International Journal of Agriculture, Environment and Biotechnology
Citation: IJAEB: 9(4): 485-491 August 2016
DOI Number: 10.5958/2230-732X.2016.00064.4

Assessment of genetic diversity in Okra (*Abelmoschus esculentus* L. Moench) for yield and yellow vein mosaic virus incidence

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Paper No. 467 Received: 17-1-2016 Accepted: 10-8-2016

Abstract

Thirteen diverse genotypes were evaluated to assess the genetic diversity in a randomized block design during 2013-14 for yield and yellow vein mosaic virus (YVMV) incidence in Okra**.** On the basis of D^2 values, the 30 genotypes were clustered into six groups. Cluster II constituted the largest group (11 genotypes) followed by cluster III and cluster VI (5 genotypes each). The cluster IV and V contain 4 genotypes each, whereas only 1 genotypes present in cluster I. The character coefficient of infection alone contributes highest percentage (51%) toward divergence, followed by number of branches per plant (24%), percentage disease incidence (12%). The first six principal components have accounted 84.00% of total variation and percent variation expected were 24.00% (PC1), 19.50% (PC2), 14.30% (PC3), 11.48% (PC4), 7.97% (PC5) and 6.80% (PC6), respectively. The PC1 has positive association with days to first picking, followed by days to first flowering and days to 50% flowering. However, PC1 has negative association for fruits per plant and fruit weight. Therefore, the traits *viz*., days to first picking, first flowering node and days to first flowering should be given top priority in diverse parent selection for attempting high yielding along with YVMV tolerant hybrids in okra.

Highlights

- Hybridization between genotypes from cluster I and V might be beneficial
- Coefficient of infection and number of branch contributes maximum diversity

Keywords: Genetic diversity, Okra, principal component, yield, YVMV

The cultivated okra is an important fruit vegetable crop cultivated in tropical, sub-tropical and mild temperate parts of the world. It belongs to Malvaceae family under the genus *Abelmoschus* and was originated in the Hindustani centre, *i.e.* India (Zeven and Zhukovsky 1975). Okra is grown for their tender pods which are cooked in curry and also in soup making. Okra fruits are nutritionally rich and contain good amount of vitamin C (30 mg $100g^{-1}$), calcium (90mg 100 g^{-1}), iron (1.5 mg $100g^{-1}$) and iodine (97mg $100g^{-1}$) (Pal *et al*. 1952).

India is leading okra producing country with 72.9 % share in world okra production and produces okra in an area of 533 thousand hectares with production of 6346 thousand tonnes and productivity of 11.9 tonnes/ha. In India West Bengal (14% share) is leading okra producer in the country followed by Bihar (12% share). (Anonymous, 2014).

One of the major limiting factors is incidence of okra yellow vein mosaic virus and its vector whitefly (*Bemisia tabaci* Gen.) for reduction of cultivation of okra. This disease is caused by a complex consisting

of the monopartite begomovirus, okra yellow vein mosaic virus (family: Geminiviridae) and a small satellite DNA b component. This disease and insect vectors cause heavy losses of crop by affecting the quality and yield of the fruits. Infection of 100% plants in a field is very usual and yield losses ranges from 50 to 94% depending on the stage of crop growth at which infection occurs (Kumar *et al.* 2015). It is quite difficult to control this disease as it is tuff to successful eliminate the white fly. This disease causes heavy loss of okra by affecting the fruit qualities as well as fruit yield (Solankey *et al.* 2014)

India is the richest country for diverse genotypes of okra. Geographically separation, genetic barriers to crossability, and different parents of evolution are the main reason of genetic diversity.

To breed desired plant type, the information about the nature and magnitude of genetic variability among base population and the degree of transmission of traits are prerequisite. The multivariate analysis is a powerful tool to estimate the degree of divergence among genotypes in the population and nature of forces operating at different levels (Coelho *et al.* 2007). Moreover, cluster analysis and principal component analysis (PCA) are most frequent genetic diversity assessing methods while securing relative basic differences between them. The cluster analysis has been most exploited for assessing family relationships (Mellingers, 1972). Hence, the present investigation was carried out to study of nature and magnitude of genetic divergence and the characters which play important role in genetic diversity of okra.

Materials and Methods

Materials for this investigation were procured from different national institutes *viz*., NBPGR, New Delhi; IIHR, Bangalore and IIVR, Varanasi. It consists of 30 okra genotypes including 4 checks (VRO 6, Pusa Sawani, Arka Anamika, and Arka Abhay). The present experiment was performed in randomize block design with three replications and germplasm evaluated at research farm of the Department of Horticulture (Vegetable & Floriculture), Bihar Agricultural College, Bihar Agricultural University, Sabour, Bhagalpur (Bihar) during Rainy season of 2013-14. Observations were recorded for 14 quantitative characters *viz*., days to first flowering, days to 50% flowering, first flowering node, days to first fruit picking, fruit length (cm), fruit diameter (cm), plant height (cm), number of branches/plant, plant canopy width (cm), number of fruits/plant, average fruit weight (g), fruit yield/plant (g) and per cent incidence of O YVMV and coefficient of infection (CI). The soil of the plot was sandy loam in texture having good fertility properly leveled and well drained. All the agronomic package and practices were adopted to raise the healthy crop.

Scoring of YVMV disease incidence was scored on 0-4 scale at the 15 days intervals (30 day, 45 day, 60 day and 75 days) after seed sowing and PDI and CI value was calculated by the procedure coined by Banerjee and Kalloo (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.

The genetic divergence among the okra genotypes was estimated by using D^2 statistics (Mahalanobis, 1936). All genotypes were clustered into different groups accomplished by Tocher's method (Rao, 1952). The average distance between the cluster and within the cluster was calculated by the statistical procedure given by Singh and Choudhary (1985).

Results and Discussion

Grouping of genotypes into different cluster

In the present research work, 30 okra genotypes were clustered for the 14 quantitative characters categorized into six groups based on Mahalanobis D^2 statistics (Table 1). Cluster II i.e. the largest group constituted 11 genotypes followed by cluster III and cluster VI that consists of 5 genotypes each. The cluster IV and V contain 4 genotypes each, whereas only one genotype presents in cluster I. The pattern of grouping genotypes into a single group does mean that they are genetically similar for most of the traits. Though they have originated from different geographical area, for example VRO-6 (from IIVR, Varanasi) and Arka Anamika (from IIHR, Bangalore) comes under cluster V. Therefore grouping of genotypes in a group is independent of their geographical origin (Kiran and Pathak, 2012). Similar statement has also stated by Oriyo

(1987). It is concluded that the genetic diversity might be due to some other factors like different genetic architect of the population, heterogeneity, selection history, and genetic drift. Kiran and Pathak (2012) stated that the genetic drift and selection in different environments may cause greater diversity than geographical distance. It revealed that the geographically isolated genotype in okra needs not to show genetic diversity (Sanwal *et al*. 2012). The similar results have also been reported by Shanthakumar and Salimath (2011). Ramya and Senthilkumar (2009) advocated dearth of clear relationship between geographical as well as genetic diversity in okra.

Table 1: Clustering pattern of diverse okra genotypes

Clusters	Number of Genotypes	Name of genotypes
I	1	IIHR-129
II	11	IIHR-43, IIHR-110, IIHR-112, IC-15537, IC-18073A, IC-99709, IC-128035, IC-43741, IC-31037A, IC-16262A, IC 43742.
III	5	IIHR-53, IIHR-120, IIHR-123 ,IIHR-113, Arka Abhay
IV	4	Pusa Sawani, IC -128065, IC-90298, IC-128037
V	4	VRO-6, IIHR-128, Arka Anamika, IC-14845B
VI	5	IC-43750, IC-14600, IC-128071, IC-90219, IC-111520

Intra and intercluster distance

The intra and inter cluster average D^2 values among the genotypes showed that (Table 2) intra cluster distances ranges from 22.69 (cluster IV) to 98.49 (cluster I). The highest values of inter cluster distances was worked out between cluster I and V (827.47), followed by cluster IV and V (674.45), cluster I and III (568.38) and cluster III and IV (499.06). From cluster mean (Table 3), it was estimated that the cluster V contributed least yield mean value (147.44), number of fruits per plant (12.86), fruit length (9.79 cm) and highest percent disease incidence (89.58), while cluster IV were found highest mean performer for fruit yield per plant (216.02 g), average fruit weight (12.33 g) and number of fruits per plant (17.26) due to comparatively less percent disease incidence (33.54%) and coefficient of infection (17.34). Cluster I contains only one entry i.e. IIHR 129 with less disease incidence. The mean performance of cluster I (184.07) and cluster III (176.28) were high with respect to yield due to comparatively high mean value for fruit length and number of branches per plant. From the cluster mean data and inter cluster distance, it assumed that the hybridization between cluster I and cluster III (inter cluster distance 568.38) and also cluster III and cluster IV (inter cluster distance 499.06) may produce high performing hybrids. Therefore, the genotypes IIHR 129, IIHR 53, IIHR 120, IIHR 123, IIHR 113 and Arka Abhay may be rewarding entries in the breeding programme for development of high yielding as well as YVMV disease tolerance. Although the cluster VI resulted in second highest mean yield value (185.83) yet a suitable cross combination with other clusters may not be rewarding due to proportionate narrow genetic diversity. Thus to obtain high heterotic hybrids, hybridization between genotypes from cluster I and V might be beneficial as due to crossing between genetically diverse parents (Figure 1). The similar results have also been observed by Dhankhar *et al.* (2008) and Singh *et al.* (2012).

Table 2: Inter and Intra cluster values for 30 okra genotypes

Cluster	I	II	II	IV	V	VI
I	22.69	148.66	568.38	102.84	827.47	323.52
II		33.29	235.78	132.73	404.55	179.52
II			38.26	499.06	161.9	368.82
IV				98.49	674.45	203.17
V					63.51	306.93
VI						42.67

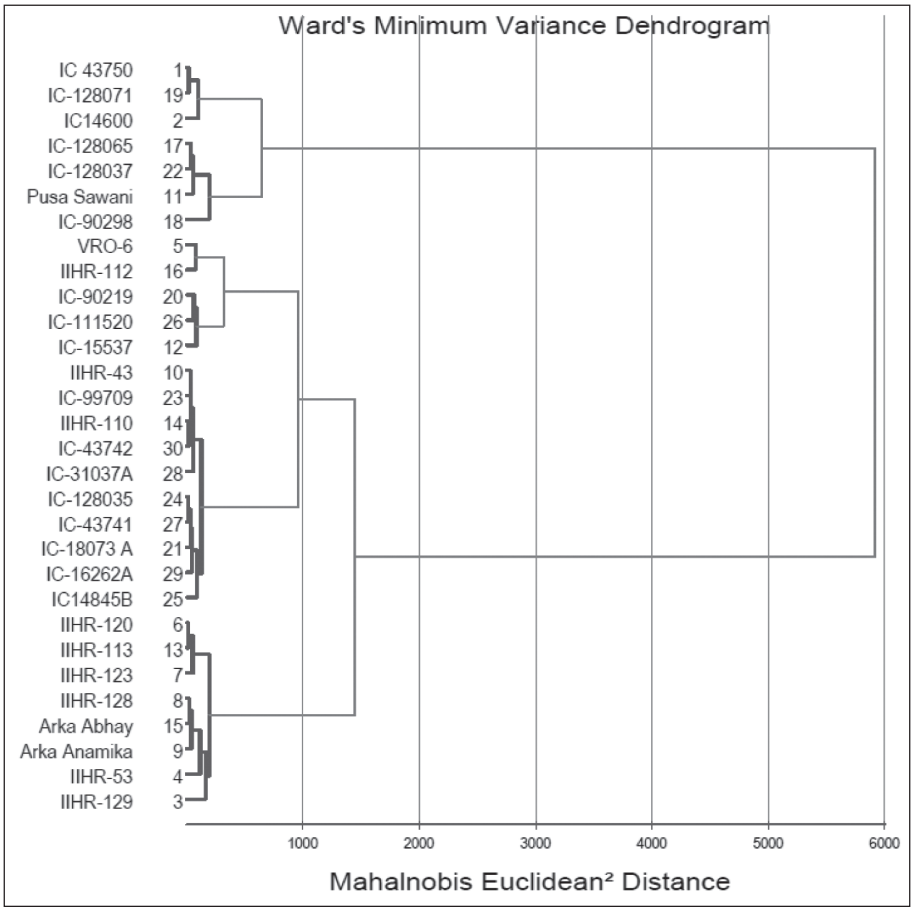

Fig. 1: Dendrogram (Tocher's method) showing clustering pattern among 30 okra genotypes

Table 3: Cluster means by using Tocher's method

Characters	Clusters					
	1	II	III	IV	V	VI
Days to First Flowering	47.22	47.10	43.89	46.71	48.17	46.67
Days to 50 % Flowering	54.33	55.27	51.89	53.54	56.17	54.33
First Flowering Node	9.00	8.07	7.00	7.75	8.08	7.67
Days to First Picking	53.67	53.37	49.89	52.46	53.92	52.50
Fruit Length (cm)	10.76	9.89	10.45	10.37	9.79	10.64
Fruit Dia (cm)	1.73	1.47	1.48	1.63	1.59	1.46
Plant Height (cm)	98.48	111.51	107.68	118.42	119.19	113.72
Branches/ Plant	3.28	3.41	3.56	2.75	1.97	1.16
Plant Canopy Width(cm)	100.67	95.37	96.67	95.88	101.50	94.67
Fruits/ Plant	15.82	13.37	15.69	17.26	12.86	14.87
Fruit Weight(g)	11.60	12.12	11.29	12.33	11.50	12.52
Fruit Yield/ Plant (g)	184.07	161.86	176.28	216.02	147.44	185.83
Percent Disease Incidence (%)	17.78	65.67	79.11	33.54	89.58	60.33
Coefficient of Infection	4.44	49.25	79.11	17.34	89.58	45.25

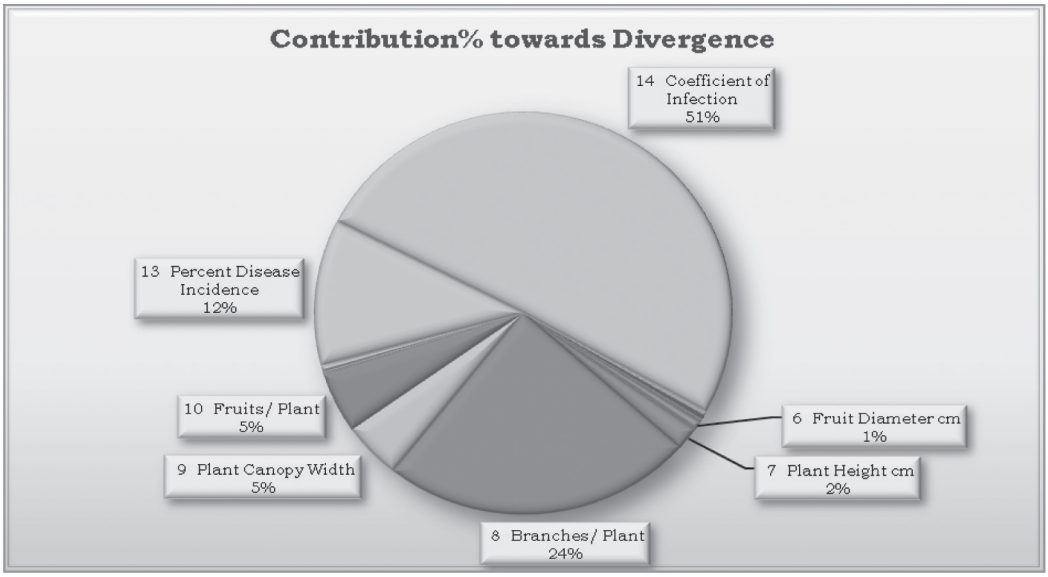

Fig. 2: Graphical representation of proportionate contribution of studied major traits (in parentheses value) towards genetic divergence in okra

Contribution of traits toward genetic diversity

Among all the yield and yield contributing traits, seven character aggregates to yield 100 % contribution towards divergence (Fig. 2.). Out of these 7 characters, coefficient of infection alone contributed highest (51%) genetic diversity followed by number of branches per plant (24%), percent disease incidence (12%), number of fruits per plant (5%) and plant canopy width (5%). It indicated that the character coefficient of infection would be the important parameter for selecting diverse okra genotypes.

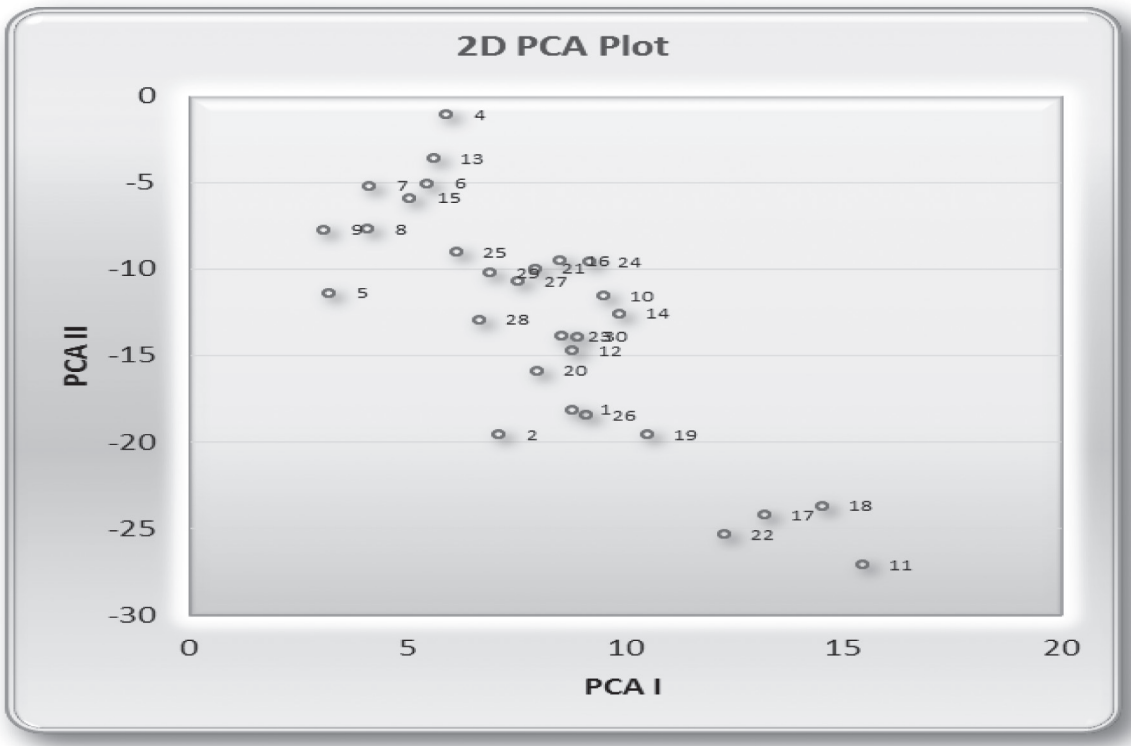

Fig. 3: Scattered diagram by using two dimentional ordination of 30 okra genotypes based on PC (principal component) axis 1 and 2

Principal component analysis

The principal component analysis (PCA) of 14 traits in 30 okra genotypes (Table 4 & Fig. 3) indicated that the first six principal components (PCs) *viz*., PC 1, PC 2, PC 3, PC 4, PC 5 and PC 6 having Eigen values of 3.60, 2.92, 2.13, 1.72, 1.19 and 1.02, respectively, moreover have accounted for 84.00% of total genetic variation. The similar results have also been obtained by Yonas *et al.* (2014). The PC 1 and PC 2 contributed 23.99% and 19.50% variation of the total variation. The two dimensional ordinations of 30 okra genotypes on PC axis 1 and 2 (Fig. 3), revealed scattered diagram of genotypic distribution pattern on axis. The first 7 principal components collectively contributed 89.38% of cumulative total variations. The first PC has associated positively to days to first picking (0.392), days to first flowering (0.376), days to 50% flowering (0.350), fruit yield per plant (0.308) and percent disease of incidence (0.276), while the negative association was observed for fruit per plant (-0.365) and fruit weight (-0.269). The second PC pointed out that the first flowering node (0.345) and number of branches per plant (0.266) has positive association while, percent disease incidence (-0.449) and coefficient of infection (-0.459) has negative association. The third PC has positive association with days to first flowering (0.358) and plant canopy width (0.355) and negative association with fruit yield per plant (-0.328) and number of branches per plant (-0.491). The positively associated characters with different PCs demonstrated major role in genetic divergence analysis. The results are in conformity with the works done by Singh *et al*. (2012) and Koundinya *et al.* (2013).

Table 4: Principal component analysis for 14 traits in 30 okra genotypes

Parameter	PC1	PC2	PC3	PC4	PC5	PC6	PC7
Eigene Value	3.600	2.926	2.139	1.722	1.195	1.020	0.806
Cumulative Eigen value	3.600	6.526	8.665	10.387	11.582	12.602	13.408
% Var. Exp.	23.998	19.504	14.260	11.479	7.966	6.798	5.371
Cum. Var. Exp.	23.998	43.502	57.763	69.242	77.208	84.006	89.377
Days to First Flowering	0.376	0.133	0.358	0.089	0.132	0.067	0.288
Days to 50 % Flowering	0.350	-0.008	-0.233	0.172	0.119	0.001	-0.446
First Flowering Node	0.076	0.345	0.067	-0.253	-0.285	0.128	-0.520
Days to First Picking	0.392	0.103	0.314	0.123	0.253	0.109	0.169
Fruit Length (cm)	-0.209	0.050	0.287	-0.498	0.161	0.308	-0.053
Fruit Diameter (cm)	0.122	0.127	-0.186	0.200	-0.729	-0.085	0.274
Plant Height (cm)	-0.181	-0.288	0.053	0.237	-0.151	0.664	0.165
Branches/ Plant	-0.072	0.266	-0.491	-0.152	0.272	-0.010	0.105
Plant Canopy Width (cm)	0.103	-0.293	0.355	-0.245	-0.360	-0.050	-0.175
Fruits/ Plant	-0.365	0.163	0.235	0.055	0.046	-0.356	0.297
Fruit Weight (g)	-0.269	-0.013	0.005	0.558	0.132	0.206	-0.283
Fruit Yield/ Plant (g)	0.308	0.100	-0.328	-0.250	-0.024	0.417	0.298
Percent Disease Incidence (%)	0.276	-0.449	-0.005	0.076	0.117	-0.081	-0.073
Coefficient of Infection	0.158	-0.459	-0.154	-0.161	0.069	-0.260	0.070

Conclusion

Availability of desirable genetic diversity is utmost important to fulfill the present research objective *i.e*. high yield as well as YVMV tolerant variety of okra. The traits like days to first picking, first flowering node and days to first flowering should be given top priority in diverse parent selection for attempting heterotic cross combination and development of high yielding and YVMV resistant hybrids/varieties in okra.

Acknowledgements

Authors acknowledge Bihar Agricultural University, Sabour, Bhagalpur (Bihar) for providing the research facility and financial support. The authors are also thankful to Director, IIVR, Varanasi, Director, NBPGR, New Delhi and Director, IIHR, Bengaluru for the provision of okra germplasm used in this study.

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