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Research Article

Performance and character contributions to variability in okra (*Abelmoschus esculentus* L. Moench) genotypes

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Okra is an important vegetable crop, but its optimal production is constrained by a myriad of problems including pests, poor agronomic practices, and improper varietal identification among others. A study was carried out to determine the field performance and contribution of agronomic characters to overall variation in eighteen okra genotypes over two locations, Teaching and Research Farms of the Federal University of Agriculture, Abeokuta, Nigeria and Rehoboth Farms Limited, Moniya, Ibadan, Nigeria. The experiments were laid down in a randomized complete block design with three replicates and data were collected on number of days to emergence, number of days to 50% flowering, number of branches per plant, pod length, pod width, number of pods per plant, plant height, pod weight, number of seeds per pod, number of ridges per pod, 100 seed weight, seed, and pod yield. The data were subjected to analysis of variance, heritability in the broad sense, principal component analysis as well as the single linkage cluster analysis. Results revealed significant (p <0.05) variation in the genotypes and high heritability estimates for most of the characters. Number of branches per plant, plant height, number of pods per plant accounted for the highest contributor to variations in the accessions while clustering analysis revealed genotypes; NGB00303, NGB00342 and NGB00346 were distant from all genotypes making them useful materials for hybridization studies.

Keywords: okra, heritability, pca, dendrogram

1 Introduction

Okra, *Abelmoschus esculentus* [L.] Moench is an important vegetable crop in West Africa, and it contributes 60% share of fresh vegetables export (Shete, 2000) and rich in essential amino acids and dietary fibre (NAP, 2006). Selection of okra plants with wide adaptability and yield potential plays a crucial role in breeding programmes (Balai et al., 2014). The choice of breeding methods is conditioned by the variability inherent in available germplasms and the target environment where they are being selected. Wray and Visscher, 2008 reported that estimation of heritability, gives an insight of variance components responsible for transmission of traits. Also, the use of numerical tools such single linkage cluster analysis (SLCA) and principal component analysis (PCA) has been valuable for classifying large number of accessions of agronomic importance (Badenes et al., 2000). The PCA allows visual differentiation among entries and identify possible associations by providing a two-dimensional scatter plot consisting of individual entries. PCA saves time and resources thereby improving the selection responses in breeding programs. The objectives of this study were to determine the performance, heritability of characters and their contribution to and relationships between the genotypes.

2 Materials and methods

2.1 Planting materials, field evaluations and data collection

Eighteen okra accessions were sourced from National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan, Nigeria. Field evaluations were carried out in the early wet season (average temperature of 26 °C, rainfall 175.26 mm, humidity of 87% and sunshine 12 hrs 26 minutes). The experiments were laid out in a Randomized Complete Block Design (RCBD) with three replicates in single row plots at the Teaching and

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Research Farms of the Federal University of Agriculture, Abeokuta, Nigeria (Latititude 7° 15′ N and longitude 3° 25 ′E) and Rehoboth Farms Limited, Moniya, Ibadan, Oyo State, Nigeria (Latitude 3° 56′ N and Longitude 3° 11′ E). Planting was done on 5 m long row with ant inter and intra row spacing of 0.75 m and 0.45 m, respectively. Weed control was done when due and NPK 16 : 16 : 16 fertilizer was applied at 60 kg.ha^{-1}. Insect pests were controlled using cypermethrin at 80 g active ingredient per ha fortnightly till harvest. Data were collected on number of days to emergence, number of days to 50% flowering, number of branches per plant, pod length (cm), pod width (mm), number of pods per plant, plant height (cm), pod weight (g), number of seeds per pod, number of ridges per pod, seed weight (g), 100 seed weight (g), seed yield (kg.ha^{-1}) and pod (kg.ha^{-1}).

2.2 Data analysis

Data collected were subjected to analysis of variance using SAS Release 8.0 (SAS Institute, 1999) and means were separated using Duncan's multiple range test. Variance components and heritability estimates were computed, while principal component analysis (PCA) and single linkage cluster analysis (SLCA) were used to determine the character contribution and variation pattern in the accessions, respectively.

3 Results and discussion

Genetic variation is an important index for yield improvement in crop plant. The genotypes performed differently with respect to characters evaluated except for pod weight and 100 seed weight, while significant genotype × interaction were observed for number of days to emergence, number of branches, plant height, number of pods per plant, pod width and pod yield (Table 1). This shows the environment effect on these characters over locations, which implies that selection for these characters based on phenotypic performance, will not be reliable as they are not stable and responsive to the environment. Accession NGB 00327 germinated earlier than all other accessions. Earliness to flowering is an important factor in selection of high yielding varieties and it was observed that NBG 00298 was the earliest flowering genotype (Table 2). Also, the high yield of NGB 00316 will make is a good material for hybridization studies. The difference between the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (PCV) for the characters (Table 3), suggests the role environment plays in expression of phenotypic characters. Generally, the higher heritability estimates for all characters with moderate for pod weight and 100 seed weight shows that these characters were less amenable by the environment. Therefore, selecting for these characters is likely to be effective. Murtadha

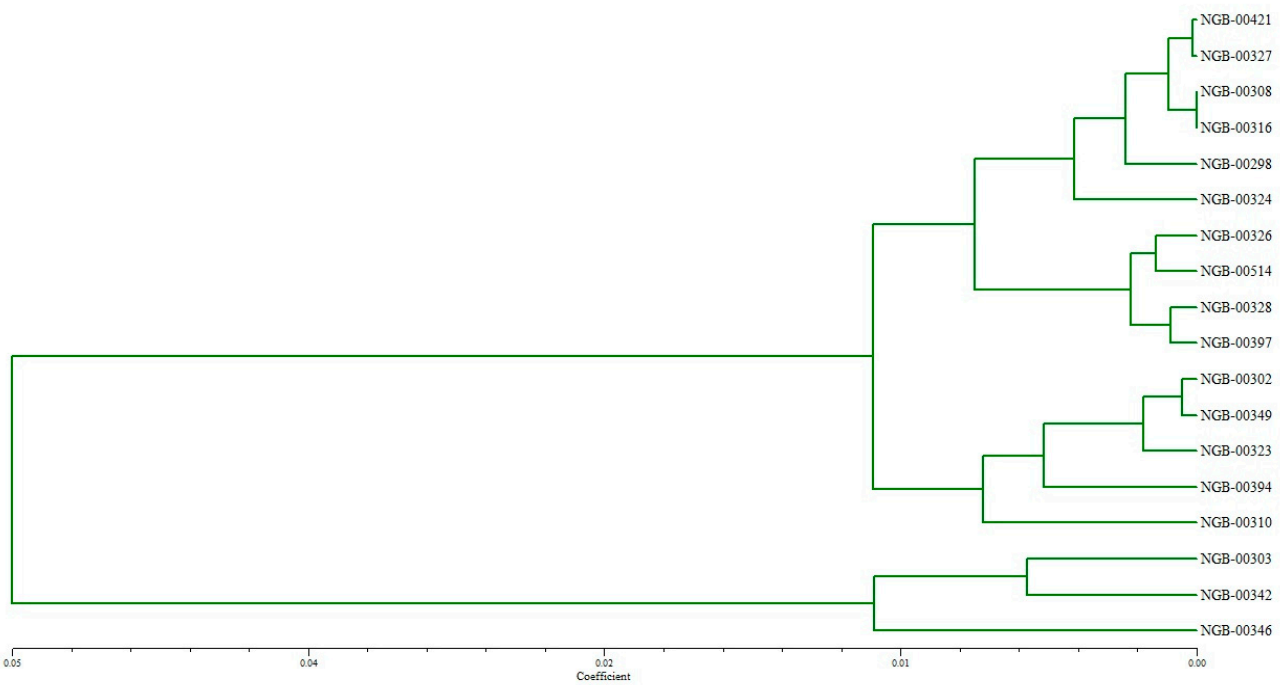

Figure 1 Dendrogram showing similarity coefficients of the okra genotypes evaluated

Table 1 Pooled analysis of variance of characters evaluated for eighteen okra genotypes

Sources of variation	*df*	Number of days to emergence	Number of days to flowering	Number of branches.plant^{-1}	Plant – height (cm)	Number of pods.plant^{-1}	Pod length (cm)	Pod width (mm)	Pod weight (g)	Number of seed.pod^{-1}	Number of ridges.pod^{-1}	100 seed weight (g)	Seed yield (kg.ha^{-1})	Pod yield (kg.ha^{-1})
Block	2	0.20	0.75	3.17	1384.07	63.37*	4.89	13.54	87.46	434.07	0.30	5.27*	29561.71	72584.47
Genotype	17	0.77**	10.35**	21.20**	5718.46**	51.44**	19.65**	94.98**	68.27	2159.76**	8.04**	1.22	52387.69**	196841.06**
Location	1	16.47**	0.27	224.20**	72763.11**	403.10**	3.13	11.03	12.52	101.45	1.02	0.38	687649.51**	3146530.91**
Gen*Loc	17	0.47*	6.68	14.12**	1389.69**	21.97*	2.92	23.54**	56.09	166.91	0.49	1.900	24910.07	78905.71*
Error	69	0.22	4.68	3.15	578.87	11.71	1.85	10.40	61.83	313.92	0.61	1.12	16855.44	43307.13

Table 2 Mean performance of the eighteen genotypes of okra for seed yield and seed related characters

Genotype	Number of days to emergence	Number of days to flowering	Number of branches.plant^{-1}	Plant height (cm)	Number of pods.plant^{-1}	Pod length (cm)	Pod width (mm)	Pod weight (g)	Number of seeds.pod^{-1}	Number of ridges.pod^{-1}	100 seed weight (g)	Seed yield (kg.ha^{-1})	Pod yield (kg.ha^{-1})
NGB 00421	6.53bc	72.50a-c	5.29c-e	158.23a-d	9.87bc	11.76c	25.15e	8.11b	69.78d-f	7.22f	5.73a	267.64a-f	592.77a-c
NGB 00298	6.83bc	70.50a	5.55d-f	175.29a	8.12b-d	10.94cd	32.47ab	13.08ab	139.15a	9.33ab	5.36a	371.71ab	717.49ab
NGB 00302	6.58bc	73.00 a-c	4.65b-e	138.93b-e	5.27c-e	10.14c-e	29.52a-d	11.13b	96.07bc	8.52a-e	6.42a	197.80b-f	426.12c-f
NGB 00303	7.08c	74.83c	3.24a-d	112.45e-g	3.33e	16.08a	30.44 a-d	11.79b	97.55bc	9.38a	6.30a	105.73f	223.62ef
NGB 00308	6.96bc	71.83 a-c	5.89sf	187.33a	10.67ab	10.79 cd	30.16 a-d	9.55b	86.50b-e	8.30b-e	6.07a	352.32a-c	728.51ab
NGB 00310	7.02bc	74.83c	2.68ab	95.25g	4.45de	10.77 cd	29.72 a-d	8.98b	89.30b-d	8.48 a-e	5.59a	116.79f	271.25de
NGB 00316	6.99bc	71.50ab	7.59fg	189.48a	14.28a	11.15 cd	32.04a-c	11.17b	91.03 b-d	8.83a-c	5.77a	391.51a	809.87a
NGB 00323	6.79bc	73.67bc	3.70a-e	103.81fg	5.23 c-e	10.58 c-e	26.71de	21.56a	91.32 b-d	7.90c-f	4.94a	154.38ef	335.58c-f
NGB 00324	6.54bc	71.50ab	4.57 b-e	135.74c-e	9.13 b-d	13.56b	18.33f	5.00b	48.43f	5.28g	4.81a	178.35c-f	448.89b-f
NGB 00326	6.89bc	71.33ab	5.84ef	173.56a	6.11b-e	10.06c-e	31.37 a-c	10.01b	76.10c-e	8.22 c-f	5.56a	301.44a-e	541.48a-d
NGB 00327	5.49a	72.00 a-c	8.54g	169.03ab	8.82 b-d	8.79e	33.21a	10.12b	83.93 c-e	8.39 a-e	5.86a	264.16a-f	597.66a-c
NGB 00328	6.99bc	72.00 a-c	8.19g	165.26a-c	10.59ab	10.20 c-e	30.48 a-d	9.97b	77.70 c-e	7.48ef	6.03a	341.67a-d	530.73b-d
NGB 00342	6.56bc	73.00 a-c	2.09a	118.42 e-g	4.73de	10.27 c-e	28.05b-e	9.51b	90.38 b-d	8.55 a-e	6.42a	99.74f	174.49f
NGB 00346	6.83bc	74.17bc	2.95a-c	129.18d-f	3.35e	9.32de	31.91 a-c	9.45b	93.87 b-d	8.20 c-f	5.94a	167.88d-f	264.49d-f
NGB 00349	6.80bc	73.83 a-c	3.13a-d	131.07d-f	6.28 b-e	11.00 cd	30.27a-d	11.11b	109.17b	8.74a-d	5.63a	221.49a-f	463.50b-e
NGB 00514	6.75bc	72.67 a-c	3.97a-e	139.06 b-e	8.59 b-d	13.96b	20.44f	6.62b	63.48ef	5.15g	5.36a	230.82a-f	386.21c-f
NGB 00394	6.83bc	74.67c	4.89 b-e	88.90g	5.73 c-e	9.57de	27.77c-e	8.60b	91.97 b-d	7.48ef	6.07a	205.06b-f	344.46c-f
NGB 00397	6.37b	73.80bc	3.49a-e	140.36 b-e	6.11 b-e	10.04 c-e	28.43b-e	9.15b	96.58bc	7.72d-f	5.76a	310.97a-e	472.68b-e

Means followed by the same alphabet along columns are not statistically different from one another

Table 3 General mean, estimate of variance components and broad sense heritability of the characters evaluated in the okra genotypes

Character	Mean	Phenotypic variance	Genotypic variance	Phenotypic coefficient of variation	Genotypic coefficient of variation	Heritability (%)
Number of days to emergence	6.72	0.77	0.70	13.06	12.43	91
Number of days to flowering	72.90	10.35	8.78	4.41	4.07	85
Number of branches.plant^{-1}	4.80	21.20	20.15	95.84	93.43	95
Plant height (cm)	142.00	5718.46	5525.50	53.26	52.35	97
Number of pods.plant^{-1}	7.26	51.44	47.53	98.84	95.01	92
Pod length (cm)	11.06	19.65	19.03	40.07	39.43	97
Pod width (mm)	28.69	94.98	91.51	33.97	33.34	96
Pod weight (g)	10.30	68.27	47.66	80.22	67.03	70
Number of seeds.pod^{-1}	88.34	2159.76	2055.13	52.61	51.32	95
Number of ridges.pod^{-1}	7.96	8.04	7.83	35.63	35.17	97
100 seed weight (g)	5.76	1.22	0.84	19.14	15.93	69
Seed yield (kg.ha^{-1})	236.36	52387.69	46769.21	96.84	91.50	89
Pod yield (kg.ha^{-1})	462.06	196841.06	182405.35	96.02	92.43	93

Table 4 Character loading, eigen values and variance components characters evaluated in both locations

Character	Component			
	1	2	3	4
Number of days to emergence	0.41	0.03	0.66	0.02
Number of days to flowering	-0.50	0.22	0.52	-0.03
Number of branches.plant^{-1}	0.80	-0.17	-0.03	-0.07
Plant height (cm)	0.87	-0.11	0.06	-0.10
Number of pods.plant^{-1}	0.81	-0.31	0.02	0.11
Pod length (m)	-0.14	-0.42	0.59	0.23
Pod width (mm)	0.29	0.77	-0.10	0.05
Pod weight (g)	0.07	0.30	-0.22	0.60
Number of seeds.pod^{-1}	0.21	0.79	0.13	0.24
Number of ridges.pod^{-1}	0.21	0.81	0.08	0.19
100 seed weight (g)	0.09	0.35	0.02	-0.70
Seed yield (kg.ha^{-1})	0.87	-0.15	0.01	-0.01
Pod yield (kg.ha^{-1})	0.93	-0.10	0.00	0.04
Eigen value	4.33	3.06	1.15	1.10
Variance (%)	30.94	21.87	8.23	7.82
Cumulative variance (%)	30.94	52.807	61.041	68.86

et al. (2000) suggested that a trait with high GCV and heritability will be a good predictor of pod yield. The high heritability and GCV observed for number of branches per plant, number of pods per plant, total seed yield and total pod yield could be attributed to additive gene action thus making selection for them simple. The lower GCV indicated for number of days to emergence and flowering, and 100 seed weight indicated them less amenable to improvement by selection. Ariyo (1989) reported the need to breed for specific environments because the response of most characters to environment was non-linear. Several investigators also studied heritability of different traits in okra crop which support the present findings. Singh et al. (2006) reported high heritability for days to flowering and pod weight. Indurani and Veeragavathatham (2005) and Singh et al. (2006) also reported moderate to high heritability for plant height. The first three principal components were the most important in discrimination accessions as reported by Clifford and Stephenson (1975). From this study, four of the 13 principal components had eigen values greater than one and accounted for 30.90%, 21.87%, 8.23% and 7.82% of the total variation, respectively and 68.86% cumulatively (Table 4). The first principal component was loaded largely with number of branches per plant, plant height, number of pods per plant, seed, and pod yield.

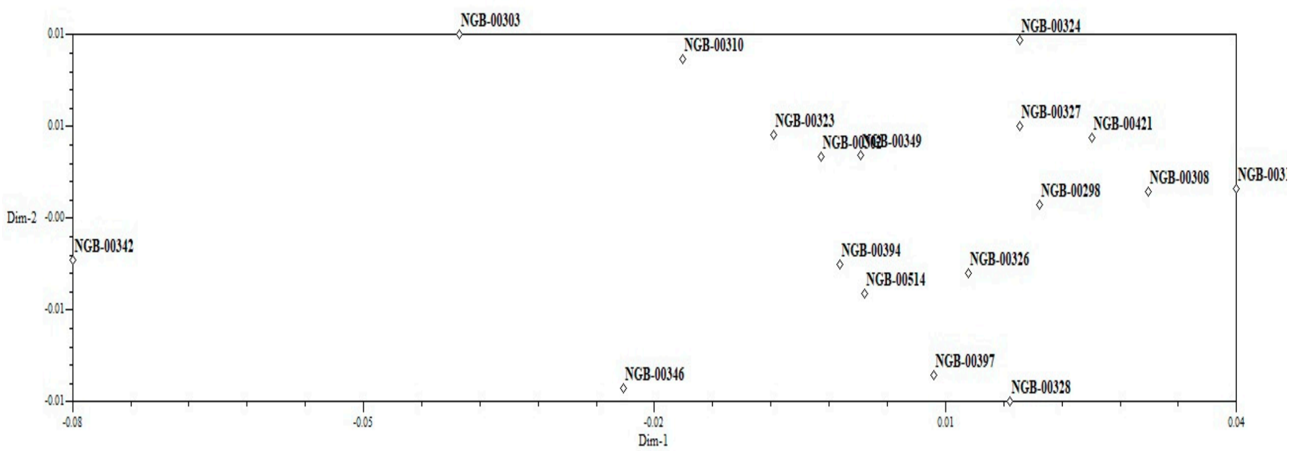

Figure 2 Two dimensions plots of the configurations of the okra genotypes

While the second principal component axis comprised pod width, number of seeds per pods and number of ridges per pod. The eigen values for axis one was high (4.33) and low (1.10) for axis four. The contributions pod and seed characters were relatively high in the principal axes 1 and 2. This agrees with the report of Ariyo and Odulaja (1991) and Ogunbodede (1997). Clustering of the accessions also suggest a close relationship between them. Aliyu and Fawole (2000) also demonstrated the importance of cluster analysis based on similarity coefficients. The genotypes were grouped into two major groups: I and II. Group I had only three genotypes which were late flowering, had fewer number of pods per plant and low yielding (Fig. 1). Genotypes NGB00303, NGB00342 and NGB00346 were the most diverse as also revealed in Fig. 2. Which makes them a useful source for hybridization with members of the other group in okra improvement programme.

4 Conclusion

This study revealed significant variability in the genotypes and characters such as plant height, number of branches and number of pods were useful in discriminating the okra genotypes. High heritability estimates were observed for pod related parameters which makes them amenable for selection. Also, distinctions of genotypes: NGB00303, NGB00342 and NGB00346 from all other genotypes will make them useful for hybridization studies.

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