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RESEARCH ARTICLE

Identification of Elite Parental Lines in Cultivated and Wild Okra (*Abelmoschus esculentus* L. Moench) Accessions for Yellow Vein Mosaic Virus Disease Resistance Using Multivariate Analysis

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ABSTRACT

Yellow vein mosaic virus (YVMV) is the most destructive viral disease of okra, has become a limiting factor in the successful cultivation and production of okra in India, resulting in yield losses ranging from 17.09 to 96.49 per cent. As a result, it is critical that breeders continue to develop superior varieties or hybrids with long-lasting resistance to overcome this major devastating disease. In this context present investigation was carried with 74 elite okra lines to discover potential parents for a resistance breeding programme. On the basis of D^2 values the 74 genotypes were divided into seven groups. Cluster I constituted the highest number of genotypes followed by cluster II, III, IV, V, VI and VII. The traits per cent disease index of YVMV contributed maximum towards divergence followed by total phenolic content, peroxidase activity, fruit yield per plant, number of primary branches and number of fruit per plant. PCA showed four principal components with Eigen values more than one *viz.,* 3.87, 3.21, 1.89 and 1.64 and accounted 81.56 per cent of the total genetic variation. Principal component analysis revealed that PC1 captured potential traits *viz.,* total phenolic content, peroxidase activity, polyphenol oxidase, number of fruits per plant, number of primary branches per plant and fruit yield per plant, which could be used in future breeding programmes for high yield and YVMV resistance. The present study it was revealed that, eleven accessions *viz.,* AE-65, AE-66, AE-CBE-921, Pusa Bhendi-5, SB-2, IC112449, AE-CBE-94, AE-CBE-943, AE-CBE-934, AE-CBE-92 and AE-CBE-93 appeared to be very promising lines for future use in resistant breeding programmes.

Keywords: *Okra; YVMV; Genetic diversity; Cluster analysis; PCA*

INTRODUCTION

Okra (*Abelmoschus esculentus* L. Moench) is a well-known and commercially useful tropical vegetable crop. It has 2n=130 chromosomal number and is a member of Malvaceae family. The nutrients vitamins, calcium, potassium, fibre, iron, and minerals are abundant in this vegetable, making it a nutrient-dense food (IBPGR, 1990). In India, okra is most frequently cultivated and popular vegetable crop leads the world in production with 60.03 lakh tonnes followed by Nigeria with 20.60 lakh tonnes (FAO, 2017). However, India's productivity (12.0 tha^{-1}) continues to lag behind that of other okra producers such as Saudi Arabia (13.30 tha^{-1}), Egypt (12.50 tha^{-1}), and Sudan (11.90 tha^{-1}). The main reasons for low productivity in India is the use of unimproved local cultivars, open-pollinated varieties and high incidence of yellow vein mosaic viral disease, which is transmitted by whitefly (*Bemisia tabaci* Genn) (Khade *et al.,* 2020). It has been demonstrated that YVMV reduces the fruit yield by 17.09 to 96.49 per cent, depending on the variety (Jamir *et al.,* 2020). It is caused by a variety of monopartite and bipartite begomoviruses and their satellite DNA pose a significant challenge to okra cultivation and production (Venkataravanappa *et al.,* 2016). To warfare this disease, India has made

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efforts to identify resistant and tolerant cultivars among cultivated and wild species (Nerkar and Jambhale, 1985).

Genetic diversity has its own importance in plant breeding programme. It is base for the survival of plant in nature and for crop improvement, diversity in plant genetic resources, enables breeders to create new and improved cultivars with desired features. Genetic variation within and between crop plant species enables breeders to identify superior genotypes for use as new varieties or as parents in hybridization programmes. To select appropriate genotypes for a planned breeding programme, it is necessary to understand the type and magnitude of diversity present in available breeding materials. Multivariate analysis is a powerful tool for estimating the degree of divergence among genotypes in a population and the nature of forces at different levels (Coelho *et al.,* 2007). The cluster analysis nd principal component analysis (PCA) are the two most commonly used methods for assessing genetic diversity. In the present scenario, available cultivars have chance to be phased out in the near future due to genetic drift and an increased risk of disease. This necessitates ongoing research and development of new high-yielding cultivars with YVMV resistance and acceptable fruit quality to replace current varieties. Therefore, the present study was carried out to assess the genetic variability for various yield component features and genotype diversity to identify acceptable parents for future use in the YVMV resistant breeding programme.

MATERIAL AND METHODS

The current study was conducted in the Department of Vegetable Science, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, India. Seventy-four elite okra accessions (Table 1) were collected from various geographical regions, National Institutes and State Agricultural Universities in India. The experiment was conducted in three replications by using Randomised Block Design (RBD). The plants were planted in a plot size of (4.5 × 1.2 m^2) with a spacing of 60 × 45 cm during the *Summer season* of 2020. All production techniques were carried out following the TNAU crop production guide. The following parameters were observed on ten randomly selected plants *viz.,* plant height (cm), node at which the first flower appears, number of primary branches per plant, fruit length (cm), fruit diameter (cm), fruit weight (g), number of ridges on fruit, number of fruits per plant, fruit yield per plant (g). The quality traits *viz.,* total phenolic content, peroxidase activity, and polyphenol oxidase were determined using the procedure of Sadasivam and Manickam's (1991). The field experiment was conducted during the summer season, during the peak pressure of the vector *Bemisia tabaci*, using an infector row technique. The planting ratio of healthy to vulnerable plants was 3:1. The susceptible varieties Arka Anamika and Parbhani Kranti were utilized as susceptible checks. Throughout the crop growth season, no chemical pesticides were sprayed. Natural pressure was permitted to operate at full capacity, allowing the diseases to spread at breakneck speed. The following disease severity scale for YVMV, as adopted by Das *et al.* (2013) was used in the study.

Disease Severity Scale	Symptoms
0	No disease
1	up to 15% of leaf area affected
3	30%–45% of leaf area affected
5	45%–60% of leaf area affected
7	greater than 60% of leaf area affected

The following scale as used to evaluate resistance and the susceptible reaction of the genotypes to YVMV disease by Percent Disease Index (PDI).

A. Resistant (R) PDI ≤ 10%,

B. Moderately resistant (MR) PDI 11 - 15%

C. Moderately susceptible (MS) PDI 16 - 45%

D. Highly susceptible (HS) PDI > 45 %

The following formula was used to calculate PDI, which was then transformed using the arcsine transformation.

$$PDI = \frac{\text{Sum of numerical rating of disease severity scale}}{\text{Highest grade of the scale} \times \text{number of plants examined}} \times 100$$

The genetic divergence among okra genotypes was determined using D^2 statistics (Mahalanobis, 1936). Tocher's method was used to sort all genotypes into different categories (Rao, 1952). The statistical approach developed by Singh and Choudhary, (1985) was used to calculate the average distance between and within clusters. The statistical analysis for D^2 statistics was carried out using the INDOSTAT software and Principal component analysis (PCA) was carried out to identify plant traits that contribute to most of the observed variations among the genotypes by XLSTAT 2016.

RESULTS AND DISCUSSION

Differentiation of genotypes into clusters

In the present study, 74 okra accessions were clustered for thirteen quantitative and quality traits including per cent disease index of YVMV and classified into seven groups using Mahalanobis D^2 statistics (Figure 1). Cluster I was the largest

group that had 54 genotypes followed by cluster II (6), cluster III (6) and cluster IV (5), while clusters V, VI and VII each had only one genotype (Table 2). The pattern of grouping genotypes into a single cluster indicates that they are genetically similar for the majority of attributes (Alake, 2020 and Balai *et al.,* 2015). On the whole, the pattern of distribution of genotypes from different geographical regions into different clusters appeared to be random in nature. This may be due to the free and regular flow of genetic materials between farmers and breeders from different geographical areas (Karthika and Maheswari, 2019). The application of differential selection pressure based on regional preference resulted in increased homogeneity in the germplasm. The geographical distance was found to have no relationship with genetic diversity, indicating that forces other than the geographic origin, such as exchange of genetic stock, mutation caused by chance or mutation caused by natural or artificial selection, were responsible for the evolution of genetic diversity. Similar finding was reported by Seth *et al.* (2016). Because of this, rather than geographic diversity, the selection of genotypes for hybridization should be based on genetic divergence.

Table 1. List of okra accessions used in study

S.No.	Accessions	Sources
1	GED-19	TNAU, Coimbatore, India
2	GED-545	TNAU, Coimbatore, India
3	GED-509	TNAU, Coimbatore, India
4	GED-15	TNAU, Coimbatore, India
5	GED-11	TNAU, Coimbatore, India
6	IC417885	TNAU, Coimbatore, India
7	NO-315	VNMKV, Parbhani, India
8	EC16394	TNAU, Coimbatore, India
9	SB-2	TNAU, Coimbatore, India
10	AE-11	TNAU, Coimbatore, India
11	AE-62	TNAU, Coimbatore, India
12	AE-63	TNAU, Coimbatore, India
13	AE-64	TNAU, Coimbatore, India
14	AE-65	TNAU, Coimbatore, India
15	AE-66	TNAU, Coimbatore, India
16	IC22237	VNMKV, Parbhani, India
17	EC755648	VNMKV, Parbhani, India
18	IC43743	VNMKV, Parbhani, India
19	EC755647	VNMKV, Parbhani, India
20	IC18960	VNMKV, Parbhani, India
21	IC417875	NBPGR, New Delhi, India
22	IC111370	NBPGR, New Delhi, India
23	IC332457	NBPGR, New Delhi, India
24	IC411880	NBPGR, New Delhi, India
25	IC433532	NBPGR, New Delhi, India
26	IC112449	NBPGR, New Delhi, India
27	*A.tuberculatus* (IC140984)	NBPGR, New Delhi, India
28	*A.ficulneus* (IC558661)	NBPGR, New Delhi, India
29	*A.tuberculatus* (IC325954)	NBPGR, New Delhi, India
30	*A.moschatus* (IC433556)	NBPGR, New Delhi, India
31	*A.callei* (IC255758)	NBPGR, New Delhi, India
32	*A.moschatus* (IC140196)	NBPGR, New Delhi, India
33	IC105675	NBPGR, New Delhi, India
34	Pusa Bhendi-5	IARI, New Delhi, India
35	IC433533	NBPGR, New Delhi, India
36	Arka Anamika	NSC, Coimbatore, India
37	KTL-1	Collection from Nagpur region of Maharashtra, India
38	AE-WR- 05	Collection from Nagpur region of Maharashtra, India
39	AE-WR-06	Collection from Nagpur region of Maharashtra, India
40	AE-RMKN-01	Collection from Chhindwara region of Madhya Pradesh, India
41	AE-RMKN-02	Collection from Chhindwara region of Madhya Pradesh, India
42	AE-BDR-01	Collection from Nagpur region of Maharashtra, India

43	AE-WR-01	Collection from Nagpur region of Maharashtra, India
44	AE-WR-02	Collection from Nagpur region of Maharashtra, India
45	AE-WR-03	Collection from Nagpur region of Maharashtra, India
46	AE-WR-04	Collection from Nagpur region of Maharashtra, India
47	AE-CBE-01	Collection from Coimbatore region, India
48	AE-CBE-02	Collection from Coimbatore region, India
49	AE-CBE-03	Collection from Coimbatore region, India
50	GED-46	TNAU, Coimbatore, India
51	GED-5	TNAU, Coimbatore, India
52	GED-4	TNAU, Coimbatore, India
53	GED-18	TNAU, Coimbatore, India
54	307-10-1	TNAU, Coimbatore, India
55	GED-25	TNAU, Coimbatore, India
56	IC10265	VNMKV, Parbhani, India
57	IC090213	NBPGR, New Delhi, India
58	AE-BR-01	Collection from Bihar, India
59	AE-BR-02	Collection from Bihar, India
60	AE-CBE-04	Collection from Coimbatore region, India
61	*A. moschatus*	IARI, New Delhi, India
62	AE-CBE-05	Collection from Coimbatore region, India
63	AE-CBE-06	Collection from Coimbatore region, India
64	AE-CBE-10	Collection from Coimbatore region, India
65	AE-CBE -91	Sambaravalli village of Coimbatore district, India
66	AE-CBE -92	Karamadai village of Coimbatore district, India
67	AE-CBE -93	Kethanur village of Tirupur district, India
68	AE-CBE -94	Ponnimandurai village of Dindigul district, India
69	AE-CBE -921	Andarkulam village of Kanyakumari district, India
70	AE-CBE -912	Palakkode village of Dharmapuri district, India
71	AE-CBE -943	Navakurichi village of Salem district, India
72	AE-CBE -934	Nadupatti village of Tiruchirapalli district, India
73	AE-CBE-08	Collection from Coimbatore region, India
74	AE-CBE-09	Collection from Coimbatore region, India

The D^2 values of Mahalanobis D^2 statistics showed that inter-cluster distances ranged from 39.40 to 156.50 (Table 3). The minimum inter-cluster distance (39.40) was found between Cluster I and V, indicated that the genotypes included in these clusters were closely related. Cluster IV and V had the highest inter-cluster score (156.50), followed by cluster IV and VII (140.96), cluster IV and VI (137.12) and cluster I and IV (132.24) indicated that the genotypes included in these clusters had the highest degree of divergence between them. The selection of parents for hybridization programmes from these diverse clusters would help get novel recombinants. Hence, these diverse clusters could be utilized in hybridization and selection for future breeding programme. Similar finding was given by Kalloo *et al.* (1980), where the recombination occurred when selected varieties from widely dispersed clusters were crossed.

Table 2. Cluster classification of seventy-four accessions of okra

Clusters	Number of accessions	Accessions
Cluster 1	54	IC411880, AE-RMKN-02, AE-RMKN-01, AE-WR-02, IC090213, AE-BR-01, IC332457, IC43743, IC111370, AE-WR-03, AE-63, IC417885, AE-CBE-06, AE-WR-06, AE-WR-04, IC18960, AE-11, AE-CBE-01, AE-WR-01, IC10265, AE-62, EC16394, GED-509, GED-545, IC433533, GED-18, GED-46, AE-WR- 05, AE-CBE-02, GED-11, 307-10-1, NO-315, AE-BR-02, IC417875, AE-64, GED-4, GED-5, GED-15, EC755648, GED-25, AE-CBE-09, IC433532, *A.callei* (IC255758), IC22237,GED-19, EC755647, AE-CBE-04, Arka Anamika, AE-CBE-03, AE-BDR-01, *A.tuberculatus* (IC140984), AE-CBE-10, AE-CBE-08, AE-CBE-05.
Cluster 2	6	AE-65, AE-66, AE-CBE-921, Pusa Bhendi-5, SB-2, IC112449
Cluster 3	6	AE-CBE -91, AE-CBE -912, *A. moschatus* (IC140196), *A. moschatus*, *Abelmoschus moschatus* (IC433556), *A. tuberculatus* (IC325954),
Cluster 4	5	AE-CBE-94, AE-CBE-943, AE-CBE-934, AE-CBE-92, AE-CBE-93
Cluster 5	1	IC 105675
Cluster 6	1	*A. ficulneus* (IC558661)
Cluster 7	1	KTL-1

From the cluster mean it was observed that, all of the characters' mean genotype cluster values differed in magnitude (Table 4). The maximum fruit yield per plant, fruit length, total phenolic content, peroxidase, polyphenol oxidase activity and negligible per cent disease incidence was observed in cluster IV. Whereas, the cluster II had minimum point for a node at which first flower appear and had least incidence of YVMV disease. Both clusters (II and IV) had a total of five ridges on the fruit, which was a positive indicator of consumer choice.

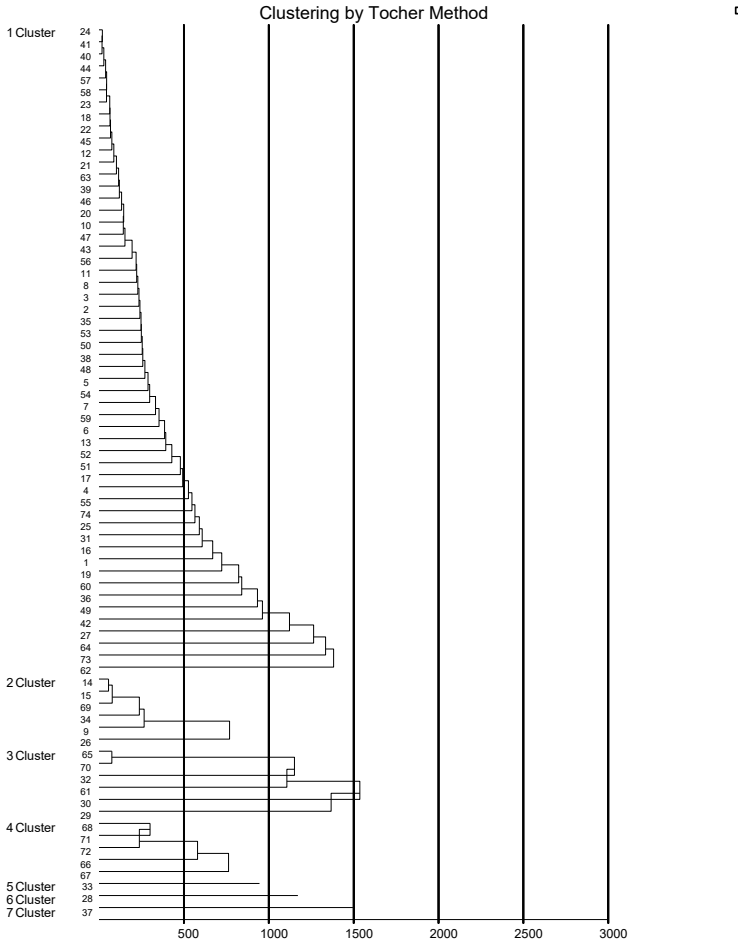

Fig 1. A dendrogram displaying the clustering pattern of seventy-four okra accessions

The maximum plant height, number of primary branches, and number of fruits per plant were observed in cluster VI. Regarding fruit diameter and weight, Cluster III and Cluster I had the highest cluster mean. From the present investigation it is revealed that, based on cluster mean value, genotypes from Cluster II were the earliest and had low prevalence of YVMV, which could be useful for developing early maturing variety, while cluster IV genotypes were high yielding and had negligible per cent disease index for YVMV. So, in future breeding operations such as, hybridization between okra genotypes belonging to Clusters II and IV, could bring together increased fruit yield and early maturity with strong resistance to the YVMV disease. A similar conclusion was made by Karthika and Maheswari, (2019) in okra.

Table 3. Inter-cluster distances between seventy-four okra accessions

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7
Cluster 1	-	84.17	47.11	132.24	39.40	69.61	51.89
Cluster 2		-	72.96	56.25	106.88	94.51	94.67
Cluster 3			-	120.94	56.51	56.35	53.75
Cluster 4				-	156.50	137.12	140.96
Cluster 5					-	72.82	56.01
Cluster 6						-	40.3
Cluster 7							-

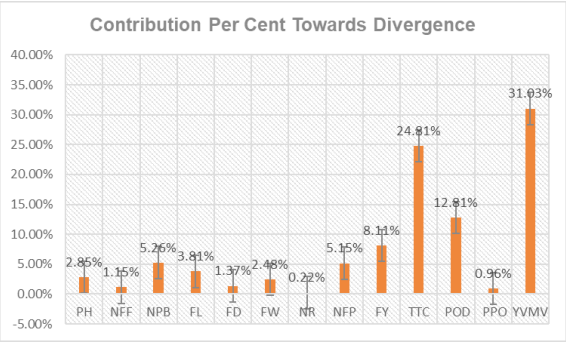

Fig 2. Graphical representation of the quantitative and quality variables that contribute to genetic diversity in okra

PH - Plant height (cm), NFF - Node at which the first flower appears, NPB - Number of primary branches per plant, FL - Fruit length (cm), FD -Fruit diameter (cm), FW - Fruit weight (g), NR - Number of ridges on fruit, NFP – Number of fruits per plant, FY - Fruit yield per plant (g), TPC - Total phenolic content, POD - Peroxidase activity, PPO - Polyphenol oxidase and YVMV - Per cent disease index of yellow vein mosaic virus

Trait contribution to genetic diversity

The per cent contribution of each character towards total divergence is presented in Figure 2. Per cent disease index of YVMV was contributed highest towards divergence, followed by total phenolic content, peroxidase activity, fruit yield per plant, number of primary branches, number of fruit per plant, fruit length, plant height, fruit weight, fruit diameter, node at first flowering, polyphenol oxidase and number of ridges on fruit. It suggested that the character of Yellow Vein Mosaic Virus would be a critical factor in selecting various okra genotypes. Whereas the traits *viz.,* total phenolic content, peroxidase activity, fruit yield per plant, number of primary branches, number of fruit per plant contributed highest towards divergence. Thus, these were the major characters that contributed to the total divergence. Hence, the selection of divergent parents based on these traits will be useful in the heterosis breeding of okra. Similar findings were reported by Prakash and Pitchaimuthu, (2010) and Kumar *et al.* (2016) in okra.

Table 4. Cluster means for seventy-four okra accessions for thirteen quantitative and quality traits

	PH	NFF	NPB	FL	FD	FW	NR	NFP	FY	TPC	POD	PPO	YVMV
Cluster 1	114.12	4	2.84	15.22	1.99	18.85	5.85	28.5	462.73	0.5	1.68	1.18	38.32
Cluster 2	115.89	3.81	3.13	14.91	1.85	16.94	5	35.18	487.02	1.72	3.16	2.54	4.54
Cluster 3	98.05	5.32	6.47	10.03	2.19	10.28	5.67	37.99	396.79	0.85	1.77	1.36	9.1
Cluster 4	92.17	4.22	3.22	15.95	2.16	18.67	5	40.77	707.29	2.41	4.32	3.13	0.34
Cluster 5	62.97	4.8	3.06	14.43	1.83	15.78	7	26.28	373.52	0.49	0.69	1.12	40.06
Cluster 6	175.76	7.88	19.9	4.32	1.87	2.71	5	104.79	256.11	0.87	1.78	1.28	23.33
Cluster 7	90.58	4.95	9.94	5.38	1.76	2.71	5	97	236.78	0.48	1.7	1.11	36.35

PH - Plant height (cm), NFF - Node at which the first flower appears, NPB - Number of primary branches per plant, FL - Fruit length (cm), FD -Fruit diameter (cm), FW - Fruit weight (g), NR - Number of ridges on fruit, NFP – Number of fruit per plant, FY - Fruit yield per plant (g), TPC - Total phenolic content, POD - Peroxidase activity, PPO - Polyphenol oxidase and YVMV – Per cent disease index of yellow vein mosaic virus

Principal component analysis (PCA)

PCA identified four principal components that had Eigen values more than one *viz.,* 3.87, 3.21, 1.89 and 1.64 together, they accounted for 81.56 per cent of the total genetic variation. PC1 and PC2 were responsible for 29.73 and 24.67 per cent of the overall variation. Okra genotypes were plotted in two dimensions on-axis PC1 against PC2 (Figure 5), revealing the pattern of genotype dispersion among the axis. The total phenolic content, peroxidase activity, polyphenol oxidase, number of fruit per plant, number of primary branches per plant, fruit yield per plant were positively associated with the PC1, while per cent disease index of YVMV was negatively associated, which contributed the most to variability (Table 5 and Figure 3). As a result, this component was associated with the traits that determined the yield level and YVMV resistance. These traits were the most involved in the divergence and carried the greatest amount of variability.

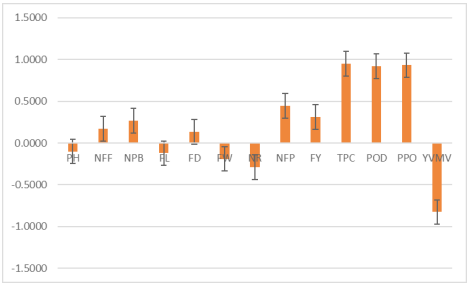

Fig 3. Graphical representation of rotated component matrix for different traits in PC1

PH - Plant height (cm), NFF - Node at which the first flower appears, NPB - Number of primary branches per plant, FL - Fruit length (cm), FD -Fruit diameter (cm), FW - Fruit weight (g), NR - Number of ridges on fruit, NFP – Number of fruits per plant, FY - Fruit yield per plant (g), TPC - Total phenolic content, POD - Peroxidase activity, PPO - Polyphenol oxidase and YVMV - Per cent disease index of yellow vein mosaic virus

Table 5. Principle components analysis of okra accessions for thirteen traits

Principle components	PC1	PC2	PC3	PC4
Eigen value	3.87	3.21	1.89	1.64
Variability (%)	29.73	24.67	14.53	12.63
Cumulative %	29.73	54.41	68.93	81.56
PH	-0.1016	-0.0200	-0.5514	0.6346
NFF	0.1711	-0.6481	0.3738	0.0722
NPB	0.2661	-0.7389	0.3366	0.3874
FL	-0.1225	0.8467	0.0391	0.1604
FD	0.1323	0.1503	0.7416	0.3561
FW	-0.1904	0.8228	0.3347	0.2538
NR	-0.2900	0.0074	0.7997	-0.2377
NFP	0.4463	-0.5641	-0.0400	0.5820
FY	0.3102	0.5968	0.0960	0.6105
TPC	0.9516	0.1408	-0.0271	-0.1444
POD	0.9204	0.2739	-0.0726	-0.1230
PPO	0.9328	0.2345	-0.0147	-0.1283
YVMV	-0.8269	-0.0120	-0.1056	0.2149

PH - Plant height , NFF - Node at which the first flower appears, NPB - Number of primary branches per plant, FL - Fruit length , FD -Fruit diameter , FW - Fruit weight , NR - Number of ridges on fruit, NFP – Number of fruit per plant, FY - Fruit yield per plant , TPC - Total phenolic content, POD - Peroxidase activity, PPO - Polyphenol oxidase and YVMV - Per cent disease index of yellow vein mosaic virus

Similar findings were reported by Seth *et al.* (2016), Kumar *et al.* (2016). The second principal component (PC2) accounted for 24.67 per cent of the total variance, with positive loadings for fruit length, fruit weight and fruit yield per plant, while node at first flowering was negatively associated (Figure 4). The PC3 was distinguished by a high loading for number of ridges on fruit, fruit diameter and the number of primary branches per plant. The PC4 was positively associated with plant height, fruit yield per plant and number of fruit per plant.

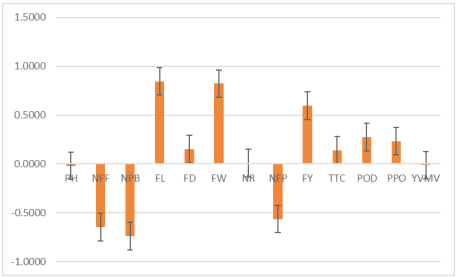

Fig 4. Graphical representation of rotated component matrix for different traits in PC2

PH - Plant height (cm), NFF - Node at which the first flower appears, NPB - Number of primary branches per plant, FL - Fruit length (cm), FD -Fruit diameter (cm), FW - Fruit weight (g), NR - Number of ridges on fruit, NFP – Number of fruits per plant, FY - Fruit yield per plant (g), TPC - Total phenolic content, POD - Peroxidase activity, PPO - Polyphenol oxidase and YVMV - Per cent disease index of yellow vein mosaic virus

The biplot of principal component analysis revealed a high degree of variation among genotypes and between parameters. I quadrant of biplot had the highest divergence towards total phenolic content, peroxidase activity, polyphenol activity, fruit yield per plant and had a negative association with per cent disease index of YVMV, as per cent disease index of YVMV is in obtuse angle with these traits. Whereas, quadrant IV had the highest divergence for number of primary branches, the node at which first flower appear and number of fruit per plant. Quadrant II had highest divergence for fruit weight and fruit length. However, the quadrant III had maximum divergence for per cent disease index of YVMV, number of ridges on fruit and plant height. From the present investigation, it was observed that quadrant I had high yielding genotypes and YVMV resistant while quadrant IV had the highest number of primary branches, number of fruit per plant, and earliness, which would be utilized in the future breeding programme for creating desirable novel segregants genotypes. A similar finding was revealed by Seth *et al.* (2016) and Alake, (2020). So, this study helps in identifying the variables that contribute to the variability and selecting suitable genotypes for YVMV disease resistance breeding.

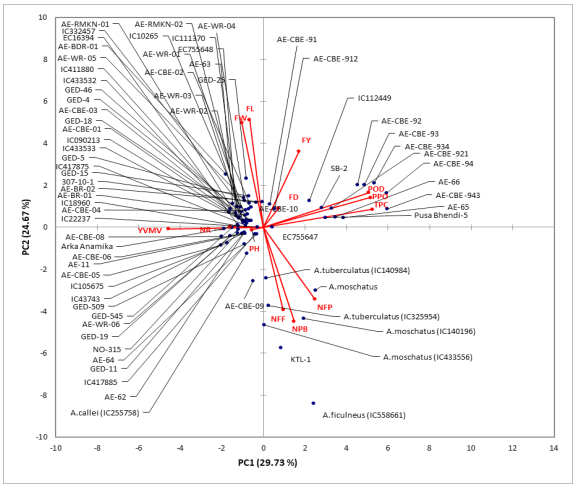

Fig 5. Biplot diagram of principal components (PC1 and PC2)

Conclusion

Cluster analysis formed seven clusters based on their degree of divergence. Cluster I constituted the maximum number of genotypes while, least in clusters V, VI and VII. The per cent disease index of YVMV contributed maximum towards divergence, followed by phenolic content, peroxidase activity, fruit yield per plant, number of primary branches and number of fruit per plant. Principal component analysis showed four main principal components which had Eigen values more than one and contributed 81.56 per cent of the total variation. Total phenolic content, peroxidase activity,

polyphenol oxidase, number of fruit per plant, number of primary branches per plant, fruit yield per plant and per cent disease index of YVMV were the potential traits captured in PC1 which could be employed in future breeding programmes. So, from the present study, it is concluded that, eleven genotypes from cluster II and IV *viz.,* AE-65, AE-66, AE-CBE-921, Pusa Bhendi-5, SB-2, IC112449, AE-CBE-94, AE-CBE-943, AE-CBE-934, AE-CBE-92, AE-CBE-93 appeared to be very promising lines for future use in resistance breeding programmes.

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Originality and plagiarism

Authors should ensure that they have written and submit only entirely original works.

Ethics statement

No specific permits were required for the described field studies because no human or animal subjects were involved in this research.

Consent for publication

All the authors agreed to publish the content.

Competing interests

There were no conflict of interest in the publication of this content

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