Original Research Paper

Diversity analysis of phenotypic traits in okra
(*Abelmoschus esculentus* L. Moench)

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ABSTRACT

It is necessary to obtain cultivars which provide high yield by exploiting desirable traits from wild genotypes of okra (*Abelmoschus esculentus* L. Moench). Okra genotypes were evaluated for phenotypic traits during 2018. High genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) occurred for nine traits 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 nine traits. Thousand seed weight had a positive, significant, correlation with yield per hectare. Plant height and number of fruits per plant had direct and positive effects towards the yield per hectare The principal component analysis indicated the first 3 principal components contributed 80.517% of total variation among traits describing genotypes. Cluster analysis indicated hybridization of genotypes among inter-cluster I and II could be used to develop stable, uniform varieties in diverse climatic conditions. EC359637 and IARI Selection 2 are distantly placed and can be used for overall improvement in further crop breeding.

Keywords: Cluster analysis, GCV, heritability, okra, PCV, principal component analysis and yield.

INTRODUCTION

Okra or ladies' finger (*Abelmoschus esculentus* L.) belongs to the mallow family i.e., Malvaceae. It is a flowering, hairy, herbaceous annual plant grown for its edible pods. Its origin is considered to be at western regions of Africa because of the presence of diverse wild species (De Candolle, 1886). The development of better-quality vegetables, has a lot higher export potential not only in India but has recently discovered a way to the African and South-Eastern Nations as compared to other field crops (Ankita *et al.,* 2021).

Okra is one of the major vegetable crops grown for its high nutritive content, high export potential and antioxidant value. Okra fruits are edible constituting a high source of protein and minerals with about 88% moisture, 7.7% carbohydrate, 2.2% protein, 1.5% iron, 1.1% fibre, 0.7% mineral matter, 0.09% calcium, 0.2% fat, 0.08% phosphorous and 41 (kcal) calorific values (Bhat and Bisht, 2006). The vitamin content is 58 IU of vitamin A, 0.06 mg vitamin B, 0.06 mg nicotinic acid, 0.06 mg riboflavin and 16 mg vitamin C per 100 grams of raw okra fruits (USDA, 2019).

The yield potential is a limiting factor because of poor yielding varieties and the incidence of different pests and diseases (Tripathi *et al.,* 2011). Crop improvement in okra focuses on plant height, higher yield, early flowering, fruit length and biotic and abiotic stress resistance (Ranga *et al.,* 2019). Assessment of genotypes for estimating genetic diversity for yield and yield contributing attributes 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. The current investigation was undertaken to assess the nature and magnitude of genetic divergence and to identify the potential okra genotypes towards yield and its association with other morphological traits.

MATERIALS AND METHODS

Planting material

The field experiment was at the Experimental Farm of the Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Phagwara, Punjab, India, during February – May 2018. The accessions were sourced from the Indian Council of Agricultural Research – National Bureau of Plant Genetic Resources, New Delhi and their details are represented in Table 1.

Field evaluation and data collection

The soil of the experimental site was loamy in origin and was ploughed before sowing. The climate of the area represents a tropical condition with semi-arid, hot and subtropical monsoon types. Before sowing, farmyard manure and urea were applied as basal doses. The recommended package of practices and plant protection measures to raise a good crop were timely and uniformly applied.

The experiment was carried out in a completely randomized block design with three replications. Each accession was soaked in water for 8 hours and sown at a spacing of 45×30 cm of 5 m length. The following observations were recorded during plant growth and development stages viz., days to 50% flowering [DF], days to 80% maturity [DM], plant height [PH (cm)], first flowering node [FFN], fruit diameter [FD (cm)], fruit length [FL (cm)], number of fruit per plant [FP], number of seed per fruit [SF], 1000 seed weight [TSW (g)], yield per plant [YP (g)] and yield per hectare [YH (t/ha)] from 5 representative plants of each genotype.

Data analysis

Data collected were subjected to ANOVA (Analysis of Variance) to evaluate the presence of statistically significant differences among genotypes for the traits studied (Panse and Sukhatme, 1954). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated as per the formula suggested by Burton, 1952. Genetic advance and heritability were calculated by using the formula of Lush, (1949) and Allard (1960). Heritability of more than 80% is considered high. Genotypic correlation coefficients, path analysis, principal component analysis (PCA) and cluster analysis were calculated using OP-STAT (Sheoran *et al.,* 1998) and PAST (Hammer *et al.,* 2001). Yield per hectare was taken as a dependent variable whereas, all other traits were considered as independent variables.

Table 1: Fifteen okra (*Abelmoschus esculentus* L. Moench) genotypes repatriated from NBPGR used in the study.

Sl. 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	-	-

RESULTS AND DISCUSSION

Analysis of variance and variability parameters

The genotypes showed high positive and significant variations for all the traits (Table S1). Yield per hectare obtained the highest positive and significant variation (73394588.940**) and the lowest was obtained for fruit diameter (0.280**). Gondane and Lal (1994) and Alam and Hossain (2008) also obtained similar results in okra.

Yield per hectare ranged from 5313.870-33714.430 kg/hectare with a mean of 20056.945 grams per genotype. Profitable yield i.e., production of 25000-30000 kg per hectare was achieved by EC305615, EC305740, IC013356 and IC0104018. In the genetic variability studies (Table 2), the phenotypic coefficient of variation (PCV) was higher than the comparing genotypic coefficient of variation (GCV) for every trait with the close relationship between them, therefore, the environment has low impact and subsequently, the phenotypic performance of traits ought to be utilized for selection. Moderate and high GCV values were observed for most of the traits except fruit diameter, days to 80% maturity and days to 50% flowering which

exhibited the presence of a high magnitude of genetic diversity in the population examined. The previous workers also observed a 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 they were comparatively stable to environmental variation (Majumdar *et al.,* 1969). However, fruit diameter and yield per hectare registered wider variation between PCV and GCV.

Heritability is a good index of transmission of traits from parents to their off-springs (Falconer, 1981). Among ten traits, nine traits displayed high heritability (low <30%, moderate 31% to 60% and high >60%) coupled with high genetic advance (low <10%, moderate 11% to 20% and high >20%) as percent over mean. This focuses on the predominance of additive gene effects for these traits; thus, crop improvement through selection based on these traits would be beneficial. Fruit girth showed low heritability accompanied with moderate genetic advance over mean portraying the role of non-additive effects and hence selection based on

Table 2. Estimates of variability parameters for various traits of okra genotypes.

Traits	Mean	Range	GCV	PCV	h²	GA	GA as % of Mean
DF	37.71	28.67-50.33	17.63	18.92	86.79	12.76	33.83
DM	76.60	54.67-100.00	16.17	16.42	97.01	25.14	32.82
PH (cm)	86.39	42.27-154.50	39.10	39.16	99.70	69.49	80.43
FFN	6.01	2.70-11.13	36.88	38.55	91.56	4.37	72.70
FD (cm)	2.00	1.50-2.43	11.35	21.00	29.21	0.25	12.64
FL (g)	14.05	7.90-18.80	21.65	22.23	94.85	6.10	43.44
FP	21.23	6.40-40.60	54.41	56.56	92.56	22.90	107.84
SF	51.24	34.00-89.60	27.31	27.56	98.19	28.57	55.75
TSW (g)	212.33	61.44-422.64	40.93	52.67	60.38	139.11	65.51
YP (g)	271.31	73.37-453.10	38.72	39.01	98.54	214.84	79.19
YH (kg/ha)	20056.94	5313.87-33714.43	17.34	34.96	24.61	3556.47	17.73

(DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height, FFN = First flowering node, FD = Fruit diameter, FL = Fruit length, FP = Number of fruit per plant, SF = Number of seed per fruit, TSW = 1000 seed weight, YP = Yield per plant and YH = Yield per hectare, h²: heritability, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, GA: Genetic advance)

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this trait may not be rewarding. High estimates of heritability and genetic advance were also reported by Nwangburuka *et al,* (2012) and Hazra and Basu (2000).

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 interrelationship of various traits (Ranga *et al.,* 2019).

In the present investigation, the genotypic and phenotypic correlation coefficient analysis is represented in Table 3 and Fig.1. Days to 80% maturity showed a highly significant and positive correlation with days to 50% flowering (0.488**, 0.427**). Plant height showed a significant and positive correlation with days to 50% flowering (0.346*, 0.318*). Fruit diameter showed a highly significant and positive genotypic correlation with days to 80% maturity (0.517**, 0.314*) and plant height (0.714**, 0.393**), and only genotypic correlation was positive and significant for day to 50% maturity (0.707**). Number of fruits per plant showed a highly
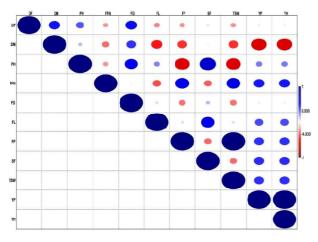

Fig. 1. Correlation coefficient studies in okra genotypes

(DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height, FFN = First flowering node, FD = Fruit diameter, FL = Fruit length, FP = Number of fruit per plant, SF = Number of seed per fruit, TSW = 1000 seed weight, YP = Yield per plant and YH = Yield per hectare)

significant and positive correlation with first flowering node (0.602**, 0.550**). Number of seeds per fruit showed a highly significant and positive correlation with plant height (0.693**, 0.684**) and fruit length (0.580**, 0.564**). 1000 seed weight showed a highly significant and positive correlation with fruit length (0.453**, 0.309*). Yield per plant showed a highly significant and positive correlation with first flowering node (0.459**, 0.442**), fruit length (0.357*, 0.355*), number of fruits per plant (0.417**, 0.395**) and number of seed per fruit (0.421**, 0.411**). Yield per hectare showed a highly significant and positive correlation with 1000 seed weight (0.391**, 0.340*). Comparable results for okra yield having a positive relationship were proposed by Ranga *et al.* (2021), Reddy *et al.* (2012), Raval *et al.* (2019) and Duggi *et al.* (2013). Yield per plant showed a highly significant and negative correlation with days to 80% maturity (-0.635**, -0.627**). Yield per hectare showed a significant and positive genotypic correlation with days to 50% flowering (-0.379*).

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 plant height (3.893, 0.239) had the highest direct positive effect towards the yield per hectare and other traits such as days to 80% maturity (0.811, 0.053), number of fruits per plant (2.871, 0.174) had direct effects. Traits such as days to 50% maturity (-0.575, -0.267), and yield per plant (-1.868, -0.197) had a direct effect with a negative sign. Residual effect (0.475, 0.800) indicated the effect of other possible independent traits, which were not included in the study, on the dependent variable i.e., yield per hectare. The results are in accordance with the findings of Ranga *et al.,* (2021); Dwivedi and Sharma (2017); Das *et al.* (2012).

Principal component analysis

Principal component analysis (PCA) reflects the importance of the largest contributor to the total variations at each axis of differentiation (Sharma,

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Table 3. Genotypic and phenotypic correlation coefficient studies in okra genotypes.
(Bold numbers indicated positive and significant correlation between two traits)

Traits		DF	DM	PH (cm)	FFN	FD (cm)	FL (cm)	FP	SF	TSW (g)	YP (g)	YH (kg/ha)
DF	rg	1.000										
	rp	1.000										
DM	rg	0.488**	1.000									
	rp	0.427**	1.000									
PH (cm)	rg	0.346*	0.141^{NS}	1.000								
	rp	0.318*	0.141^{NS}	1.000								
FFN	rg	-0.205^{NS}	-0.294*	-0.215^{NS}	1.000							
	rp	-0.218^{NS}	-0.290^{NS}	-0.205^{NS}	1.000							
FD (cm)	rg	0.707**	0.517**	0.714**	0.009^{NS}	1.000						
	rp	0.285^{NS}	0.314*	0.393**	-0.085^{NS}	1.000						
FL (cm)	rg	-0.253^{NS}	-0.462**	0.244^{NS}	-0.353*	-0.150^{NS}	1.000					
	rp	-0.218^{NS}	-0.443**	0.237^{NS}	-0.340*	-0.064^{NS}	1.000					
FP	rg	-0.226^{NS}	-0.415**	-0.627**	0.602**	-0.370*	-0.093^{NS}	1.000				
	rp	-0.210^{NS}	-0.389**	-0.603**	0.550**	-0.208^{NS}	-0.089^{NS}	1.000				
SF	rg	0.080^{NS}	-0.044^{NS}	0.693**	-0.323*	0.183^{NS}	0.580**	-0.295*	1.000			
	rp	0.078^{NS}	-0.040^{NS}	0.684**	-0.305*	0.113^{NS}	0.564**	-0.293^{NS}	1.000			
TSW (g)	rg	-0.171^{NS}	-0.090^{NS}	0.036^{NS}	-0.244^{NS}	-0.206^{NS}	0.453**	0.066^{NS}	0.110^{NS}	1.000		
	rp	-0.112^{NS}	-0.052^{NS}	0.022^{NS}	-0.249^{NS}	0.022^{NS}	0.309*	0.026^{NS}	0.098^{NS}	1.000		
YP (g)	rg	-0.064^{NS}	-0.635**	0.262^{NS}	0.459**	0.099^{NS}	0.357*	0.417**	0.421**	-0.162^{NS}	1.000	
	rp	-0.050^{NS}	-0.627**	0.259^{NS}	0.442**	-0.002^{NS}	0.355*	0.395**	0.411**	-0.144^{NS}	1.000	
YH (kg/ha)	rg	-0.379*	0.047^{NS}	0.108^{NS}	0.054^{NS}	0.258^{NS}	0.116^{NS}	0.021^{NS}	0.067^{NS}	0.391**	-0.194^{NS}	1.000
	rp	-0.201^{NS}	0.045^{NS}	0.047^{NS}	-0.013^{NS}	0.109^{NS}	0.044^{NS}	0.004^{NS}	0.033^{NS}	0.340*	-0.107^{NS}	1.000

(DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height, FFN = First flowering node, FD = Fruit diameter, FL = Fruit length, FP = Number of fruit per plant, SF = Number of seed per fruit, TSW = 1000 seed weight, YP = Yield per plant and YH = Yield per hectare; rg = genotypic correlation coefficient, rp = phenotypic correlation coefficient)

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Table 4. Genotypic and phenotypic path coefficient analysis for various okra genotypes.
(Diagonal and bold values indicate direct effect of traits on yield per plant)

Traits		DF	DM	PH (cm)	FFN	FD (cm)	FL (cm)	FP	SF	TSW (g)	YP (g)	Correlation of YH (kg/ha)
DF	gp	**-0.575**	0.395	1.347	0.011	-0.701	-0.375	-0.650	-0.120	0.169	0.119	**-0.379***
	pp	**-0.267**	0.023	0.076	-0.013	0.029	0.009	-0.037	0.002	-0.033	0.010	**-0.201ᴺˢ**
DM	gp	-0.281	**0.811**	0.547	0.016	-0.512	-0.683	-1.191	0.065	0.089	1.186	**0.047ᴺˢ**
	pp	-0.114	**0.053**	0.034	-0.018	0.032	0.018	-0.068	-0.001	-0.015	0.123	**0.045ᴺˢ**
PH	gp	-0.199	0.114	**3.893**	0.011	-0.708	0.361	-1.800	-1.038	-0.035	-0.490	**0.108ᴺˢ**
(cm)	pp	-0.085	0.008	**0.239**	-0.012	0.040	-0.010	-0.105	0.017	0.007	-0.051	**0.047ᴺˢ**
FFN	gp	0.118	-0.239	-0.838	**-0.053**	-0.009	-0.522	1.728	0.484	0.242	-0.858	**0.054ᴺˢ**
	pp	0.058	-0.016	-0.049	**0.061**	-0.009	0.014	0.096	-0.007	-0.074	-0.087	**-0.013ᴺˢ**
FD	gp	-0.407	0.419	2.779	0.000	**-0.991**	-0.222	-1.064	-0.274	0.203	-0.186	**0.258ᴺˢ**
(cm)	pp	-0.076	0.017	0.094	-0.005	**0.103**	0.003	-0.036	0.003	0.006	0.000	**0.109ᴺˢ**
FL	gp	0.146	-0.374	0.948	0.019	0.148	**1.480**	-0.267	-0.869	-0.448	-0.666	**0.116ᴺˢ**
(cm)	pp	0.058	-0.024	0.057	-0.021	-0.007	**-0.040**	-0.015	0.014	0.092	-0.070	**0.044ᴺˢ**
FP	gp	0.130	-0.336	-2.440	-0.032	0.367	-0.138	**2.871**	0.442	-0.065	-0.778	**0.021ᴺˢ**
	pp	0.056	-0.021	-0.144	0.034	-0.021	0.004	**0.174**	-0.007	0.008	-0.078	**0.004ᴺˢ**
SF	gp	-0.046	-0.035	2.696	0.017	-0.181	0.858	-0.847	**-1.499**	-0.109	-0.787	**0.067ᴺˢ**
	pp	-0.021	-0.002	0.163	-0.019	0.012	-0.023	-0.051	**0.024**	0.029	-0.081	**0.033ᴺˢ**
TSW	gp	0.098	-0.073	0.140	0.013	0.204	0.670	0.189	-0.165	**-0.988**	0.303	**0.391****
(g)	pp	0.030	-0.003	0.005	-0.015	0.002	-0.012	0.005	0.002	**0.297**	0.028	**0.340***
YP	gp	0.037	-0.515	1.021	-0.024	-0.099	0.528	1.197	-0.631	0.160	**-1.868**	**-0.194ᴺˢ**
(g)	pp	0.013	-0.034	0.062	0.027	0.000	-0.014	0.069	0.010	-0.043	**-0.197**	**-0.107ᴺˢ**

gp residual effect: 0.475

pp residual effect: 0.800

(DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height, FFN = First flowering node, FD = Fruit diameter, FL = Fruit length, FP = Number of fruit per plant, SF = Number of seed per fruit, TSW = 1000 seed weight, YP = Yield per plant and YH = Yield per hectare); gp = genotypic path coefficient, pp = phenotypic path coefficient)

1998). PCA (Table 5 and Table S2) was performed to provide partial visualization of the data set in a reduced dimension and first three principal components have Eigenvalues>1 and contributed to 80.517 percent variation. From the loading of the variables in PC I, it was found that days to 50% flowering, days to 80% maturity and plant height were the dominant features that contributed to 36.662 percent of the total variation. In PCA II, plant height, fruit length, number of seed per fruit, yield per plant and yield per hectare exerted a maximum influence which accounts for 27.862 percent of the total variation. Days to 50 percent

flowering, days to 80% maturity, first flowering node and fruit diameter were the dominant features in PCA III which accounted for 15.993 percent of the total variation. Ranga *et al.* (2021), Ahiakpa *et al.* (2013) and Amoatey *et al.* (2015) also indicated high genetic diversity using PCA. Few traits *viz.,* fruit length, 1000 seed weight, number of seed per fruit and fruit yield per plant offered more towards variation as accounted for by different scientists in okra (Bhardwaj *et al.,* 2021; Ahiakpa *et al.,* 2013; Amoatey *et al.,* 2015; Nwangburuka *et al.,* 2012).

Table 5. Eigen value and percent variation explained by first 5 principal components and correlations between PC scores and quantitative traits.

(Bold values indicate traits which are heavy contributors in the particular principal component)

Sr. No.	Traits	PC I	PC II	PC III	PC IV	PC V	Eigen Value
1.	**DF**	**0.221**	0.061	**0.472**	**0.528**	**0.446**	**4.033**
2.	**DM**	**0.365**	-0.188	**0.265**	0.168	-0.072	**3.065**
3.	**PH (cm)**	**0.237**	**0.443**	0.173	-0.256	0.077	**1.759**
4.	**FFN**	**-0.338**	-0.076	**0.360**	**-0.506**	0.026	0.781
5.	**FD (cm)**	0.205	0.170	**0.499**	-0.013	**-0.746**	0.501
6.	**FL (cm)**	-0.056	**0.375**	**-0.430**	**0.301**	**-0.383**	0.476
7.	**FP**	**-0.436**	-0.148	0.141	**0.349**	-0.142	0.190
8.	**SF**	0.084	**0.484**	-0.102	0.187	0.114	0.131
9.	**TSW (g)**	**-0.436**	-0.148	0.141	**0.349**	-0.142	0.064
10.	**YP (g)**	**-0.328**	**0.394**	0.177	-0.030	0.127	0.000
11.	**YH (kg/ha)**	**-0.328**	**0.394**	0.177	-0.030	0.127	0.000
Percent of Total Variance Explained		**36.662**	**27.862**	**15.993**	7.100	4.552	
Cumulative Variation		**36.662**	**64.524**	**80.517**	**87.617**	**92.169**	

(DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height, FFN = First flowering node, FD = Fruit diameter, FL = Fruit length, FP = Number of fruit per plant, SF = Number of seed per fruit, TSW = 1000 seed weight, YP = Yield per plant and YH = Yield per hectare)

A biplot was drawn using the values of PC I and PC II (Figure 2). The greater the angle between the traits, the lesser the association between them. Placement of genotypes in quadrants signifies variability. Accessions are placed in quadrants using vector scores of PC I and PC II. However, no obvious grouping of genotypes was observed, and some overlapping occurred among groups the relatedness of the genotypes across the collection. In the biplot graph of
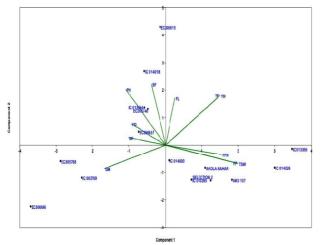
PCA, quadrant I (+,+) consists of zero accessions formed the cluster 1 which were highly influenced by three traits characters viz. fruit length, yield per plant and yield per hectare through genotypes spread towards midway through X and Y-planes of quadrant-I. The cluster II corresponding to the quadrant II (-,+) contained 5 genotypes, which were influenced by number of seeds per plant, plant height, fruit diameter and days to 50% maturity. Similarly, the cluster III corresponding to quadrant III (-,-) consisted also of 3 genotypes which were influenced by days to 80% maturity only whereas the cluster IV corresponding to quadrant IV (+,-) also consisted of 7 genotypes which were influenced by first flowering node, number of fruits per plant and 1000 seed weight, respectively.

Cluster analysis

The hierarchical cluster analysis among genotypes for yield and yield contributing traits grouped genotypes into 2 major clusters (Figure 3). Clustering was not based on a similar geographical origin. Cluster I accommodated 5 genotypes (EC359637, IC013664, EC306696, EC305768, IC003768) and cluster II comprised 10 genotypes (EC305615, EC305740, IC014018, IC010265, IC014600, IC013356,

Fig. 2. Biplot between PC1 and PC2 showing contribution of various traits responsible for variability in okra.
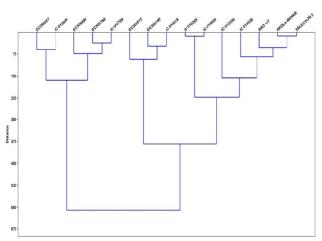
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Fig. 3. Dendrogram showing the genetic relationship among fiteen orka genotypes based on quantitative traits

(DF = Days to 50% flowering, DM = Days to 80% maturity, PH = Plant height, FFN = First flowering node, FD = Fruit diameter, FL = Fruit length, FP = Number of fruit per plant, SF = Number of seed per fruit, TSW = 1000 seed weight, YP = Yield per plant and YH = Yield per hectare)

IC014026, AKO107, Akola-Bahar and IARI Selection 2). In order to determine diversity among genotypes, and verify genotypes by distance, cluster analysis placed the genotypes in a single group (Sokal and Sneath, 1973). Genotypes that are located far from each other have more variation between them and can be used to obtain improved cultivars. Genotypes which distantly placed are more diverse; those which are closer are similar morphologically. The maximum intra-cluster distance was observed for EC359637 and IC003769 in sub-cluster 1 and EC305615 and IARI Selection 2 in sub-cluster 2 while maximum inter-cluster distance was observed for EC359637 and IARI Selection 2.

CONCLUSION

Higher variations were observed for number of fruits per plant, yield per plant, yield per hectare and 1000 seed weight displaying a wide range showing the distinction of genotypes in breeding programs. Yield per hectare showed a highly significant and positive correlation with 1000 seed weight. Hence, it can be used for developing high-yielding and bold seeded cultivars resistant to biotic and biotic stress. Plant height and number of fruits per plant had direct and positive effects on the yield per hectare. The first three principal components accounted for a cumulative

variance to be 80.517 % of the total variation and traits *viz.* fruit length, plant height, days to 80% maturity and days to 50% flowering assorted for more than 50 % phenotypic variations. Since EC359637 and IARI Selection 2 are distantly placed, therefore, they can be used for overall improvement in further breeding programs.

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