Original Research Article

Exploring Genetic Distance and Diversity Analysis in Okra (*Abelmoschus esculentus* L. Moench): A Comprehensive Study on the Genetic Variation within Cultivars

Comment [Ma1]: Genetic distance is a component of genetic diversity analysis. Consider the more general term in your title

Abstract

An experiment was conducted at the experimental field of Genetics and Plant Breeding Department of Sher-e-Bangla Agricultural University, Dhaka Bangladesh from~~during~~ March ~~2017~~ to July 2017. The experiment was laid out ~~conducted~~ in a randomized complete block design with three replications. Twenty eight genotypes of okra were used in this study which w*ere*~~as~~ collected from Bangladesh Agricultural Research Institute (BARI), Gazipur and local market. Genetic distance among the~~of~~ 28 okra genotypes was measured using Euclidean distance based on 11 traits.. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization It is shown that Plant height, fruits per plant and fruit weight contributed maximum towards fruit yield improvement. So, divergent genotypes are recommended to use as parents in future hybridization program.

Comment [Ma2]: Can you make into a problem statement/objective. Abstract typically should include problem statement, objectives, methods, results, and conclusion. Kindly include all the component chronologically. PCA is totally missing in this account

Keywords: Euclidean distance, Diversity Analysis, Hybridization, Okra

Introduction

Okra (*Abelmoschus esculentus* (L.) Moench) also? ~~is~~known as lady's finger or~~,~~Dherosh in Bangladesh, is a commercial vegetable crop and belongs to the family Malvaceae. Not only it has industrial value, but also it has both medicinal and nutritional values**[1]**. It has a vital role in human diet and is a good source of vitamin A, B, and C and also rich in protein, minerals and iodine **[2]**. The main origin of okra is Ethiopia and, then it is widely spread~~ed~~ all over tropical, subtropical and warm temperate regions of the World**[3]**. Total area under okra cultivation in Bangladesh is estimated to be 30118.73 acres yielding about 70242.27 tons of green pods**[4]**.

The average yield of okra in Bangladesh is 2332.28 Kg acr-1 which is very low as compared to other okra growing countries. At present time, enormous amount of commercial cultivars including F1 hybrids of okra is available in the market. But all these are not adapted and suited to all the regions of the country. Further, no specific recommendation about the suitability of genotypes for a particular area is available**[5]**.Genetic diversity knowledge within okra germplasms play significant role in breeding program. This helps to develop varieties with desired traits. Most importantly it is a prerequisite to develop high yielding okra varieties like in all other crop improvement. This is important for selecting parents in combination breeding and to obtain transgressive segregants **[6]**. The knowledge of pattern of inheritance of various characters are important consideration while, determining the most approximate breeding procedures applicable to any particular crop.

Comment [Ma3]: Can you please give more details. There are lots of information in literature including different methods and approaches

Comment [Ma4]: Was this addressed in your study. I think not. Are you able to do a brief review on previous genetic diversity studies in okra and justify why the current study is necessary? You may lay emphasis on the need for your study in Bangladesh.

MATERIALS AND METHODS

Experimental Site

The experiment was conducted at the experimental field of Genetics and Plant Breeding Department of Sher-e-Bangla Agricultural University, Dhaka Bangladesh during March 2017 to July 2017.

Plant Materials

Twenty eight genotypes of okra were used in this study which was collected from Bangladesh Agricultural Research Institute (BARI), Gazipur and local market (Table 1).

Comment [Ma5]: Are they all commercial varieties or a few are breeding lines? Please indicate

Experimental Design

The experiment was conducted in randomized complete block design with three replications. In each block, each genotype was planted in one row of 8.4 m length and 1 m width, maintaining a plant to plant spacing of 0.6 m and accommodated 14 plants per plot.

Field Management~~s~~

The recommended dosage of Urea, TSP, and MP was applied in field at the rate of 150, 100, 150 Kg/ha respectively. Irrigation was applied once a week at emergence and every two weeks at flowering and pod production. Chemicals and cultural practices were applied to control insect pest.

Comment [Ma6]: Please state the full meaning at first mention

Comment [Ma7]: Please state this was a supplement to rainfall. Certainly, your plants will not survive this watering regime. Are you able to give details on the amount of rainfall during the growth period?

Observations recorded

Observations were recorded on five plants in each genotype in each replication for all the characters studied. The observations are given below-

Comment [Ma8]: Were these competitive plants? Please give clear details on your methods

Days to first flowering,Days to 50% flowering,Days to maturity,Plant height (cm),Number of primary branches per plant,Fruit character and yield,Fruit length (cm),Fruit diameter (mm),Average fruit weight (g),Number of tender fruits per plant,Number of seeds per pod,Hundred seed weight (g),Fruit yield per plant (g)

Comment [Ma9]: Please mention if the pods were harvested dried, fresh or both

Table 1.Details of Experimental Materials

GENOTYPES	NAME OF GENOTYPES	SOURCE
G1	BARI Dheros1	Bangladesh Agricultural Research Institute
G2	BARI Dheros2	Bangladesh Agricultural Research Institute
G3	BD-1928	Bangladesh Agricultural Research Institute
G4	BD-1929	Bangladesh Agricultural Research Institute
G5	BD-1930	Bangladesh Agricultural Research Institute
G6	BD-1931	Bangladesh Agricultural Research Institute
G7	BD-1932	Bangladesh Agricultural Research Institute
G8	BD-1933	Bangladesh Agricultural Research Institute

G9	BD-1934	Bangladesh Agricultural Research Institute
G10	BD-1935	Bangladesh Agricultural Research Institute
G11	BD-1936	Bangladesh Agricultural Research Institute
G12	BD-1937	Bangladesh Agricultural Research Institute
G13	BD-1938	Bangladesh Agricultural Research Institute
G14	BD-1939	Bangladesh Agricultural Research Institute
G15	BD-1940	Bangladesh Agricultural Research Institute
G16	BD-1941	Bangladesh Agricultural Research Institute
G17	BD-1942	Bangladesh Agricultural Research Institute
G18	OrkaOnamika	Krishibid Seed Limited
G19	Ladies Finger	Krishibid Seed Limited
G20	Kohnur	Krishibid Seed Limited
G21	Mukta	Krishibid Seed Limited
G22	Soft Finger	Krishibid Seed Limited
G23	KS-3	Krishibid Seed Limited
G24	KS-1201	Krishibid Seed Limited
G25	Shruti-16	Local Market
G26	Preeti-72	Local Market
G27	NF-1003	Local Market
G28	SONIYA-86	Local Market

Result and Discussions

Comment [Ma10]: Please give a full account of your methodology. Statistical analysis from which you got your result is conspicuously missing. Please see literatures for guidance

Genetic distance

Genetic distance of 28 okra genotypes was measured using Euclidean distance based on 11 traits and the result is presented (Table 2). The genetic distances for all possible pairs of 28 okra genotypes ranged from 0.19 to 4.09 with mean and standard deviation of 1.47 and 0.66, respectively. The most distant genotypes were G1 and G28 (4.09) followed by G1 and G27 (3.32), G1 and G23 (3.60), G1 and G14 (3.37) and G1 and G17 (3.00). The lowest genetic distance was exhibited between G10 and G24 (0.19) followed by G10 and G22 (0.32), G10 and G20 (0.37), G6 and G20 (0.39) and G10 and G25 (0.39). This suggested that the higher chance of improving the crop production through collection, characterization, evaluation and selection or hybridization of okra genotypes from different regions even from other countries. The extent of diversity present between genotypes determines the extent of improvement gained through selection and hybridization. The more divergent the two genotypes are the more will be the probability of improving through selection and hybridization. This result is supported by Prakash et al, Kamalpreet et al.who reported that presence of genetic diversity for okra collection[6][7].

Comment [Ma11]: Are you able to put this into context? For instance, does the GD reflect the genetic background of the genotypes? Please do attempt to further characterize the genotypes to really show the differences among them. Importantly, show your ANOVA, to statistically show differences among your genotypes for the trait measured.

Comment [Ma12]: Is this across all traits or specific traits. More results are required. Consider grouping the genotypes into clusters

Table 2.Genetic Euclidean distances and mean Euclidean distance of 28 genotypes based on 11 traits

Genotypes	Squared Euclidean Distance														
	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10	G11	G12	G13	G14	G15
G2	1.08														
G3	2.83	0.62													
G4	0.88	0.83	1.76												
G5	1.98	1.36	1.83	1.53											
G6	2.14	0.65	0.47	0.81	1.65										
G7	1.84	0.90	1.03	1.48	0.49	1.19									
G8	2.73	2.33	2.86	0.84	2.45	1.62	2.59								
G9	0.92	0.56	1.16	0.59	0.95	0.53	0.78	1.89							
G10	1.33	0.77	1.50	0.44	1.26	0.76	1.44	0.97	0.44						
G11	1.32	0.74	1.41	1.50	1.25	1.63	0.85	2.71	1.08	1.28					
G12	1.49	1.17	2.21	0.90	0.81	1.82	1.32	1.58	1.20	0.77	1.84				
G13	1.57	1.57	2.26	1.35	1.09	1.69	1.21	2.26	0.70	0.88	0.90	1.89			
G14	3.37	1.64	1.73	1.53	1.87	1.36	2.55	1.44	1.88	0.83	2.55	1.12	2.65		
G15	2.04	0.94	1.30	1.41	1.72	1.01	0.99	1.82	0.92	1.01	0.67	2.23	1.01	2.44	
G16	2.79	1.25	1.59	1.62	1.75	1.18	1.64	1.34	1.46	0.92	1.68	1.50	2.28	1.13	0.86
G17	3.00	1.09	0.76	2.09	0.88	0.99	0.55	2.44	1.16	1.39	1.19	1.74	1.70	1.73	0.79
G18	1.27	0.55	1.12	1.52	1.43	1.66	1.19	2.94	1.19	1.19	0.72	1.15	1.61	1.88	1.66
G19	3.09	1.83	1.99	2.56	0.55	2.04	0.78	2.74	1.53	1.69	1.67	1.44	1.64	2.17	1.42

G20	1.57	0.51	1.03	0.61	2.07	0.39	1.88	1.45	0.61	0.37	1.53	1.55	1.58	1.09	1.08
G21	1.51	0.58	1.24	1.40	0.52	1.10	0.52	2.89	0.44	0.93	0.93	1.13	1.02	2.03	1.04
G22	2.16	1.53	2.33	1.11	1.43	1.62	2.00	0.95	1.21	0.32	1.80	0.79	1.21	0.77	1.45
G23	3.60	1.44	0.98	2.06	1.37	0.66	1.62	2.56	1.27	1.43	2.20	2.30	2.15	1.25	1.66
G24	1.66	1.13	1.83	0.61	1.73	0.90	1.92	0.62	0.79	0.19	1.53	1.23	1.11	0.97	0.94
G25	1.59	1.46	2.22	0.68	1.25	1.40	1.45	0.46	0.98	0.39	1.38	0.82	1.00	1.27	1.03
G26	2.46	1.75	2.82	1.30	2.00	1.92	2.42	0.99	1.65	0.60	1.81	1.31	1.79	1.13	1.28
G27	3.32	2.14	2.00	2.02	2.65	1.64	2.90	1.53	1.94	0.97	2.17	2.24	2.09	0.89	1.86
G28	4.09	1.97	2.10	2.66	2.92	1.66	2.46	2.44	1.94	1.41	2.34	2.98	2.47	2.12	0.90

	G16	G17	G18	G19	G20	G21	G22	G23	G24	G25	G26	G27
G17	0.711											
G18	1.984	1.505										
G19	1.151	0.412	1.870									
G20	1.124	1.614	1.333	2.480								
G21	1.353	0.722	1.123	0.818	1.236							
G22	0.964	1.623	1.569	1.443	1.002	1.461						
G23	1.243	0.741	2.360	1.413	1.216	1.150	1.857					
G24	0.800	1.567	1.614	1.883	0.410	1.464	0.312	1.499				
G25	0.879	1.459	1.586	1.405	1.128	1.503	0.332	2.063	0.302			
G26	0.594	1.853	2.306	1.945	1.255	1.770	0.466	2.212	0.534	0.542		
G27	1.226	1.848	1.926	2.436	1.281	2.623	0.907	1.855	0.756	1.052	1.257	
G28	0.610	1.250	3.073	1.963	1.558	1.833	1.599	1.780	1.387	1.789	1.061	1.787

Contribution of different characters to total diversity

The relative contribution of eleven different characters intakes in the evaluation of 28 genotypes towards the expression of genetic divergence is given in Table 3. The percent contribution of component characters ranged from 0.010 to 26.74 percent. The studies revealed that more or less contributions of similar characters towards total divergence was also been discussed byDhaduk et al, Mamta and Choudhury, Patel et al, and Singh and Jain **[8,9,10,11]**

Principal components analysis (PCA) results of 11 quantitative traits are presented (Table 3). The PCA analysis results includes the factor scores of each character among the 28 okra accessions, Eigen values, percentage total variance accounted for by eight principal components (PCs). This principal component analysis resulted in eleven principal components (PC1 to PC11) with Eigen values ranged from 0.012 to 2.941. The eleven principal components accounted varied percentage of total variance ranged from 0.1 to 26.74%. Cumulative percent of total variation up to PCA five with eigen value more than unity accounted 80.67%. Ahiakpa, Nwangburukaet al and Mihretu et al who reported that principal component axes contributed 64.32%, 78.51% and 83% variation, respectively**[12,13,14].** The first five components were retained in analysis because eigen values are >1. The others factors having eigen value < 1 were ignored. These were ignored due to Gutten's lower bound principle that eigen values <1 should be ignored**[15]**.

Comment [Ma13]: This was neither mentioned in your abstract nor in your methodology

Comment [Ma14]: The loadings or contributions of each character to the PCs are completely missing. Consider including them and remove the redundant principal axes. I did a quick check online and thought this : https://www.researchgate.net/publication/303852745_Discrimination_of_maize_Zea_mays_L_inbreds_for_morphophysiological_and_yield_traits_byD2_statistics_and_principal_component_analysis_PCA might be helpful. There are several others.

Comment [Ma15]: Therefore do not include them in the table. Consider removing them.

The first three principal components PC1, PC2 and PC3 with values of 26.74%, 18.15% and 14.84%, respectively, contributed more to the total of 59.73% variation. Similar result was reported by Amoateyet al and Ahiakpa that the first principal component (PC1) recording the highest (32.44%) variance**[12,16].** According to Chahal and Gosal , characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. **[17]**

Table 3. Eigen values and yield percent contribution of 11 characters of 28 genotype

Principal component axes	Eigen values	Percent variation	Cumulative % of percent variation
I	2.941	26.74	26.74
II	1.996	18.15	44.89
III	1.632	14.84	59.73
IV	1.292	11.75	71.48
V	1.011	9.19	80.67
VI	0.780	7.09	87.76
VII	0.690	6.28	94.04
VIII	0.297	2.70	96.74
IX	0.213	1.94	98.68
X	0.135	1.22	99.9
XI	0.012	0.10	100

Conclusion

Results of the present studies indicated significant variation among the genotypes for all the characters studied. Plant height, fruits per plant and fruit weight contributed maximum towards fruit yield improvement. Twenty eight okra genotypes formed five different clusters. Considering genetic variability, diversity and other agronomic performance selection of genotypes G1 and G18 could be selected for earliness and high fruit yield and genotypes G6 and G20 selected for less seeds per fruit for future breeding program. High genotypic distance observed between G1 and G28, G27, G23, G14, G17, respectively.

Reference

1.Chauhan, DVS. Vegetable Production in India. 3rd edn.Ramprasad and Sons. Agra. 1972; 275-333.

2.Singh P, Chauhan V, Tiwari BK, Chauhan SS, Simon S, Bilal S, Abidi AB. An overview on okra (Abelmoschusesculentus) and it’s importance as a nutritive vegetable in the World. International Journal of Pharmacy and Biological Sciences. 2014; 4(2):227-233.

3.Baloch AF, Qayyum SM, Baloch MA. Growth and yield performance of okra (Abelmoschus esculentus L.) cultivars.Gomal University Journal of Research.1990;10:191.

4.BBS, 2020-2021. Statistical Year Book of Bangladesh. Bangladesh Bureau of Statistics, Planning Division, Ministry of Planning, Dhaka, Bangladesh,

5.Syfullah, K., Sani, M. N. H., Nasif, S. O., Parvin, S., Rony, M. M. H., Islam, M. S., & Hossain, M. S. (2018). Genetic Variability, Heritability, Character Association and Morphological Diversity in Okra (Abelmoschus esculentus L. Moench). International Journal of Plant & Soil Science, 25(6), 1-11. https://doi.org/10.9734/IJPSS/2018/45828

6.Prakash K, Pitchaimuthu M, Ravishankar Assessment of genetic relatedness among okra genotypes [Abelmoschus esculentus (L) Moench] using rapd markers. Electronic Journal of Plant Breeding. 2011;2(1):80-86.

7.Kamalpreet, K., Mamta, P., Satinder, K., Dharminder, P. and Neena, C. (2013). Assessment of morphological and molecular diversity among okra [Abelmoschus esculentus (L.) Moench.] germplasm. Academic J. 12 (21): 3160-3170.

8.Dhaduk, L.K., Mehta, D.R. and Patel, K.D. (2004). Genetic diversity in okra. Orissa. Hortic. 32 (1): 70-72.

9.Mamta Kumari and Choudhury, D.N. (2006). Genetic divergence in okra [Abelmuschusesculentus (L.) Moench]. Veg. Sci. 33 (1): 71-72.

10.Patel, K.D. Dhaduk, L.K. Mehta, D.R. and Pandya, H.M. (2006). A multivariate analysis of okra genotypes. Agril. Sci. Digest. 26 (1): 45-47.

11.Singh SP and Singh JP. (2006). Variability, heritability and scope of improvement for yield components in okra [Abelmoschus esculentus (L.) Moench]. Intl. J. Plant Sci. 1 (2): 154-155.

12.Ahiakpa, J.K. (2012). Characterization of twenty-nine (29) accessions of okra [AbelmoschusSpp (L.) Moench] in Ghana. Master of Philosophy, University of Ghana, Ghana.

13.Nwangburuka, C.C., Kehinde,O.B., Ojo, D.K., Denton O.A., and Popoola A.R. (2011). Morphological classification of genetic diversity in cultivated okra [Abelmoschus esculentus (L.) Moench] using principal component analysis (PCA) and single linkage cluster analysis (SLCA). African J. Biotechnol.10 (54): 11165-11172.

14.MihretuYonas, WeyessaGaredew and AdugnaDebela, (2014a). Multivariate analysis among Okra [Abelmoschus esculentus (L.) Moench] collection in South. Western Ethiopia. J. Plant Sci. 9: 43-50.

15. Kumar, R.P., Vashisht, R., Gupta, K., Singh, M. and Kaushal, S. (2011). Characterization of European carrot genotypes through principal component analysis and regression analysis. Intl. J. Veg. Sci.17: 3-?

16.Amoatey, HM., GYP Klu, Quartey, EK, Doku, HA., Sossah, FL., Segbefia, MM. and Ahiakpa. JK. (2015). Genetic diversity studies in 29 accessions of okra (Abelmoschusspp (L.) using 13 quantitative traits. American J. Experiment. Agric.5 (3): 217-225.

17. Chahal, GS and Gosal SS. (2002). Principles and procedures of plant breeding biotechnology and conventional approaches. Narosa Publishing House, New Delhi. Pp 604.

Comment [Ma16]: Where is the b? Please remove the a if this is the only citation from the same authors in the same year