DISCUSSION

Analysis of Variance and Variability Parameters

The accessions showed highly positive and significant variations for all the traits under study. Yield per plant observed highest positive and significant variation and the lowest was reported for fruit diameter. Alake (2020) also reported similar results in okra. Yield per plant ranged from 43.32g (EC 305768) to

221.660g (AKO 107) with a mean of 142.760 g. In the genetic variability studies (Table 2), phenotypic coefficient of variation (PCV) was higher than the comparing genotypic coefficient of variation (GCV) for most traits with the close relationship between them, therefore, the environment has low impact and subsequently phenotypic performance of traits ought to be utilized for selection. High PCV and GCV values were observed for most of the traits whereas fruit diameter, days to 80% maturity and days to 50% flowering were moderate which exhibited the presence of high magnitude of genetic diversity in the population examined. The previous workers also observed similar trend of greater magnitude of PCV and GCV (Ranga *et al.*, 2021; Shanthakumar and Salimath, 2010; Prakash *et al.*, 2011). Narrow differences between the phenotypic and genotypic coefficient of variation in most of the traits indicated that these were comparatively stable to environmental variation.

Table 2: Estimates of variability parameters for various traits of okra accessions

Traits	Mean	Range	GCV	PCV	h^2	GA	GAM
DF	48.190	33.000-59.790	15.520	15.680	97.890	15.240	31.620
DM	94.010	76.720-130.420	15.650	15.950	96.370	29.760	31.660
PH	27.740	16.600-43.500	31.870	32.260	97.590	18.000	64.870
FN	10.980	7.500-15.680	21.900	22.070	98.510	4.920	44.780
FD	1.760	1.300-2.410	18.380	18.610	97.590	0.660	37.400
FL	6.890	3.310-14.310	40.310	40.400	99.540	5.710	82.850
FP	9.880	4.970-18.300	47.020	47.130	99.510	9.540	96.610
SF	25.130	17.100-38.700	25.630	25.790	98.760	13.190	52.470
SW	6.750	3.380-14.070	41.160	41.260	99.500	5.710	84.570
YP	142.760	43.320-221.660	44.960	45.020	99.740	132.050	92.500

Where, DF: Days to 50% flowering, DM: Days to 80% maturity, PH: Plant height (cm), FN: First flowering node, FD: Fruit diameter (cm), FL: Fruit length (cm), FP: Number of fruit per plant, SF: Number of seed per fruit, SW: 100 Seed weight(g), YP: Yield per plant (g), GCV: Genotypic coefficient of variation (%), PCV: Phenotypic coefficient of variation (%), h^2 : Heritability (%), GA: Genetic advance (%) and GAM: Genetic advance as per cent of mean

Heritability is a good index of transmission of traits from parents to their offsprings (Falconer, 1981). All the ten traits displayed high heritability (>60%) coupled with high genetic advance (>20%) as percent over mean. This focuses on the pre-dominance of additive gene effects for these traits; thus, crop improvement through selection based on these traits would be beneficial.

Genotypic and Phenotypic Correlation Coefficient Analysis

The correlation is the overall or net impact of the segregating genes; few genes may increase both the traits leading to the positive correlation, whereas the others might increase the one and decrease the other, causing the negative correlation (Falconer, 1981). Thus, to accumulate an optimum combination of yield contributing traits in a single genotype, it is essential to know the implication of the inter-relationship of various traits (Ranga *et al.*, 2019).

Table 3: Genotypic (rg) and phenotypic (rp) correlation coefficient analysis for various traits of okra accessions

TRAITS		DF	DM	PH	FN	FG	FL	FP	SF	SW	YP
DF	rg	1.000									
	rp	1.000									
DM	rg	0.045	1.000								
	rp	0.039	1.000								
PH	rg	0.466**	0.219	1.000							
	rp	0.463**	0.212	1.000							
FN	rg	-0.116	0.092	-0.128	1.000						
	rp	-0.113	0.093	-0.125	1.000						
FG	rg	-0.536**	-0.084	-0.478**	0.603**	1.000					
	rp	-0.529**	-0.082	-0.472**	0.599**	1.000					
FL	rg	0.614**	-0.027	0.301*	-0.430**	-0.418**	1.000				
	rp	0.595**	-0.019	0.291*	-0.422**	-0.408**	1.000				
FP	rg	0.315*	0.151	0.334*	0.073	0.001	0.264	1.000			
	rp	0.311*	0.145	0.327*	0.072	0.002	0.258	1.000			
SF	rg	0.072	-0.215	0.003	-0.092	0.024	-0.288	0.211	1.000		
	rp	0.069	-0.211	0.003	-0.091	0.023	-0.280	0.212	1.000		
SW	rg	-0.079	0.080	-0.174	-0.290	-0.107	0.022	-0.521**	-0.605**	1.000	
	rp	-0.081	0.077	-0.169	-0.289	-0.105	0.029	-0.515**	-0.600**	1.000	
YP	rg	-0.215	0.054	-0.004	0.582**	0.529**	-0.496**	0.210	0.563**	-0.552**	1.000
	rp	-0.211	0.054	-0.003	0.579**	0.527**	-0.488**	0.209	0.560**	-0.547**	1.000

*, ** Significant at 5% and 1% levels, respectively.

Where, DF: Days to 50% flowering, DM: Days to 80% maturity, PH: Plant height (cm), FN: First flowering node, FG: Fruit diameter (cm), FL: Fruit length (cm), FP: Number of fruit per plant, SF: Number of seed per fruit, SW: 100 Seed weight(g), YP: Yield per plant (g), rg: Genotypic correlation coefficient and rp: Phenotypic correlation coefficient

In the present investigation, the genotypic and phenotypic correlation coefficient analysis is represented in Table 3. A genotypic correlation coefficient analysis plot has been represented in Figure 1. All traits were significant at both genotypic and phenotypic levels (except fruit length). The plant height showed a highly significant and positive correlation with days to 50% flowering. Fruit diameter showed significant and positive correlation with first flowering node. Fruit length showed significant positive correlation with days to 50% flowering and plant height (only at genotypic level). Number of fruits per plant have significant and positive correlation with days to 50% flowering and plant height.

Yield per plant has significant and positive correlation with first flowering node, fruit diameter, and number of seed per fruit. Comparable results for okra yield having positive relationship were proposed by Ranga *et al.*, (2021), Alam *et al.*, (2021) and Raval *et al.*, (2019). Fruit diameter had significant and negative correlation with days to 50% flowering and plant height. Fruit length had significant and negative correlation first flowering node and fruit diameter. 100 seed weight had significant and negative correlation number of fruits per plant and number of seeds pre fruit. Yield per plant had significant and negative correlation with fruit length and 100 seed weight.

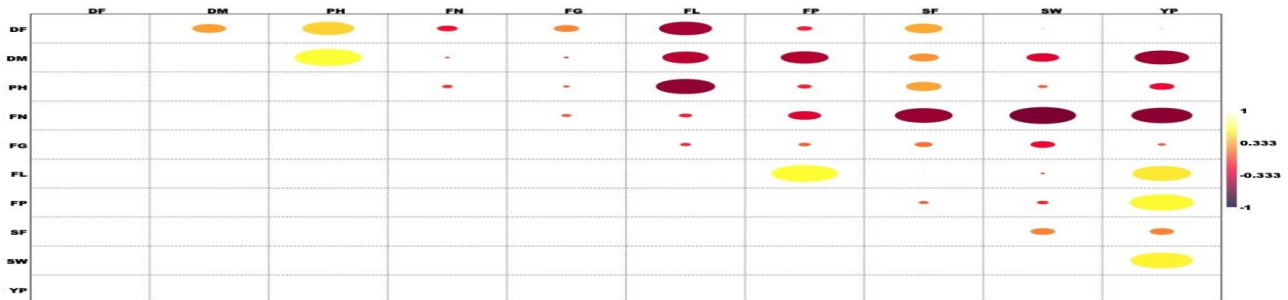


Figure 1: Genotypic correlation studies in Okra accessions

Genotypic and Phenotypic Path Coefficient Analysis

Path analysis provides information about the cause and effect in understanding the association between two variables. It allows the assessment of the direct effects of different traits on crop yield just as their indirect effects by means of other component traits. Hence, it gives a premise for the selection of predominant genotypes from diverse populations (Komolafe *et al.*, 2021). The genotypic and phenotypic path coefficient analysis is represented in Table 4 and the data revealed that number of seed per fruit

had the highest direct positive effect towards the yield per plant followed by first flowering node, fruit length, 100 seed weight, plant height, days to 80% maturity and number of fruits per plant. Traits such as days to 50% flowering and fruit diameter had a direct but negative effect. Residual effect ($rg=0.135$, $rp=0.173$) indicated the effect of other possible independent traits, which were not included in the study, on the dependent variable i.e. yield per plant. The results are in accordance with findings of Ranga *et al.*, (2021), Dwivedi and Sharma (2017) and Hallur *et al.*, (2016).

Table 4: Genotypic and phenotypic path coefficient analysis showing direct (diagonal and bold) and indirect effect of different traits on yield per plant for various okra accessions

TRAITS		DF	DM	PH	FN	FG	FL	FP	SF	SW
DF	gp	-0.723	0.006	0.121	-0.126	0.053	0.376	0.028	0.087	-0.039
	pp	-0.400	0.005	0.113	-0.083	-0.059	0.158	0.012	0.060	-0.017
DM	gp	-0.032	0.143	0.057	0.100	0.008	-0.016	0.014	-0.258	0.039
	pp	-0.015	0.126	0.052	0.069	-0.009	-0.005	0.006	-0.184	0.016
PH	gp	-0.337	0.031	0.260	-0.139	0.048	0.184	0.030	0.004	-0.085
	pp	-0.185	0.027	0.244	-0.092	-0.053	0.078	0.012	0.002	-0.036
FN	gp	0.084	0.013	-0.033	1.088	-0.060	-0.264	0.007	-0.110	-0.142
	pp	0.045	0.012	-0.031	0.736	0.067	-0.112	0.003	-0.079	-0.061
FG	gp	0.388	-0.012	-0.124	0.657	-0.100	-0.256	0.000	0.029	-0.053
	pp	0.211	-0.010	-0.115	0.441	0.111	-0.109	0.000	0.020	-0.022
FL	gp	-0.444	-0.004	0.078	-0.468	0.042	0.612	0.024	-0.347	0.011
	pp	-0.238	-0.002	0.071	-0.311	-0.045	0.266	0.010	-0.244	0.006
FP	gp	-0.228	0.022	0.087	0.080	0.000	0.161	0.090	0.254	-0.256
	pp	-0.124	0.018	0.080	0.053	0.000	0.069	0.038	0.184	-0.109
SF	gp	-0.052	-0.031	0.001	-0.100	-0.002	-0.177	0.019	1.202	-0.297
	pp	-0.028	-0.027	0.001	-0.067	0.003	-0.075	0.008	0.872	-0.127
SW	gp	0.057	0.011	-0.045	-0.315	0.011	0.013	-0.047	-0.728	0.491
	pp	0.033	0.010	-0.041	-0.213	-0.012	0.008	-0.020	-0.524	0.212

[Residual (rg) are 0.13536 Residual (rp) are 0.17354]

Where, DF: Days to 50% flowering, DM: Days to 80% maturity, PH: Plant height (cm), FN: First flowering node, FG: Fruit diameter (cm), FL: Fruit length (cm), FP: Number of fruit per plant, SF: Number of seed per fruit, SW: 100 Seed weight (g), gp: genotypic path coefficient and pp: phenotypic coefficient

Principal Component Analysis

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variation at each axis of differentiation. PCA (Table 5; Table 6) was performed to provide partial visualization of the data set in a reduced dimension and first three principal components have eigen values >1 and contributed to 69.371 per cent variation. From the loading of the variables in PC I, it was found that days to 50% flowering, days to 80% maturity, plant height, fruit length, number of fruits per plant and yield per plant were the dominant features which contributed to 31.601 per cent of the total variation. In PC II, days to

50% flowering, plant height, first flowering node, number of seeds per fruit, 100 seed weight and yield per plant exerted maximum influence which accounts to 24.171 per cent of the total variation. Fruit diameter, number of fruits per plant and 100 seed weight were the dominant features in PCA III which accounted to 13.599 per cent of the total variation. Bhardwaj *et al.*, 2021, Ranga *et al.*, (2021) and Amoatey *et al.*, (2015) also indicated high genetic diversity using PCA. Few traits viz., plant height, 100 seed weight, days to 50% flowering and fruit yield per plant offered more towards variation as accounted for by different scientists in okra (Ranga *et al.*, 2022; Bhardwaj *et al.*, 2021; Amoatey *et al.*, 2015).

Table 5: Eigen value and percentage of variation explained by first five principal components and correlations between PC scores and agro-morphological traits

TRAITS	PC I	PC II	PC III	PC IV	PC V
DF	0.240	-0.370	0.233	-0.291	-0.347
DM	0.424	-0.158	0.031	0.468	0.159
PH	0.333	-0.348	0.061	0.188	-0.428
FN	0.223	0.500	0.131	-0.099	-0.117
FG	0.044	-0.056	0.639	-0.502	0.360
FL	-0.449	0.134	0.154	0.375	0.158
FP	-0.381	-0.055	0.437	0.280	-0.464
SF	0.008	-0.481	0.184	0.268	0.513
SW	-0.217	-0.367	-0.514	-0.300	0.040
YP	-0.454	-0.277	0.053	-0.133	-0.149
Eigenvalues	3.160	2.417	1.360	0.968	0.708
Total variation (%)	31.601	24.171	13.599	9.678	7.079
Cumulative variation(%)	31.601	55.772	69.371	79.049	86.128

Where, DF: Days to 50% flowering, DM: Days to 80% maturity, PH: Plant height (cm), FN: First flowering node, FG: Fruit diameter (cm), FL: Fruit length (cm), FP: Number of fruit per plant, SF: Number of seed per fruit, SW: 100 Seed weight(g), YP: Yield per plant (g) and PC: Principal component

A scree plot was drawn between all principal component and the total variation

caused by them (Figure 2).

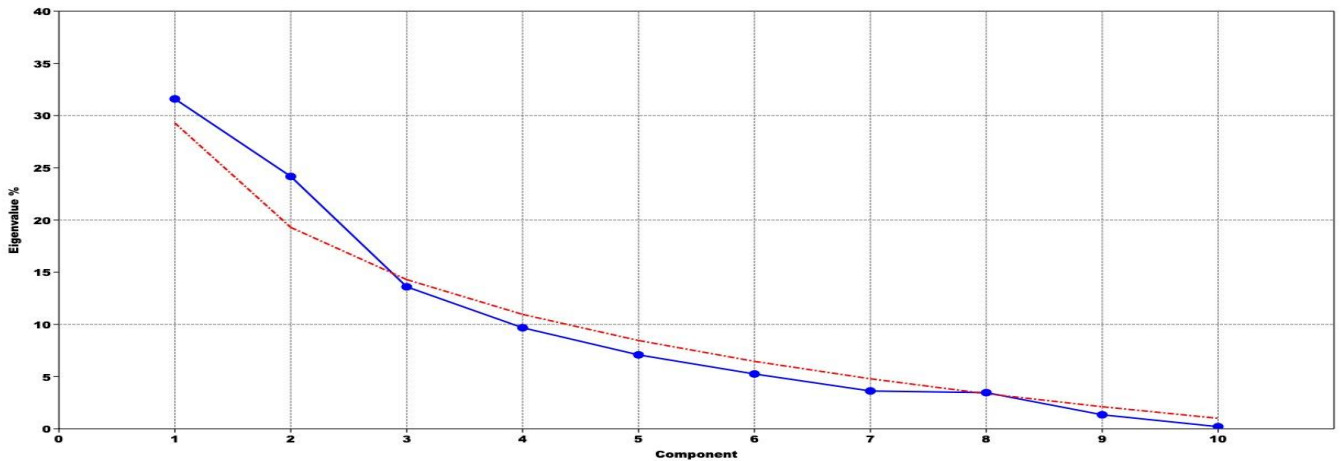


Figure 2: Scree plot depicting total variation caused by each component

A biplot was drawn using the values of PC I and PC II (Figure 3). The greater the angle between the traits, the lesser the correlation between them. Placement of accessions in quadrants signifies variability. Accessions are placed in quadrants using vector scores of PC I and PC II. However, no obvious grouping and overlapping of accessions was observed demonstrating the distinctness of the accessions across the collection. In biplot graph of PCA, the quadrant I (+,+) consisting of four accessions formed the cluster 1, which were highly influenced by three traits viz. 100 seed weight, yield per plant and number of fruits per plant

through accessions spread towards midway through X and Y-planes of quadrant-I. The cluster II corresponding to the quadrant II (-,+) contained two accessions, which were influenced by number of seed per fruit, fruit diameter, days to 50% flowering, plant height and days to 80% maturity. Similarly, the cluster III corresponding to quadrant III (-,-) consisted also of five accessions which were influenced by first flowering node only whereas the cluster IV corresponding to quadrant IV (+,-) also consisted of four accessions which were influenced by fruit length, respectively.

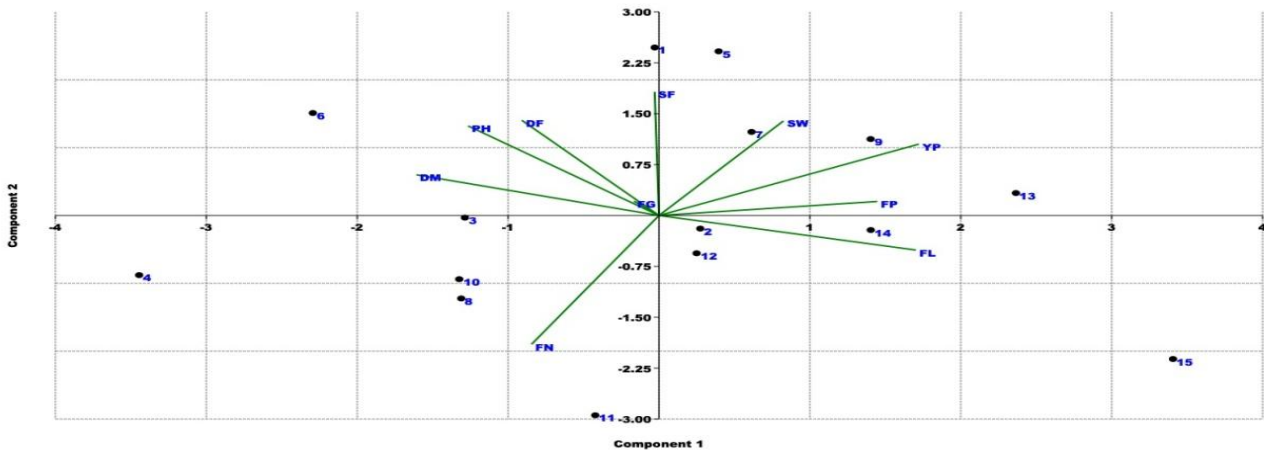


Figure 3: Biplot between PC I and PC II showing contribution of various traits responsible for variability in diverse okra accessions

Table 6: Vector scores of accessions on the basis of principal components

Accession	PC I	PC II	PC III	PC IV	PC V	PC VI	PC VII	PC VIII	PC IX	PC X
EC305615	0.016	-1.592	1.365	-1.058	1.588	-0.448	0.744	-0.240	-0.691	1.29
EC305740	-0.154	0.124	0.210	-0.320	0.424	-1.669	1.671	1.368	1.502	-1.238
EC305768	0.724	0.020	-0.527	0.989	1.204	-0.902	-1.546	0.433	-1.803	-0.735
EC306696	1.938	0.565	0.674	-0.586	-1.349	-0.030	0.584	0.964	-1.251	1.059
EC359637	-0.222	-1.556	-1.276	1.260	-0.190	0.967	1.837	-1.091	-0.582	-0.138
IC 003769	1.290	-0.971	0.290	1.252	0.066	1.487	-1.011	1.092	1.729	0.25
IC 010265	-0.345	-0.792	1.093	-0.419	-2.109	0.225	-0.339	-0.746	-0.142	-1.231
IC 013356	0.737	0.786	-0.587	-0.241	-0.372	-0.831	-0.352	-1.497	1.521	1.531
IC 013664	-0.789	-0.725	-2.277	-2.101	-0.155	0.307	-0.931	0.761	0.069	0.375
IC 014018	0.745	0.603	-0.290	-0.511	0.723	0.766	0.216	0.201	0.138	-1.704
IC 014026	0.238	1.894	0.061	-0.724	0.616	1.237	0.486	-1.299	-0.347	-0.575
IC 014600	-0.140	0.358	-0.350	1.213	0.482	-1.140	-0.221	-1.024	0.335	0.341
Akola Bahar	-1.331	-0.213	1.615	-0.333	0.480	0.309	-1.315	-0.569	0.375	-0.265
IARI Selection 2	-0.790	0.138	-0.226	0.652	-1.420	-1.294	-0.325	0.213	-0.544	-0.22
AKO 107	-1.916	1.360	0.228	0.928	0.010	1.015	0.502	1.432	-0.309	1.261

Cluster Analysis

The hierarchical cluster analysis among accessions for yield and yield contributing traits were grouped accessions into 2 major clusters (Figure 4). Clustering shows that each group is homogeneous with respect to certain characteristics and each group should be different from the other groups with respect to the same characteristics (Melaku *et al.*, 2022). Clustering was not based on a similar geographical origin. Cluster I accommodated 7 accessions (EC 305768, EC306696, IC 003769, IC 013356, IC 014018, IC 014026 and IC 014600) and cluster II comprised of 8 accessions (EC 305615, EC 305740, EC 359637, IC 010265, IC 013664, Akola Bahar, IARI

Selection 2 and AKO 107). These were further divided into two sub-clusters. In order to determine diversity among accessions, and verifying accessions by distance, cluster analysis placed the accessions in a single group (Sneath and Sokal, 1973). Accessions which are located far from each other have more variation between them and can be used to obtain improved cultivars. Accessions which are distantly placed are more diverse; those which are closer are morphologically similar. The maximum intra-cluster distance was observed for IC 0104018 and IC014600 in cluster 1 and IARI Selection 2 and AKO 107 in cluster 2 while maximum inter-cluster distance was observed for IC 014600 and IARI Selection 2.

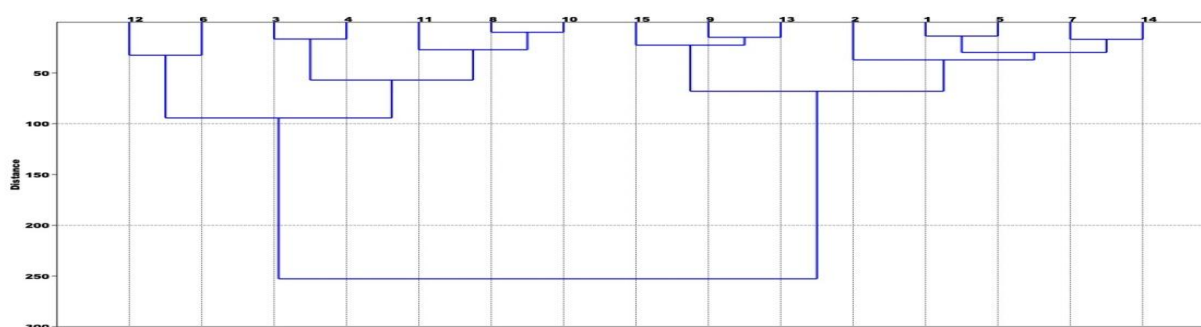


Figure 4: Dendrogram showing genetic relationship among various okra accessions

CONCLUSION

Higher variations were observed for yield per plant, plant height and days to 50% flowering displaying a wide reach showing the handiness of accessions in breeding programmes. Yield per plant showed positive correlation with first flowering node, fruit diameter and number of seed per fruit, hence, it can be used for developing high yielding. Days to 80% maturity, plant height, first flowering node, fruit length, number of fruits per plant, number of seed per fruit and 100 seed weight had direct positive effect towards the yield per plant. The first three principal components accounted cumulative variance to be 69.371% of the total variation and traits *viz.* days to 50% flowering, days to 80% maturity, plant height, 100 seed weight and yield per plant assorted for more than 50 % phenotypic variation. IC 014600 and IARI

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Selection 2 were distantly placed, indicating maximum differences between them, hence, they can be further used in breeding programme.

CONFLICT OF INTEREST

All authors declare that they agree on all parameters and have no conflict of interest.

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