Electronic Journal of Plant Breeding, 6(3): 663-667 (Sep 2015)
ISSN 0975-928X

Research Article

Assessment of morphological variation among Okra [*Abelmoschus esculentus* L. (moench)] accessions to aid selection of ideal parents

Olayiwola, M.O.*, Dabo, O.A. and Ariyo, O.J.
Department of Plant Breeding and Seed Technology Federal University of Agriculture, Abeokuta, Ogun State, Nigeria
*E-mail:ollyrichie@gmail.com

(Received:24 Feb 2015 ; Accepted:24 Mar 2015)

Abstract
A total of ten Okra [*Abelmoschus esculentus* L. (Moench)] accessions were evaluated over 2 years to determine the genetic diversity present in the germplasm accessions so that parents could be chosen for use in hybridization. Observations on days to flowering, number of branches and pods per plant, height at flowering, final plant height, pod length, pod width, and pod yield were recorded. There was a large degree of variability among genotypes for all traits and the metroglyph analysis classified the genotypes into 6 groups based on morphological differences. Genotype NHGB/09/008(B) had the highest total index. Groups II and V had the largest within group variation indicating that within group improvement was possible. Hybridization between Group III and Groups II and VI could yield desirable hybrids useful in Okra breeding program.

Key words
Abelmoschus esculentus, clustering, germplasm, metroglyph.

Introduction

A detailed understanding of the pattern and magnitude of genetic diversity within germplasm accessions is necessary in any crop improvement. Ariyo (1987) reported that a diverse germplasm collection was a valuable source of supply of parental strains for hybridization and development of improved genotypes. Information on the choice of parents is essential as it is a basic component of breeding (Aremu*et al*., 2007; Rahim *et al*., 2010), and provides for creating useful variations in subsequent progenies (Aremu,2011). Identification of genotypes resistant to environmental stresses under various conditions has increased crop production (Fu and Somers, 2009). Mohammadi *et al*. (2010) reported that appropriate parental combinations through efficient diversity study increased the crop yield. Aremu (2011) reported that existing cultivar populations have narrow genetic bases and there is a need to create variability among cultivars after analyzing the genetic diversity.

The decline in okra [*Abelmoschus esculentus* L. (Moench)] yield necessitates evaluation of the germplasm accessions for existing variability (FAOSTAT, 2012). The need to encourage research that would aid development of new and superior genotypes to replace the old and low yielding has been emphasized (Kumar *et al*., 2010; Alake *et al*., 2012) in okra. Bisht *et al*. (1995) and Omohinmin and Osarawu (2005) stated that wide genetic diversity existed among cultivated *Abelmoschus spp*. Large genetic variability has also been reported among okra germplasm accessions (Dhankhar and Dhankhar, 2002; Nwangburuka *et al*., 2012;Vandana *et al*., 2014 and Salameh, 2014).

Multivariate methods have been used to study variability in okra (Omohinmin and Osarawu, 2005; Nwangburuka *et al*., 2012). Anderson (1957) proposed metroglyph analysis for genetic diversity studies. The technique reveals patterns of morphological variation in crop species by reducing the complex inter-relationship among accessions into a pictorial scatter diagram. The efficiency of the technique as a tool for diversity study has been reported in different crops *viz*., Venkatarao *et al.* (1973) in tobacco, Singh and Chaudhary (1974) in green gram, Akoroda (1983) in yellow yam, Singh *et al*. (1986) in lowland rice cultivars and Ariyo (1987) in okra. This study was undertaken to assess the magnitude of genetic variations among okra accessions to provide information on choice of parents to be used in hybridization programmes. This would aid decision on the strategy to be adopted in improving okra yield.

Materials and Methods

Okra accessions were evaluated at the Teaching and Research Farm of the Federal University of Agriculture, Abeokuta ($7^{o}38'$N, $3^{o}88'$E; 450 m above sea level), south-western Nigeria in September 2011 and 2012. Abeokuta is a transition zone between rainforest and derived savannah with a humid tropical climate and a mean annual rainfall of 1200 mm. The soil was a Arenic Plinthic Kand indalf(Busari,2011). The accessions NHGB/09/017, NHGB/09/015, NHGB/09/008(B), NHGB/09/114,

NG/SA/DEC/09/0528, NHGB/09/008(A), NG/TO/JUN/09/007 and NG/SA/DEC/07/0522 were obtained from the National Centre for Genetic Resources and Biotechnology; the accessions FUNAAB 11325 and FUNAAB 2241 were obtained from the Federal University of Agriculture, Abeokuta. The accessions were evaluated in two-row plots, each 4.5 m long and 90 cm apart, arranged in a randomized complete block design with 3 replications. In each year, recommended agronomic practices were used for optimum crop stand.

In each accession, the inner 18 plants from the two rows were sampled. Observations were made on eight morphological traits such as days to flowering, number of branches per plant, number of pods per plant, height at flowering, final plant height, pod length, pod width, and pod yield. Data were then subjected to analysis of variance and metroglyph analysis (Anderson, 1957) to reveal patterns of variation among accessions. Accession means were averaged over years and means of each trait averaged over accessions. Range, variance and standard deviation were calculated for each trait and the coefficient of variation (CV) for each determined. The two most variable characters were selected based on magnitude of their CV and used as coordinates on the graph and the point of intersection represents the marker (glyph) for each accession. The other characters were represented by rays at different positions on the glyph with rays from the same character occupying the same position on each glyph. The range of variability among accessions for each trait was represented by ray length. Depending on index score, ray length may be short, longer or longest with scores 1, 2 and 3, respectively. Genotype with a low value for a character had no ray; medium values had relatively medium length rays and those with high values had the longest rays. Using suitable class intervals, the range of variability, with regards to a character, was classified into 3 groups. The index score of characters for each genotype were summed as the total index score and represented as the value of the genotype. Based on positions on the pictorial scatter diagram genotypes were classified into groups. The distribution of the total index score and average index score for each cluster was determined and represented as the average worth of each group for each character.

Results and Discussion

Analysis of variance showed highly significant genotypic effect for all characters (Table 1) indicating that there was large degree of divergence among accessions. Dhankhar and Dhankhar (2002) and Nwangburuka *et al*. (2012) found wide genetic variations among *A. esculentus* accessions. Pod yield and number of pods per plant had the highest coefficient of variations (Table 2). The performance of accessions varied for each character (Table 3). Genotype NHGB/09/017 flowered earlier, while, NHGB/09/015 flowered late. Genotype NG/TO/JUN/09/007 was the shortest plants at flowering, while NHGB/09/008(B) was the tallest at flowering. Genotype FUNAAB 11325 had the lowest pod yield and NHGB/09/008(B) had the highest pod yield. Genotype NHGB/09/015 had the lowest number of pods; NHGB/09/008(B) had the highest number of pods. Genotype NHGB/09/015 had the shortest pods; NG/TO/JUN/09/007 had the longest pods. The pods were thinner in FUNAAB 11325, and wider in NG/SA/DEC/07/0528. Genotype NG/TO/JUN/09/007 had the shortest plants at maturity; NHGB/09/008(B) had the tallest final plant height. Genotype NHGB/09/114 had the lowest number of branches; NG/SA/DEC/09/0528 had the most branches. Genotype NHGB/09/114 had the highest total index; NG/TO/JUN/09/007 had the lowest. The variability observed in these genotypes justifies further analysis to clarify grouping patterns.

The metroglyph analysis (Fig. 1) indicated pod yield and number of pods per plant were the most variable among characters and used as Y and X coordinates, respectively. The largest divergence among genotypes was between NHGB/09/008(B) and NHGB/09/015. The metroglyph showed that accessions fell into 6 groups represented by the big oval shapes (Fig. 1) indicating that variability was well captured. Genotypes belonging to the same group were morphologically similar. With the exception of Group I, III and VI, other groups exhibited low within group variation. Group V contained NHGB/09/017, NG/TO/JUN/09/007 and NG/SA/DEC/07/0522; Group IV and Group II had NHGB/09/008(A) and NG/SA/DEC/07/0528, and NHGB/09/114 and NHGB/09/015, respectively; Groups I, III and VI all had a single member, FUNAAB 11325, FUNAAB 2241, NHGB/09/008(B), respectively (Table 4). The frequency distribution of index scores and the average index score of the groups varied (Table 5). Among groups with more than a single accession, Group V had the highest within group variation; overall, Groups III and VI had the highest average index. Group V had the least average index score (Table 5).The genotype NHGB/09/008(B) had the highest total index and could be considered for further improvement. Accessions in Groups I, III, IV and VI could be subjected to selection, within group crosses and development of populations that could be a source of quality pure lines. Success in hybridization depends on the genetic constitution of potential parents and parents are chosen based on the extent of dissimilarity. Falconer (1981) advanced that heterosis was highly correlated with heterozygosity and information on genotypic differences has aided decisions on choice of parents (Akotkar *et al*., 2010; Nwangburuka *et al*.,

2011; Olayiwola *et al*., 2014). Differences among groups could be explored for heterosis breeding and trangressive segregation in the direction desired by the breeder. A cross between Group III accessions (seed source) and Group VI (pollen source) could result in tall, high yielding, plants with robust pods and extra early hybrids. Hybrids from Group III × Group II could be early, tall with long and robust pods. The best accession in each group could be recombined to form a composite presenting a broad based population to be used for further improvement.

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Table 1. Mean squares of agronomic characters estimated in 10 okra accessions

Source	Days to flowering	Plant height at flowering	Pod yield	Number pods per plant	Pod length	Pod width	Final plant height	Number branches per plant
Genotype (G)	75.5*	1509.8***	44671.2***	17.7***	7.7***	4.0*	2919.8***	23.2***
Year (Y)	375.0**	375.0*	402.1	3.9*	41.4***	60.0***	396.7**	0.6
G×Y	24.3	31.7	111.3	0.2	1.0	0.9	31.2	0.4

***, **, * significant at P<0.001, P<0.01 or P<0.05.

Table 2. Range, coefficient of variation (CV) and index score for eight agronomic characters

Character	Range	CV(%)	Index score		
			1	2	3
Days to flowering	49.4-58	5.06	≤52.3	52.4-55.2	≥55.3
Plant height at flowering (cm)	40.1-99.6	21.72	≤59.93	59.94-79.77	≥79.78
Pod yield (g)	60-339.9	47.92	≤153.3	153.4-246.7	≥246.8
Number of pods per plant	1.9-7.2	40.22	≤3.67	3.68-5.45	≥5.46
Pod length (cm)	6.8-10.55	12.04	≤8.05	8.06-9.3	≥9.4
Pod width (cm)	8.78-10.6	5.68%	≤9.39	9.4-10.01	≥10.02
Final plant height (cm)	45.9-116.6	26.57%	≤69.47	69.48-93.05	≥93.06
Number of branches	1.93-3.56	17.96%	≤2.47	2.48-3.02	≥3.03

Table 3. Mean values of characters with the index score for each character in parenthesis

Genotypes	Days to flowering	Plant height at flowering (cm)	Pod yield (g)	Number of pods per plant	Pod length (cm)	Pod width (cm)	Final plant height (cm)	Number of branches	Total index score
NHGB/09/114	57a (3)	69.2c (2)	113.0f (1)	2.2gh(1)	10.2a (3)	10.1a(3)	92.8bc(3)	1.93d(1)	17
NHGB/09/015	58a (3)	68.2c (2)	68.2g (1)	1.9h(1)	6.8c (2)	9.8a	84.3de(2)	3.0ab(2)	14
NHGB/09/017	49.5b(1)	50.8d (1)	197.9b-d(2)	4.7cd(2)	9.7a (3)	9.8ab(2)	51.7g(1)	2.7bc(2)	14
NHGB/09/008(B)	50.6b(1)	99.6a (3)	339.9a(3)	7.2a(3)	10.0a (3)	9.7ab (2)	116.6a(3)	2.8b(2)	20
NG/SA/DEC/07/0528	54.1a (2)	65.8c (2)	117c-e(1)	2.9fg(1)	8.9ab (2)	10.6a (3)	77.5ef(2)	3.6a(3)	16
NG/TO/JUN/09/007	51.8b(1)	40.1e (1)	221.1b(2)	4.3de(2)	10.5a (3)	8.9b(1)	45.9g(1)	2.3c (1)	12
NG/SA/DEC/07/0522	52.3b(1)	80.9b (3)	210.7bc(2)	5.3bc(2)	9.8a (3)	9.3ab (1)	99.4b(3)	3.5a(3)	14
NHGB/09/008(A)	51.7b(1)	71.8bc (2)	167.7de (2)	3.7ef (2)	9.8a (3)	9.7ab (2)	88.2dc (2)	2.8b(2)	16
FUNAAB11325	54.2ab(2)	66.0c (2)	60.0g(1)	6.2ab (3)	8.1b (2)	8.8b (1)	71.6f(2)	2.8bc(2)	15
FUNAAB2241	52.3b(1)	68.6c (2)	149.4ef(1)	6.1ab (3)	9.1a (2)	10.1ab(3)	101.3b(3)	3.1ab(3)	18

Means with similar alphabets along the same column are not significantly different from each using DMRT (P<0.05)

Table 4. Okra Group Means for evaluated characters

Character	Group I	Group II	Group III	Group IV	Group V	Group VI
Days to flowering	54.2	57.5	52.3	52.9	51.2	50.6
Plant height at flowering	66	68.7	68.6	68.8	57.3	99.6
Pod yield	60	90.6	149.4	172.4	209.9	339.9
Number of pods per plant	6.2	2.05	6.1	3.3	4.8	7.2
Pod length	8.13	8.5	9.13	9.4	10	10.02
Pod width	8.79	9.94	10.08	10.16	9.36	9.7
Final plant height	71.6	88.6	101.3	82.9	65.7	116.6
Number of branches per plant	2.75	2.47	3.1	3.16	2.83	2.78

Table 5. Frequency distribution of index score and average index score for the six groups of okra genotypes.

Group	Genotype	Distribution	Average index score
I	FUNAAB 11325	15	15
II	NHGB/09/114, NHGB/09/015	14-17	15.5
III	FUNAAB 2241	18	18
IV	NG/SA/DEC/07/0528 NHGB/09/008(A)	16	16
V	NHGB/09/017, NG/TO/JUN/09/007, NG/SA/DEC/07/0522	12-14	13
VI	NHGB/09/008(B)	20	20

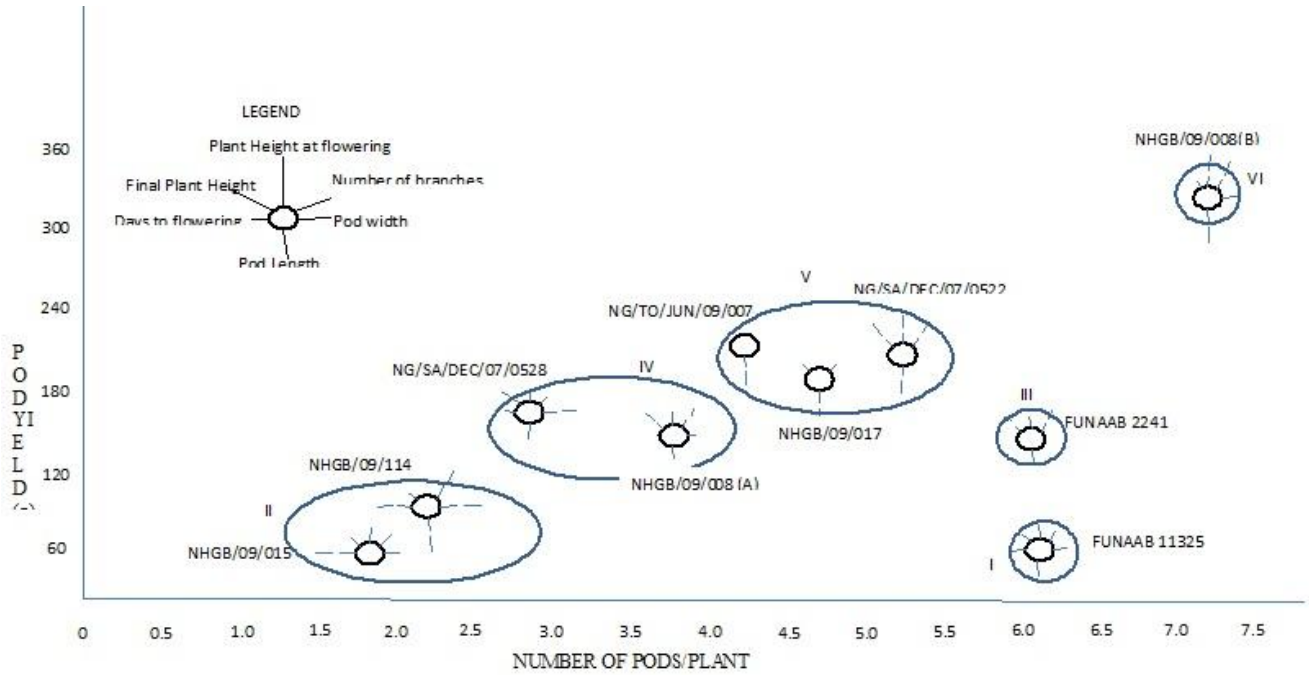

Figure 1. Metroglyph analysis of okra accessions (represented by glyph) on agronomic characters with values indicated by rays.