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Diversity Analysis in Okra [*Abelmoschus esculentus* (L.) Moench] Genotypes under Saline Situation

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ABSTRACT: Salinity is one of the major abiotic stresses that limits okra production as its deleterious effect persist throughout the plant life cycle. Okra is an important, high-value vegetable and it contains high nutritional value but yield of okra is low due to soil salinity. Extensive evaluation is essential to develop salt tolerant lines which can withstand the salinity stress. This study was conducted to assess the varietal performance and correlation and morphological diversity of pod yield and other related characters among twenty five okra genotypes under salinity stress. GCV and PCV values were high for fresh fruit yield per plant followed by number of fruits per plant and number of seeds per fruit. High heritability coupled with high genetic advance as percentage of mean was observed in fresh fruit yield per plant, number of fruits per plant, germination percentage and number of seeds per fruit. Germination percentage, plant height, number of leaves per plant, leaf length, fruit length, fruit diameter, fruit weight, number of fruits per plant, number of seeds per fruit and thousand seed weight exhibited significant positive correlation co-efficient with fresh fruit yield per plant. Considerable diversity within and between clusters were noted and Cluster III followed by Cluster V was deemed best for selecting diverse accessions. Cluster analysis and it's inter and intra distances will help in narrowing down the selection of the genotypes suitable for breeding strategies with an eye on salinity tolerance The genotypes under these clusters hold great promise as parents in future hybridization program to obtain accessions tolerant to salinity.

Keywords: Correlation, genetic advance, heritability, okra, path analysis, salinity.

INTRODUCTION

Plants have to experience a series of environmental stresses in terms of biotic and abiotic during the entire life span. Abiotic stresses are the most deleterious one which causes nearly 50% of yield reduction and it seems to be a potential threat to the global food security in the coming decades. More than 30% of the irrigated land and 6% of the total world's land (Chaves *et al*., 2009; Parihar *et al*., 2015) have been affected by salinity. Salinity tolerance in plants is mostly influenced by the environmental condition and it also varies among different plant species. The factors related to plants like soil, water and climate interact with each other and affect the salinity tolerance in plants and that is why the plant's reaction to a particular salt concentration cannot be predicted appropriately.

Exposure of plants to saline situation has adverse effects during various developmental stages, however the sensitivity of one stage varies from another growth stage. Salinity tolerance during seedling emergence stage depends on the survivability rate of the plants whereas this stage is resolute on the basis of growth or yield reduction (Gregorio *et al.,* 1997). Seedling stage is considered to be more critical to salt stress as compared to other developmental stages. Plants have been classified according to their adaptation ability to salinity stress in two groups such as glycophytes and halophytes. Most of the plants are glycophytes and sensitive to salt stress among which NaCl-salinity is responsible for modifications of physiological,

biochemical processes, morphological characteristics and it also causes anatomical changes which leads to restricted root growth (Lopez and Satti 1996) and depletion of shoot growth (Misra *et al*., 1995). Some agronomic practices such as selection of salt tolerant cultivars, irrigation practices, sowing date and nutrient management are some of the beneficial tools that are adapted on a short-term basis and for long-term effect alteration of plant genome.

Okra is an important annual, herbaceous vegetable crop in India, West Africa, South-East Asia, U.S.A., Brazil and Turkey. Okra (*Abelmoschus esculentus* (L.) Moench), belonging to the family Malvaceae, is extensively grown in the tropical and subtropical parts of the world. It is one of the most important nutritious vegetable crops grown around the year in India (Sanjay *et al*., 2021). Its origin is believed to be near Ethiopia and being considered as a high-value vegetable, it serves as a great source of vitamins, minerals, carbohydrates and fats. Although, it contains high nutritional value and consumer demand per hectare, yield of okra is low due to several reasons, soil salinity being one of them. Use of underground saline water for irrigation is one of the causes of salt deposition in the crop apart from these industrial effluents in the canal used for irrigation also serves as a source of salts in irrigation water. Application of this saline water to the crop decreases the rate of transpiration which leads to the disruption of evapo-transpiration rate and causes yield reduction (Dudley *et al.*, 2008). Being moderately salt tolerant crop okra could tolerate the salinity level up to $2dsm^{-1}$ or $20mMl^{-1}$ (Minhas and Gupta 1993; Abid *et al.,* 2002). As okra plays an important role in economy of nations among annual crops, further consideration should be given to choosing of varieties of higher yield for edible and seed pods. Previous researchers found that the salinity tolerance level in plant depends highly on its developmental stage (Chinnusamy *et al.,* 2005) that means a genotype which can tolerate at one life stage may not be able to tolerate at earlier or later stages. Thus, to identify salt tolerant genotypes more credibly evaluation of plant genotypes needs to be done at every stage of plant ontogeny starting from the germination till its reproductive phase. Extensive evaluation is essential to develop near to completely salt tolerant lines which can withstand the salinity stress at each developmental stage. This study was conducted to assess the varietal performance and correlation and morphological diversity of pod yield and other related characters of okra cultivars under salinity stress.

MATERIALS AND METHODS

The present experiment was carried out at Agricultural Experimental Farm, University of Calcutta, situated at Baruipur, South 24 Parganas, West Bengal, India during summer-rainy season of 2018 and 2019. Twenty-five accessions (Table 1) of okra were evaluated in Randomized Block Design having three replicates. The pre-soaked seeds of twenty-five genotypes were sown at field with a spacing of 40 × 40 cm between row to row and plant to plant respectively ensuring 14 plants in each plot. After the seed sowing, insecticide carbaryl was broadcasted into the experimental field for avoiding the jassids and red spider mites. Requisite amount of NaCl salt solution was added to raise the desired salinity level as per our plan of work. The salt solution prepared in Hoagland base (Table 2a and b) and applied to the field soil with a 50 mM basal dose and then gradually scaled upto 200 mM. Five plants were selected randomly from each plot to evaluate the quantitative characters. Data were recorded on days to first germination, germination percentage, plant height (cm), number of branches per plant, internodal length (cm), node number to which first flower appeared, days to 50% flowering, number of leaves per plant, leaf length, days to attain edible fruit maturity, fruit length (cm), fruit diameter (cm), number of fruits per plant, fruit weight (g), number of seeds per fruit, thousand seed weight(g) and fresh yield per plant (g). The statistical analysis for various parameters was executed in the Department of Horticulture, Institute of Agricultural Science, University of Calcutta using the statistical package SPAR II (ICAR-IASRI) utilizing the pooled data over the years.

RESULTS AND DISCUSSION

A. GCV and PCV study

In the present study, twenty–five genotypes of okra were evaluated (Burton, 1952). The analysis of variance revealed significant differences among all the characters under study (Table 3). This suggests the presence of significant variability among the genotypes selected for the study. Substantial variability as evidenced from range, PCV and GCV was noted for morphological and yield traits (Table 3). GCV and PCV were calculated by the formula given by Burton (1952). Several workers like Ibrahim *et al.* (2013), have reported presence of good amount of variability in this crop. The magnitude of PCV was slightly higher than the GCV for all the characters under study which indicates that the apparent variation is not only due to the genotype but also due to environmental influence, the findings being similar to Kumari *et al*. (2022); Reddy *et al*. (2012); Adekoya *et al*. (2014) who reported that most of the traits exhibited higher phenotypic variance than their respective genotypic variances. Among yield related traits, highest GCV and PCV were observed for fresh fruit yield per plant (52.39 and 54.94). Higher the coefficient of genetic variation, more are the chances of improvement in that character (Nanohar *et al.,* 1986). GCV and PCV were considered to be low (<10%), moderate (10-20%) and high (>20%) according to Sivasubramanian and Menon (1973). GCV and PCV were high (>20%) for fresh fruit yield per plant followed by number of fruits per plant and number of seeds per fruit. Similar observations had been reported by Mehta *et al.* (2006); Magar and Madrap (2009); Akotkar *et al.* (2010). Moderate GCV and PCV (10-20%) were observed in thousand seed weight followed by plant height and fruit length. The results are synonymous to those of Reddy *et al.* (2012); Das *et al.* (2012). Low GCV and PCV (<10%) were

found in traits like days to fifty percent flowering, days to attain edible fruit maturity, fruit diameter, indicating lower variability of these traits. The result collaborates with the previous findings of Jaiprakashnarayan *et al.* (2006). In this study GCV and PCV (Fig. 1) was high for most of the traits except leaf length (20.12%). The proportion of GCV in PCV ranged from 75.71 % for fruit diameter to 97.85% for germination percentage. In this study, most of the traits had high GCV and PCV values thus these traits are reliable for selection.

B. Heritability and Genetic Advance

Heritability according to Johnson *et al*. (1955), was categorized as low (0-30%), medium (31-60%) and high (61% and above). Genetic Advance as percentage of mean was categorized according to Johnson *et al*. (1955) which was high ≻20%, moderate-10 to 20% and low-≺10%. In this study, most of the yield and yield related traits were found to have moderate to high heritability (Table 3) which ranged from 34.24 (days to 50% flowering) to 95.78 (germination percentage). Heritability coupled with genetic advance is more important than heritability alone in anticipating resultant effect to select the best individuals. High heritability coupled with high genetic advance as percentage of mean (Fig. 2) (heritability-61% and above; GA- more than 20%) was observed in fresh fruit yield per plant, number of fruits per plant, germination percentage and number of seeds per fruit. The characters which possess high heritability coupled with high genetic advance reveals that these traits are controlled by additive gene action (Panse, 1957) and consequently a high genetic advance may be expected from selection of these traits. Similar findings were reported by Jayapandi and Balakrishnan (1992); Pal *et al.* (2010); Guddadamath *et al.* (2011); Choudhary *et al*. (2022). Other characters like fruit girth, days to attain edible fruit maturity and days to 50% flowering exhibited low to moderate genetic advance as per cent of mean. The high heritability and low to moderate genetic advance values were observed for characters like days to first germination, number of branches per plant and days to attain edible fruit maturity, indicating that expression of these characters was regulated by non-additive gene action and can be utilized for heterosis breeding (Kandasamy, 2015).

C. Correlation studies

Association analysis of different traits with fruit yield of okra genotypes and their inter-relationships were evaluated through the study of both phenotypic and genotypic correlation co-efficient. In the present study, 17 characters were recorded and their genotypic and phenotypic correlation co-efficient were analysed. In general, phenotypic and genotypic correlation co-efficient agreed very closely but the genotypic correlations were slightly higher than phenotypic correlations in most of the cases. This may occur as the genes governing two traits were similar and environmental influence was less in the expression of the traits (Das *et al.,* 2012). Out of seventeen characters (Table 4a and b), ten characters namely germination percentage, plant height, number of leaves per plant, leaf length, fruit length, fruit diameter, fruit weight, number of fruits per plant, number of seeds per fruit and thousand seed weight exhibited significant positive correlation co-efficient with fresh fruit yield per plant. Besides, character like number of branches per plant showed positive but non-significant correlation with fresh fruit yield per plant. However, days to first germination, days to 50% flowering and days to attain edible fruit maturity exhibited significant negative correlation with fruit yield per plant (Prasath *et al.,* 2001). This indicates that early germination, 50% flowering and faster edible fruit maturity attainment helped in improving fruit yield of okra. These findings were in conformation to the work of Das *et al*. (2012). The significant positive association of fruit yield with the parameters viz. germination percentage, plant height, numbers of leaves per plant, leaf length, fruit length, fruit weight and number of fruits per plant revealed that preference of genotypes with more of these traits will lead to better yield realization. The significant negative association of days to first germination, days to 50% flowering and days to attain edible fruit maturity revealed that the genotypes having lesser value of these traits gave higher fruit yield. Similar results have been reported by Modi and Sharma (2021); Gogineni *et al*. (2015); Kumar and Reddy (2016); Kerure *et al*. (2017) for number of fruits per plant, Gogineni *et al*. (2015); Kumar and Reddy (2016) for plant height, Gogineni *et al*. (2015); Aminu *et al*. (2016); Kerure *et al*. (2017) for fruit weight and Mehta *et al*. (2006) for fruit length.

D. Path Analysis

Days to attain edible fruit maturity had the highest direct contribution towards yield followed by number of primary branches per plant and fruit diameter (Table 5). Days to 50% flowering and days to first germination showed high indirect effect to yield via days to attain edible fruit maturity. Node number to which first flower appeared, fruit weight, number of seeds per fruit showed high indirect effect through number of primary branches per plant. Our findings could be related partially to Ahamed *et al.* (2015); Gangashetty *et al.* 2010; Kerure *et al.* (2017); Reddy *et al.* (1985). The residual effect of path analysis was low suggesting inclusion of maximum fruit yield influencing characters in the analysis. It can be depicted from the above results that under 200 mM NaCl, the genotypes which completed their life cycle earlier may have higher yield potential. It may be concluded from the above results that selection based on characters having higher positive and direct effects on total fruit yield per plant viz. internodal length, leaf length, days to attain edible fruit maturity, number of fruits per plant and number of seeds per fruit are more accountable for improvement of the crop to bring in more yield potential under saline situation.

E. Genetic Divergence

Based on Mahalanobis D^2 statistics (Mahalanobis, 1936) (Table 6), twenty-five accessions were grouped into 9 clusters among which maximum number of accessions (10) were assembled under cluster II. Cluster

IV consisted of 4 accessions. Cluster I, cluster III, cluster V and cluster VI, each had 2 accessions. Cluster VII, cluster VIII and cluster IX had solitary accession, in each.

F. Inter relationship of clusters

Intra cluster distance. Cluster IV showed the maximum intra cluster distance (22.450) followed by cluster II (21.672) and cluster VI (20.618) (Table 7). Intra cluster distances suggested that cluster IV was having the highest distance from rest of the clusters and genotypes present in this cluster are more diverse (Madhuri *et al.,* 2019).

Inter cluster distance. Inter cluster divergence depicts the distance between the accessions falling under different clusters. The maximum inter cluster distance was found in between cluster IV and IX (38.198) followed by cluster I and IX (35.197). Presence of single genotype in a cluster stipulated uniqueness of that accession from other accessions. Genotypes belonging to the cluster with maximum inter cluster distance are genetically more divergent and hybridization between genotypes of divergent cluster is likely to produce wide variability (Table 7).

Cluster mean analysis. The cluster wise mean value (Table 8; Fig. 3) showed that the difference in cluster means were substantially high for germination percentage, plant height, days to fifty percent flowering, days to attain edible fruit maturity, thousand seed weight and fruit yield per plant. Cluster III had the highest mean value for yield per plant. Cluster III also had the highest mean values for fruit length, number of fruits per plant and fruit weight. Least mean values for days to first germination, days to 50% flowering and days to attain edible fruit maturity were observed in cluster V, which depicted earliness.

Table 1: Okra genotypes along with their place of collection.

Sr. No.	Name of the genotypes	Brand &Place of collection
1.	Shakti (F_1)	Bayer, Jharkhali, South 24 Parganas
2.	Samrat (F_1)	Bayer, Jharkhali, South 24 Parganas
3.	Sartaj (F_1)	Bayer, Jharkhali, South 24 Parganas
4.	Rohini 1001 (F_1)	Nuzivedu, Raidighi, South 24Parganas
5.	Gunjan (F_1)	Kalash, Kakdweep, South 24 Parganas
6.	Raj-333 (F_1)	Pear, Kakdweep, South 24 Parganas
7.	Divya-192 (F_1)	Calyx, Kakdweep, South 24 Parganas
8.	Arka Ankita (F_1)	Shriram, Amtala, South 24 Parganas
9.	Jhilmil (F_1)	Shriram, Amtala, South 24 Parganas
10.	Hybrid-302 (F_1)	Bio-seed, Bhangar, South 24 Parganas
11.	Special Hariyali (F_1)	JK seed, Bhangar, South 24 Parganas
12.	Durga (F_1)	JK seed, Kakdweep, South 24 Parganas
13.	Raj Vendi (F_1)	PAN, Bhangar, South 24 Parganas
14.	Mayna (F_1)	Mahyco, Amtala, South 24 Parganas
15.	Shivani (F_1)	Rashi seed, Raidighi, South 24 Parganas
16.	Arka Anamika (OP)	Annapurna, Amtala, South 24 Parganas
17.	Suhani (OP)	Shriram, Amtala, South 24 Parganas
18.	Novo-62 (OP)	Novo, Kakdweep, South 24 Parganas
19.	Vaner (OP)	Golden, Jharkhali, South 24 Parganas
20.	Jhar Pankaj (OP)	Debgiri, Jharkhali, South 24 Parganas
21.	Satdhari (OP)	Bakra, Jharkhali, South 24 Parganas
22.	Japani Jhar (OP)	A.K. Laskar & Co., Jharkhali, South24Parganas
23.	Calyx- 303 (OP)	Calyx, Kakdweep, South 24 Parganas
24.	Adharsa Jhar (OP)	Indo-Hybrid, Amtala, South 24 Parganas
25.	Super Green (OP)	V.N.R. , Bhangar, South 24 Parganas

Table 2a: Composition of Hoagland Solution.

Salt Solution	g/ 100 ml
1. $Ca(No_3)$, $4H_2O$	23.61
2. KNO_3	10.11
3. KH_2PO_4	13.61
4. $MgSO_4$, $7H_2O$	24.65
Trace Elements	**g/ 100 ml**
1. $MnCl_2$	0.28
2. $ZnSO_4$, H_2O	0.18
3. $CuSO_4$	0.022
4. Na_2MoO_4	0.01
Fe – EDTA	**g/ 100 ml**
1. EDTA, 2Na	1.04
2. $FeSO_4$, $7H_2O$	0.78
3. KOH	5.61

Cluster I, cluster II, cluster VI and cluster VII did not show any high mean value. Cluster IV had the highest mean value for number of seeds per fruit. Cluster V had the highest mean values for germination percentage, plant height and leaf length. Cluster VIII had the highest mean value for number of leaves per plant. Cluster IX had the least mean value for node number to which first flower appeared and highest mean values for fruit diameter and thousand seed weight. It can be concluded that cluster III followed by cluster V under 200 mM NaCl was deemed best for selecting diverse accessions. Hence, selection of divergent parents based on these characters can be useful for heterosis breeding in okra as well as serve a broader spectrum for favourable genetic variability in segregating generation for improvement of fruit yield in okra. In general, the pattern of distribution of accessions from a different region to different cluster was random. Partially similar findings were observed by Koundinya *et al.* (2013) in okra.

Table 2b: Working Concentration of Hoagland Solution.

Component	Volume for 1000 ml solution
1.$Ca(NO_3)_2$, $4H_2O$	7 ml
2.KNO_3	5 ml
3.KH_2PO_4	2 ml
4.$MgSO_4$, & H_2O	2 ml
5.Trace Elements	1 ml
6.Fe- EDTA	1 ml

Table 3: Genotypic and Phenotypic Coefficient of Variation, heritability (h^2 %) and Genetic Advance as percent of mean for seventeen characters among twenty-five genotypes of okra [*Abelmoschus esculentus* (L.) Moench] under 200 mM NaCl.

Characters	Mean	Range	GCV(%)	PCV(%)	GCV: PCV	h^2(%)	GA as % of mean
Days to first germination	7.24	6.28-8.52	9.66	11.60	83.27	69.27	16.55
Germination percentage	51.87	28.49-70.76	22.84	23.34	97.85	95.78	46.05
Plant height (cm)	61.51	41.64-76.27	15.73	16.49	95.39	90.93	30.89
Number of branches per plant	3.99	2.97-5.45	11.99	14.90	80.46	64.72	19.87
Intermodal length (cm)	5.13	3.77-6.23	12.35	12.86	96.03	92.17	24.42
Node number to which first flower appeared	5.27	4.17-6.44	13.36	13.87	96.32	92.75	26.50
Days to 50% flowering	48.41	39.70-59.98	6.83	11.67	58.52	34.24	8.23
Number of leaves per plant	28.10	18.19-36.22	13.36	15.99	83.55	69.76	22.98
Leaf length (cm)	13.43	10.42-17.41	13.08	14.09	92.83	86.28	25.03
Days to attain edible fruit maturity	50.20	42.42-57.11	6.53	8.22	79.44	63.08	10.68
Fruit length (cm)	10.03	7.76-12.12	12.11	14.67	82.54	68.14	20.59
Fruit diameter (cm)	4.88	4.10-5.63	7.14	9.43	75.71	57.36	11.14
Number of fruits per plant	11.13	1.64-23.22	49.99	54.52	91.69	84.10	94.45
Fruit weight (g)	11.01	4.23-17.52	28.55	31.64	90.23	81.41	53.06
Number of seeds per fruit	20.70	3.77-41.22	43.10	45.86	93.98	88.31	83.43
Thousand seed weight (g)	42.35	27.02-52.69	15.99	17.64	90.64	82.17	29.85
Fresh fruit yield per plant (g)	140.86	21.79-300.50	52.39	54.94	95.35	90.95	102.93

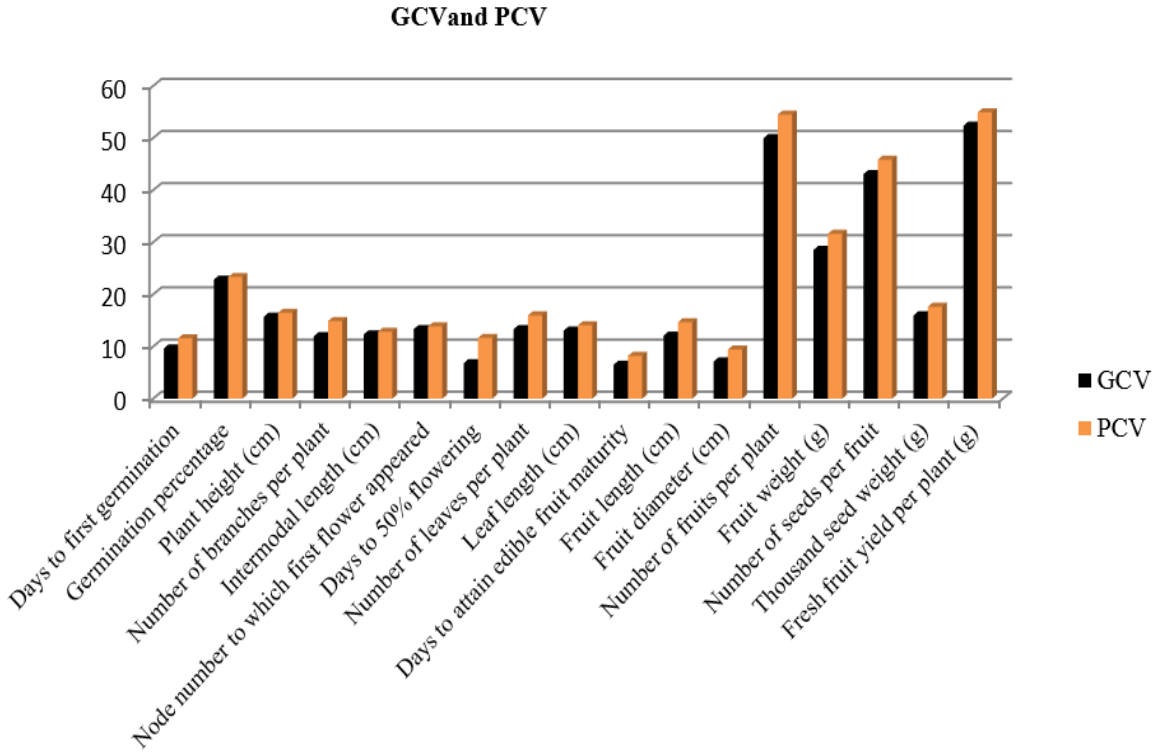

Fig. 1. Graphical representation of genotypic and phenotypic coefficient of variation for the traits under study in *Abelmoschus esculentus* (L.) Moench.

Table 4a: Genotypic Correlation studies among seventeen characters in Okra [*Abelmoschus esculentus* (L.) Moench] under 200 mM NaCl.

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	1.000	-0.805**	-0.481*	-0.151	-0.005	0.121	1.019**	-0.556**	-0.351	0.745* *	-0.709**	-0.300	-0.884**	-0.819**	-0.267	-0.257	-0.871**
2		1.000	0.551**	0.203	0.134	-0.105	-0.963**	-0.323	0.335	-0.836**	0.701**	0.409*	0.871**	0.599**	0.371	0.515**	0.849**
3			1.000	0.125	-0.128	-0.561**	-0.644**	0.492*	0.392	-0.533**	0.493*	0.150	0.645**	0.301	0.043	0.609**	0.542**
4				1.000	0.203	0.546**	0.004	0.338	-0.151	-0.027	0.209	0.079	0.217	0.505*	0.484*	-0.202	0.260
5					1.000	-0.064	0.259	-0.340	-0.010	0.034	0.138	-0.046	-0.042	0.096	0.002	-0.135	-0.030
6						1.000	0.316	0.116	-0.349	0.342	-0.174	-0.050	-0.240	0.058	0.406*	-0.331	-0.138
7							1.000	-0.683**	-0.703**	1.121**	-0.488*	-0.312	-1.104**	-0.796**	-0.308	-0.312	-1.076**
8								1.000	0.294	-0.463*	0.250	0.204	0.471*	0.358	0.265	0.180	0.521**
9									1.000	-0.541**	0.369	0.018	0.605**	0.362	0.155	0.368	0.529**
10										1.000	-0.471*	-0.419*	-1.001**	-0.563**	-0.375	-0.285	-0.928**
11											1.000	0.470*	0.837**	0.790**	0.382	0.352	0.789**
12												1.000	0.527**	0.303	0.296	-0.163	0.594**
13													1.000	0.715**	0.474*	0.520**	1.014**
14														1.000	0.355	0.061	0.729**
15															1.000	-0.035	0.490*
16																1.000	0.425*
17																	1.000

Note:1. Days to first germination**2**. Germination percentage**3.** Plant height (cm) **4.** Number of primary branches per plant**5.** Internodal length (cm) **6**. Node number to which first flower appeared **7**. Days to 50% flowering **8.** Numberof leaves per plant **9.** Leaf length (cm) **10.** Days to attain edible fruit maturity **11.** Fruit length (cm) **12.** Fruit diameter (cm)**13.** Numberof fruits per plant**14**.Fruit weight (g)**15.** Number of seeds per fruit**16.** Thousand seed weight (g) **17**. Fresh yield per plant (g)

Table 4b: Phenotypic Correlation studies among seventeen characters in Okra [*Abelmoschus esculentus* (L.) Moench] under 200 mM NaCl.

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	1.000	-0.742**	-0.501**	-0.362	-0.100	0.156	0.754**	-0.397	-0.370	0.753**	-0.711**	-0.344	-0.768**	-0.793**	-0.356	-0.359	-0.822**
2		1.000	0.562**	0.234	0.150	-0.114	-0.631**	0.251	0.339	-0.740**	0.651**	0.368	0.815**	0.576**	0.388	0.516**	0.838**
3			1.000	0.189	-0.078	-0.551**	-0.440*	0.390	0.382	-0.533**	0.498*	0.193	0.598**	0.322	0.093	0.601**	0.552**
4				1.000	-0.061	0.377	-0.221	0.264	-0.022	-0.241	0.363	0.171	0.255	0.537**	0.531**	0.030	0.312
5					1.000	-0.091	0.006	-0.238	0.026	-0.070	0.190	0.028	-0.001	0.126	0.061	-0.054	0.020
6						1.000	0.250	0.091	-0.348	0.302	-0.171	-0.115	-0.237	0.023	0.325	-0.318	-0.159
7							1.000	-0.406*	-0.473*	0.824**	-0.460*	-0.335	-0.711**	-0.505**	-0.347	-0.401*	-0.757**
8								1.000	0.211	-0.344	0.258	0.076	0.279	0.265	0.233	0.101	0.404*
9									1.000	-0.526**	0.381	0.087	0.538**	0.384	0.205	0.386	0.522**
10										1.000	-0.554**	-0.486*	-0.793**	-0.538**	-0.410*	-0.377	-0.820**
11											1.000	0.442*	0.670**	0.713**	0.436*	0.394	0.729**
12												1.000	0.453*	0.246	0.305	-0.033	0.513**
13													1.000	0.660**	0.476*	0.523**	0.935**
14														1.000	0.392	0.156	0.706**
15															1.000	0.070	0.520**
16																1.000	0.452*
17																	1.000

**= significant at 1% level, *= significant at 5% level

Note: 1. Days to first germination, **2**. Germination percentage, **3**. Plant height (cm), **4.** Number of primary branches per plant, **5.** Internodal length (cm), **6**. Node number to which first flower appeared, **7**. Days to 50% flowering, **8.** Number of leaves per plant, **9**. Leaf length (cm), **10.** Days to attain edible fruit maturity, **11**. Fruit length (cm), **12.** Fruit diameter (cm), **13.** Nusmber of fruits per plant, **14**. Fruit weight (g), **15.** Number of seeds per fruit, **16.** Thousand seed weight (g), **17**. Fresh yield per plant (g).

Table 5: Path values among sixteen characters in Okra [*Abelmoschus esculentus*. (L.) Moench] under 200 mM NaCl (Dependent variable: Total fruit yield per plant).

Traits	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	**-7.665**	0.0625	1.687	-0.678	-0.006	-0.566	0.817	0.299	-0.879	3.998	3.961	-1.026	-1.372	1.688	-0.421	-0.770
2	6.172	**-0.077**	-1.934	0.910	0.153	0.489	0.773	-0.173	0.837	-4.486	-3.915	1.400	1.352	-1.234	0.586	1.542
3	3.687	-0.042	**-3.508**	0.559	-0.146	2.620	-0.517	-0.264	0.980	-2.860	-2.751	0.512	1.000	-0.620	0.068	1.824
4	1.158	-0.015	-0.437	**4.489**	-0.233	-2.550	-0.003	-0.181	-0.377	-0.146	-1.168	0.270	0.366	-1.041	0.765	-0.604
5	0.042	-0.010	0.448	-0.912	**1.147**	0.297	0.207	0.182	-0.024	0.184	-0.772	-0.156	-0.064	-0.198	0.002	-0.403
6	-0.928	0.008	1.967	2.450	-0.072	**-4.673**	0.253	-0.062	-0.874	1.835	0.972	-0.169	-0.373	-0.120	0.641	-0.993
7	-7.807	0.074	2.260	-0.018	0.296	-1.474	**0.803**	0.367	-1.759	6.019	2.725	-1.068	-1.712	1.641	-0.487	-0.993
8	4.262	-0.025	-1.726	1.516	-0.389	-0.540	-0.548	**-0.538**	0.736	-2.483	-1.394	0.700	0.731	-0.738	0.418	0.540
9	2.692	-0.026	-1.373	-0.676	-0.011	1.632	-0.564	-0.158	**2.503**	-2.904	-2.062	-0.063	0.938	-0.746	0.245	1.102
10	-5.709	0.064	1.869	-0.122	0.039	-1.597	0.900	0.248	-1.354	**5.368**	2.628	-1.433	-1.553	1.169	-0.592	-0.854
11	5.436	-0.054	-1.728	0.939	0.158	0.813	-0.391	-0.134	0.924	-2.526	**-5.585**	1.609	1.298	-1.628	0.603	1.055
12	2.297	-0.031	-0.525	0.354	-0.052	0.231	-0.250	-0.110	-0.046	-2.247	-2.625	**3.423**	0.817	-0.623	0.468	-0.486
13	6.778	-0.067	-2.261	0.972	-0.047	1.123	-0.886	-0.253	1.515	-5.374	-4.675	1.804	**1.551**	-1.473	0.748	1.559
14	6.280	-0.046	-1.055	2.269	0.110	-0.272	-0.639	-0.192	0.906	-3.045	-4.413	1.036	1.108	**-2.061**	0.560	0.183
15	2.046	-0.028	-0.152	2.174	0.002	-1.896	-0.247	-0.142	0.388	-2.012	-2.132	1.014	0.734	-0.731	**1.580**	-0.106
16	1.971	-0.039	-2.135	-0.906	-0.154	1.548	-0.250	-0.097	0.921	-1.531	-1.967	-0.556	0.807	-0.126	-0.056	**2.996**

Residual Effect:0.651

Note: 1. Days to first germination, **2**. Germination percentage, **3.** Plant height (cm), **4.** Number of primary branches per plant, **5.** Internodal length (cm), **6**. Node number to which first flower appeared, **7**. Days to 50% flowering, **8.** Number of leaves per plant, **9**. Leaf length (cm), **10.** Days to attain edible fruit maturity, **11**. Fruit length (cm), **12.** Fruit diameter (cm), **13.** Number of fruits per plant, **14**. Fruit weight (g), **15.** Number of seeds per fruit, **16.** Thousand seed weight (g), **17**. Fresh yield per plant (g).

Table 6: Grouping of twenty-five genotypes of Okra [*Abelmoschus esculentus*. (L.) Moench] in clusters grown under 200 mM NaCl.

Cluster I	Vaner, Jhar-Pankaj
Cluster II	Shakti (F_1), Samrat(F_1), Sartaj(F_1), Rohini(F_1), Gunjan (F_1), Raj-333 (F_1), Divya-192 (F_1), Arka Anamika, Arka Ankita (F_1), Jhilmil (F_1)
Cluster III	Shivani Hybrid, Japani Jhar
Cluster IV	Hybrid-302, Special Hariyali, Durga(F_1), Calyx-303
Cluster V	Mayna, Suhani
Cluster VI	Raj-Vendi, Satdhari
Cluster VII	Adharsa-Jhar
Cluster VIII	Super Green
Cluster IX	NOVO-62

Table 7: Inter and intra cluster distances among twenty-five genotypes of okra under 200 mM NaCl.

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Cluster I	8.193	23.987	26.119	22.623	31.240	17.225	29.747	18.002	35.197
Cluster II		21.672	22.841	27.251	24.898	27.453	32.124	23.199	29.817
Cluster III			16.450	25.957	23.114	29.291	23.659	25.928	34.091
Cluster IV				22.450	34.051	27.493	24.948	24.057	38.198
Cluster V					20.299	29.876	32.281	33.205	27.525
Cluster VI						20.618	29.789	26.169	30.918
Cluster VII							0.000	30.275	34.409
Cluster VIII								0.000	35.110
Cluster IX									0.000

Table 8: Cluster mean value for seventeen characters in okra grown under 200 mM NaCl.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
Cluster I	8.208	39.045	56.698	4.090	5.345	5.823	56.275	25.980	12.538	55.865	9.210	4.408	3.700	9.715	13.780	38.272	26.870
Cluster II	7.139	54.384	66.901	4.124	4.732	5.140	46.073	30.260	14.015	48.457	10.085	4.907	13.700	11.417	22.694	44.933	174.189
Cluster III	6.372	64.813	57.565	4.275	5.325	5.983	44.465	29.305	14.372	47.717	11.417	5.307	17.983	15.592	28.873	40.750	243.462
Cluster IV	7.815	49.249	57.713	3.870	5.398	5.368	52.086	25.368	12.151	52.189	9.788	5.026	8.079	7.595	29.040	40.077	102.757
Cluster V	6.097	67.647	71.818	3.693	5.523	4.320	42.500	27.970	16.580	45.147	11.092	4.820	17.648	13.538	16.157	47.200	206.970
Cluster VI	7.725	38.685	57.255	4.203	5.935	4.740	53.388	23.510	12.233	53.890	9.480	4.552	4.423	11.725	10.310	36.658	56.847
Cluster VII	6.810	50.690	41.645	3.310	6.230	6.335	49.690	27.120	11.125	51.920	9.595	4.590	7.110	10.675	17.300	39.050	115.490
Cluster VIII	7.420	39.420	45.715	4.145	3.775	6.440	48.780	30.540	11.215	54.035	7.765	4.365	1.640	9.360	15.145	36.940	26.350
Cluster IX	7.205	45.380	63.825	3.235	4.965	4.280	49.515	27.260	13.320	50.580	11.020	5.560	12.625	9.525	3.770	47.400	158.470

Note: 1. Days to first germination, **2.** Germination percentage, **3.** Plant height (cm), **4.** Number of primary branches per plant, **5.** Internodal length (cm), **6.** Node number to which first flower appeared, **7**. Days to 50% flowering, **8.** Number of leaves per plant, **9**. Leaf length (cm) **10.** Days to attain edible fruit maturity, **11**. Fruit length (cm), **12.** Fruit diameter (cm), **13.** Number of fruits per plant, **14**. Fruit weight (in g), **15.** Number of seeds per fruit, **16.** Thousand seed weight (g), **17**. Fresh yield per plant. (g).

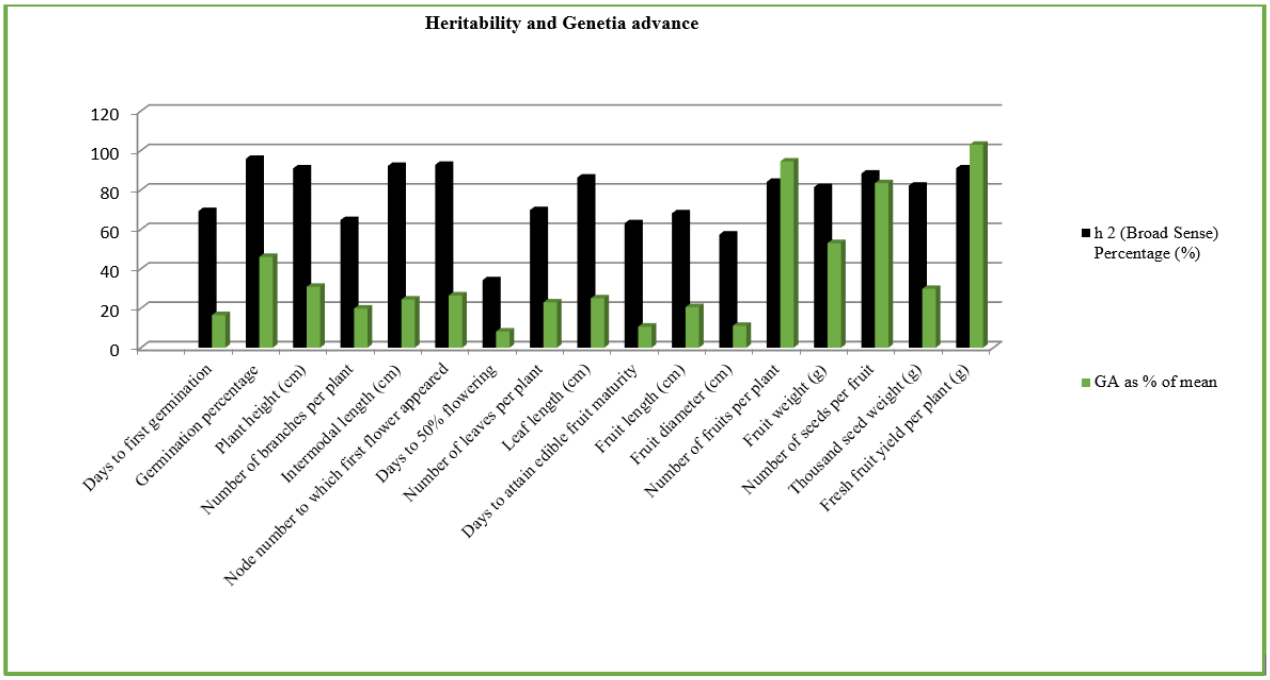

Fig. 2. Graphical representation of heritability (h^2 broad sense) and genetic advance as percent of mean.

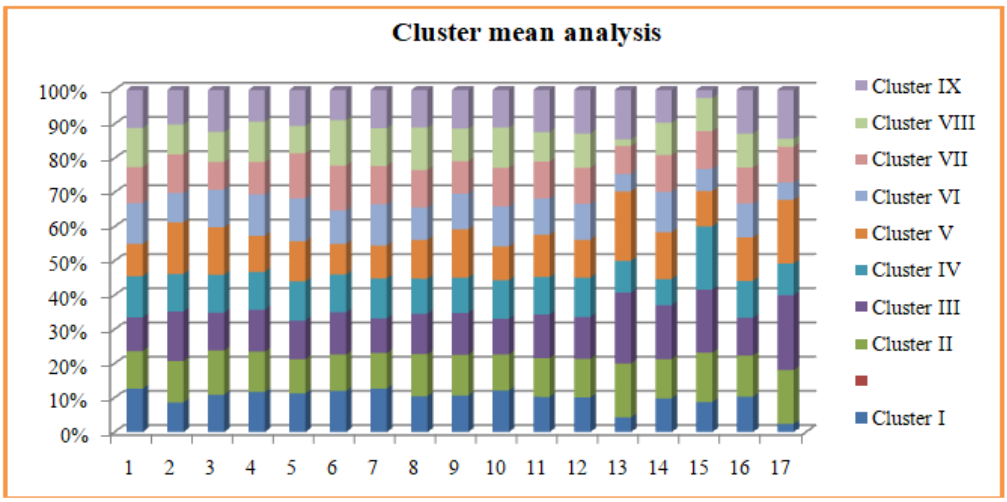

Fig. 3. Graphical representation of cluster means analysis for seventeen characters in *Abelmoschus esculentus* (L.) Moench.

CONCLUSIONS

Good amount of variation for the set of characters under study among the utilized okra germplasm was observed which depicts that gene pool of okra towards salinity tolerance is available. On the basis of heritability coupled with genetic advance ample scope remains for selection of the promising types based on traits having high to moderate heritability as well having good presence of genetic advance. Correlation and path coefficient analysis will help us in simplified screening through weightage on traits which are having positive and significant correlation with yield. Cluster analysis and it's inter and intra distances will help in narrowing down the selection of the genotypes suitable for breeding strategies with an eye on salinity tolerance. In our ensuing experiment, genotypes falling under cluster III (Shivani Hybrid and Japani Jhar) and cluster V (Mayna and Suhani) could be exploited in the near future keeping in mind their sustainability of morphological and yield related traits under saline conditions.

FUTURE SCOPE

This investigation will help to identify promising okra germplasm having desirable tolerance towards salinity that can be utilized as donor parents for future hybridization program. Molecular studies will help in detecting the gene(s) and their corresponding loci which may help in establishing a QTL map. Further, the traits which are linked to salinity stress can be given due weightage while going for future screening of okra.

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Conflict of Interest. None.

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