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Assessment of genetic diversity among okra (*Abelmoschus esculentus*) genotypes for quality traits

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ABSTRACT

Thirty diverse genotypes of okra (*Abelmoschus esculentus*) were evaluated during *kharif* 2013 in Randomized Complete Block Design with three replications. The mature fruits (seven days after anthesis) were analysed for 19 quality traits. Dietary fibre content was recorded maximum in genotype Arka Abhay (0.09 g/g), while genotype USDO 2546 was found good source of dietary fibre (0.09 g/g) as well as protein (2.75%). Mucilage content was found maximum in genotype Punjab Padmini (6.10 %) and least mucilage was recorded in genotype DOV 26 (3.35%). Maximum iron content was recorded in genotype DOV 66 (1.71ppm) followed by DOV 27 (1.60ppm) and DOV 24 (1.53ppm). However, high calcium content was recorded in Arka Abhay and DOV 23. Genotype P 7 (13.33µg/g), DOV 2 and DOV 4 (i.e. 13.04 µg/g each) were found high in ascorbic acid. Total leaf carotenoid content was maximum in Pusa A 4 (3.35 mg/g). Total leaf chlorophyll and carotenoid content was maximum in Pusa A 4 (3.35 mg/g and 3.06 mg/g, respectively). Based on Mahalanobis D^2 analysis 30 genotypes were grouped into 7 divergent clusters. Cluster VII had maximum (7) genotypes followed by cluster III and V (6 genotypes in each). Maximum inter cluster distance (6.44) was recorded between genotypes of cluster IV and VII. Cluster IV recorded maximum cluster mean for sugar (5.36%), ascorbic acid content (11.42 mg/g), ash content (1.57%), protein content (2.54%) and Mn content (0.29ppm). In principal component analysis of morphological traits, a total of 82.33% variability was contributed by 7 principal components out of 20 principal components.

Key words: *Abelmoschus esculentus*, Genetic diversity, Nutritional analysis, Okra, Principal component analysis

Okra [*Abelmoschus esculentus* (L.) Moench] 2n=2x=130), is one of the important vegetable crops grown worldwide. India is the largest producer of okra with 6.35 million tonnes production (72.9% of total world production) from 0.53 million ha area (NHB Database 2014). Tender pods of okra are used as delicious vegetable. Okra is often included in weight reducing diet as it is almost free from fat and cholesterol and rich in fibre. It is a rich source of protein, calcium and potassium. Okra mucilage is potentially used as food, non-food products and medicinal purposes (Kumar *et al*. 2009). High level of dietary fibre and low caloric value and rich source of minerals, like Ca, P, K and Mg regulates blood pressure. Seven days old fresh okra pods have the highest concentration of nutrients (Agbo *et al*. 2008). Keeping its nutritional values and to address the problem of malnutrition of growing population, it is imperative to identify the nutritionally rich genotypes to develop the varieties by using appropriate breeding techniques. Multivariate analysis of elite genotypes is prerequisite for choosing promising genetically diverse lines for desirable traits. For this, cluster analysis based on D^2 statistic and Principal Component (PC) analysis are the important genetic diversity measuring tools employed to assess the nature and magnitude of genetic divergence. It also helps in solving taxonomical problem in biological population of inter varietal, sub-species and species level. Study of genetic diversity in okra may play significant role in identification of desirable genotypes which will be helpful in development of resistant variety/hybrids and pre breeding lines with desirable fruit quality traits. In the past, limited attempt has been made to estimate genetic divergence in okra genotypes on the basis of quality traits. The present study was, therefore, conducted to estimate the genetic divergence on the basis of biochemical traits in 30 genotypes of okra which had been released as resistant to Yellow Vein Mosaic Virus disease (YVMV).

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MATERIALS AND METHODS

The present investigation was carried out by utilizing

30 promising and diverse lines/varieties of okra developed as YVMV resistant by various institutes/SAU of the country. The crop was raised following the standard cultivation practices during the *kharif* season of 2013. Fruits for biochemical analysis for 19 traits were harvested after seven days of anthesis as per standard procedure mentioned by Ranganna (2012). Mineral content in okra pod was determined by atomic absorption spectrophotometer (Model-GBC, 904AA) according to Jackson (1980). The texture of pod were measured using the methodology described by Bouvier *et al*. (1997) using the texture analyzer (Model: *TA+HDi,* Stable Micro Systems, UK) attached with 500 kg load cell. The biochemical data of three replications were subjected to various statistical analysis. The clustering analysis and PC analysis in 30 genotypes of okra was estimated based on biochemical data to assess the magnitude of genetic variation following Mahalanobis D^2 statistics (Generalized distance as suggested by Rao 1952). Based on D^2 values (Mahalanobis 1936) lines were grouped into a number of clusters. D^2 being treated as the square of generalized distance, according to the method described by non-hierarchical Euclidean cluster analysis. Average intra and inter-cluster distances and clustering patterns among 30 okra genotypes exhibiting dendogram were assessed by using Tocher's method.

RESULTS AND DISCUSSION

Analysis of variance revealed highly significant mean sum of square due to treatments for all the traits, suggested thereby the presence of substantial amount of genetic diversity in the material under study.

A critical perusal of Table 1 showed that genotype VRO 21 (9.66), DOV 22 (8.91) and DOV 64 (8.73) had high value for texture showing that these genotypes had better fruit texture quality. There was little variability for dietary fibre amongst the genotypes, however, dietary fibre content was recorded maximum in genotype Arka Abhay (0.09 g/g) and USDO 2546 (0.09 g/g), while it was low in DOV 26, DOV 29, P 7, Varsha Uphar and VRO 6 (0.03 g/g in each). Protein content, an important character from nutrition point of view, was found maximum in USDO 2546 (2.75%) andminimum in DOV 26 (1.37 %) with mean value of 1.78 %. High protein content was also recorded in several genotypes, viz. Hisar Unnat (2.49%), USDO 2730 (2.45%), DOV 62 (2.42%), Punjab Padmini (2.39%) and DOV 4 (2.38%). Sugar content ranged from 1.31% (DOV 23) to 6.55 % (USDO 2546). It was clearly shown that genotypes with high sugar content had high value of mucilage. Ash content (%) ranged from 0.60 to 2.00. Mucilage content was found maximum in genotype Punjab Padmini (6.10 %) and least mucilage was recorded in genotype DOV 26 (3.35%). Similarly Ahikpa *et al.* (2014) also reported high variation for mucilage in okra.

There was less variation in Mg content among the genotypes under study, however it ranged from 1.66ppm (DOV 12) to 2.87ppm (DOV 27). Genotypes, namely DOV 66 (1.77 ppm), DOV 27 (1.60 ppm) and DOV 24 (1.53 ppm) recorded high value of iron. High calcium content was recorded in Arka Abhay (6.75ppm) and DOV 23 (5.47ppm), DOV 152 (5.22ppm) and Hisar Unnat (5.12ppm). Most of the genotypes recorded low content of CU and Mn. The mean value of ascorbic acid content (µg/g) was found high in genotype P 7 (13.33), DOV 2 and DOV 4 (13.04 each). Quite high genotypic differences were recorded in phenol content,which ranged from 5.74 (DOV 2) to 25.05 mg/g (Varsha Uphar). Total leaf chlorophyll and leaf carotenoid content were maximum in Pusa A-4 (3.35 mg/g and 3.06 mg/g, respectively). The high total leaf carotenoid and chlorophyll content of Pusa A-4 should have been reflected in its heavy fruiting ability, but due to YVMV incidence it could not be converted in total fruit yield, therefore, in YVMV free season and places, Pusa A-4 may be able to give high yield. Nwachukwu *et al*. (2014) also found significant differences for various nutritional and biochemical traits in Malaysian okra varieties.

Plant genetic resources are the most valuable and essential basic raw materials for the current and future need of crop improvement programmes (Paroda and Arora 1991). Assessing potential genotypes for further hybridization work to get desirable recombinants, identification of good genotypes from the germplasm sources is a prerequisite. This can be done with the help of assessment of genetic diversity. In Mahalanobis D^2 study, 30 okra genotypes were categorised into distinct clusters and their Euclidian distance using D^2 statistics based on 19 quality traits. A total of 7 clusters were formed for grouping of 30 genotypes. Cluster VII contains maximum genotypes (7), all of them also showed high degree of resistance to YVMV, while cluster I, IV and VI had equal no. of 3 genotypes in each cluster (Table 2). Cluster III and V were represented by 6 genotypes in each. Cluster II consisted only two genotypes (Pusa Sawani and Arka Abhay) based on biochemical traits. Data presented in Table 3 showed that Intra-cluster distance was maximum in cluster II (3.24) showing the existence of maximum variability among the genotypes of this cluster which comprised Pusa Sawani and Arka Abhay (Table 2). Maximum inter-cluster distance was found between cluster IV and VII (6.44) followed by cluster IV and VI (5.85) suggesting that the genotypes belonging to above clusters are more divergent than the rest of the clusters, hence can be undertaken in hybridization programme for evolving good hybrids or segregates (Table 2). Based on quality traits, Arka Anamika and Arka Abhay were grouped in two different clusters, while, Parbhani Kranti, P 7 and Punjab Padmini were grouped in the same cluster. Therefore, cluster analysis was useful in forming core subsets for grouping the genotypes with similar characters into homogeneous categories. Similar studies in okra have been done by Kumar *et al.* (2011) and Reddy *et al.* (2012). In general, the genotypes grouped together in one cluster were less divergent for quality traits than those which were placed in different clusters. Further, higher intra-cluster distance indicates high degree of divergence within that cluster.

Table 1 Mean performance of 30 okra genotypes for quality traits

Genotype	Texture	Dietary fiber (g/g)	Protein (%)	Moisture (%)	Sugar (%)	Ash (%)	Mucilage (%)	Mg (ppm)	Fe (ppm)	Ca (ppm)	CU (ppm)	Mn (ppm)	Ascorbic acid (µg/g)	Phenol (mg/g)	Flavanol (mg/g)	Chlor ophyll a(mg/g)	Chloro phyll b(mg/g)	Total chloro-phyll (mg/g)	Carot-enoid (mg/g)	Yield/ plant(g)
ArkaAbhay	3.58	0.09	1.92	84.76	4.96	1.65	4.39	2.48	1.27	6.75	0.26	0.20	9.39	11.02	1.08	0.91	0.48	1.39	1.14	91.33
ArkaAnamika	6.74	0.06	1.49	89.46	4.64	1.25	4.61	2.68	1.33	4.36	0.49	0.18	9.95	15.34	1.46	0.91	0.82	1.73	1.43	91.33
DOV 11	5.42	0.08	1.47	90.81	4.44	0.92	4.70	2.05	1.36	3.58	0.43	0.29	11.06	21.02	3.01	0.80	0.57	1.37	1.20	157.67
DOV 2	7.65	0.06	1.90	92.31	2.62	0.77	3.51	2.29	1.45	4.03	0.42	0.31	13.04	5.74	0.53	0.19	0.60	0.79	0.13	148.00
DOV 4	7.85	0.05	2.38	87.49	4.64	1.40	3.89	2.47	1.11	3.97	0.44	0.30	13.04	16.12	1.33	0.70	0.25	0.95	0.69	149.33
DOV 62	8.19	0.07	2.42	85.53	4.51	1.29	4.99	2.35	1.12	4.63	0.51	0.30	8.61	18.83	3.57	0.82	0.75	1.57	1.29	149.33
DOV 64	8.73	0.04	1.54	90.53	1.96	0.74	3.58	2.33	0.96	3.87	0.44	0.30	9.16	11.68	1.58	0.19	0.19	0.37	0.10	155.67
DOV 66	7.51	0.04	1.70	89.93	3.33	0.98	3.65	2.32	1.71	3.92	0.38	0.29	10.72	13.85	2.04	0.19	0.18	0.37	0.10	163.67
HissarUnnat	6.48	0.08	2.49	85.66	4.89	1.38	4.22	2.26	1.22	5.12	0.33	0.31	12.82	15.37	1.46	0.96	0.30	1.27	1.03	152.67
DOV 152	6.62	0.04	1.74	89.40	3.85	0.98	4.35	2.14	0.85	5.22	0.44	0.30	11.16	8.84	1.27	0.19	0.57	0.76	0.15	147.33
DOV 26	8.10	0.03	1.37	91.82	3.81	0.91	3.35	2.51	0.92	4.12	0.46	0.28	7.39	18.42	3.00	0.18	0.35	0.54	0.03	133.00
DOV 29	7.90	0.03	1.66	90.89	2.52	0.70	3.41	2.84	0.83	3.38	0.34	0.26	10.38	23.37	3.35	0.99	0.75	1.74	1.50	137.67
IC 09491	8.13	0.04	1.78	90.86	3.83	1.01	4.42	2.17	1.42	3.63	0.49	0.27	7.28	15.13	2.04	0.86	0.83	1.69	1.33	88.00
USDO 2546	7.79	0.09	2.75	82.37	6.55	1.94	4.76	2.17	0.96	3.70	0.53	0.26	8.39	11.59	1.93	0.24	0.19	0.43	0.13	80.00
USDO 2730	6.02	0.07	2.45	88.26	5.12	1.30	3.98	1.78	0.95	4.88	0.40	0.25	9.28	11.59	1.92	1.00	0.65	1.65	1.45	74.00
P 7	6.10	0.03	1.40	93.76	2.52	0.66	3.51	2.33	0.87	3.47	0.48	0.26	13.33	17.81	3.07	0.25	0.89	1.14	0.15	75.00
P 8	6.93	0.07	1.90	88.96	4.27	1.21	4.86	2.39	0.95	4.65	0.69	0.25	7.72	22.57	3.01	0.92	0.65	1.57	1.32	78.67
Parbhani Kranti	8.45	0.04	1.29	90.78	3.83	1.06	4.31	1.77	0.87	3.30	0.38	0.27	8.72	17.39	4.15	1.01	0.95	1.96	1.74	108.00
Punjab Padmini	6.36	0.08	2.39	87.44	3.48	2.06	6.10	2.47	1.29	3.32	0.44	0.23	7.94	15.68	3.86	1.07	0.99	2.06	1.84	114.00
Pusa A4	8.39	0.08	1.94	88.94	3.14	1.18	3.83	2.28	0.76	4.29	0.41	0.28	11.60	18.79	1.99	1.99	1.37	3.35	3.06	140.00
DOV 24	8.25	0.04	1.61	90.33	3.25	0.83	3.50	2.39	1.53	3.37	0.50	0.29	7.06	10.52	1.98	0.99	0.75	1.73	1.47	174.67
DOV 23	7.30	0.08	1.64	89.48	1.31	1.18	4.62	1.84	0.83	5.47	0.44	0.23	9.73	5.81	0.46	0.50	0.34	0.84	0.58	66.00
DOV 12	5.27	0.06	1.42	93.63	3.16	0.77	4.94	1.66	1.46	2.84	0.47	0.32	11.83	12.95	2.41	0.79	0.48	1.27	1.09	149.00
DOV 27	7.71	0.06	1.58	89.51	4.31	0.85	4.67	2.87	1.60	3.57	0.54	0.21	7.83	16.03	1.70	0.91	0.58	1.49	1.28	149.67
Varsha Uphar	5.03	0.03	1.83	88.39	2.43	1.36	4.54	2.27	0.95	4.14	0.48	0.25	8.72	25.05	3.41	0.67	0.49	1.16	0.95	142.33
VRO 21	9.66	0.06	1.46	90.39	2.08	1.01	4.18	2.73	0.49	3.04	0.49	0.27	10.72	24.34	3.70	0.91	0.88	1.79	1.46	153.00
VRO 5	4.03	0.04	1.54	90.37	6.91	0.89	5.15	2.57	0.89	4.06	0.50	0.28	10.60	14.71	1.98	1.30	1.20	2.51	2.10	139.33
VRO 6	8.65	0.03	1.49	89.84	1.98	0.61	3.75	2.57	0.76	3.37	0.37	0.27	9.49	16.24	1.70	0.92	0.65	1.57	1.34	148.33
DOV 22	8.91	0.04	1.60	90.29	2.73	0.87	3.97	2.53	0.83	3.50	0.40	0.24	8.72	22.49	3.48	1.03	0.90	1.92	1.70	149.00
Pusa Sawani (c)	6.73	0.04	1.61	90.67	1.99	1.41	4.45	2.	0.85	4.22	0.37	0.20	7.94	17.74	1.94	1.08	0.95	2.02	1.78	125.00
CD (P=0.05)		0.55	0.03	.42	1.8	0.49	0.49	1.28	.35	.32	0.43	0.18	0.05	1.11	1.36	0.19	0.04	s0.19	0.18	0.01

Table 2 Group constellation of the 30 okra genotypes based on Mahalanobis D2 statistics of 19 quality traits

Cluster	No of genotype number	Name of the genotypes
I	3	DOV 62 ,P 8 , DOV 12
II	2	Arka Abhay, Pusa Sawani
III	6	DOV 11, IC 09491, Pusa A 4, DOV 24, VRO 6, DOV 22
IV	3	DOV 4, Hissar Unnat, USDO 2546
V	6	DOV 2, DOV 64, DOV 66, DOV 15, DOV 2, USDO 2730
VI	3	Arka Anamika, DOV 23, Varsha Uphar
VII	7	DOV 29, P 7, Parbhani Kranti, Punjab Padmini, DOV 27, VRO 21, VRO 5

Table 3 Estimates of average intra (diagonal) and inter-cluster distance for different clusters for 30 okra genotypes of 19 quality traits

	I	II	III	IV	V	VI	VII
I	3.07						
II	5.14	3.24					
III	4.15	5.27	3.07				
IV	4.65	4.56	5.09	3.06			
V	5.66	5.66	3.39	5.17	2.97		
VI	3.90	5.34	4.22	5.85	5.62	3.02	
VII	4.28	6.15	3.52	6.44	5.18	4.35	3.08

Cluster means of quality traits (Table 4) showed that cluster I had maximum mean value for phenol (20.53 mg/g) and flavonol (3.46 mg/g), while cluster II had maximum mean value for Ca (5.70 ppm) and cluster III for iron (1.35 ppm). Cluster IV comprises maximum cluster mean for sugar % (5.36), ascorbic acid (11.42µg/g), ash (1.57%), protein content (2.54%) and Mn (0.29ppm), while cluster VI has maximum cluster mean for mucilage content (5.14%), Mg content (2.70ppm) and Cu content (0.51ppm). Cluster V showed lowest cluster mean for mucilage (3.66 %), while highest cluster mean for mucilage content was recorded in cluster VI (5.14%). Most of the clusters recorded low cluster mean for dietary fibre content. The highest cluster mean for fruit texture (8.39), chlorophyll a (1.13), chlorophyll b (0.92), total chlorophyll (2.05) and carotenoid content (1.80) was found in cluster VII. The highest cluster mean 142.72 for yield (q/ha) was found in cluster III. In general, no two clusters taken together had the similar pattern for all the traits indicating wide diversity in the experimental material for majority of the traits. Maximum intra-cluster value of cluster shows that genotypes of that cluster are very diverse. Maximum inter-cluster value suggested that genotypes of that cluster can be used for hybridization. Therefore, for getting better heterosis, the genotypes from higher degree of divergence with high mean performance may be the best combination of parents for improvement of various economic characters. Thus, cluster VII consisted of better yield and quality traits may be utilized for hybridization.

Clustering pattern of 30 genotypes assessed by Tocher's method exhibiting dendogram showing diversity has been

Table 4 Cluster mean of quality traits of 30 genotypes of okra

Cluster traits	I		II		III		IV		V		VI		VII	
	Mean	SE±	Mean	SE±	Mean	SE±	Mean	SE±	Mean	SE±	Mean	SE±	Mean	SE±
Texture	6.62	1.31	5.63	1.89	7.42	1.71	7.37	0.78	7.45	0.96	6.16	1.91	8.39	0.91
Dietary fiber (g/g)	0.06	0.02	0.08	0.01	0.05	0.02	0.07	0.02	0.04	0.01	0.05	0.01	0.05	0.02
Protein (%)	2.14	0.31	2.00	0.42	1.60	0.13	2.54	0.19	1.61	0.21	1.54	0.05	1.58	0.20
Moisture (%)	87.58	1.50	87.50	2.45	90.67	1.78	85.17	2.59	91.29	1.64	89.78	0.51	90.26	0.68
Sugar (%)	3.67	0.94	3.80	2.15	3.39	0.70	5.36	1.04	3.02	0.77	5.29	1.41	2.61	0.69
Ash (%)	1.48	0.39	1.37	0.24	0.95	0.19	1.57	0.32	0.84	0.13	1.00	0.22	0.98	0.28
Mucilage (%)	5.03	0.50	4.33	0.32	4.01	0.77	4.29	0.44	3.66	0.35	5.14	0.87	3.99	0.36
Mg (ppm)	2.37	0.08	2.03	0.39	1.95	0.30	2.30	0.16	2.32	0.12	2.70	0.15	2.41	0.37
Fe (ppm)	1.08	0.16	1.01	0.23	1.35	0.24	1.10	0.13	1.13	0.36	1.28	0.36	0.77	0.13
Ca (ppm)	4.18	0.63	5.70	0.96	3.58	0.54	4.27	0.75	4.10	0.59	4.00	0.40	3.58	0.48
CU (ppm)	0.53	0.11	0.37	0.09	0.44	0.06	0.44	0.10	0.44	0.03	0.51	0.03	0.40	0.05
Mn (ppm)	0.26	0.03	0.23	0.03	0.29	0.02	0.29	0.03	0.29	0.02	0.23	0.05	0.26	0.03
Ascorbic acid (µg/g)	8.25	0.49	9.46	0.24	9.64	2.18	11.42	2.63	10.80	2.27	9.46	1.45	9.65	1.30
Phenol (mg/g)	20.53	4.12	9.47	3.19	15.41	4.45	14.36	2.43	12.73	4.99	15.36	0.66	20.05	3.26
Flavanol (mg/g)	3.46	0.36	1.15	0.73	2.39	0.49	1.57	0.31	1.92	1.00	1.71	0.26	2.90	0.99
Chlorophyll a (mg/g)	0.87	0.17	0.80	0.26	0.85	0.08	0.63	0.36	0.20	0.02	1.04	0.230	1.13	0.38
Chlorophyll b (mg/g)	0.72	0.21	0.49	0.15	0.62	0.14	0.25	0.06	0.46	0.28	0.87	0.31	0.92	0.23
Total chlorophyll (mg/g)	1.59	0.37	1.29	0.41	1.46	0.21	0.88	0.42	0.66	0.30	1.91	0.53	2.05	0.59
Carotenoid (mg/g)	1.35	0.37	1.06	0.44	1.22	0.17	0.62	0.45	0.11	0.04	1.60	0.44	1.80	0.58
Yield /plant	121.08	32.14	77.11	12.95	142.72	29.26	127.33	41.03	137.11	32.09	126.78	31.13	137.29	15.93

Table 5 Principal component analysis for quality traits in 30 okra genotypes

Parameter	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14	PC15	PC16	PC17	PC18	PC19	PC20
Eigen value (root)	4.54	4.42	1.94	1.69	1.57	1.20	1.12	0.92	0.58	0.52	0.46	0.35	0.25	0.16	0.14	0.07	0.06	0.04	0.00	0.00
Cumulative eigen value	4.54	8.96	10.90	12.59	14.15	15.35	16.47	17.39	17.97	18.48	18.94	19.29	19.54	19.70	19.84	19.90	19.96	20.00	20.00	20.00
Explained variation (%)	22.68	22.12	9.68	8.45	7.84	5.99	5.57	4.60	2.90	2.59	2.30	1.74	1.23	0.79	0.70	0.32	0.31	0.17	0.01	0.00
Cumulative explained variation (%)	22.68	44.80	54.48	62.93	70.77	76.76	82.33	86.93	89.83	92.42	94.72	96.46	97.69	98.48	99.18	99.50	99.81	99.98	99.99	99.99
Eigen vectors																				
Texture	-0.07	0.43	-0.17	-0.13	0.10	-0.14	-0.04	-0.22	0.07	0.23	-0.48	0.16	-0.25	-0.33	0.11	0.26	0.14	0.22	0.20	0.14
Dietary fiber (g/g)	-0.04	-0.29	-0.55	0.13	0.21	-0.54	0.09	0.16	-0.20	-0.20	0.11	0.13	-0.10	0.01	0.31	0.05	0.02	0.04	-0.05	0.09
Protein (%)	0.03	0.41	-0.40	0.07	0.03	0.09	0.05	-0.19	-0.35	0.12	-0.16	0.13	0.41	0.42	-0.08	-0.13	-0.03	-0.10	-0.14	-0.19
Moisture (%)	-0.36	-0.15	0.43	0.19	-0.23	-0.42	0.11	-0.07	-0.42	0.17	-0.32	-0.21	0.07	0.02	0.03	0.03	-0.07	-0.01	0.02	-0.16
Sugar (%)	0.20	-0.15	-0.12	0.27	-0.21	0.30	0.16	0.07	-0.10	0.07	0.06	-0.23	0.13	0.12	0.23	0.37	0.30	0.37	0.38	-0.15
Ash (%)	0.15	0.15	0.30	0.10	-0.27	-0.08	0.37	-0.03	0.05	-0.25	0.01	0.51	0.16	0.19	0.17	0.10	-0.10	0.02	0.07	0.46
Mucilage (%)	-0.08	-0.07	0.17	0.04	0.17	0.09	-0.02	-0.71	-0.16	-0.21	0.29	0.23	-0.27	0.05	0.17	-0.01	0.12	0.05	0.04	-0.31
Mg (ppm)	0.15	0.32	0.16	-0.18	-0.02	0.04	0.10	0.39	-0.56	0.07	0.35	0.17	-0.14	-0.33	-0.01	-0.04	0.17	0.05	-0.07	-0.12
Fe(ppm)	-0.35	0.51	0.11	0.15	0.16	-0.05	0.10	0.19	0.30	-0.30	0.12	-0.28	0.10	0.01	0.41	-0.03	0.03	-0.01	-0.05	-0.21
Ca(ppm)	0.50	0.08	0.11	-0.11	0.03	-0.48	0.25	-0.02	0.29	-0.08	-0.05	-0.01	0.03	0.07	-0.30	0.03	0.15	0.09	-0.01	-0.46
CU (ppm)	-0.02	-0.01	0.04	-0.29	-0.01	-0.24	-0.15	-0.13	0.15	0.52	0.44	0.06	0.39	-0.04	0.27	0.19	-0.22	0.02	0.08	-0.03
Mn (ppm)	0.51	0.05	0.15	-0.13	-0.06	-0.04	-0.52	0.00	-0.19	-0.25	-0.25	-0.17	0.01	0.06	0.44	-0.01	-0.17	-0.09	-0.02	0.00
Ascorbic acid (µg/g)	0.24	0.02	-0.17	0.30	-0.33	0.11	0.32	-0.11	0.13	0.30	-0.02	-0.03	-0.28	-0.26	0.29	-0.18	-0.29	-0.25	-0.22	-0.17
Phenol (mg/g)	-0.02	-0.10	0.17	-0.08	0.08	0.00	-0.04	0.21	0.14	0.40	-0.12	0.19	-0.25	0.46	0.31	-0.28	0.46	0.03	-0.16	0.00
Flavanol (mg/g)	-0.18	-0.21	-0.04	-0.51	0.04	0.25	0.27	0.22	-0.01	-0.13	-0.28	0.24	-0.03	0.08	0.16	0.16	-0.32	-0.05	0.12	-0.40
Chlorophyll a(mg/g)	0.12	-0.08	0.22	0.53	0.55	0.10	-0.14	0.20	0.03	0.16	-0.13	0.34	0.14	-0.13	-0.03	0.12	-0.20	-0.02	0.04	-0.17
Chlorophyll b (mg/g)	0.20	-0.10	0.12	-0.19	0.52	0.10	0.49	-0.18	-0.14	0.08	-0.09	-0.36	0.17	-0.11	0.14	-0.15	0.06	-0.07	-0.01	0.29
Total chlorophyll (mg/g)	-0.06	-0.22	-0.04	-0.04	-0.18	0.06	-0.06	-0.07	0.10	-0.15	-0.18	0.23	0.51	-0.48	0.15	-0.25	0.40	0.03	-0.18	-0.12

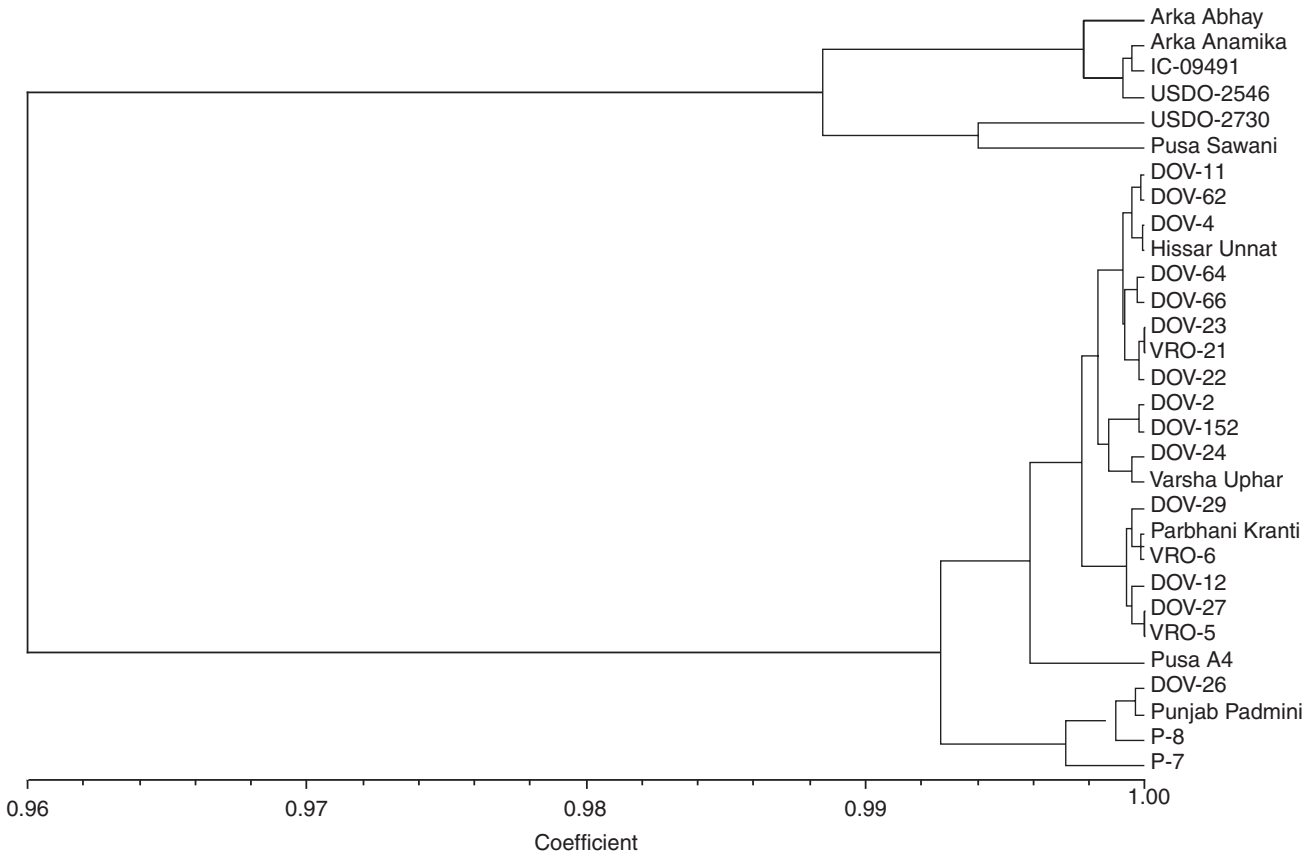

Fig 1 Dendrogram showing clustering pattern among 30 genotypes of okra for 19 quality traits

shown in Fig 1. The PCA of the traits are shown in Table 5. The first 7 PC's having Eigen value greater than one accounted for 82.33 % of total variation based on 19 quality traits. The first 8 principal components explained 86.93% total variation based on quality traits with proportionate contribution of 22.68%, 22.12%, 9.68%, 8.45%, 7.84%, 5.99%, 5.57% and 4.60%, respectively. PC1 showed positive factor loading for sugar content (0.20), ascorbic acid (0.24), ash % (0.15), protein content (0.03), Mg (0.15), Mn(0.51) and Ca(0.50). PC2 showed highest positive factor loading for Fe (0.51), proteincontent (0.41) and Mg (0.32).

Based on overall study, genotypes namely DOV 2, DOV 11, DOV 24, DOV 66, and DOV 12 were found resistance to bhendi YVMV disease, apart from high yielding and good in quality traits. Many genotypes were found susceptible to bhendi YVMV disease, which resulted in their poor fruit yield, though they had high content of quality attributes/ minerals.

The selection of parents for hybridization depends on genetic diversity of parents. Appropriate information on the nature and degree of genetic divergence would help the plant breeder in selecting the suitable parents for hybridization. In general, the level of heterosis increases with increase in parental diversity up to some extend and decreases with further increase in parental diversity owing to crossability barriers. Thus maximum heterosis occurs at an optimal or intermediate level of parental diversity. Further, the occurrence of heterosis cannot be predicted on the basis of genotypic divergence alone (Matzinzer and Werusman 1958). Apart from the higher degree of divergence, the mean performance of genotypes and the characters with maximum contribution, and the best combination of parents for improvement in various economic traits can be recommended on the basis of per se performance of the genotypes and inter-cluster divergence.

REFERENCES

Agbo A E, Gnakri D, Beugre G M, Fondio L, Kouame C. 2008. Maturity degree of four okra fruit varieties and their nutrients composition. *Electronic Journal of Food Plant Chemistry* **5**: 1–4.

Ahiakpa J K, Amoatey H M, Amenorpe G, Apatey J, Ayeh E A, Quartey E K and Agbemavor W S K. 2014. Mucilage contents of 21 accessions of okra (*Abelmoschus spp* L.). *Scientia Agriculturae* **2**(2): 96–101.

Bouvier J M, Bonneville R and Goullieux A. 1997. Instrumental methods for the measurement of extrudate crispness. *Agro-Food-Industry Hi-Techology* **8:** 16–9.

Jackson M L. 1980. *Soil Chemical Analysis,* p 452. Prentice Hall of India Pvt Ltd, New Delhi.

Kumar R, Patil M B, Patil S R and Paschapur M S.2009. Evaluation of *Abelmoschus esculentus* mucilage as suspending agent in paracetamol suspension. *International Journal of PharmTech Research* **1**: 658–65.

Kumar Vijay, Kumar Amit and Gayen Rajshree. 2011. Estimation of genetic parameters in okra for quantitative traits. *Indian Journal of Horticulture* **68**(3): 336.

Mahalanobis P C. 1936. On the generalized distance in statistics. *Proceedings of National Institute of Sciences*, India **12**: 49–55.

Matzinger D R and Werusman F A. 1958. Four cycles of mass selection in a synthetic variety of an autogamous species, *Nicotiana tobaccum* L. *Crop Science* **8**: 239–43.

MOA. 2014. National Horticulture Database 2014, Ministry of Agriculture, Government of India, p 286.

Nwachukwu Emmanuel Chika, Nulit R and Rusea G O. 2014. Nutritional and biochemical properties of Malaysian okra variety. *Advancement in Medicinal Plant Research* **2**(1): 16–9.

Paroda R S and Arora R K. 1991. Plant genetic resources: conservation and management. Concepts and approaches. International Board for Plant Genetic Resources, Regional Office for South and Southeast Asia, New Delhi, p 247–72.

Ranganna S. 2012. Handbook of Analysis and Quality Control for Fruit and Vegetable Products, p 1 112. Tata McGraw Hill Education Pvt Ltd, New Delhi.

Rao C R. 1952. Advanced Statistical Methods in Biometrical Research, pp 357–63. John Wiley and Sons, Inc., New York.

Reddy M T, Haribabu K, Ganesh M, Chandrasekhar Kand Begum H. 2012. Genetic divergence analysis of indigenous and exotic collections of okra (*Abelmoschus esculentus* (L.) Moench). *Journal of Agricultural Technology* **8**(2): 611–23.