

AGROMORPHOLOGICAL CHARACTERIZATION OF TWELVE OKRA (*Abelmoschus esculentus* (L.) Moench) GENOTYPES FROM SOUTH-WESTERN NIGERIA

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ABSTRACT

As part of efforts to expand and document the horticultural germplasm repository at the National Horticultural Research Institute (NIHORT), Ibadan, eleven okra genotypes collected from farmers' fields in south-west Nigeria were characterized alongside one improved variety in an open field experiment for eight important agro-morphological characters: plant height, number of days to flowering, pod length, pod width, fruit pedicel length, number of pods per plant, number of seeds per pod, and 1000-seed weight. Significant variations were observed among cultivars for most of the traits except days to flowering and number of seeds per pod. Moderate to high heritability estimates in the broad sense recorded for seven of the eight traits; suggest that environmental influence on the traits were minimal. Number of pods per plant had moderate to high positive genotypic and phenotypic correlations with plant height, pod length and pedicel length. Principal component analysis (PCA) revealed that the first three principal components accounted for 87.45% of the total variation based on the eight characters observed. The PCA suggested that pod width, number of seeds per pod, plant height, fruit pedicel length, number of pods per plant, pod length, 1000-seed weight and days to flowering contributed significantly to the total variation observed. This study reveals the potential of the genotypes to enhance NIHORT's okra improvement and genetic conservation research.

Key words: Okra, genotypic correlation, phenotypic correlation, principal component analysis, genetic conservation

Introduction

Okra (*Abelmoschus esculentus* L. Moench), also known as lady finger, is an important vegetable crop cultivated mainly in the tropics (Schippers, 2000). It belongs to the family *Malvaceae*, and is believed to have originated in Africa (Aladele *et al.*, 2008). It is widely grown as a garden or commercial crop for its fresh leaves, buds, flowers, stems, pods and seeds (Schippers, 2000). Nutritionally, tender pods of okra are good sources of vitamin C (30 mg/100 g), calcium (90 mg/100 g) and iron (1.5 mg/100 g). The edible fruit is widely grown from Africa to Asia, in Southern Europe, the Mediterranean and South America (Oyelade *et al.*, 2003). Total commercial production of okra in the world is

estimated at over 4.8 million tons with India and Nigeria as the leading producers followed by Sudan (Gulsen *et al.*, 2007; Varmudy, 2011). Okra cultivation and production is widely practiced across all agro-ecological zones of Nigeria because of its importance to food security, and can be found in almost every market in the country (Christo and Onuh, 2005). According to Daramola (2005), okra production contributes significantly to the economic stability of rural dwellers (mostly the women) in West Africa. Despite the nutritional and economic importance of this crop, limited efforts have been directed towards conservation and genetic improvement of this crop for increased fruit yield and, tolerance to biotic and abiotic stresses

hindering its production in Nigeria. Thus, there is the need to initiate breeding programs geared towards developing new resilient okra varieties that can withstand the dynamics associated with climate change, and also exhibit farmers preferred traits. Assembling, characterization, evaluation and conservation of new genetic materials in addition to the existing genetic resources of a plant increase the frequencies of desirable alleles existing within germplasm collections, thus maximizing their utilization in any crop improvement programme (Onwueme and Sinha, 1991). Numerous landraces and cultivars differing in fruit shape, fruit colour, plant architecture, mucilaginous properties, and days to maturity with varying levels of tolerance to biotic and abiotic factors affecting okra production can be found in Nigeria due to preferential selection over the years by farmers. Understanding the nature and extent of variation within new germplasm collections is an important prerequisite to identifying superior cultivars for hybridization. Trait improvement through selection is futile unless the trait of interest is under genetic control and heritable. According to Hanson *et al.* (1956), the heritability of a trait gives insight into the proportion of phenotypic variance that is due to genetic factors, and which is also transferable to the next generation of progenies. Genotypic and phenotypic association among measured traits indicate the level of interrelationship between two or more plant characters which can be exploited by the breeder through indirect selection during a breeding program. Indirect selection can be deployed to select for traits that are costly to measure or easily influenced by the environment. National Horticultural Research Institute (NIHORT), Ibadan has the mandate for horticultural crop improvement research. As an important focus, NIHORT aims at developing high yielding and acceptable okra varieties with good fruit quality traits. Thus, the objective of this study described here was to characterize okra cultivars selected from farmers' fields in south-west Nigeria for fruit yield, fruit quality and plant growth attributes under field conditions.

Materials and Methods

The experiment was conducted at the experimental field of National Horticultural Research Institute, Ibadan. The materials characterized in this study comprised of eleven

adapted cultivars and landraces selected from farmers' fields in Ogun State, south-west Nigeria alongside a popular improved variety, V 35, which was included as a check. The collected genotypes were designated IK 1 to IK 11. Seeds from the twelve okra accessions were first treated with an anti-pest dressing (*DressForce*, Jubaili Agrotech) prior to planting. Three seeds per hill were planted directly in 3cm holes under field conditions, and later thinned to one plant per hill after seedling establishment. The experiment was laid out in a Randomized Complete Block Design with three replications. Each replicate consisted of two rows of 25 plants for each genotype. Plants were spaced 60 cm between and within rows. Agronomic maintenance carried out included manual weeding at two and four weeks after planting; NPK 15:15:15 fertilizer was applied in split at 60 Kg/ha first at three weeks after planting and later at flowering. Data were recorded from five plants randomly selected from the middle section of each plot on the following agronomic attributes: Number of days to flowering, plant height at flowering (cm), number of pods per plant, pod length (cm), pod width (cm), number of seeds per pod (average of three fruits) and weight (g) of 1000 seeds (1000-seed weight, obtained by weighing two lots of 100 seeds and multiplying by five). Data from means for each plot were analyzed using Plant Breeding Tools software to estimate the heritability, principal component analysis, genotypic and phenotypic correlation coefficients. Broad-sense heritability (H) was computed as:

$$H = \frac{V_g}{V_g + V_e/r}$$

Where V_g is genetic variance, V_e is error variance, and r is the number of replications. Mean separation was carried out using the least significant difference (LSD) test at probability of 0.05.

Results and Discussion

Variation among genotypes

The mean performance of the okra accessions evaluated using eight agronomic traits showed significant differences among the accessions for most of the attributes studied, except days to flowering and number of seeds per pod (Table 1). The range of number of days to flowering of the accessions was 52.74 – 54.93 with the earliest average reproductive maturity (number of days to first flower opening) observed in IK 1 at 52.74

days, while the last to attain reproductive maturity was IK 2 with a mean of 54.93 days. Improved cultivar V35 recorded the longest pod length (11.40 cm), fruit pedicel length (3.86 cm) and number of pods per plant (12), showing its uniqueness above the landraces/accessions. Among the accessions collected, IK1 had a combination of good attributes for pod length, number of pods per plant and number of seeds per

pod. Genotype IK 8 showed the least values for most of the parameters observed in this study (Table 1). High heritability in the broad sense (>70%) was recorded for six of the traits, while days to flowering (22%) and number of seeds per pod (52%) recorded low and moderate heritability estimates, respectively (Table 1). The highest heritability estimate of 97% was recorded for 1000SW (Table 1).

Table 1: Means and heritability estimates of twelve okra genotypes

Lines	DTF (days)	1000SW (g)	PH (cm)	PL (cm)	PW (cm)	FP (cm)	NPP	NSP
IK1	52.74	5	126.43	9.43	11.66	2.06	8	82
IK2	54.93	6	79.44	7.9	11.47	2.96	7	64
IK3	54.27	6	98.61	8.56	12.23	2.06	7	78
IK4	53.29	6	86.92	9.22	11.66	2.29	7	69
IK5	53.84	5	69.08	9.22	11.1	2.51	7	68
IK6	53.51	5	97.84	8.56	11.47	2.06	5	70
IK7	53.62	5	100.64	9	11.66	2.06	6	71
IK8	52.96	4	58.87	7.03	10.53	2.96	6	63
IK9	54.82	5	82.8	10.53	10.53	3.41	7	70
IK10	53.73	6	79.37	7.9	11.85	2.06	6	70
IK11	54.38	7	102.74	9	11.66	2.96	7	69
V35	53.4	5	105	11.4	10.91	3.86	12	72
Prob. level	0.683	0.001	0.001	0.001	0.022	0.0003	0.004	0.218
SED	3.065	0.369	14.397	0.709	0.826	0.688	0.907	8.304
Heritability	0.22	0.97	0.94	0.87	0.75	0.9	0.83	0.52

DTF=Days to 50% flowering; 1000SW= 1000 seed weight; PHT= Plant height; PL= Pod length; PW= Pod width; FP= Fruit pedicel; NPP= Number of pods per plant; NSP=Number of seeds per pod; P=0.5.

Traits influencing variability among genotypes

The results of principal component analysis (PCA) carried out are shown in Table 2. The first three principal components (PC) contributed 87.45% of the total variation available in the germplasm. Pod width, number of seeds per pod, plant height and fruit pedicel length are the important traits that largely influenced the 34.07% variation contributed by PC1 to the total

variation within the accessions. The second principal axis (PC2) contributed 32.49% to the total variation among the accessions. Pod length and number of pods per plant were largely responsible for the 32% of the total variation with moderate contributions from fruit pedicel length and plant height. Days to flowering and 1000seed weight were the dominant parameters in PC3 which accounted for 21% of the total variation.

Table 2: Contribution of the first three principal component axes to variation in okra genotypes

Parameters	PC1	PC2	PC3
1000 seed weight	0.2790	0.0964	0.6276
Days to 50% flowering	-0.1162	0.0658	0.6779
Fruit pedicel length	-0.4091	-0.3930	0.2420
Number of pods per plant	-0.0177	-0.5537	0.0949
Number of seeds per pod	0.4818	-0.2649	-0.1835
Plant height	0.4749	-0.3187	-0.0235
Pod length	0.0389	-0.5569	0.0952
Pod width	0.5308	0.2087	0.1889
Eigen value	2.7250	2.5990	1.6720
Percentage	34.0700	32.4900	20.8900
Cumulative	34.0700	66.5600	87.4500

Relationships among agronomic and growth traits

The genotypic and phenotypic correlations among studied traits are shown in Table 3. Days to flowering exhibited low to high positive genotypic and phenotypic correlations with 1000seed weight (0.9850) and pedicel length (0.3671), but correlated negatively with the other attributes measured in this study, even though the coefficients were low. Plant height showed negative genotypic correlation with days to flowering (-0.4398) and pedicel length (-0.2169) but had positive association with 1000 seed weight (0.9850), pod length, pod width, number of pods per plant (0.4318) and number of seeds

per pod (0.9850). There was high positive genotypic correlation between number of pods per plant and pod length and pedicel length, and moderate and positive relationship between number of pods per plant and plant height. Days to flowering recorded negative genotypic correlation with pod length (-0.3671) and pod width (-0.1996) but showed very low positive phenotypic correlation with the same traits at (0.0500) and (0.0358) correlation coefficient respectively. Positive but low genotypic correlation (0.2256) coupled with negative phenotypic correlations (-0.0878) was also observed between number of pods per plant and days to flowering.

Table 3. Genotypic and phenotypic association among 12 okra accessions

Traits		DTF	1000SW	PHT	PL	PW	FP	NPP	NSP
DTF	G		0.9850	-0.4398	-0.3671	-0.1996	0.6063	0.2256	-0.0290
	P		0.8317	-0.2078	0.0500	0.0358	0.2992	-0.0878	-0.2991
1000SW	G			0.3709	0.1866	0.9850	0.2630	0.1576	0.1408
	P			0.3587	0.1746	0.9720	0.2496	0.1432	0.1014
PHT	G				0.5344	0.5554	-0.2169	0.4318	0.9850
	P				0.4824	0.4699	-0.1865	0.3731	0.8115
PL	G					-0.3324	0.5857	0.8954	0.5650
	P					-0.2472	0.4915	0.6921	0.4105
PW	G						-0.9222	-0.1490	0.9892
	P						-0.7260	-0.2085	0.4577
FP	G							0.7756	-0.3728
	P							0.6551	-0.3502
NPP	G								0.3975
	P								0.2792

DTF=Days to 50% flowering; 1000SW= 1000 seed weight; PHT= Plant height; PL= Pod length; PW= Pod width; FP= Fruit pedicel; NPP= Number of pods per plant; NSP=Number of seeds per pod

The magnitude of genetic variability available in a germplasm and the extent to which these desirable characters are heritable is an important consideration in a breeding programme. Good understanding of the nature

and behavior of the characters under consideration is one of the prerequisites that determine the success of crop genetic improvement programmes. The genetic materials evaluated in this study exhibited

significant phenotypic variation for most of the traits. This indicates the presence of an appreciable level of genetic variability that can be exploited by breeders through selection. Numerous researches have also reported significant variations among okra accessions (Bisht *et al.*, 1995; Nwangburuka *et al.*, 2012; Aminu *et al.*, 2017). Genotype V35 with the highest mean values for fruit pedicel, number of pods per plant and pod length; accessions IK 1 and IK 11 with superior values for number of seeds per pod and 1000-seed weight, respectively is an indication that selection focusing on the above traits within these genetic materials can be exploited for hybridization by the breeder. Although IK 8 recorded the least value for most of the parameters observed in this study, it can be used as a donor parent in breeding programmes aiming to develop semi-dwarf okra varieties as a result of its reduced height. Moderate to high heritability estimates recorded for 1000-seed weight, plant height, pod length, pod width, fruit pedicel, number of pods per plant and number of seeds per pod indicates that most of these traits are under genetic control. This suggests that selection for these traits will be effective since environmental factors may have less influence on their overall phenotypic performance. This is largely in agreement with the findings of Ariyo, (1990) and Nwangburuka *et al.* (2012). The observed low heritability in days to flowering is expected as this trait is largely environment-influenced. Bello *et al.* (2015) also reported low heritability estimate for days to flowering as was observed in this study. Higher genotypic correlation over phenotypic correlation recorded for most of the traits in these collections further confirms strong genetic association and less environmental influence on the expression of these traits. This agrees with earlier reports by Ibrahim and Hussein (2006) and Nwangburuka *et al.* (2012) that positive genetic association between most of the characters studied among evaluated okra germplasm. The positive, moderate to high genotypic and phenotypic correlations between number of pods per plant, plant height, pod length and fruit pedicel suggests that selection in favor of these traits might lead to increase in number of pods per plant. This also agrees with Adeniji and Aremu (2007) who reported positive and significant phenotypic and

genotypic correlation between plant height at maturity, days to flowering seeds per pod and pods per plant. However, low but negative genotypic and phenotypic association between number of pods per plant and days to flowering indicates that selections favouring increased days to flowering might result in reduced number of pods per plant in this new germplasm.

The principal components (PCs) revealed the contribution of characters to the total variation existing in the germplasm. The first three principal components (PCs) were considered in this study and they accounted for 87% of the total variance in this germplasm. According to the Kaiser criterion (Kaiser, 1960) which suggested that only PCs with Eigen values greater than one should be presented, only the first three PCs had Eigen values greater than one and were retained. Sharma and Prasad (2010) used the first two principal components which accounted for 62.83% of the total variation existing in a germplasm of 20 okra genotypes in India. Principal component analysis indicated that first three principal components contributed 60% of the total variation among 36 okra accessions evaluated in India (Shivaramgowda *et al.*, 2016). The PCA showed the existence of high genetic diversity among the okra germplasm, which is in accordance with the report of Sharma and Prasad (2010). Other researchers have also reported high genetic diversity and the contribution of different traits to the total variation existing among okra germplasm based on PCA. The three important component axes identified traits that are mainly responsible for the variability that exists among the accessions. Characters with high variability as identified by the PCA are expected to respond more to selection during breeding programs (Gana, 2013; Aliyu *et al.*, 2000).

Conclusion

The findings of this study reveal that there exists ample heritable variation in farmers' cultivars and landraces that could be exploited for genetic improvement of okra. The addition of these eleven accessions to NIHORT's genebank is a further step at continually expanding a well-documented horticultural germplasm repository for conservation. It

enhances the potential for okra improvement research currently and in the future.

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