J. Agr. Sci. Tech. (2016) Vol. 18: 751-762

Selecting Parental Lines among Cultivated and Wild Species of Okra for Hybridization Aiming at YVMV Disease Resistance

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ABSTRACT

Yellow Vein Mosaic Virus (YVMV) disease of okra is the single major production constraint and causes yield loss to the tune of 50-90% in India. Hence continuous search for new sources of resistance and development of better varieties/hybrids with durable level of resistance should receive attention of breeder. An attempt was made to screen twenty-six advanced lines/varieties of okra in one of the hot spots of YVMV disease in eastern India to identify suitable parents for resistant breeding program. The study revealed high magnitude of genetic variability and high degree of transmission of majority of the growth, earliness, and yield component traits under consideration. Based on the degree of divergence, the genotypes were grouped into four clusters. Hybridization between genotypes belonging to Cluster II and Cluster III could combine early maturity, higher yield, and having high tolerance against YVMV disease. Dendrogram among the genotypes also revealed high diversity along with strong inter cluster relationships. Based on averages and principal component analysis, six genotypes *viz*., BCO-1, *A. caillei*, *A. manihot*, 11/RES-6, VNR Green and 12/RES-2 appeared very promising candidates for future use in resistant breeding programs.

Keywords: Genetic diversity, PCA analysis, Resistant breeding, Tolerance against YVMV.

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench), mainly grown for its tender fruit, is an important warm season vegetable crop grown in tropical and subtropical parts of the world (Das *et al*., 2013). Okra is a surprising versatile vegetable for its easily digestible fibre content, low in calories and fat free (Kumar and Sreeparvathy, 2010; Reddy *et al.,* 2013).

India ranks first in production (5.78 mt) of okra in the world and accounts for 60 % of the total exported fresh vegetables (NHB, 2011). However, the productivity in India (11.60 t ha^{-1}) is still lagging behind the other okra producing countries like Saudi Arabia (13.30 t ha^{-1}), Egypt (12.50 t ha^{-1}) and Sudan (11.90 t ha^{-1}). West Bengal, a State of eastern India, is the forerunner in okra production (0.862 million tons), but the productivity is less than other Indian States. One of the main reasons for low productivity is growing of local unimproved cultivars/OP varieties by the farmers and very high incidence of Yellow Vein Mosaic Virus (YVMV) disease which is transmitted through whitefly (*Bemisia tabaci* Genn.) (Arora *et al*., 2008). Cent per cent infection of plants in a field is usual in the Gangetic

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plains of West Bengal and yield losses range from 50 to 94% depending on stage of crop growth at which infection occurs (Sastry and Singh, 1974). The disease is caused by a complex consisting of the monopartite begomovirus BYVMV and a small satellite DNA β component (Jose and Usha, 2003).

Earlier workers reported a complex genetic control of resistance to YVMV disease (Dhankhar *et al*., 2005; Arora *et al*., 2008). Efforts were made in India for the identification of resistant/tolerant cultivars among cultivated (Tiwari *et al*., 2012) and wild species (Prabu *et al*., 2007) against this disease as well as to transfer genes for tolerance to YVMV from related wild species to susceptible cultivated varieties (Nerkar and Jambhale, 1985).

The existing variability present in okra has been exploited in various breeding programs, resulted in the development and release of a good number of varieties. However, the released varieties cannot be continued longer due to genetic drift and susceptibility to various diseases, especially the YVMV. This demands continuous development and replacement of current varieties by new high yielding varieties having durable resistance to YVMV with acceptable fruit quality.

The importance of genetic diversity for selecting parents in combination breeding of okra to obtain transgressive segregants has been very well emphasized (Das *et al.,* 2012b). Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. To elucidate the basis of resistance to YVMV disease, some morphological characters confer resistance to whitefly that has been studied by many workers (Butter and Vir, 1989; Wilson *et al*., 1993). One of the reasons for whitefly flare up is the cultivation of pubescent genotypes which are conducive for higher rate of oviposition and population build up. Hair density and leaf thickness are positively correlated with the population of whitefly. The thinner and glabrous leaved genotypes confer resistance to whitefly. Screening of okra genotypes in order to reveal the biochemical basis of YVMV disease resistance indicated that higher amount of phenols in the leaves may be responsible for reduced virus multiplication which finally could have lead to resistant reaction in okra (Sharma *et al*., 1981; Prabhu and Warade, 2009).

Knowledge and the nature and magnitude of variation existing in available breeding materials are requisite to choose characters for effective selection of desirable genotypes to undertake planned breeding program. Further, to improve the productivity, information about the nature and magnitude of genetic divergence would help selection of diverse parents, which upon hybridization might lead to effective gene recombination. The present study was, therefore, undertaken to evaluate the genetic variability for different yield component characters and diversity of genotypes for identification of suitable parents for future use in YVMV resistant breeding programme.

MATERIALS AND METHODS

Plant Material and Field Growing

The investigation was carried out during *kharif* season (July to September), 2012 at research plot of All India Coordinated Research Project on Vegetable Crops, Bidhan Chandra Krishi Viswavidyalaya, Kalyani, Nadia, West Bengal, India, situated at 23.5° N latitude and 89° E longitude with above mean sea level of 9.75 m. Twenty-six advanced lines/varieties of okra developed by different Indian Council of Agricultural Research Institutes/ State Agricultural Universities were collected from Indian Institute of Vegetable Research, Varanasi, India for the present study. Seed of twenty-six okra genotypes comprising twenty-four of *Abelmoschus esculentus*, one each of *Abelmoschus manihot* and *Abelmoschus caillei*, after treatment with Thiram (3 g kg^{-1} of seed), were sown following RBD with three replications, during the 1st week of

July, at 2.5 cm deep furrows with 60×30 cm spacing in 3.0×2.5 m plots. Fertilizer at the rate of 60:60:60 kg N: P: K ha^{-1} was applied along with 15 tons of FYM ha^{-1} as basal to the soil. Top dressing of nitrogen at 60 kg ha^{-1} was applied in two equal split doses at 30 and 55 days after sowing. Management practices for cultivation were followed as advised by Chattopadhyay *et al.* (2007). No plant protection measures against sucking insect pest of okra were taken. At the same time, susceptible variety Pusa Sawani was grown in the screening plot to ensure viral load as well as symptom development.

Field Observation

Ten randomly selected plants from each replication were taken to record nine quantitative traits *viz.,* plant height (cm), days to 1st flowering, 1st flowering node, days to 50 % flowering, fruit length (cm), fruit girth (cm), average fruit weight (g), and number of marketable fruits per plant, and marketable fruit yield per plant (g). Fruit characters of each genotype were taken after six days of anthesis by tagging the flowers.

YVMV Disease Incidence

Disease incidence and severity data were recorded at five different growth stages at an interval of 15 days starting from 30 Days After Sowing (DAS) to 90 DAS. The Percent Disease Index (PDI) was expressed as percentage from all 45 plants in a replication using disease severity scale (0-9) for single plant through visual evaluation as suggested by Das (2011).

Scale	Description of symptom
0	No disease
1	Up to 15% leaf area affected of a plant
3	15-30% leaf area affected of a plant
5	30-45% leaf area affected of a plant
7	45-60% leaf area affected of a plant
9	Greater than 60% leaf area affected of a plant

Numbers of plants infected in each entry were recorded and *PDI* (%) was calculated by the following formula:

$$PDI = \frac{\sum N}{H \times T}$$

Were N is numerical ratings, H is Highest grade of rating and T is total number of plants of the entry examined. This formula should be multiplied with 100, since PDI is calculated as percentage.

On the basis of *PDI* value of YVMV disease, six resistant genotypes and three susceptible genotypes were selected out of twenty-six genotypes to take the following morphological and biochemical characters in order to have the basis of resistance to this disease and their degree of association.

Population Count of White Fly (Adult)

White fly populations were monitored from July to September and were recorded on five leaves, two each from lower, middle and one from upper canopy of the plants between 5.30 and 6 a.m. from 5 randomly selected tagged plants of each plot at 7-day-intervals after sowing.

Total Phenol Content in Leaf

In order to reveal the biochemical basis of disease resistance, the total phenol content from the middle portion of leaf of both resistant/susceptible genotypes at 90 DAS was estimated as per the standard procedure (Sadasivam and Manickam, 1991).

Leaf Thickness

In order to reveal the morphological basis of disease resistance, the thickness of the leaves from lower, middle, and upper portion of the canopy of both resistant/susceptible genotypes at 90 DAS was measured by digital slide callipers.

Statistical Analysis

Data were subjected to analysis of variance (Panse and Sukhatme, 1984). The Genotypic Co-efficient of Variation (GCV) and Phenotypic Co-efficient of Variation (PCV) were calculated by the formula given by Burton (1952). For the estimates of heritability (broad sense) and genetic advance as percentage of mean, the method of Hanson *et al*. (1956) was followed. *K*-Means clustering was performed for 26 genotypes in order to categorize the genotypes having similar characteristics as well as to judge the variability amongst different clusters. Subsequently hierarchical cluster analysis was done with those same genotypes in order to observe the degree of association according to their characteristics that was expressed in dendrogram following Ward's (1963) method. Correlations between YVMV disease causing variables among nine selected genotypes based on their *PDI* (%) values were tested for significance (Gomez and Gomez, 1984). Principal Component Analysis (PCA), as the method of identifying the factor dimension of the data, was used to summarize varietal information in a reduced number of factors (whitefly population, percent disease index, leaf thickness and phenol content in leaf) for selection of the best performing genotype(s). Statistical analyses were done using SAS 9.3 Professional Version and SPSS Professional Version 13.0.

RESULTS AND DISCUSSION

Genetic Variability and Heritability Analysis

The variance analysis showed that genotypes differed significantly among themselves for all the characters under study. *PCV* agreed closely with the *GCV* for all the characters except 1st flowering node, fruit length, fruit girth, average fruit weight, and number of marketable fruits per plant indicated

Table 1. Mean, range, and estimates of genetic parameters of twenty-six okra genotypes.

Characters	Mean	Range	*GCV* (%)	*PCV* (%)	*GCV* : *PCV*	Heritability (%) in bs	Genetic advance as (%) of mean
Plant height (cm)	129.65	60.00 – 207.33	21.62	21.86	98.90	97.80	44.05
1st flowering node	5.25	3.66 – 17.00	49.01	50.61	96.83	93.79	97.78
Days to 1st flowering	40.84	30.00 – 71.00	22.36	22.87	97.77	95.62	45.06
Days to 50% flowering	49.33	38.00 – 80.00	18.32	18.62	98.38	96.82	37.14
Fruit length (cm)	8.21	3.58 - 9.44	13.20	14.82	89.06	79.37	24.23
Fruit girth (cm)	1.25	1.10 - 2.24	16.59	18.43	90.01	81.00	30.76
Average fruit weight (g)	8.20	3.54 - 12.51	19.41	20.94	92.69	85.89	37.05
Number of marketable fruits/Plant	14.09	5.63 - 27.56	37.61	38.68	97.23	94.51	75.31
Marketable fruit yield (g plant^{-1})	110.57	47.60 - 213.57	30.81	30.89	99.74	99.47	63.30

that the environmental influence was very low (Table 1). In general, the magnitude of *PCV* was higher than *GCV* for all the nine characters under study, indicated that the apparent variation was not only due to genotype but also due to the favourable influence of environment and selection for these traits sometimes may be misleading. The *GCV* ranged from 13.20 to 49.01%, while *PCV* ranged from 14.82 to 50.61%. High proportion of *GCV* to *PCV* is desirable in selection process because it depicts that the traits are much under the genetic control rather than the environment (Kaushik *et al*., 2007). The *PCV* and *GCV* values were classified as low (< 10.00 %), moderate (10.00-20.00%) and high (> 20.00%) as suggested by Sivasubramanian and Menon (1973). High *GCV* and *PCV* values (> 20.00%) were found for plant height, 1st flowering node, days to 1st flowering, number of marketable fruits per plant, marketable fruit yield per plant and indicating the potential of simple selection for the improvement of these characters. These observations find support from the previous workers (Reddy *et al*., 2012; Das *et al*., 2012a). On the other hand, moderate *PCV* and *GCV* values (10.00-20.00%) were shown by days to 50% flowering, fruit length, fruit girth and average fruit weight. Similar findings had been reported by Reddy *et al*. (2012) and Das *et al*. (2012a). The proportion of *GCV* in *PCV* observed in this study was generally high ranging from 89.06% in fruit length to 99.74% in marketable fruit yield per plant. These traits are reliable for selection in genetic improvement of the okra genotypes. Traits whose expressions are environmentally dependent may not be reliable descriptors for morphological characterization (Pandey *et al.,* 2008). However, in this study, the proportion of genetic contribution to the overall phenotypic expression of most of the traits was very high. Therefore, their use as important discriminatory variable for okra classification studies seemed relatively reliable.

Traits with high broad sense heritability estimates suggest that they have high genetic potential; the effect of the environment in determining them is low. Higher estimates of broad sense heritability (more than 60%) coupled with the higher genetic advance as per cent of mean (more than 20%) were found for all the characters under study, which indicated additive genetic control of these traits and selection based on these parameters would be more reliable. Johnson *et al.* (1955) suggested that high *GCV* along with high heritability and genetic advance gave better picture for the selection of the genotypes rather than heritability values alone.

High magnitude (> 60.00%) of heritability estimates had also been reported for plant height (Das *et al*., 2012a; Reddy *et al.,* 2012), days to 1st flowering (Das *et al.,* 2012a), days to 50% flowering and 1st flowering node (Das *et al.,* 2012a; Reddy *et al.,* 2012), all fruit traits [fruit length, width and weight], number of marketable fruits per plant (Das *et al.,* 2012a) and marketable fruit yield per plant (Das *et al.,* 2012a; Reddy *et al.,* 2012).

High magnitude (> 20.00%) of genetic advance as per cent of mean was observed for plant height (Das *et al.,* 2012a), days to 1st flowering (AdeOluwa and Kehinde, 2011), days to 50% flowering (Bello *et al.,* 2006), fruit length and weight (Das *et al.,* 2012a), number of marketable fruits per plant (Das *et al.,* 2012a; Reddy *et al.,* 2012), marketable fruit yield per plant (Das *et al.,* 2012a).

Genetic Diversity through Multivariate Analysis

The selection of parents on large phenotypic differences may be useful but there are several instances where a single gene can provide large scale differences in height, maturity and yield. Therefore, measures based on genetic criteria qualifying diversity have become important in classifying the material for use by the breeders. Assessment of divergence for a set of characters utilizing different multivariate analyses has been effectively utilized in vegetable crops with diverse breeding

system (Murthy, 1979). Kalloo *et al.* (1980) suggested that the crosses between selected genotypes from widely separated clusters were most likely to give desirable recombinants.

Based on the determination of divergence, all the twenty six genotypes could meaningfully be grouped into four clusters (Table 2). Cluster I had the maximum of 16 genotypes, Cluster II comprised 2 genotypes, while Cluster III and Cluster IV had 4 genotypes each. The genetic divergence among okra genotypes through cluster analysis was reported by previous workers (Akotkar *et al.,* 2010; Das *et al.,* 2012b). In general, the pattern of distribution of genotypes from diverse geographical region into different clusters was random. It might be due to free and frequent exchange of genetic materials among the farmers and breeders of different regions. Differential selection pressure according to regional preference also produced greater uniformity in the germplasm. The absence of relationship between genetic diversity and geographical distance indicated that forces other than geographical origin such as exchange of genetic stock, genetic drift, spontaneous mutation, natural and artificial selection were responsible for genetic diversity. Therefore, the selection of genotypes for hybridization should be based on genetic divergence rather than geographic diversity. Environmental influence on the composition of cluster was also recorded earlier in different self-pollinated crops like tomato (Peter and Rai, 1976), pea (Kalloo *et al.,* 1980) and cowpea (Hazra *et al.,* 1992).

The inter-cluster distance among twenty-six genotypes revealed that the minimum value was observed between Cluster I and IV (57.008) indicating close relationship among the genotypes included in these clusters (Table 3). The maximum inter-cluster value was observed between cluster III and IV (130.216) followed by 124.790 between Cluster II and IV, which indicated that the genotypes included in these clusters had the maximum divergence. Hence, intermating between the genotypes included in these clusters was expected to give transgressive segregates in the advanced generation. Kalloo *et al*. (1980) suggested that the crosses between selected varieties from widely separated clusters were most likely to give desirable recombinants.

K-Means algorithm was performed for the 26 genotypes and arranged in four distinct clusters in order to judge the homogeneity within the cluster and variability between the clusters. The cluster means of genotypes (Table 4) showed that the mean values of the clusters varied in magnitude for all the characters. Plant height attained the maximum cluster centres (182.83) in cluster II. On the

Table 2. Cluster classification of twenty six genotypes of okra.

Cluster with number of genotype in parentheses	Name of the genotype
I (16)	10/RES-1, 10/RES-2, 10/RES-3, 10/RES-4, 10/RES-5, 10/RES-6, 10/RES-7, 10/RES-9, 11/RES-2, 11/RES-4, 11/RES-5, 12/RES-3, 12/RES-4, 12/RES-5, 12/RES-6, VRO-6
II (2)	*Abelmoschus manihot*, *Abelmoschus caillei*
III (4)	12/RES-2, 11/RES-6, VNR Green, BCO-1
IV (4)	10/RES-8, Arka Anamika, Pusa Sawani, Arka Abhoy

Table 3. Inter cluster distances of twenty six genotypes of okra.

Cluster	I	II	III	IV
I	-	97.737	83.773	57.008
II		-	104.148	124.790
III			-	130.216
IV				-

Table 4. Cluster means of ten characters of okra.

Characters	Cluster			
	1	2	3	4
Plant height (cm)	130.27	182.83	122.75	107.53
1st Flowering Node	4.63	13.00	4.00	5.17
Days to 1st flowering	39.71	69.84	33.42	38.34
Days to 50% flowering	47.73	77.50	41.33	49.67
Fruit length (cm)	8.27	6.52	8.45	8.58
Fruit girth (cm)	1.19	1.76	1.23	1.27
Average fruit weight (g)	7.88	8.03	8.74	9.05
Number of marketable fruits/Plant	14.12	17.61	19.39	6.93
Marketable fruit yield (g plant^{-1})	111.36	96.53	163.58	61.45
PDI (%) of YVMV disease	70.99	2.50	6.76	84.50

other hand, node at 1st flowering, days to 1st flowering as well as days to 50% flowering achieved the minimum point (4.00, 33.42 and 41.33, respectively) in cluster III. Highest cluster centres for fruit length and fruit weight (8.58 and 9.05, respectively) belonged to cluster IV, while fruit girth registered its maximum association in cluster II (1.76). Number of marketable fruits per plant (19.39) and marketable fruit yield per plant exhibited highest cluster centre (163.58) in cluster III. The PDI values of YVMV disease showed the lowest level of cluster centre (2.50) in cluster II. Therefore, genotypes belonging to Cluster III had taken the earliest days to reaching flowering and yielded more, which could be helpful for breeding an early high yielding genotype. On the other hand, genotypes belonging to cluster II possessed low incidence of YVMV disease. Thus**,** hybridization between genotypes belonging to Cluster II and Cluster III could combine higher fruit productivity with early maturity having high tolerance against YVMV disease of okra in future breeding programs.

In further study of dendrogram following Ward's (1963) method (Figure 1) by using squared Euclidean distance registered the fact that genotypes belonging to cluster II (*Abelmoschus manihot* and *Abelmoschus caillei*) and cluster III (11/RES-6, BCO-1, VNR Green and 12/RES-2) were identified as the genetically more diverse featuring unique characteristics as they associated with the rest of genotypes at the farthest rescaled distance (25.0 scale).

Correlation Study

Percent Disease Index (PDI) of YVMV disease of okra is dependent on many variables. However, we have considered few factors like whitefly (adult) population per leaf, leaf phenol content, and leaf thickness which have a direct bearing with the YVMV disease incidence. The correlation study (Table 5) clearly depicted that *PDI* was positively and significantly correlated with whitefly population and leaf thickness, which corroborated the findings of previous workers (Butter and Vir, 1989; Wilson *et al.,* 1993). Significant negative correlation existed between *PDI* and leaf phenol content which justified the previous study of Sharma *et al.* (1981), Prabhu and Warade (2009).

Principal Component Analysis (PCA)

PCA was performed to obtain a simplified view of the relationship between disease causing variables and variable loadings for components PC1 (PDI%) and PC2 (Whitefly population) were extracted in Table 6. These components were chosen because their eigenvalues exceeded 1.0 and explained 99.98% of the total variance. The first component explained 99.12% of total accounted for variance in which an increase in *PDI%* leads to increase in whitefly population and leaf thickness and decrease

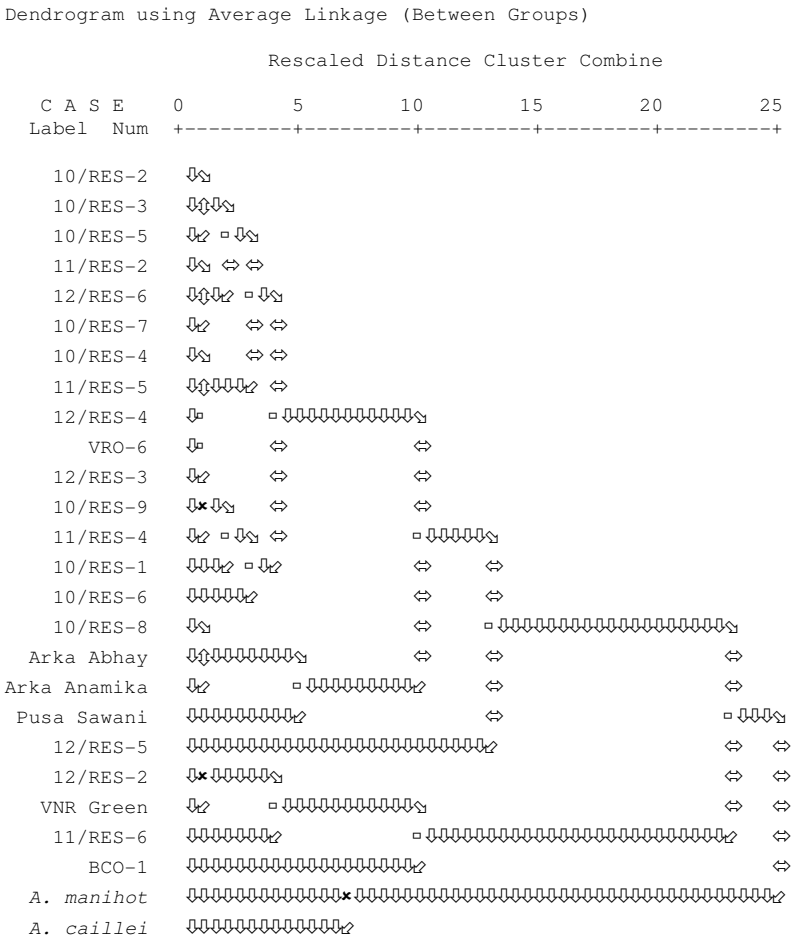

Figure 1. Dendrogram of 26 genotypes of okra following Ward's method.

Table 5. Pearson correlation matrix between YVMV disease causing variables.

Variable	PDI	Whitefly population	Phenol content	Leaf thickness
PDI	1.000	0.958**	-0.977**	0.855**
Whitefly population		1.000	-0.965**	0.905**
Phenol content			1.000	-0.881**
Leaf thickness				1.000

** Means significant at 1% level.

Table 6, Results of Principal Component Analysis (PCA) for YVMV disease causing factors in okra.

Principal component	Eigenvalue %	% Variance	% Cumulative variance
Eigenvalues and variance accounted for (%) by PCA based on correlation matrix			
PC1	2298.25	99.12	99.12
PC2	20.03	0.86	99.98
PC3	0.47	0.02	100.00
PC4	0.003	0.00	100.00

Variables	PC1	PC2	PC3	PC4
Factor loadings due to PCs with eigenvalues greater than 1				
PDI (%)	0.86	0.50	-0.02	0.01
Whitefly population per leaf	0.05	-0.05	0.99	-0.04
Leaf phenol content (mg 100 g^{-1})	-0.49	0.86	0.07	0.01
Leaf thickness (mm)	0.01	-0.01	0.04	0.99

in phenol content. The second component (PC2) explained an additional 0.86% of the variance in which an increase in *PDI%* and phenol content of leaf were associated with decrease in whitefly population and leaf thickness.

The scattered diagram (Figure 2) clearly depicted that the six out of nine genotypes had similar features and formed a separate cluster, while Arka Abhay, Pusa Sawani and Arka Anamika registered distinct differences of their genotypic characters and belonged to farthest distances from the other genotypes in the plot.

Based on PCA and average values (Table 7), six genotypes (BCO-1 , *A. caillei*, *A. manihot* , 11/RES-6, VNR Green and 12/RES-2) possessed the optimum combination of all variables and these lines should be considered for use in YVMV

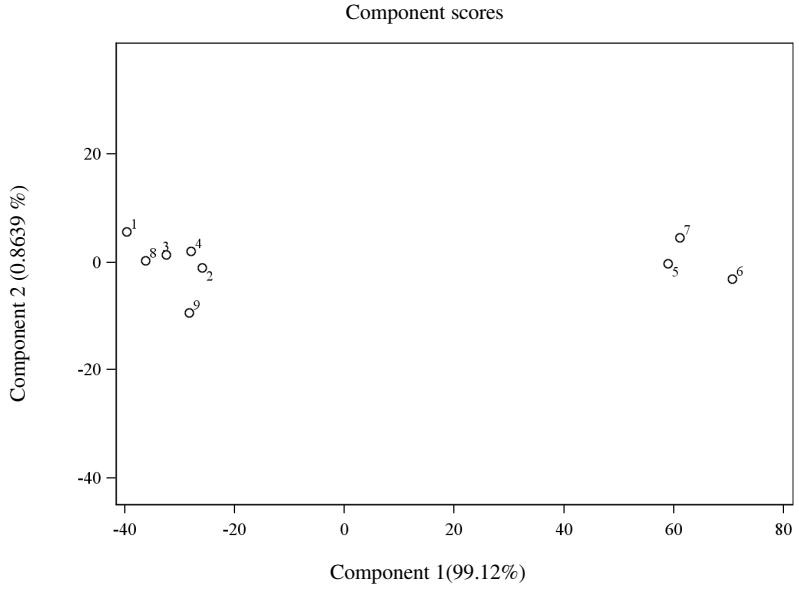

Figure 2. Scatter diagram of regression factor scores for the first two components produced by PCA. Genotypes: 1: BCO-1; 2: 12/RES-2; 3: 11/RES-6; 4: VNR Green; 5: Arka Abhay; 6: Pusa Sawani; 7: Arka Anamika; 8: *A. manihot*, and 9: *A. caillei.*

Table 7. Range of values for YVMV disease causing factors in nine okra genotypes, average of three replicates.

Variables	Maximum	Minimum	Average	Genotypes with below average value	Genotypes with above average value
PDI (%) of YVMV disease	1.20	92.30	32.74	BCO-1 (1.20), *A. caillei* (1.50), *A. manihot* (3.50), 11/RES-6 (5.35), VNR Green (9.50) and 12/RES-2 (9.80)	Arka Abhay (83.60), Arka Anamika (87.90) and Pusa Sawani (92.30)
Whitefly population per leaf	0.30	7.55	2.59	BCO-1 (0.30), *A. caillei* (0.35), *A. manihot* (0.80), 11/RES-6 (1.05), VNR Green (1.30) and 12/RES-2 (1.50)	Arka Anamika (4.35), Arka Abhay (6.15) and Pusa Sawani (7.55)
Leaf phenol content (mg 100 g^{-1})	32.54	94.94	70.29	Pusa Sawani (32.54), Arka Abhay (40.76) and Arka Anamika (43.72)	BCO-1 (94.94), *A. caillei* (88.60), 11/RES-6 (87.62), VNR Green (86.00), 12/RES-2 (82.35) and *A. manihot* (76.06)
Leaf thickness (mm)	0.52	0.91	0.71	*A. caillei* (0.52), BCO-1 (0.56), 11/RES-6 (0.63), *A. manihot* (0.66)	Arka Anamika (0.80), Arka Abhay (0.85) and Pusa Sawani (0.91)

resistant breeding programs to develop improved lines.

CONCLUSIONS

The pattern of distribution of genotypes from diverse geographical region into different clusters was random. In spite of huge diversity among the genotypes, relatively small number of clusters indicated either common character constellation or mutual balancing of characters among the genotypes. However, intermating between highly divergent parents belonging to different clusters is expected to give transgressive segregates in the advanced generation. Mean results of the experiment along with PCA indicated that six genotypes (BCO-1, *A. caillei*, *A. manihot*, 11/RES-6, VNR Green and 12/RES-2) had the highest levels of disease resistance along with desirable attributes. These cultivars could be used as donor parents in future resistant breeding programs.

ACKNOWLEDGEMENTS

First author wishes to acknowledge the financial help rendered by Department of Science and Technology, Government of India in the form of INSPIRE fellowship to carry out this study.

REFERENCES

1. AdeOluwa, O. O. and Kehinde, O. B. 2011. Genetic Variability Studies in West African Okra (*Abelmoschus caillei*). *Agri. Biol. J. N. Am.,* **2(10):** 1326-1335.
2. Akotkar, P. K., De, D. K. and Pal, A. K. 2010. Genetic Variability and Diversity in Okra (*Abelmoschus esculentus* L. Moench). *Electron. J. Plant Breed.,* **1(4):** 393-398.
3. Arora, D., Jindal, S. K., and Singh, K. 2008. Genetics of Resistance to Yellow Vein Mosaic Virus in Inter-Varietal Crosses of Okra (*Abelmoschus esculentus* L. Moench). *SABRAO J. Breed. Genet*., **40(2):** 93-103.
4. Bello, D., Sajo, A. A., Chubado, D. and Jellason, J. J. 2006. Variability and Correlation Studies in Okra (*Abelmoschu esculentus* L. Moench). *J. Sustain. Deve. Agri. Environ.,* **2(1):** 120-126.
5. Burton, G. W. 1952. Quantitative Inheritance in Grasses. *Proc. 6th Intl. Grassland Congr*., **1:** 277-283.
6. Butter, N. S. and Vir, B. K. 1989. Morphological Basis of Resistance in Cotton to the Whitefly *Bemisia tabaci*. *Phytoparasitica,* **17**: 251-261.
7. Chattopadhyay, A., Dutta, S., Bhattacharya, I., Karmakar, K. and Hazra, P. 2007. *Technology for Vegetable Crop Production*. Published by All India Coordinated Research Project on Vegetable Crops, Directorate of Research, Bidhan Chandra Krishi Viswavidyalaya, Kalyani-741235, Nadia, West Bengal, India
8. Das, S. 2011. Genetic Variability, Yield Components, Heterosis and Gene Action in Okra (*Abelmoschus esculentus* L. Moench). Dissertation, Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, Nadia, India.
9. Das, S., Chattopadhyay, A., Chattopadhyay, S. B., Dutta, S. and Hazra, P. 2012b. Characterization of Okra Germplasm and Their Genetic Divergence in the Gangetic Alluvium of Eastern India. *Vegetos,* 25(2):86-94.
10. Das, S., Chattopadhyay, A., Chattopadhyay, S. B., Dutta, S. and Hazra, P. 2012a. Genetic Parameters and Path Analysis of Yield and Its Components in Okra at Different Sowing Dates in the Gangetic Plains of Eastern India. *African J. Biotech.,* **11(95):** 16132-16141.
11. Das, S., Chattopadhyay, A. Chattopadhyay, S. B., Dutta, S. and Hazra, P. 2013. Breeding Okra for Higher Productivity and Yellow Vein Mosaic Tolerance. *Intern. J. Veg. Sci.,* **19:** 58–77.
12. Dhankhar, S. K., Dhankhar, B. S. and Yadava, R. K. 2005. Inheritance of Resistance to Yellow Vein Mosaic Virus in an Inter-specific Cross of Okra (*Abelmoschus esculentus*). *Indian J. Agric. Sci.,* **75:** 87-89.
13. Gomez, K. A. and Gomez, A. A. 1984. *Statistical Procedures for Agricultural Research*. 2nd Edition, John Wiley and Sons. New York. 680 PP.
14. Hanson, C.H., H.F. Robinson and R.E. Comstock 1956. Biometrical studies of yield in segregating population of Korean lespedza. *Agron. J*., 48:268-272.

15. Hazra, P., Som, M. G. and Das, P. K. 1992. Selection of Parents for Vegetable Cowpea Breeding by Multivariate Analysis. *Veg. Sci.,* **19:** 166-173.
16. Johnson, H. W., Robinson, R. W. and Comstock, R. E. 1955. Estimate of Genetic and Environmental Variability in Soybean. *Agron. J.,* **47:** 314-318.
17. Jose, J. and Usha, R. 2003. Bhendi Yellow Vein Mosaic Disease in India Is Caused by Association of DNA β Satellite with a Begomovirus. *Virol.,* **205(2):** 310–317.
18. Kalloo, G., Singh, V. P., Dudi, B. S. and Pratap, P. S. 1980. Analysis of Variation and Genetic Diversity in Garden Peas. *J. Res. Haryana Agric. Univ*., **10:** 540-546.
19. Kaushik, N., Kumar, K., Kumar, S., Kaushik, N. and Roy, S. 2007. Genetic Variability and Divergence Studies in Seed Traits and Oil Content of Jatropha (*Jathropha curcas* L.) Accessions. *Biomass Bioener.,* **31:** 497-502.
20. Kumar, P. S. and Sreeparvathy, S. 2010. Studies on Heterosis in Okra (*Abelmoschus esculentus* (L.) Moench). *Electron. J. Plant Breed.,* **1(6):** 1431-1433.
21. Murthy, B. R. 1979. Selection of Parental Material, Breeding Methods and Evaluation Procedures in Developing Improved Crop Varieties. *Indian J. Genet.,* **39:** 305-315.
22. Nath, V., Lal, H., Rai, M., Rai, N. and Ram, D. 2009. Hierarchical Clustering and Character Association Studies in Cowpea [*Vigna unguiculata* (L.) Walp.]. *Indian J. Plant Genet. Resour*., **22:** 22-25.
23. National Horticulture Board (NHB). 2011. *Indian Horticulture Database.* Ministry of Agriculture, Gurgaon, India.
24. Nerkar, Y. S. and Jambhale, N. D. 1985. Transfer of Resistance to Yellow Vein Mosaic from Related Species into Okra (*Abelmoschus esculentus* (L.) Moench). *Indian J. Genet*., **45(2):** 261-270.
25. Pandey, S., Kumar, S., Rai, M., Mishra, U. and Singh, M. 2008. Assessment of Genetic Diversity in Indian Ash Gourd (*Benincasa hispida*) Accessions Using RAPD Markers. 1. *Cucurbitaceae* (Genetics and Breeding of *Cucurbitaceae). Proceedings of the IX*th *EUCARPIA,* INRA, May 21-24th, Avignon, France.
26. Panse, V. G. and Sukhatme, P. V. 1984. *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research, New Delhi, India.
27. Peter, K. N. and Rai, B. 1976. Genetic Divergence in Tomato. *Indian J. Genet.,* **36**: 379-383.
28. Prabhu, T., Warade, S. D. and Ghante, P. H. 2007. Resistant to Okra Yellow Vein Mosaic Virus in Maharashtra. *Veg. Sci.,* **34(2):** 119-122.
29. Prabhu, T. and Warade, S. D. 2009. Biochemical Basis of Resistance to Yellow Mosaic Virus in Okra. *Veg. Sci.,* 36(3): 283-287.
30. Reddy, M. T., Babu, K. H., Ganesh,M., Begum, H., Reddy, R. S. K. and Babu, J. D. 2013. Exploitation of Hybrid Vigour for Yield and Its Components in Okra [*Abelmoschus esculentus* (L.) Moench]. *Amer. J. Agric. Sci. Tech.,* **1:** 1-17.
31. Reddy, M. T., Babu, K. H., Ganesh, M., Reddy, C. K., Begum, H., Reddy, P. B. and Narshimulu, G. 2012. Genetic Variability Analysis for the Selection of Elite Genotypes Based on Pod Yield and Quality from the Germplasm of Okra (*Abelmoschus esculentus* L. Moench). *J. Agric. Tech.,* **8(2):** 639-655.
32. Sadasivam, S. and Manikam, A. 1991. *Biochemical Methods for Agriculture Science*. Wiley Eastern Limited, New Delhi, PP. 106-108.
33. Sastry, K. S. M. and Singh, S. J. 1974. Effect of Yellow Vein Mosaic Virus Infection on Growth and Yield of Okra Crop. *Indian Phytopath.,* **27:** 294-97.
34. Sharma, B. R., Kumar, V. and Bayay, K. L. 1981 Biochemical Basis of Resistance to Yellow Vein Mosaic Virus in Okra. *Genet. Agrar.,* **35(2):** 121-130.
35. Sivasubramanian, S. and Menon, M. 1973. Heterosis and Inbreeding Depression in Rice. *Madras Agric. J.,* **60**: 1139.
36. Tiwari, A., Singh, B., Singh, T. B., Sanval, S. K. and Pandey, S. D. 2012. Screening of Okra Varieties for Resistance to Yellow Vein Mosaic Virus under Field Condition. *HortFlora Res. Spectrum,* **1(1):** 92-93.
37. Ward, J. H. Jr. 1963. Hierarchial Grouping to Optimize an Objective Function. *J. Amer. Statist. Assoc.,* **58:** 236-44.
38. Wilson, F. D., Flint, H. M., Stapp, B. R. and Parks, N. J. 1993. Evaluation of Cultivars, Germplasm Lines, and Species of Gossypium for Resistance to Biotype "B" of Sweetpotato Whitefly (Homoptera: Aleyrodidae). *J. Econ. Entomol*., **86:** 1857-1862.

گزینش رگه های والد در بین گونه های کشت شده و وحشی بامیه برای دو رگ گیری با هدف مقاومت در برابر مرض YVMV

ت. ست، ا. چاتوپاتهی، س. چاترجی، س. دوتا، و ب. سینگ

چکیده

ویروس موزائیک رگبرگ زرد (YVMV) بامیه تنها عامل محدود کننده اصلی تولید این محصول است که در هندوستان خساراتی در حد ۹۰-۵۰٪ به بار می آورد.از این رو، کاوش پیوسته برای یافتن منابع مقاومت به آن و اصلاح رقم ها و هیبرید های دارای مقاومت پایدار، نیازمند توجه بهنژاد گران است. در این رابطه، تلاش شد تا با غربال گری ۲۶ رگه و رقم پیشرفته بامیه در یکی از مناطق اصلی مرض YVMV در شرق هند، والد های مناسب برای برنامه بهنژادی به منظورایجاد مقاومت به این ویروس شناسایی شود. نتایج حاکی از تنوع ژنتیکی زیاد و درجه بالایی از انتقال در مورد بیشتر صفات رشد، زود رسی، و اجزای عملکرد بود. نیز، بر اساس درجه تفرق، ژنوتیپ های مورد مطالعه در چهار خوشه دسته بندی شدند. دردو رگ گیری بین ژنوتیپ های خوشه II و خوشه III، صفات زود رسی،عملکرد بیشتر، و مقاومت به YVMV در هم آمیختند. دندروگرام ژنوتیپ ها نیز تنوع زیاد و رابطه هایی قوی بین خوشه ها آشکار ساخت. بر مبنای میانگین داده های آزمون و تجزیه اجزای اصلی، شش ژنوتیپ شامل BCO-1، *A. caillei*، *A. manihot*، 11/RES-6، VNR Green، و 12/RES-2 برای کاربرد در برنامه های ژنتیکی ایجاد مقاومت، گزینه های بسیار امید بخشی به نظر می آیند.