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Genetic Diversity Analysis Based on Variability Parameters Principal Component and Cluster Analysis of Okra (*Abelmoschus Esculentus* L. Moench)

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ABSTRACT

The present investigation was entitled to study the effect of seasonal change with respect to genetic parameters on growth and yield of okra (*Abelmoschus esculentus*). Twelve diverse genotypes were grown in two different growing season in 2018 at Lovely Professional University, Punjab. All the genotypes under both the seasons are significantly differed. The results of PCV and GCV indicated that the value of PCV higher than the GCV. The value of GCV and PCV were high for fruit number plant^{-1}, test weight and yield plant^{-1} in both the seasons which indicates the presence of sufficient genetic variability for selection in these traits. Fruit girth, days to flowering, fruit size and fruit seed number plant^{-1} are positively and significantly correlated with each other. Genotypes in the present investigation showed significant variation at each axis through Principal component analysis which is the great tool to screen out the genotypes based on breeding objectives. Principal component analysis indicated that two important components accounted for about 78.8% of the total variation among traits in okra genotypes.

Key words: GCV, PCV heritability, Principle component analysis, Okra

INTRODUCTION

Okra (*Abelmoschus esculentus*), commonly known as ladies fingers or ochro, is a flowering, herbaceous, hairy annual plant of the mallow family (Malvaceae). It is native to the tropics of the Eastern Hemisphere and is widely cultivated or naturalized in the tropics and subtropics of the

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Western Hemisphere i.e. of West African, Ethiopian and South Asian origins for its edible green fruit. The plant is cultivated in tropical, subtropical and warm temperate regions around the world.

India is the leader in the world in area and production of okra with 61.26 lakh tonnes of production obtained from an area of 51.40 lakh ha under the crop with a productivity of 11.91 tonnes per hectare (Horticultural Statistics, 2017). The yield potential is very low attributing to poor yielding varieties and incidence of various pests and diseases. At edible stage, okra is good source of protein and minerals with about 88% moisture, 7.7% carbohydrate, 2.2% protein, 1.5% iron, 1.1% fiber, 0.7% mineral matter, 0.09% calcium, 0.2% fat, 0.08% phosphorous and 41 (k.cal) calorific values. The vitamin content is 58 IU vitamin A, 0.06 mg vitamin B, 0.06 mg Nicotinic acid, 0.06 mg Riboflavin and 16 mg vitamin C.

In okra the main breeding objectives for crop improvement needs to focus on plant height, higher yield, early flowering, number of branching, fruit size , diameter of fruit, inter-nodal length, and the fruits number plant^{-1}. The basic need in any crop improvement programme is to improve the yield potential of the any crop. Yield is a complex and polygenic trait, which depends on different factors and evaluation of all important factors is a prime breeding objectives in okra (Darvhankar *et al.,* 2016). Estimation of variability parameter under different dates or environments also provides useful information regarding pattern of changing variability under varied condition. By using such valuable information, breeding programme can become more systematic and sound (Sandhu *et al* 2018).

Extent and continuous breeding practices result in loss of genetic diversity of the okra germplasm and its adaptation (Zhang et al., 2005). Genetic diversity for germplasm is a pre-requisite material for screening promising lines for trait of interest (Ali et al., 2008). Genetically diverse parents is important for exploiting trangressive segregation as well as for securing useful heterosis in the progeny (Joshi et al., 2004). Principal Component Analysis and Cluster analysis

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(PCA) are the most common diversity assessing methods. The cluster analysis has opened a new possible way of assessing family relationships (Rogers, 1972). The main objectives of the present investigation is to sort out genetically diverse parents for exploiting high yielding okra germplasm.

METHODOLOGY

Plant material: Twelve diverse genotypes of okra (Collected from NBPGR, New Delhi) were used for the present investigation. These 12 lines of okra were evaluated under Rrandomized Block Design (RBD) with three replications at Experimental site, Lovely Professional University, Jalandhar, Punjab. Each genotypes were grown in a single line with the spacing of 45 X 30 cm. The seeds were soaked in water for six hours to remove any inhibiting materials on the seed coat soluble in water (Alabi, D.A., 1981).

Data Collection: As a measure of yield and yield contributing characters data were collected from two different growing seasons Kharif (S1) and Rabi (S2) seasons of the year 2018. Ten different morphological characters *viz,* plant height (PH), fruit girth (FG), days to flowering (DF), fruit number plant^{-1} (FN), fruit size (FL), maturity (80%)(DM), fruit seed number (SF), test weight (TW), first flowering node (FN) and yield plant^{-1} (YP) were recorded from both the seasons. The observations *viz*., days to flowering and maturity (80%) were recorded on plot basis from each seasons while rest characters were recorded by randomly selecting five plants from each replications and each seasons.

Statistical analysis:

Variance analysis: The analysis of variance was performed following the standard procedures given by Panse and Sukhatme (1985).

Variability parameters: The PCV and GCV was computed as per method described by Burton and DeVane (1953). Heritability estimate was computed by dividing the genotypic variance with phenotypic variance and then multiplying by 100 as suggested by Warner (1952). Correlation

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coefficient at genotypic and phenotypic level was computed according to Al-Jibouri *et al.*, (1958).

Principal component: Principal component analysis (PCA) was performed based on pooled data of both the seasons as proposed by Jeffers (1967) using software PAST (Hammer et al., 2001). A bi-plot display of the first two components was used for grouping genotypes illustrating the relationship between the genotypes and indices.

Cluster Analysis: Cluster analysis was performed as proposed by Tryon and Robert C. (1939) and a dendrogram was constructed using Ward linkage based on all morphological traits under study.

RESULTS AND DISCUSSION

Variability estimates

Analysis of variance was carried out for 10 different characters in okra. All the genotypes of present investigation are significantly differed for all the characters which indicates existence of large variability in the genotypes. Wide range of variations were observed for PH, DF, FP, DM, SF and YP indicating further scope of improvement in these traits. Maximum range was observed for YP followed by DM and PH, while lowest was in FB for both of the seasons.

The high value of GCV were observed for FP (54.89, 46.92), TW (49014, 47.50), FN (41.02, 24.92) YP (43.25, 50.98) for both the seasons. The high value of PCV were observed for FP (55.18, 47.85), TW (50.05, 47.70), FN (42.75, 24.96) and YP (43.56, 51.05). From the value of GCV and PCV it is observed that the value of PCV always higher than the value of GCV which indicates the magnitude of variation. Our results are in accordance with the results of Joshi et al., 2004, Darvhankar et al., 2016 and Sandhu et al., 2018. The high value of heritability and genetic advance were observed for all the characters under study except fruit girth for both the seasons. The high value of heritability and genetic advance suggest that the selection of the characters for next generation can be effective.

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Correlation Coefficient

PH were significantly correlated with DF (0.447, 0.725), DF with DM (0.507, 0.488), FP with YP (0.603, 0.524), FL with YP (0.524, 0.370), SF with YP (0.415, 0.382) and FN with YP (0.623, 0.441) for both seasons.

Principal Component Analysis and Cluster Analysis

Principal component analysis a new promising tool to screen diverse parents reflects the importance of the largest contribution to the total variation for each axis (Sharma, 1998). In this study, Eigen value > 1 was observed in three principal components (PCs) out of 10 extracted. These three PCs contributed 78.18% and the remaining 21.82% of total variability amongst the genotype assessed (Table. 4). The PC1 contributed maximum towards variability (32.89%) followed by PC2 (30.76%) and PC3 (14.53%). The traits like PH, SF, HW and FL showed considerable positive loadings on PC1. The PC2 was related to diversity due to DF, DM and FG with their considerable positive and FN with negative loadings.

The principal component analysis bi-plot of 10 yield related characters revealed the coefficient of correlation among them. In the bi-plot diagram the angle between PH, SF, HW and FL characters is acute angle, therefore they have positive correlation which confirmed by correlation analysis (Fig. 1).

The PC1 and PC2 axis which justify 78.18% of total variation mainly distinguish the indices of different group. PH, SF, HW and FL refer to group 1 (G1). The PC's axis separated indices like DF, DM and FG in group 2 (G2). FN was separated as group 3 (G3) and FP as a group 4 (G4). The most prominent relations reveal a strong negative association between DF, DM and FG with FP as indicated by the large obtuse angles between their vectors. A strong positive correlation could be expected between PH, SF, HW and FL with DF, DM and FG as these indices formed acute angle between themselves. These, bi-plot graph supported the relationship between traits revealed in correlation analysis.

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Bi-plot display based on the first two component genotypes were placed in four main groups depicted earlier. G1 with higher values for component 1 and component 2 includes genotypes 1, 10, 3, 5, and 9. G2 with higher values for component 2 and lower value of component 1 includes genotypes 2, 6 and 4. On the other hand G3 and G4 had lower values for both the component includes genotypes 11 and 12 (G3) and 7 (G4).

In order to determine the variation among different genotypes and determination of the genotypes far or nearness, cluster analysis was applied to place the similar genotypes in one group (Sajad Bokaei et al, 2008). 12 genotypes were subjected to cluster analysis using all ten characters under the study and genotypes were grouped into two major clusters based on various morphological traits (Figure. 1).

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Table.1 Mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as per cent of mean for ten characters of okra

SN	CH	MEAN		RANGE		GCV		PCV		Heritability		GA%	
		S1	S2	S1	S2	S1	S2	S1	S2	S1	S2	S1	S2
1	**PH**	95.51	44.04	55.50-154.50	31.83-55.33	32.92	15.21	32.99	15.97	99.59	90.66	67.69	29.84
2	**FG**	1.98	1.63	1.50-2.53	1.07-2.30	8.1	25.92	24.32	28.8	11.1	80.95	5.56	48.04
3	**DF**	37.44	50.64	28.67-50.33	34.33-65.00	18.63	15.44	19.48	16.09	91.52	92.06	36.73	30.52
4	**FP**	17.38	7.69	6.40-35.03	3.20-16.83	54.89	46.92	55.18	47.85	98.95	96.15	112.48	94.79
5	**FL**	13.97	5.6	7.90-18.80	3.17-8.17	24.05	30.98	24.67	31.82	95.05	94.74	48.32	62.12
6	**DM**	76.89	98.31	54.50-100.00	72.67-127.67	18.15	16.25	18.37	16.48	97.66	97.18	36.96	33
7	**SF**	52.89	24.53	34.00-89.60	13.87-47.67	28.82	41.16	28.98	41.21	98.9	99.75	59.05	84.7
8	**TW**	7.51	6.49	4.90-15.63	3.43-13.10	49.14	47.5	50.05	47.7	96.41	99.18	99.4	97.46
9	**FN**	6.09	11.27	2.70-11.13	8.00-18.20	41.02	24.92	42.75	24.96	92.09	99.67	81.1	51.25
10	**YP**	273.71	124.69	73.37453.10	32.63-207.47	43.25	50.98	43.56	51.05	98.54	99.7	88.44	104.86

CH: Character, S1: Kharif Season, S2: Rabi Season, PH: Plant Height, FG: Fruit Girth, DF: Days to flowering, FP: Fruits number plant^{-1}, FL: Fruit length, DM: Days to maturity, SF: Fruit seed number, TW: Test weight, FN: First flowering node and YP: Yield plant^{-1}

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Table. 2: Kharif Correlation Coefficient for 10 different characters of okra in season 1 and season 2

		PH	FG	DF	FP	FL	DM	SF	TW	FN	YP
PH	**S1**	1.00	0.460**	0.447**	-0.382*	0.351*	0.143	0.689**	0.003	-0.294	0.282
	S2	1.00	-0.188	0.725**	-0.165	-0.2	0.573**	-0.009	-0.419*	-0.219	-0.338*
FG	**S1**		1.00	0.313	-0.118	-0.074	0.226	0.176	-0.197	-0.113	0.04
	S2		1.00	-0.14	-0.229	-0.247	0.318	-0.19	-0.225	0.215	-0.505**
DF	**S1**			1.00	-0.368*	-0.182	0.507**	0.12	-0.358*	-0.242	-0.054
	S2			1.00	-0.124	-0.005	0.488**	0.229	-0.182	-0.495**	0.068
FP	**S1**				1.00	-0.21	-0.512**	-0.173	-0.448**	0.848**	0.603**
	S2				1.00	0.274	-0.342*	0.155	0.156	-0.046	0.524**
FL	**S1**					1.00	-0.456**	0.621**	0.644**	-0.338*	0.370*
	S2					1.00	-0.357*	0.641**	0.281	-0.089	0.393*
DM	**S1**						1.00	-0.055	-0.349*	-0.293	-0.632**
	S2						1.00	0.135	-0.375*	-0.168	-0.481**
SF	**S1**							1.00	0.358*	-0.337*	0.415*
	S2							1.00	0.357*	-0.505**	0.382*
TW	**S1**								1.00	-0.627**	-0.13
	S2								1.00	-0.518**	0.623**
FN	**S1**									1.00	0.441**
	S2									1.00	-0.491**
YP	**S1**										1.00
	S2										1.00

CH: Character, S1: Kharif Season, S2: Rabi Season, PH: Plant Height, FG: Fruit Girth, DF: Days to flowering, FP: Fruits number plant^{-1}, FL: Fruit length, DM: Days to maturity, SF: Fruit seed number, TW: Test weight, FN: First flowering node and YP: Yield plant^{-1}

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Table 3: Principal component analysis of different physiological traits of okra

PC	Eigen Value	% Variance	Cumulative %
1	3.28	32.89	32.89
2	3.07	30.46	63.35
3	1.45	14.53	77.88
4	0.72	7.21	85.09
5	0.5	5.06	90.15
6	0.44	4.41	94.56
7	0.28	4.86	99.42
8	0.12	1.22	100.64
9	0.07	0.71	101.35
10	0.03	0.31	101.66

Figure 1: Bioplot between PCI and PC2 showing contribution of various traits in variability of okra on pooled basis

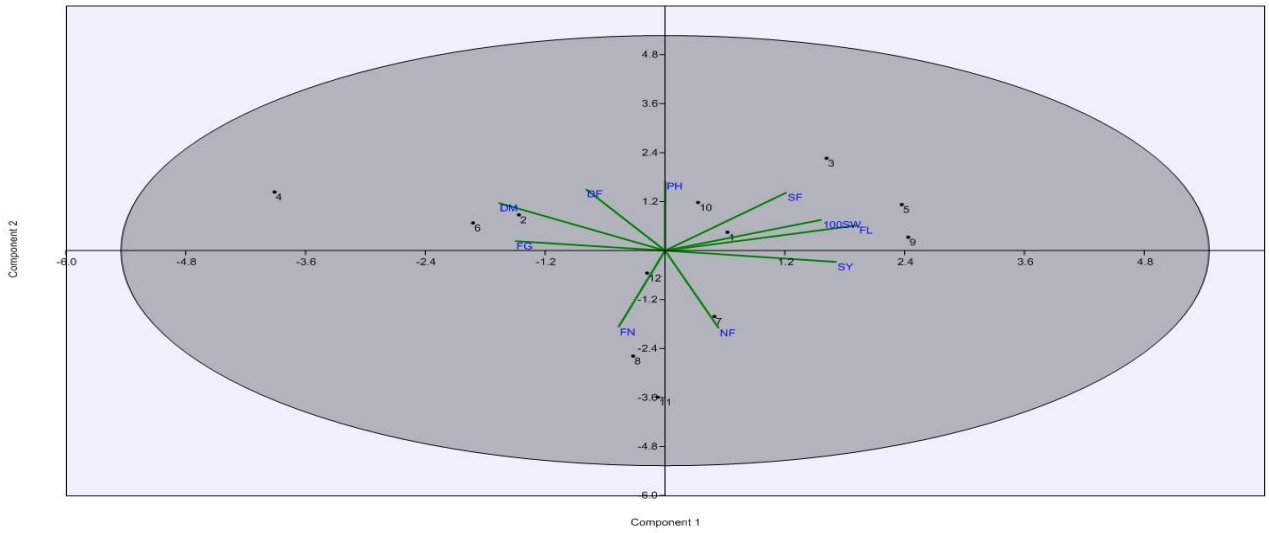

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Figure 2: Dendogram using Ward method showing classification of groundnut genotypes based on 10 traits