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Genetic Evaluation and Bi-plot Analysis in Okra Hybrids for Yield, Quality Components and YVMV Resistance

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ABSTRACT

Fifty-one okra F_1 hybrids (using 17 lines as female and 3 testers as male parent) were evaluated in RCBD design during two different consecutive seasons (summer and rainy). The phenotypic coefficient of variability (PCV) was higher than the genotypic coefficient of variability (GCV) for all studied character exhibiting environmental effects on the expression of characters. Heritability (h^2b) along with genetic advance per cent of mean was found highest for character YVMV (86.95% and 150.61%). All the 51 okra hybrids were grouped into 4 distinct clusters in which Cluster II was the largest cluster having 28 F_1s (54.90% of total F_1s) followed by Cluster I with 14 F_1s (27.45% of total F_1s). Out of the major 6 PCs, 4 principal components (PC1, PC2, PC3, and PC4) accounted with proportionate values of 22.61, 17.22, 11.87 and 10.63%, respectively and contributed 62.33 % of the cumulative variation having Eigen value more than one. Moreover, based on PCs and genetic divergence in Cluster I and Cluster IV for plant height, YVMV and number of fruit per plant are important to identify the best cross combination (Arka Abhay × Arka Anamika) in okra. Therefore, the best cross combinations for improvement in various economic traits can be recommended on the basis of genetic divergence and principal component analysis in okra.

Keywords: F_1 hybrid, Genetic diversity, Okra, Principal components, YVMV

INTRODUCTION

Okra (Abelmoschus esculentus L. Moench) is widely grown throughout India both in summer as well as in rainy season. Moreover, India is the largest producer of okra in the world with total area of 0.52 Mha and production 6.26 MT green pods whereas productivity of the crop is 12.1 MT ha-1 (Anonymous, 2013). Despite these, okra suffered mainly due to lack of high yielding hybrid in conjunction with resistance to yellow vein mosaic virus (YVMV). Various approaches are being used to overcome this problem, one of them considered as heterosis breeding. However, it should also be kept in mind that due to high chromosome number and polygenic control of major economic traits, therefore 100% homozygosity in the parents is difficult to achieve (Dhankar and Mishra, 2006).

Okra is basically categorized under often-cross-pollinated group and showed easy emasculation and a high number of seed production in single pollination. Heterosis breeding is a frequently used breeding procedure where the distant genotypes are brought together in a specific pattern to express their ability to make a dramatic shift in the magnitude of a particular trait. The genetical studies revealed that yield and its components are most assessing in nature and magnitude of gene effect and important for increasing the yield potential along with disease resistance. The economic yield in the majority of crops is a complex entity whose manifestation results from multiplicative interaction of several yield components. Therefore, for attaining higher yield levels along with resistance to YVMV, the breeder is required to simplify this complex situation through handling of the major yield components. To breed desired plant type, the information about the nature and magnitude of genetic variability among the base population and the degree of transmission of traits are prerequisite. For creating variability, crossing among parental lines is the most potent and assured method. Genetic study based on the multivariate analysis is a powerful tool for determining the degree of divergence between populations and the relative contribution of different components to the total divergence and the nature of forces operating at different levels (Singh et al., 2012). Cluster analysis and principal component analysis (PCA) are the most frequent genetic diversity assessing methods while securing relative basic differences between them. The cluster analysis has been most exploited for assessing family relationships. Therefore, expecting relative genetic potential differences, an attempt was made in the present study to group 51 hybrids of okra on the basis of their degree of total genetic divergence measured by multivariate analysis.

MATERIALS AND METHODS

Plant material and experimental conditions

Twenty diverse okra genotypes were received from Indian Institute of Vegetable Research, Varanasi (India) and evaluated at the Vegetable Research Farm, Institute of Agricultural Sciences, BHU, Varanasi, India. Crosses were made in 'line × tester' mating design, using 17 lines as female (IC 128883, VRO 5, VRO 6, AC 108, IC 45806, IC 218877, IC 218844, Arka Abhay, IC 43720, IIVR 342, IC 140906, IIVR 198, EC 305612, IIVR 435, IIVR 401, SA 2 and IC 140934) and 3 testers as male [Arka Anamika (AA), Pusa Sawani (PS) and

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Parbhani Kranti (PK)]. A total of fifty-one okra F1 hybrids were made to study heterosis. These 51 F1's were evaluated during two different consecutive seasons (summer and rainy) in two sessions. The experiments were laid out in a randomized complete block design (RCBD) with three replications at the row to row and plant to plant spacing of 45 cm and 15 cm, respectively. All the environmental observation in open field conditions such as rainfall, humidity, temperature, and sunshine of both summer and rainy season were recorded till the harvesting date. Observations were recorded in every cropping season for eight characters on 10 randomly selected plants, viz., plant height, number of fruits/plant, number of branches per plant, days to 50% flowering, number of fruits per plant, fruit length (cm), fruit diameter (cm), fruit yield per plant (g), number of seeds per fruit, ascorbic acid content (mg/100g) and yellow vein mosaic virus incidence (%).

Data analysis and its measurement

The genotypic and phenotypic variances were calculated according to Johnson et al. (1955) and Comstock and Rabinson (1952). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was calculated by the method suggested by Singh and Chaudhary (1985) whereas heritability in a broad sense for yield its and yield components were worked out by using formula suggested by Hanson et al. (1956). Genetic advance (GA) per cent of the mean was calculated by the method suggested by Johnson et al. (1955). Cluster analysis of 51 okra hybrids based on 10 quantitative traits to assess the magnitude of genetic variation was performed by using statistical software NTYSYSpc version 2.01 (Roulf, 2002) and a dendrogram was constructed (Fig.1). Euclidean distance coefficient values were made for all paired genotypes which result in euclidean dissimilarity coefficients. It is most frequently used to evaluate the relationship among the entries with a cluster analysis. The statistical tool STATISTICA version 10.0 was utilized for principal component analysis. Through, Principal component analysis (PCA), total explained variation was depicted in Fig.2 using studied yield components revealing extreme genetic variability among okra hybrids.

Scoring of YVMV disease incidence was scored on 0 – 4 scale (Table 1) at the 15 days intervals (30 day, 45 day, 60 day and 75 days) after sowing and per cent disease infection (PDI) and coefficient of infection (CI) value was calculated by the procedure coined by Banerjee and Kaloo (1987).

$$\text{PDI (\%)} = \frac{\text{Number of infected plants}}{\text{Total number of plants observed}} \times 100$$

$$\text{CI} = \text{RV} \times \text{PDI}$$

Where, RV = Response value

PDI = per cent disease infection.

Table 1: Scale for classifying disease reaction in okra to YVMV disease

Symptoms	Severity grade	Response value	Coefficient of infection	Reaction
Symptoms absent	0	0	0 – 4	HR
Very mild symptoms up to 25% leaves	1	0.25	4.1 – 9	R
Appearance of disease between 26-50% leaves	2	0.50	9.1 – 19	MR
Symptom between 51-75% leaves	3	0.75	19.1 – 39	MS
Severe disease infection at 75% leaves	4	1.00	39.1 – 69	S
Above 75% leaves	>4	>1.00	69.1 – 100	HS

R = Resistant, S = Susceptible, H R = Highly resistant, H S = Highly susceptible,
M R = Moderately resistant, M S = Moderately susceptible

RESULTS AND DISCUSSION

In the present experiment, 51 okra F_1 hybrids were analyzed for character association, cluster and principal component analysis (PCA) for yield, quality components, and YVMV resistant. The phenotypic coefficient of variability (PCV) was higher than the genotypic coefficient of variability (GCV) for all studied character exhibiting environmental effects on the expression of characters. Highest PCV was observed for YVMV (104.52%), number of seed per fruit (39.84%), ascorbic acid content (37.95%) and a number of branches per plant (30.45%) in consonance with Singh *et al.* (2012) (Table 2). It expressed the presence of extreme genetic variability among okra hybrids. Heritability (h^2b) was found highest for character YVMV (86.95%) followed by plant height (67.56%), a number of branches per plant (66.67%) and fruit length (47.06%). Highest heritability (h^2b) along with maximum genetic advance per cent of the mean was observed for YVMV (86.95% and 150.61%) followed by a number of branch per plant (66.67% and 31.21%) and number of seed per plant (46.21% and 32.87%) (Table 2).

It indicated that the presence of additive genetic effects for expression of these characters. Considering the characters under selection parameters would be effective. Fruit yield per plot was significantly and positively associated with a number of fruit per plant (0.654) and ascorbic acid content (0.327) (Table 3). It suggests that the characters should be included for genetic improvement. A negatively significant correlation (-0.343) was observed between fruit length and plant height as similarly reported by Duzyaman (2005); Reddy *et al.* (2012); Kiran and Pathak (2012);

Table 2: Genetic variability, heritability and genetic advance for 10 characters in 51 Okra hybrids

Characters	Means	St. Deviation	σ^2P	σ^2G	PCV (%)	GCV (%)	h^2b (%)	Genetic advance percent of the mean (%)
PH	109.105	12.608	145.52	98.32	11.96	9.82	67.56	15.39
NBP	2.41	0.569	0.30	0.20	30.45	23.21	66.67	31.21
D50%F	51.804	2.752	9.33	0.73	5.98	1.67	7.86	0.95
NFPP	11.643	1.402	2.27	0.57	15.54	7.63	25.00	6.66
FL	10.321	0.68	0.57	0.27	7.33	5.16	47.06	7.07
FD	1.575	0.093	0.01	0.00	7.69	3.54	25.00	3.78
FYPP	115.351	20.813	421.37	119.17	22.25	11.83	28.28	10.37
NSPF	56.554	7.567	381.28	176.18	39.84	27.08	46.21	32.87
AA	10.287	1.418	12.77	5.07	37.95	23.91	39.69	28.40
YVMV	19	18.997	255.22	221.92	104.52	97.47	86.95	150.61

Where, PH-Plant height, NBP-Number of branches per plant, D50%F- Days to 50% flowering, NFPP-Number of fruits per plant, FL- Fruit length (cm), FD- Fruit diameter (cm), FYPP-Fruit yield per plant (g), NSPF-Number of seeds per fruit, AA-Ascorbic Acid content (mg/100g), YVMV-Yellow vein mosaic virus incidence (%).

Solankey *et al*. (2013)- Yellow vein mosaic virus (YVMV) showed a negative association with days to 50% flowering, ascorbic acid content and fruit yield per plant (Table 3).

Table 3: Character association between 51 Okra F_1's hybrid for ten studied characters.

Character	PH	NBP	D50%F	NFPP	FL	FD	FYPP	NSPF	AA	YVMV
PH	1.000	0.061	0.002	-0.104	-0.343*	-0.206	-0.140	0.012	-0.262	-0.050
NBP	0.061	1.000	0.051	0.028	-0.011	-0.079	0.068	0.023	-0.146	-0.059
D50%F	0.002	0.051	1.000	0.271	0.069	-0.040	0.255	0.152	-0.039	-0.244
NFPP	-0.104	0.028	0.271	1.000	0.081	-0.078	0.654*	0.091	0.317*	-0.199
FL	-0.343*	-0.011	0.069	0.081	1.000	0.179	0.243	-0.091	0.254	0.192
FD	-0.206	-0.079	-0.040	-0.078	0.179	1.000	0.183	-0.137	-0.047	0.288*
FYPP	-0.140	0.068	0.255	0.654*	0.243	0.183	1.000	-0.096	0.327*	-0.150
NSPF	0.012	0.023	0.152	0.091	-0.091	-0.137	-0.096	1.000	0.140	0.045
AA	-0.262	-0.146	-0.039	0.317*	0.254	-0.047	0.327*	0.140	1.000	-0.237
YVMV	-0.050	-0.059	-0.244	-0.199	0.192	0.288*	-0.150	0.045	-0.237	1.000

*Significant at 5 % level of significance.

Where, PH-Plant height, NBP-Number of branches per plant, D50%F- Days to 50% flowering, NFPP-Number of fruits per plant, FL- Fruit length (cm), FD- Fruit diameter (cm), FYPP-Fruit yield per plant (g), NSPF-Number of seeds per fruit, AA-Ascorbic Acid content (mg/100g), YVMV-Yellow vein mosaic virus incidence (%).

Genetic divergence analysis

All the 51 okra hybrids were grouped into 4 distinct clusters through STATISTICA V.10 (Fig.1).

Fourteen F_1s were classified in cluster I accounted for 27.45% of total F_1s. The average value of the cluster I hybrids for YVMV (44.69), number of seeds per fruit (57.90) and plant height (110.31) are above the mean of all hybrids and for fruit yield per plot (111.93) and ascorbic acid content (9.42) below the mean of all hybrids representing poor in yield and disease resistance potential. The best cross combination (Arka Abhay × Arka Anamika) is also coming under cluster I. Out of 51 okra hybrids, 28 F_1s was grouped in cluster II accounted for 54.90% of total F_1s i.e. largest cluster. The average value of the cluster II hybrids for fruit yield per plant (111.97) and YVMV (4.98) are below the mean of all hybrids representing poor in yield but an excellent source for YVMV disease resistance. Six F_1s were classified in cluster III accounted for 11.76 % of total F_1s. The average value of the cluster III hybrids for fruit yield per plot (129.87), number of seeds per plant (57.91) and ascorbic acid content (11.33) are higher the mean of all hybrids representing better yield potential (Table 4). Cluster IV has only 3 hybrids accounting for 5.88 % of total okra hybrids. The average value of the cluster IV hybrids for fruit yield per plot (133.87), number of seeds per plant (57.61), ascorbic acid content (11.91) and YVMV (30.67) are higher than the mean of all hybrids

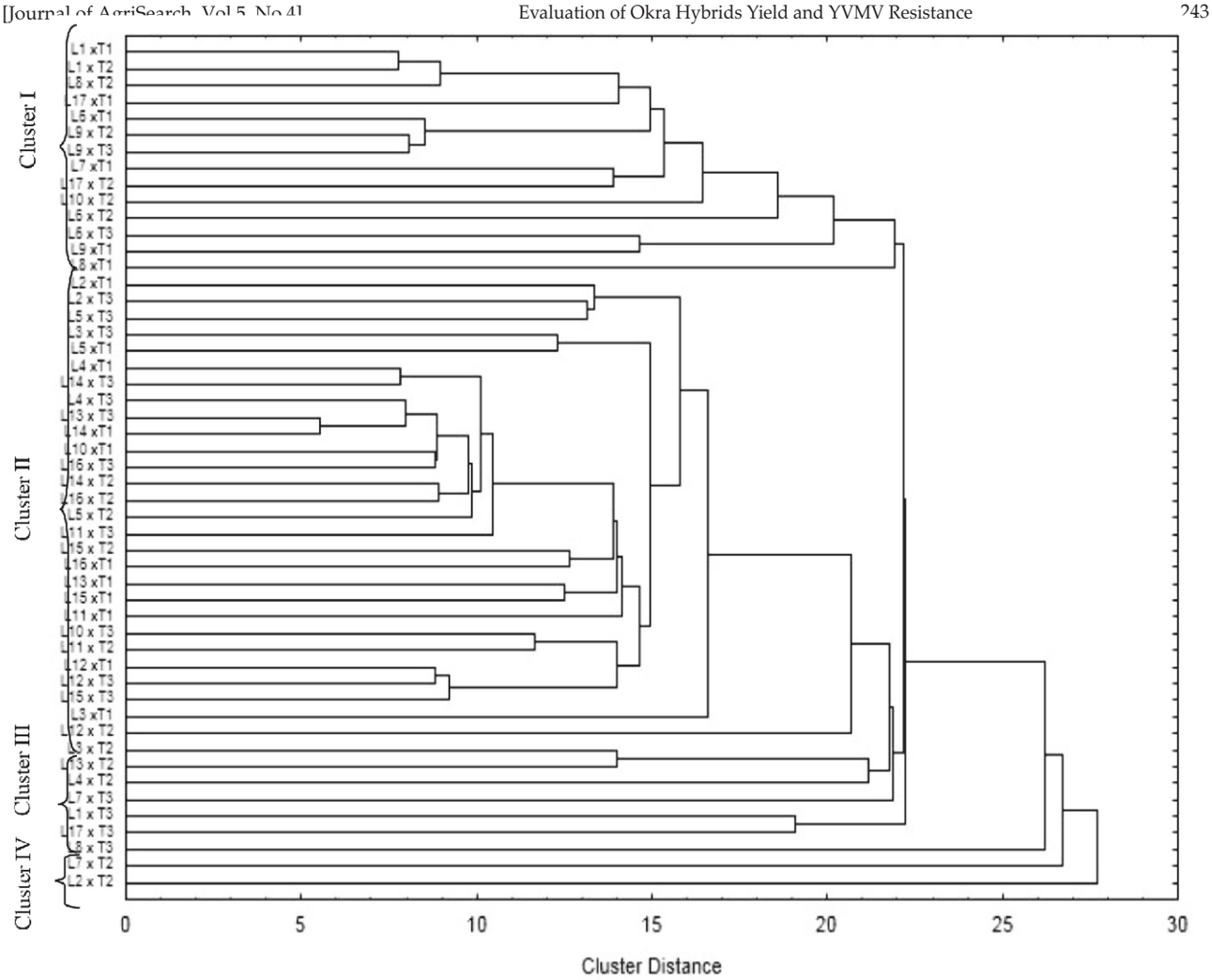

Fig 1: Dendrogram depicting clustering pattern of 51 okra hybrids

representing better yield potential but poor source of YVMV disease resistance potential (Table 4). The findings are in close conformity with the report of Hazara *et al.* (2002), Bendal *et al.* (2008), Singh *et al.* (2012), Kiran and Pathak (2012) and Singh *et al.* (2014).

Table 4: Average of traits for each cluster (above number) and its deviation from the total mean (below the number). Where, PH-Plant height, NBP-Number of branches per plant, D50%F- Days to 50% flowering, NFPP-

Cluster	PH	NBP	D50%F	NFPP	FL	FD	FYPP	NSPF	AA	YVMV
Cluster1	110.31	2.42	51.22	11.45	10.49	1.62	111.93	57.90	9.42	44.69
	1.20	0.01	-0.59	-0.19	0.17	0.05	-3.42	1.34	-0.87	25.69
Cluster2	110.10	2.45	52.13	11.64	10.18	1.55	111.97	55.48	10.32	4.98
	0.99	0.04	0.33	0.00	-0.14	-0.02	-3.38	-1.08	0.04	-14.02
Cluster3	103.78	2.12	52.50	12.28	10.67	1.57	129.87	57.91	11.33	18.67
	-5.33	-0.29	0.70	0.64	0.35	-0.01	14.52	1.36	1.04	-0.34
Cluster4	104.90	2.55	50.11	11.29	10.12	1.60	133.87	57.61	11.91	30.67
	-4.21	0.14	-1.69	-0.36	-0.20	0.03	18.52	1.06	1.62	11.67

Number of fruits per plant, FL- Fruit length (cm), FD- Fruit diameter (cm), FYPP-Fruit yield per plant (g), NSPF-Number of seeds per fruit, AA-Ascorbic Acid content (mg/100g), YVMV-Yellow vein mosaic virus incidence (%)

Principal components analysis (PCA)

PCA is usually used for data reduction for synchronizing two or more characters by linear transformation of the original variables into a novel group of unrelated variables regarded as principal components (PCs) (Wiley, 1981). Six major PCs (PC1 to PC6) from the original data explained 80.45% of the total variation as similarly reported by Singh *et al.* (2012). Out of the major 6 PCs, 4 principal components (PC1, PC2, PC3and PC4) accounted with proportionate values of 22.61, 17.22, 11.87 and 10.63 %, respectively and contributed 62.33 % of the cumulative variation having Eigen value more than one (Table 5). Two-dimensional depictions of 51 okra hybrids on PC axis 1 and 2 represented the existence of extreme genetic diversity among present hybrids set (Fig 2).

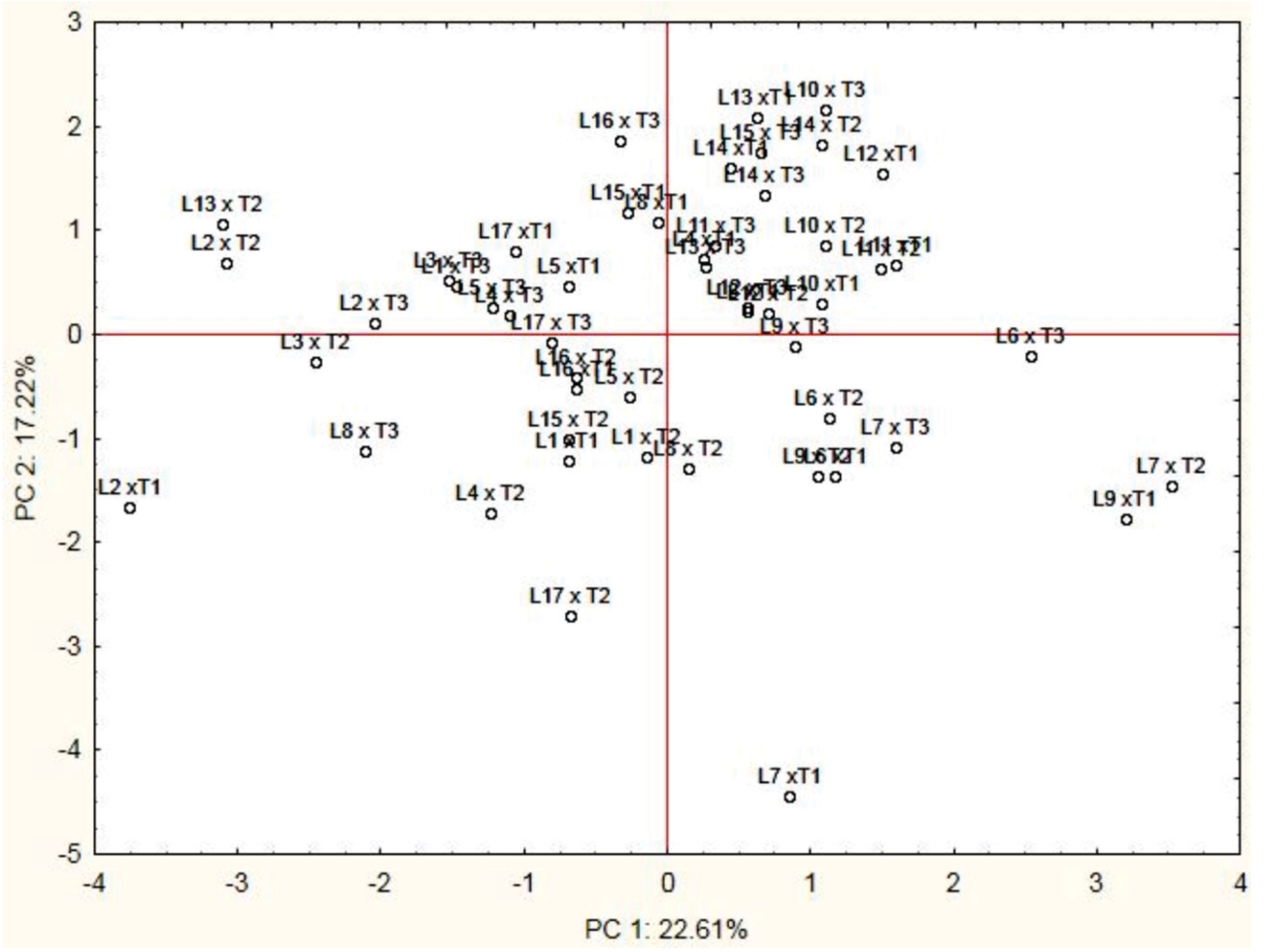

Fig. 2: Scattered plot depicting 51 okra Hybrid on Principal component (PC) axis 1 and PC2 using 10 characters

The first principal component has high positive component value for plant height and YVMV. PC1 has negative component value for fruit yield per plant, number of fruit per plant, ascorbic acid content, fruit length and days to 50% flowering as similarly reported by Duzyaman (2005) The second principal component has high positive component value for plant height, days to 50 % flowering, number of fruit per plant and number of seed per fruit and high negative component value for fruit length, fruit diameter and YVMV (Table 5).

Table 5: Principal component analysis in Okra hybrids for ten characters

Variables	PC1	PC2	PC3	PC4	PC5	PC6
Eigen value	2.26	1.72	1.19	1.06	0.95	0.86
Cumulative	2.26	3.98	5.17	6.23	7.18	8.04
% Total	22.61	17.22	11.87	10.63	9.52	8.60
Cumulative	22.61	39.83	51.70	62.33	71.85	80.45

Characters	Eigen vector					
PH	0.27	0.39	-0.22	0.09	0.27	0.36
NBP	0.01	0.17	-0.48	-0.24	-0.76	0.17
D50%F	-0.27	0.27	-0.30	-0.36	0.29	-0.61
NFPP	-0.52	0.19	-0.11	-0.01	0.14	0.35
FL	-0.28	-0.43	0.00	-0.14	-0.29	-0.25
FD	-0.06	-0.50	-0.31	-0.06	0.33	0.05
FYPP	-0.54	-0.01	-0.30	0.10	0.12	0.28
NSPF	-0.04	0.21	0.39	-0.77	0.08	0.18
AA	-0.42	-0.04	0.53	0.14	-0.15	0.16
YVMV	0.21	-0.47	-0.10	-0.40	0.12	0.38

Where, PH-Plant height, NBP-Number of branches per plant, D50%F- Days to 50% flowering, NFPP-Number of fruits per plant, FL- Fruit length (cm), FD- Fruit diameter (cm), FYPP-Fruit yield per plant (g), NSPF-Number of seeds per fruit, AA-Ascorbic Acid content (mg/100g), YVMV-Yellow vein mosaic virus incidence (%).

The studied characters having either high positive or negative component value exhibited tremendous genetic variability and perform significant impact during clustering. The third principal component has high positive component value for a number of seed per fruit and ascorbic acid content and high negative component value for number of branches per plant, days to 50% flowering, plant height, fruit diameter and fruit yield per plant as similar reported by Singh *et al.* (2012). The fourth principal component has high positive component value for ascorbic acid content and fruit yield per plant and high negative component value for number of seeds per fruit, YVMV, number of branches per plant, days to 50 % flowering and fruit length. The depiction of component characters on PC1 and PC2 axis represented that fruit yield per plant is positively related with number of fruit per plant, ascorbic acid content and days to 50% flowering and negative related with YVMV. It also revealed that the number of branches per plant, number of seeds per fruit and plant height has negative relationship with fruit length and diameter (Fig. 3).

CONCLUSION

In this way, genetic variability and principal component analysis are most reliable selection parameters for electing promising traits *viz*., plant height, YVMV and number of fruit per plant in okra. Apart from the high degree of divergence (Cluster I and Cluster IV) for these traits, the mean performance of genotypes and the traits with a maximum contribution towards divergences should also be given due consideration. Thus, the best cross combination (Arka Abhay × Arka Anamika) in cluster I for improvement for various yield and quality components can be recommended on the basis of genetic divergence and principal component analysis.

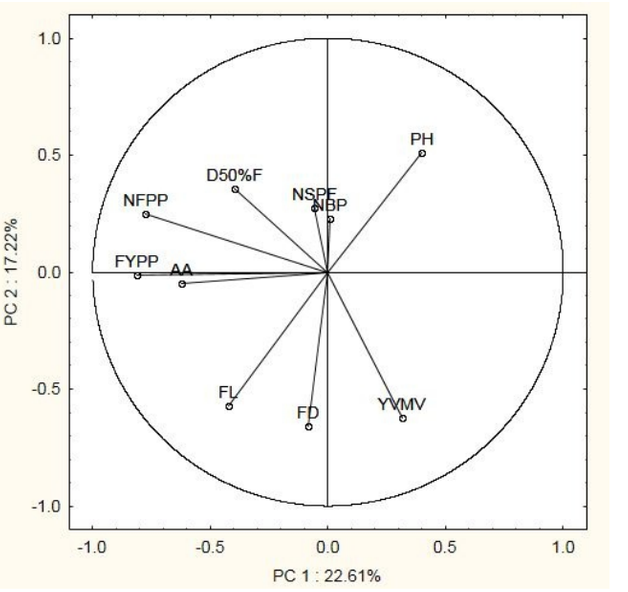

Fig 3: Scattered diagram of first two Principal components exhibiting contribution of studied characters in separation of 51 okra hybrids.

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