Received: 04 May 2023 | Revised: 04 Dec 2023 | Accepted: 29 Dec 2023

Electronic Journal of Plant Breeding

Research Article

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

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Abstract
Seventy five okra genotypes were examined for genetic divergence for fruit yield and its contributing traits during summer,2020 at Regional Horticultural Research & Training Station, Jachh, Nurpur, Himachal Pradesh. Higher PCV and GCV values were observed for fruit weight, days to 50 per cent flowering, internodal length and fruit production/ plant. High heritability along with genetic advance was observed for days to 50 per cent flowering, the first fruiting node, internodal length, fruit weight, number of seeds/fruit, plant height, and fruit yield/plant. Fruit weight, first fruiting node, number of ridges/fruit, days to 50 per cent flowering, fruit diameter, number of fruits/plant and leaf width recorded positive and significant phenotypic as well as genotypic correlation with fruit yield/plant. The path coefficient study revealed that fruit weight had the greatest positive direct impact on fruit yield/plant; followed by number of fruits/plant, first fruiting node, days to 50 per cent flowering, leaf width and hundred seed weight. Based on genetic divergence, the genotypes were divided into five clusters, with cluster I having the highest intra-cluster distance whereas, the lowest was observed in Cluster II. Clusters I and V showed the greatest inter-cluster distance, while the Clusters III and V showed the lowest. Therefore, to develop successful recombinant segregants, it would be advantageous to use genotypes from such clusters, depending on the distances between them.

Keywords: Correlation, genotypes, heritability, path coefficient, okra

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is a member of the Malvaceae family and has the chromosome number 2n = 130. It is also recognized by names such as Lady's finger, Bhindi, Gumbo Okra, Okura, Okro, Quiabos and Ochro in many countries (Kumar *et al*, 2013). Okra has a variety of geographical origins including West African, Ethiopian and South Asian. India is known to be world's largest okra producing country (Ranga *et al.,* 2019). Okra grows well in a variety of soils, but it prefers a friable and well-manured soil (Ray *et al*., 2020).

Awareness of genetic variation is a fundamental requirement in any crop improvement program (Kumar *et al.*, 2015). Furthermore, since selection progress is dependent on heritability, selection strength, and genetic advance of the character, the

variability should be highly heritable. In breeding for quantitative traits, a quantitative measure of genetic variability would be incredibly beneficial. One of the most important methods for measuring genetic variability in both cross and self-pollinated crops is genetic diversity (Sharma and Prasad 2010). The correlation analysis will aid in recognizing traits that have a close association with yield. Therefore, understanding the relationships between different characters aids the breeder in deciding the relative importance of yield components to consider in order to increase yield. The primary objective of any crop improvement programme is to increase economic yield, which is a complex dependent trait that is largely inherited quantitatively and is determined by a range of yield components that are heavily influenced by environmental conditions (Ranga and Darvhankar 2022).

MATERIALS AND METHODS

The current research was carried out at the Experimental Farm of the Department of Vegetable Science, Regional Horticultural Research & Training Station, Dr Yashwant Singh Parmar University of Horticulture and Forestry, Jachh, Nurpur, Himachal Pradesh, India during the Summer season of 2020. The experimental site is located at an altitude of 428 meters above mean sea level at a latitude of 32º16'54.02" N and longitude of 75º51'4.38" E. It falls within the Sub Mountains and low hill subtropical agro-climatic zone (Zone 1) of Himachal Pradesh. The soil structure at the experimental farm is sandy loam with a pH of approximately 7.5.

The trial involving 75 genotypes (**Table 1**) , was laid out in a randomized complete block design with three replications with a spacing of 45 cm × 15 cm. The recommended package of practices of Dr. Yashwant Singh Parmar University of Horticulture and Forestry for vegetable crops was followed for better crop stand. Five random plants of each genotype were selected for various traits *viz*., days to 50 per cent flowering (DTFPF), first fruiting node (FFN), internodal length [IL (cm)], number of ridges/fruit (NRPF), fruit length [FL (cm)], fruit diameter [FD (cm)], fruit weight [FW (g)], number of fruits/plant (NFPP), number of seeds/ fruit (NSPP), hundred seed weight [HSW (g)], leaf length [LL (cm)], leaf width [LW (cm)], plant height [PH (m)] and fruit yield/ plant [FYPP (g)].

Formula proposed by Burton (1952) was used to calculate the coefficient of variability. The broad sense heritability and genetic advance was computed according to Johnson *et al.* (1955). The method described by Al-Jibouri *et al*. (1958) was used to determine the phenotypic and genotypic correlation coefficients. Path coefficient analysis was carried out as per the method given by Dewy and Lu (1959). Mahalanobis D^2 statistics was used to find out the genetic divergence as indicated by Rao (1952).

RESULTS AND DISCUSSION

The phenotypic, as well as genotypic coefficient of variability (PCV and GCV), has been depicted in **Table 2**. For all the traits studied, the magnitude of PCV was greater than the GCV however the difference was low in the majority of cases. PCV and GCV were found higher for FW (40.25 %, 39.78 %), DTFPF (33.41 %, 33.10 %), IL (32.24 %, 31.3 7 %), FYPP (31.64 %, 31.31 %) and FFN (30.12 %, 29.76 %) whereas PH (27.36 %, 27.35 %), NSPF (26.68 %, 26.29 %), NFPP (21.52 %, 18.82 %), HSW (20.20 %, 19.53 %), FL (18.42 %, 17.81 %), NRPF (17.33 %, 17.13 %) and FD (16.24 %, 15.41 %) were observed with moderate coefficients of variability. Low phenotypic coefficient of variability was recorded for LW (14.73 %, 14.36 %) and LL (12.55 %, 11.65 %). Genetic variability parameters showed that the magnitude of phenotypic coefficient of variability (PCV) were higher than that of genotypic coefficient of variability (GCV) for most of the traits. The difference among PCV and GCV was low which indicated that the traits are less influenced by environmental factors. Such close association among PCV and GCV for the traits showed that their performance is stable under several environmental conditions. Therefore, selection can be made from the phenotypic performance of these traits. Similar findings for FYPP were examined by Ahamed *et al.* (2015) and for FW by Nwangburuka *et al*. (2012).

High heritability was recorded for PH (99.18 %), DTFPF (98.16 %), FYPP (97.96 %), NRPF (97.79 %), FW (97.68 %), FFN (97.66 %), NSPF (97.09 %), LW (95.01 %), IL (94.70 %), HSW(93.53 %), FL (93.40 %), FD (90.05 %) and LL(86.27 %), while it was low for FPP (76.51 %). Similar results were reported by Das *et al.* (2012) for FFN, FD, NRPF and FW; Ahamed *et al.* (2015) for PH, FYPP NSPF, FL, LL, LW and HSW. Phanikrishna *et al.* (2015) reported similar results for IL and DTFPF. FW (80.99%), DTFPF (67.56%), FYPP (63.84%), IL (62.89%), FFN (60.59%), PH (55.91%) and NSPF (53.36%) were reported to have higher genetic advance as a per cent of mean (**Table. 2, Fig. 1**). However, moderate genetic gain was reported by HSW (38.91 %), FL (35.45 %), NRPF (34.90 %), NFPP (33.92 %), FD (30.12 %) and LW (28.83 %) and for LL (22.30 %) the lowest genetic gain was revealed. High heritability for the traits under study revealed that the phenotypic variation for the traits is the result of genetic influence with preponderance of additive gene effect. Selection should be made for such traits in accordance with their phenotyping performance. High genetic advance was reported for several traits which show the degree of improvement achieved for improving the traits. Heritability coupled with high genetic advance shows additive as well as epistatic gene effect which offers desirable degree of gain that is fixable and helps plant breeders to identify the traits of interest which enables the selection of superior genotypes. Prakash and Pitchaimuthu (2010) reported similar results for FL, FD, FFN, NFPP, NSPF and HSW; Nwangburuka *et al.* (2012) for FW and PH; Bello *et al.* (2015) for NFPP, FL and FYPP. Significant and positive genotypic and phenotypic

Table 1 List of okra genotypes used for the present study along with their collection sources

S.No.	GERMPLASM	SOURCE	S.No.	GERMPLASM	SOURCE
1	IC 1543	ICAR-NBPGR, New Delhi	39	EC 305741	ICAR-NBPGR, New Delhi
2	IC 3307	ICAR-NBPGR, New Delhi	40	EC 305745	ICAR-NBPGR, New Delhi
3	IC 3759	ICAR-NBPGR, New Delhi	41	LC- 44-1	BILASPUR
4	IC 3769	ICAR-NBPGR, New Delhi	42	LC-46-1	BILASPUR
5	IC 4328	ICAR-NBPGR, New Delhi	43	LC-47-1	BILASPUR
6	IC 4378	ICAR-NBPGR, New Delhi	44	LC-49-1	BILASPUR
7	IC 4507	ICAR-NBPGR, New Delhi	45	LC-51-1	BILASPUR
8	IC 6485	ICAR-NBPGR, New Delhi	46	LC-53-1	BILASPUR
9	IC 7452	ICAR-NBPGR, New Delhi	47	LC-54-2	HAMIRPUR
10	IC 7472	ICAR-NBPGR, New Delhi	48	LC-55-2	HAMIRPUR
11	IC 7473	ICAR-NBPGR, New Delhi	49	LC-57-2	HAMIRPUR
12	IC 7952	ICAR-NBPGR, New Delhi	50	LC-58-2	HAMIRPUR
13	IC 8991	ICAR-NBPGR, New Delhi	51	LC-59-2	HAMIRPUR
14	IC 9327	ICAR-NBPGR, New Delhi	52	LC-60-2	HAMIRPUR
15	IC 9856	ICAR-NBPGR, New Delhi	53	LC-62-3	GANGATH,KANGRA
16	IC 11533	ICAR-NBPGR, New Delhi	54	LC-66-3	GANGATH,KANGRA
17	IC 12933	ICAR-NBPGR, New Delhi	55	LC-68-3	GANGATH,KANGRA
18	IC 12934	ICAR-NBPGR, New Delhi	56	LC-73-3	GANGATH,KANGRA
19	IC 15540	ICAR-NBPGR, New Delhi	57	LC-76-3	GANGATH,KANGRA
20	IC 27875	ICAR-NBPGR, New Delhi	58	LC-77-3	GANGATH,KANGRA
21	EC 305609	ICAR-NBPGR, New Delhi	59	LC-78-4	CHATROLI, KANGRA
22	EC 305612	ICAR-NBPGR, New Delhi	60	LC-79-4	CHATROLI, KANGRA
23	EC 305613	ICAR-NBPGR, New Delhi	61	LC-80-4	CHATROLI, KANGRA
24	EC 305634	ICAR-NBPGR, New Delhi	62	LC-81-4	CHATROLI, KANGRA
25	EC 305635	ICAR-NBPGR, New Delhi	63	LC-83-4	CHATROLI, KANGRA
26	EC 305643	ICAR-NBPGR, New Delhi	64	LC-84-4	CHATROLI, KANGRA
27	EC 305652	ICAR-NBPGR, New Delhi	65	LC-85-5	JACHH, KANGRA
28	EC 305653	ICAR-NBPGR, New Delhi	66	LC-90-5	JACHH, KANGRA
29	EC 305664	ICAR-NBPGR, New Delhi	67	LC-91-5	JACHH, KANGRA
30	EC 305672	ICAR-NBPGR, New Delhi	68	LC-92-5	JACHH, KANGRA
31	EC 305675	ICAR-NBPGR, New Delhi	69	LC-93-5	JACHH, KANGRA
32	EC 305685	ICAR-NBPGR, New Delhi	70	LC-94-5	JACHH, KANGRA
33	EC 305687	ICAR-NBPGR, New Delhi	71	LC-95-6	NURPUR, KANGRA
34	EC 305689	ICAR-NBPGR, New Delhi	72	LC-106-6	NURPUR, KANGRA
35	EC 305691	ICAR-NBPGR, New Delhi	73	LC-107-6	NURPUR, KANGRA
36	EC 305694	ICAR-NBPGR, New Delhi	74	LC-113-6	NURPUR, KANGRA
37	EC 305714	ICAR-NBPGR, New Delhi	75	Pusa Bhindi-5 (Check)	ICAR-IARI, New Delhi
38	EC 305716	ICAR-NBPGR, New Delhi			

correlation coefficient was observed for DTFPF (0.314**, 0.320**), FFN (0.411**, 0.425**), NRPF (0.346**, 0.353**), FL (0.249**, 0.260**), FD (0.309**, 0.330**), FW (0.558**, 0.570**), NFPP (0.323**, 0.356**), LW (0.293**, 0.304**) whereas it was negative and significant for HSW (-0.140*, -0.146*). NSPF (0.019, 0.017), LL (0.091, 0.092), and PH (0.038, 0.036) showed positive and non-significant correlation coefficient while it was negative and non-significant for IL (-0.055, -0.056). This is due to the fact that some genotypes had a higher number of fruits and smaller seed size, whereas, others had a lower number of fruits but larger seed size. The magnitude of genotypic correlation coefficient was higher than the phenotypic correlation coefficient for most of the traits representing the inherent genetic relation. In correlation, segregating genes shows major effect as positive correlation occurs

Table 2. Estimates of phenotypic and genotypic coefficients of variability, heritability, genetic advance and genetic gain of different traits in okra

Characters	Range	Mean ± SE(d)	Heritability (%)	Coefficient of variations (%)		Genetic advance	Genetic advance (%)
				Genotypic	Phenotypic		
Days to 50 % flowering	29.00-91.67	47.17 ± 1.74	98.16	33.10	33.41	31.87	67.56
First fruiting node	4.22-14.44	6.71 ± 0.25	97.66	29.76	30.12	4.07	60.59
Internodal length (cm)	2.42-11.67	5.86 ± 0.35	94.70	31.37	32.24	3.69	62.89
Number of ridges per fruit	5.00-9.00	5.54 ± 0.11	97.79	17.13	17.33	1.93	34.90
Fruit length (cm)	11.93-24.66	16.99 ± 0.65	93.40	17.81	18.42	6.02	35.45
Fruit breadth (cm)	1.43-2.74	1.83 ± 0.07	90.05	15.41	16.24	0.55	30.12
Fruit weight (g)	13.22-67.89	25.49 ± 1.27	97.68	39.78	40.25	20.64	80.99
Number of fruits/plant	7.00-26.99	18.05 ± 1.53	76.51	18.82	21.52	6.12	33.92
Number of seed per fruit	22.11-93.11	54.03 ± 2.00	97.09	26.29	26.68	28.83	53.36
100 seed weight (g)	3.33-8.00	5.63 ± 0.23	93.53	19.53	20.20	2.19	38.91
Leaf length (cm)	13.12-21.52	17.10 ± 0.64	86.27	11.65	12.55	3.81	22.30
Leaf width (cm)	15.34-31.77	22.71 ± 0.61	95.01	14.36	14.73	6.55	28.83
Plant height (m)	44.89-175.89	88.98 ± 1.80	99.18	27.25	27.36	49.75	55.91
Fruit yield/plant	154.89-65	300.68 ± 11.10	97.96	31.31	31.64	191.97	63.84

Table 3 Phenotypic and genotypic coefficients of correlation among different quantitative traits in okra

Traits		DTFPF	FFN	IL	NRPF	FL	FD	FW	NFPP	NSPF	HSW	LL	LW	PH	FYPP
DTFPF	P	1.000	0.693**	0.243**	0.653**	-0.186**	0.593**	0.512**	-0.184**	0.222**	-0.148*	0.122	0.079	0.152*	0.314**
	G	1.000	0.708**	0.253**	0.666**	-0.195**	0.631**	0.522**	-0.211**	0.229**	-0.159*	0.131	0.081	0.154*	0.320**
FFN	P		1.000	0.109	0.625**	0.079	0.509**	0.584**	-0.083	0.193**	-0.138*	0.345**	0.310**	0.276**	0.411**
	G		1.000	0.116	0.636**	0.081	0.533**	0.596**	-0.082	0.198**	-0.143*	0.371**	0.322**	0.281**	0.425**
IL	P			1.000	0.110	-0.310**	0.111	0.17	-0.041	0.130	-0.100	0.133*	-0.090	0.289**	-0.055
	G			1.000	0.118	-0.324**	0.124	0.025	-0.042	0.137*	-0.109	0.157*	-0.091	0.302**	-0.056
NRPF	P				1.000	0.051	0.648**	0.654**	-0.180**	0.224**	-0.135*	0.118	0.198**	0.086	0.346**
	G				1.000	0.053	0.688**	0.667**	-0.203**	0.230**	-0.141*	0.133*	0.206**	0.087	0.353**
FL	P					1.000	0.174**	0.472**	0.133*	0.029	-0.082	0.322**	0.415**	0.008	0.249**
	G					1.000	0.177**	0.482**	0.114	0.034	-0.089	0.349**	0.430**	0.009	0.260**
FD	P						1.000	0.746**	-0.195*	0.164*	-0.180**	0.205**	0.151*	0.158*	0.309**
	G						1.000	0.781**	-0.201**	0.179**	-0.190**	0.212**	0.164*	0.163*	0.330**
FW	P							1.000	-0.130	0.196**	0.197**	0.305**	0.401**	0.161*	0.558**
	G							1.000	-0.160*	0.202**	-0.206**	0.331**	0.412**	0.161*	0.570**
NFPP	P								1.000	-0.159*	-0.097	0.104	0.140*	0.034	0.323**
	G								1.000	-0.180**	-0.113	0.085	0.145*	0.040	0.356**
NSPF	P									1.000	-0.046	-0.005	-0.096	-0.027	0.019
	G									1.000	-0.051	0.003	-0.098	-0.030	0.017
HSW	P										1.000	0.088	0.227**	0.279**	-0.140*
	G										1.000	0.108	0.241**	0.288**	-0.146*
LL	P											1.000	0.621**	0.479**	0.091
	G											1.000	0.656**	0.516**	0.092
LW	P												1.000	0.470**	0.293**
	G												1.000	0.481**	0.304**
PH	P													1.000	0.038
	G													1.000	0.036
FYPP	P														1.000
	G														1.000

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

Where, DTFPF = Days to fifty percent flowering, FFN = First fruiting node, IL = Internodal length, NRPF = Number of ridges per fruit, FL = Fruit length, FD = Fruit diameter, FW = Fruit weight, NFPP = Number of fruits per plant, NSPF = Number of seeds per fruit, HSW = Hundred seed weight, LL = Leaf length, LW = Leaf width, PH = Plant height, FYPP = Fruit yield per plant

Table 4. Estimates of direct and indirect effect of different traits contributing towards fruit yield per plant in okra at genotypic level

Traits	DTFPF	FFN	IL	NRPF	FL	FD	FW	NFPP	NSPF	HSW	LL	LW	PH	FYPP
DTFPF	**0.104**	0.118	-0.005	-0.055	0.025	-0.187	0.487	-0.104	-0.012	-0.014	-0.029	0.005	-0.012	**0.320****
FFN	0.073	**0.167**	-0.002	-0.053	-0.010	-0.158	0.555	-0.040	-0.010	-0.013	-0.082	0.019	-0.021	**0.425****
IL	0.026	0.019	**-0.020**	-0.010	0.041	-0.037	0.024	-0.021	-0.007	-0.010	-0.035	-0.005	-0.023	**-0.056**
NRPF	0.069	0.106	-0.002	**-0.083**	-0.007	-0.204	0.622	-0.100	-0.012	-0.013	-0.030	0.012	-0.007	**0.353****
FL	-0.020	0.014	0.006	-0.004	**-0.126**	-0.053	0.449	0.056	-0.002	-0.008	-0.078	0.026	-0.001	**0.260****
FD	0.065	0.089	-0.002	-0.057	-0.022	**-0.296**	0.729	-0.099	-0.009	-0.017	-0.047	0.010	-0.012	**0.330****
FW	0.054	0.100	-0.001	-0.055	-0.061	-0.231	**0.933**	-0.079	-0.011	-0.019	-0.073	0.025	-0.012	**0.570****
NFPP	-0.022	-0.014	0.001	0.017	-0.014	0.059	-0.149	**0.492**	0.009	-0.010	-0.019	0.009	-0.003	**0.356****
NSPF	0.024	0.033	-0.003	-0.019	-0.004	-0.053	0.189	-0.089	**-0.052**	-0.005	-0.001	-0.006	0.002	**0.017**
HSW	-0.017	-0.024	0.002	0.012	0.011	0.056	-0.192	-0.056	0.003	**0.090**	-0.024	0.014	-0.022	**-0.146***
LL	0.014	0.062	-0.003	-0.011	-0.044	-0.063	0.308	0.042	0.000	0.010	**-0.222**	0.039	-0.039	**0.092**
LW	0.008	0.054	0.002	-0.017	-0.054	-0.049	0.385	0.071	0.005	0.022	-0.146	**0.060**	-0.036	**0.304****
PH	0.016	0.047	-0.006	-0.007	-0.001	-0.048	0.150	0.020	0.002	0.026	-0.115	0.029	**-0.076**	**0.036**

Residual effect: 0.3671

Where, DTFPF = Days to fifty percent flowering, FFN = First fruiting node, IL = Internodal length, NRPF = Number of ridges per fruit, FL = Fruit length, FD = Fruit diameter, FW = Fruit weight, NFPP = Number of fruits per plant, NSPF = Number of seeds per fruit, HSW = Hundred seed weight, LL = Leaf length, LW = Leaf width, PH = Plant height, FYPP = Fruit yield per plant

when several genes can enhance both the characters and negative correlation initiates when rest of the genes may enhance only one trait and decrease others. The results are similar to the findings of Ranga and Darvhankar (2022), Mohammad and Marker (2017), Nwangburuka *et al.* (2012), Kumar and Patil (2020), Reddy *et al.* (2013) and Yonas *et al.* (2014).

Path coefficient analysis revealed the effect of independent character either alone or in association with other characters on expression of fruit yield. It allows the analysis of direct and indirect effect of several traits on fruit yield at genotypic level. Hence, it allows the selection of superior performing genotypes from large population for further improvement programme. The findings of path coefficient analysis revealed that FW (0.935) had greater positive direct impact on FYPP which was succeeded by NFPP (0.492), FFN (0.167), DTFPF (0.103), HSW (0.089) and LW (0.059) whereas in IL (-0.019) lower negative indirect impact was revealed which was followed by NSPF (-0.052), PH (-0.075), NRPF (-0.083), FL (-0.126), LL (-0.221) and FD (-0.296). Similar findings were reported by Yonas *et al.* (2014) and Kumar *et al.* (2020). The residual effect was observed to be 0.367 which revealed that characters under study contributed to about 65 percent of the expressed variability in the dependent trait. Similar results were reported by Dwivedi and Sharma (2017) & Ranga and Darvhankar (2022).

To show the significance of the major contribution to the overall variance, principal component analysis (PCA) was utilized (**Table 5**). From the variable loadings of PC I; it was observeed that DTFPF, FFN, NRPF, FD, LL, LW, FW and FYPP were the dominant features that contributed to 31.091 per cent of the total variation. In PC II; DTFPF, NFPP, FL, LL, LW, PH and HSW had the most impact *i.e.* 16.06 per cent of the total variation. In PCA III; IL, FL, PH and HSW were the predominant traits *i.e.* 12.43 per cent of the observed total variation while in PC IV, IL, NFPP, HSW and FYPP had the most impact i.e. 8.94 of the observed total variation. Amoatey *et al.* (2015) and Bhardwaj *et al.* (2021) also observed high genetic diversity using PCA. A biplot was created (**Fig. 1**) using the values of PC I and PC II. The clustering pattern of 75 different okra genotypes is furnished in **Table 6**. All of the genotypes were divided into five groups. Cluster III (27) had the highest number of genotypes; followed by cluster II (22), cluster V (22), cluster IV (3), and cluster I (1). It was evident from the distinct cluster patterns that there was no parallelism between the patterns and the geographical diversity. Priyanka *et al.* (2017) and Waskar *et al.* (2017) also found the group constellation of okra by genetic divergence. Between clusters I and V, the inter-cluster distance was revealed to be the maximum (21.17) while between clusters III and V it was the minimum (8.70). Chaurasia *et al.* (2011) reported a broad range of variations for intra-cluster and inter-cluster in between the okra genotypes. The average values of inter and intra-cluster divergence (D^2) are depicted in **Table 7**. Cluster I (18.23) had the maximum intra-cluster distance, whereas Cluster II (10.33) had the smallest value. Cluster means for different traits among the 75 genotypes of okra are depicted in **Table 8.** Since there is minimal likelihood of diverse populations emerging through hybridization between parents inside a cluster, it would be advantageous to use

Table 5. PC scores, Eigen value and the amount of variance described by the first five main components

Characters	PC I	PC II	PC III	PC IV	PC V	PC VI	PC VII	PC VIII	PC IX	PC X	PC XI	PC XII	PC XII	PC XIV
DTFPF	0.352	-0.291	0.143	0.107	0.209	0.029	-0.225	0.011	0.025	-0.248	-0.108	-0.612	0.465	0.014
FFN	0.391	-0.063	0.070	0.085	0.124	0.071	-0.483	-0.144	-0.178	-0.157	0.490	0.096	-0.500	-0.029
IL	0.077	-0.163	0.446	0.400	-0.394	-0.102	0.430	-0.345	0.246	0.002	0.212	-0.128	-0.119	-0.059
NRPF	0.378	-0.210	-0.016	-0.069	0.171	0.004	0.016	0.128	0.374	0.590	0.269	0.318	0.310	-0.068
FL	0.143	0.356	-0.399	-0.284	-0.340	-0.082	0.158	-0.017	-0.040	-0.107	0.509	-0.291	0.225	-0.241
FD	0.382	-0.158	-0.044	-0.098	0.015	-0.205	0.319	0.515	0.086	-0.251	-0.249	0.027	-0.354	-0.387
FW	0.424	0.010	-0.194	-0.137	-0.064	-0.086	0.285	-0.077	-0.070	-0.039	-0.089	0.011	-0.096	0.801
NFPP	-0.046	0.275	-0.233	0.639	-0.018	0.287	-0.038	0.484	0.258	0.000	0.125	-0.127	-0.066	0.194
NSPF	0.119	-0.221	0.053	-0.234	-0.532	0.738	-0.090	0.086	-0.053	0.070	-0.161	0.005	-0.034	-0.033
HSW	-0.076	0.247	0.342	-0.331	0.465	0.425	0.316	0.002	0.282	-0.281	0.215	-0.015	-0.038	0.064
LL	0.226	0.405	0.230	-0.002	-0.283	-0.149	-0.328	-0.030	0.328	-0.366	-0.206	0.407	0.264	0.020
LW	0.235	0.489	0.072	-0.071	0.070	0.015	-0.110	-0.221	0.153	0.466	-0.355	-0.388	-0.306	-0.135
PH	0.167	0.303	0.481	0.108	-0.011	-0.003	0.144	0.319	-0.653	0.192	0.076	0.069	0.203	0.004
FYPP	0.268	0.091	-0.337	0.345	0.229	0.311	0.270	-0.423	-0.217	-0.132	-0.199	0.276	0.164	-0.282
Eigen Value	4.353	2.248	1.740	1.251	0.973	0.846	0.605	0.443	0.413	0.339	0.294	0.229	0.173	0.093
Total variance (%)	31.091	16.056	12.431	8.937	6.950	6.040	4.324	3.163	2.947	2.425	2.100	1.635	1.238	0.663
Cumulative Variation (%)	31.091	47.147	59.578	68.515	75.465	81.505	85.829	88.992	91.940	94.364	96.464	98.099	99.337	100.000

Where, DTFPF = Days to fifty percent flowering, FFN = First fruiting node, IL = Internodal length, NRPF = Number of ridges per fruit, FL = Fruit length, FD = Fruit diameter, FW = Fruit weight, NFPP = Number of fruits per plant, NSPF = Number of seeds per fruit, HSW = Hundred seed weight, LL = Leaf length, LW = Leaf width, PH = Plant height, FYPP = Fruit yield per plant

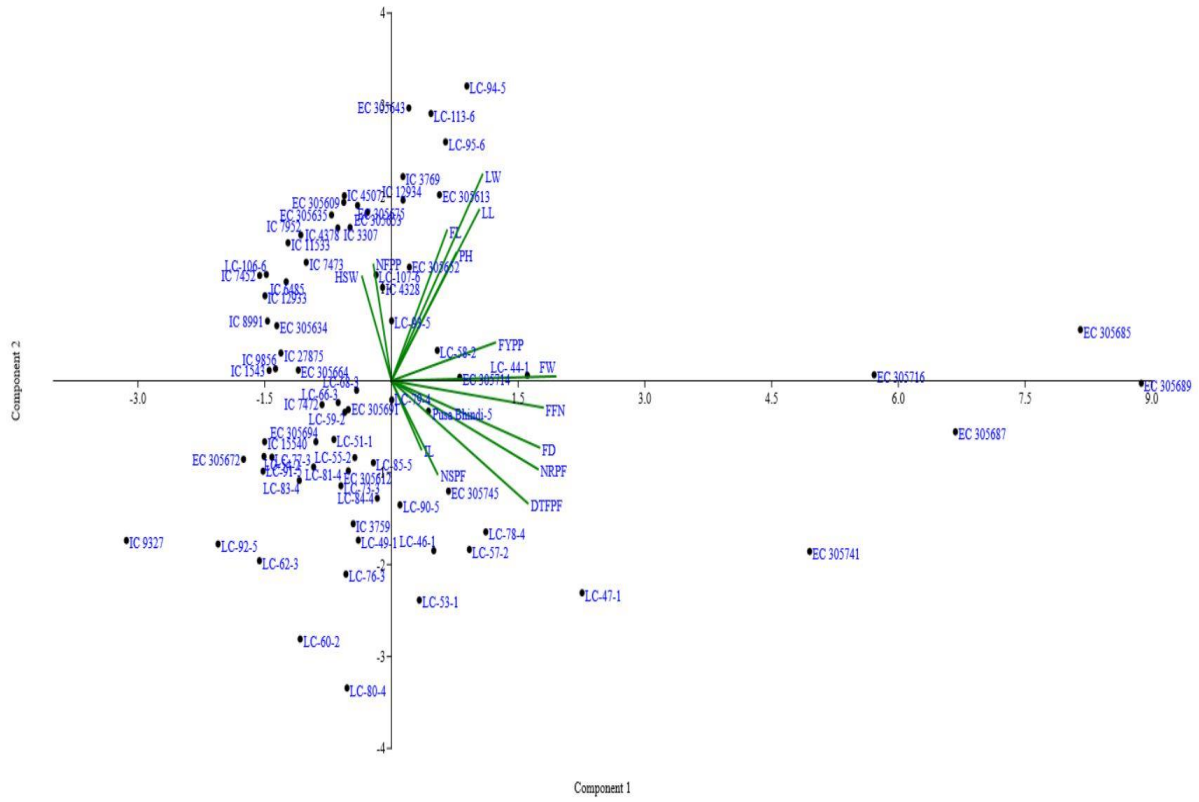

Fig. 1. Biplot between PC I and PC II depicting contribution of different traits causing variability between okra genotypes

Table 6. Clustering pattern of 75 genotypes of okra on the basis of genetic divergence

Clusters	Number of genotypes in Clusters	Name of genotypes
I	1	EC 305689
II	22	IC 3769, IC 4378, IC 7472, IC 7473, IC 11533, EC 305643, EC 305675, EC 305691, LC-44-1, LC-47-1, LC-49-1, LC-55-2, LC-59-2, LC-66-3, LC-73-3, LC-78-4, LC-79-4, LC-81-4, LC-83-4, LC-91-5, LC-107-6, LC-113-6
III	27	IC 3759, IC 4507, IC 9856, IC 12933, IC 12934, IC 15540, IC 27875, EC 305609, EC 305634, EC 305635, EC 305652, EC 305653, EC 305672, EC 305716, EC 305741, Pusa Bhindi-5, LC-46-1, LC-54-2, LC-57-2, LC-58-2, LC-60-2, LC-68-3, LC-76-3, LC-80-4, LC-85-5, LC-94-5, LC-95-6
IV	3	EC 305613, EC 305685, EC 305687
V	22	IC 1543, IC 3307, IC 4328, IC 6485, IC 7452, IC 7952, IC 8991, IC 9327, EC 305612, EC 305664, EC 305694, EC 305714, EC 305745, LC-51-1, LC-53-1, LC-62-3, LC-77-3, LC-84-4, LC-90-5, LC-92-5, LC-93-5, LC-106-6

Table 7. Average inter and intra cluster distance (D^2)

Clusters	I	II	III	IV	V
I	**18.23**				
II	16.72	**10.33**			
III	19.35	9.88	**11.70**		
IV	11.59	12.30	15.70	**12.59**	
V	21.17	13.14	8.70	17.94	**15.01**

Table 8. Cluster means for different characters among 75 genotypes of okra

Characters	Clusters				
	I	II	III	IV	V
Days to 50 per cent flowering	91.67	45.55	46.63	71.00	44.18
First fruiting node	13.11	6.26	6.54	11.63	6.41
Internodal length (cm)	4.72	6.08	6.11	5.35	5.46
No. of ridges per fruit	9.00	5.25	5.58	7.33	5.37
Fruit length (cm)	23.87	16.54	17.26	19.32	16.48
Fruit diameter (cm)	2.52	1.76	1.88	2.33	1.75
Fruit weight (g)	67.33	25.03	25.15	49.70	21.16
No. of fruits per plant	19.00	19.72	17.93	18.22	16.46
No. of seed per fruit	93.11	54.18	50.24	46.29	57.80
100 seed weight (g)	3.77	5.68	5.44	5.77	5.88
Leaf length (cm)	18.89	16.82	17.09	18.87	17.06
Leaf width (cm)	31.77	22.36	22.71	27.67	21.96
Plant height (m)	97.66	87.87	90.67	99.48	86.21
Fruit yield per plant (g)	646.00	376.92	279.48	523.19	204.43

genotypes from different clusters, depending on the distances between them, to produce desired segregants. The significance of genetic divergence was also reported by Balai *et al.* (2015).

From current analysis, the performance of genotypes *viz.,* EC 305689, EC 305685, EC 305687, EC 305613 and LC-59-2 for fruit yield per plant was observed superior which also exceeds the check variety (Pusa Bhindi-5). Fruit weight, days to 50 per cent blooming, internodal length, and fruit yield per plant recorded higher phenotypic and genotypic coefficients of variation, indicating that there was more scope for further improvement due to the high variability. Higher estimates of heritability coupled with genetic gain was examined for days to 50 per cent flowering, first fruiting node, internodal length, fruit weight,

number of seeds per fruit, plant height and fruit yield per plant. Hence, effective selection can be made by using these traits for improvement programme. Fruit yield per plant was found to have a positive and significant correlation with fruit weight, first fruiting node, number of ridges per fruit, number of fruits per plant, days to 50 per cent flowering, fruit diameter, and leaf width using phenotypic and genotypic correlation coefficients across several characters. Fruit weight had the greatest positive direct impact on fruit yield per plant during path coefficient analysis, followed by number of fruits per plant, first fruiting node, days to 50 per cent flowering, hundred seed weight, and leaf width. Principal component analysis showed that first four principal components were significant, explaining 68.51 per cent of the variation in total. In addition, clusters I and V had the maximum inter-cluster distance, while clusters III and V had the minimum.

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