

Assessment of genetic variability among accessions of okra (*Abelmoschus esculentus* L. Moench)

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Okra yields are low in West and Central Africa and factors including narrow genetic base of available germplasm have been implicated. An assessment of genetic variability among germplasm from various sources and knowledge of trait contributions to these variations is crucial to the success of okra breeding program. Eighteen okra accessions were evaluated during the 2020 cropping season in Nigeria to assess the genotypes for genetic diversity, group the accessions into clusters and identify traits that chiefly accounted for the variations among the genotypes. Data obtained were subjected to analysis of variance (ANOVA), metroglyph and principal component analyses (PCA). ANOVA revealed significant accession mean squares for majority of the measured traits. Metroglyph analysis grouped the accessions into four clusters with members of Cluster IV generally high-yielding, early-maturing and short genotypes. NGB00353 and NGB00356 that were among genotypes with high total index scores were members of Cluster IV. The first four principal components (PCs) accounted for 80% of the total observed variation. PC1 with the highest discriminatory power was loaded with days to budding, internode length, pod yield.plot⁻¹ and the number of pods.plant⁻¹. The variation within and between clusters could be explored in okra breeding program.

Keywords: clusters, early-maturing, high yield, okra germplasm, variations

1 Introduction

Okra is one of the most important fruit vegetable crops and a source of calorie for human consumption (Nwangburuka et al., 2012). It is a multipurpose vegetable due to the various uses of the fresh leaves and immature fruits which are consumed as vegetables, salads, soup and stew (Rashwan, 2011). Though okra worldwide production and total area of cultivation area has increased over the years, low yields are still being recorded on farmers' fields particularly in West Africa (Olayiwola et al., 2015). Ahiakpa et al. (2013) identified lack of adapted cultivars, narrow genetic base of germplasm collections as well as disease and pest incidence to be responsible for the relatively lower yields in the sub-region. Kumar et al. (2010) and Alake et al. (2012) advocated for the need to develop new and superior genotypes to replace existing older and low-yielding genotypes. Plant

breeders select and develop superior genotypes from existing variability within the germplasm. Omonhinmin and Osarawu (2005) reported high genetic variability within *Abelmoschus* spp. However, Kumar et al. (2010) noted that much of the variability was yet to be explored due to the relatively lower breeding activities on okra. A detailed understanding of the magnitude and pattern of genetic variability is required for the improvement of any crop. Plant breeders have thus employed several multivariate techniques including Metroglyph and Principal Component Analyses (PCA) to profile the variability within the germplasm of different crops (Aremu, 2011; Nwangburuka et al., 2011; Osarawu et al., 2013). Anderson (1960) proposed Metroglyph analysis, a technique that reveals patterns of morphological variation in crop species by reducing the complex inter-relationship among accessions into a pictorial scatter

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diagram showing clusters based on relatedness and genotype superiority based on trait profiles. Olayiwola et al. (2015) concluded that information from metroglyph analysis could guide breeders on the choice of parents for hybridization. PCA partitions total variation into components and identifies trait(s) that chiefly account(s) for the observed variability among genotypes (Bhusal et al., 2016). The current study aimed to determine the relationships among the evaluated okra accessions and identify trait(s) responsible for the variations among the genotypes.

2 Materials and methods

2.1 Experimental site and planting materials

The study was carried out at the Teaching and Research Farm of College of Agricultural Sciences, Yewa Campus (7° 12' N; 3° 3' E), Olabisi Onabanjo University. Eighteen (18) accessions of okra were sourced from National Centre for Genetic Resources and Biotechnology (NACGRAB), Ibadan.

2.2 Field preparation, layout and evaluation

The land was cleared, ploughed and harrowed. The experiment was laid out in a Randomized Complete Block Design and was replicated thrice. Each of the accessions was sown on a single-row plot that was 4.5 m long. The inter-row spacing was 0.45 m while within-row spacing was 0.45 m giving a total of eleven plants per plot. Two seeds were planted per hole but were later thinned to one per stand. All recommended agronomic practices required for optimum performance of the crop were followed.

2.3 Data collection and analysis

Observations were made on days to budding, days to 50% Flowering, plant height at flowering, internode length (cm), number of branches/plant, days to maturity, plant height (cm), number of pods, pod width (cm), pod length (cm), pod weight (kg) and pod yield.plot⁻¹ (kg)

The data were subjected to Analysis of Variance (ANOVA) and significantly different means were separated by Duncan multiple range test (DMRT) on SAS Institute Inc. (2001). Furthermore, data were subjected to Metroglyph analysis (Anderson, 1960) as earlier described by Olayiwola et al. (2015) and Adeniji et al. (2020). Briefly, coefficient of variation (CV) was determined for each of the traits. Two traits with the highest CV were used as coordinates (Y- and X-axes) on the scatter diagram and the point of intersection was the marker (glyph) for each accession. The other traits were then represented by rays at different points on the glyph. Rays for a particular trait maintained similar positions on each glyph. The range of values for each trait was grouped into three classes with each class having an associated index score. The index score determined the length of the rays and total sum of the scores represented the value or worth of the evaluated accessions for the measured traits. Based on positions on the scatter diagram the accessions were grouped into clusters. Data were also subjected to principal component analysis to identify the traits that mostly accounted for the total variation observed.

3 Results and discussion

The significant accession mean squares for most of the measured characters (Table 1) underscored the large genetic divergence among the okra accessions (Nwangburuka et al., 2012). This variability could thus be explored to develop superior genotypes. The highest coefficients of variation (CVs) were associated with pod yield and number of pods.plant⁻¹ (Table 2). The two traits thus the Y and X axis of the metroglyph scatter diagram (Adeniji et al., 2020). NGB00355 was the earliest to flower and was significantly different from NGB00314 and three other accessions (Table 3). This implies that NGB00355 could be a potential source of alleles for earliness in okra breeding programme (Olayiwola et al., 2015). NGB00644 had the tallest plants and could therefore be targeted for tallness in a breeding scheme. NGB00353 had the highest yield among the accessions and could thus be considered

Table 1 Analysis of variance of nine characters measured on eighteen accessions of okra

Sources of variation	Df	Days to 50% flowering	Plant height	Plant height at flowering	Days to budding	Days to podding	Number of branches.plant ⁻¹	Internode length	Number of pods.plant ⁻¹	Pod length	Pod width	1000-seed weight	Pod yield.plot ⁻¹
Rep	2	73.11	3,687.22**	2,107.39	58.68	21.85	1.19	18.21	40.07	73.58	146.51	0.99	16,673.65
Accession	17	133.78	3,907.88**	1,507.14	80.11	150.72**	3.09	7.65*	360.86**	83.63	146.83	6.71	83, 119.04**
Error	34	78.81	429.12	842.68	64.88	53.98	1.72	3.21	87.07	83.16	134.89	5.48	22,260.72

*, **: significant at $P \leq 0.05$ and 0.01 , respectively

Table 2 Range, mean, coefficient of variation in percentage (CV (%)), index scores and position of characters on the glyph

	Range	Mean	CV (%)	Index scores			Positions
				1	2	3	
Days to 50% flowering	56.00–73.93	64.19	8.84	56.00–63.08	63.09–70.17	≤73.93	↑
Plant height	66.07–176.17	113.57	30.98	66.07–102.76	102.76–139.46	≤176.17	↓
Plant height at flowering	49.99–120.77	80.00	27.23	49.99–73.57	73.57–97.19	≤120.77	↗
Days to budding	47.17–64.10	55.19	8.75	47.17–52.81	52.81–58.45	≤64.10	↖
Days to podding	56.53–78.33	67.71	9.47	56.53–63.43	63.43–70.88	≤78.33	←
Number of branches.plant¹	4.83–8.17	6.25	15.76	4.83–5.93	5.94–7.05	≤8.17	→
Internode length	4.17–9.50	6.95	22.33	4.17–5.94	5.95–7.71	≤9.50	↗
Number of pods.plant¹	3.67–39.00	16.17	65.94	3.67–15.44	15.45–27.22	≤39.00	y-axis
Pod length	6.40–29.67	8.83	58.09	6.40–14.15	14.16–21.90	≤29.67	↘
Pod width	8.23–11.90	11.73	57.96	8.23–9.44	9.45–10.67	≤11.90	↘
1000-seed weight	12.63–18.90	15.4	9.45	12.63–14.71	14.72–16.80	≤18.90	←
Pod yield.plot¹	56.00–520.83	256.55	63.05	56.00–210.93	210.94–365.89	≤520.83	x-axis

Table 3 Mean performance of the evaluated 18 okra accessions with their index scores for each character in parenthesis

Accession	Days to 50% flowering	Plant height	Plant height at flowering	Days to budding	Days to podding	Number of branches.plant ⁻¹	Internode length	Number of pods.plant ⁻¹	Pod length	Pod width	1000-seed weight	Pod yield.plot ⁻¹	Total index score
NGB00314	72.27 ^{a(-3)}	155.03 ^{ab(2)}	104.93 ^{ab(3)}	61.27 ^{ab(-3)}	77.70 ^{a(-3)}	6.67 ^{a-d(2)}	9.50 ⁽³⁾	11.33 ^{c-e(1)}	7.90 ^{b(1)}	39.50 ^{a(1)}	17.17 ^{a-c(3)}	188.9 ^{b-e(1)}	8
NGB00342	60.33 ^{a-c(-1)}	102.57 ^{c-f(2)}	96.20 ^{ab(3)}	56.00 ^{ab(-2)}	75.65 ^{ab(-3)}	5.00 ⁽²⁾	7.67 ^{a-d(1)}	4.0 ^{e(1)}	7.50 ^{b(3)}	10.70 ^{b(1)}	14.00 ^{bc(1)}	56.0 ^{e(1)}	9
NGB00380	73.93 ^{a(-3)}	174.50 ^{a(3)}	120.77 ^{a(3)}	64.10 ^{a(-3)}	78.33 ^{a(-3)}	7.33 ^{a-d(3)}	9.50 ⁽¹⁾	3.67 ^{e(1)}	8.40 ^{b(1)}	10.30 ^{b(2)}	15.03 ^{a-c(2)}	68.9 ^{e(1)}	8
NGB00387	73.60 ^{a(-3)}	97.27 ^{c-f(1)}	105.50 ^{ab(3)}	60.67 ^{ab(-3)}	75.75 ^{ab(-3)}	5.75 ^{a-d(1)}	7.57 ^{a-d(2)}	4.50 ^{e(1)}	7.10 ^{b(1)}	10.75 ^{b(3)}	15.15 ^{a-c(2)}	68.1 ^{e(1)}	6
NGB00302	72.77 ^{a(-3)}	121.40 ^{bc(2)}	119.27 ^{a(3)}	62.83 ^{ab(-3)}	75.50 ^{ab(-3)}	6.17 ^{a-d(2)}	8.50 ^{a-c(3)}	7.33 ^{de(1)}	6.40 ^{b(1)}	8.23 ^{b(1)}	12.63 ^{c(1)}	119.7 ^{de(1)}	6
NGB00373	68.70 ^{a-d(-2)}	87.57 ^{c-f(1)}	76.30 ^{ab(2)}	55.20 ^{ab(-2)}	69.17 ^{a-c(-2)}	8.17 ^{a(3)}	5.50 ^{b-d(1)}	24.67 ^{a-d(2)}	6.87 ^{b(1)}	9.20 ^{b(1)}	15.57 ^{a-c(2)}	373.9 ^{a-d(3)}	10
NGB00297	67.37 ^{a-d(-2)}	66.07 ^{f(1)}	52.77 ^{b(1)}	55.267 ^{ab(-2)}	66.03 ^{a-c(-2)}	6.67 ^{a-d(2)}	4.17 ^{d(1)}	21.33 ^{a-e(2)}	7.17 ^{b(1)}	11.90 ^{b(3)}	16.43 ^{a-c(2)}	319.6 ^{a-e(2)}	9
NGB00298	60.75 ^{a-d(-1)}	164.00 ^{a(3)}	67.50 ^{ab(1)}	58.50 ^{ab(-3)}	66.75 ^{a-c(-2)}	5.50 ^{b-d(1)}	9.0 ^{ab(3)}	4.0 ^{e(1)}	7.50 ^{b(1)}	11.00 ^{b(3)}	14.00 ^{bc(1)}	72.0 ^{e(1)}	9
NGB00421	65.67 ^{a-d(-2)}	108.93 ^{c-e(2)}	61.27 ^{b(1)}	54.20 ^{ab(-3)}	67.93 ^{a-c(-2)}	5.33 ^{cd(1)}	6.167 ^{a-d(2)}	9.67 ^{c-e(1)}	10.50 ^{b(1)}	10.33 ^{b(2)}	15.83 ^{a-c(2)}	151.0 ^{de(1)}	6
NGB00323	62.43 ^{a-d(-1)}	76.43 ^{d-f(1)}	53.07 ^{b(1)}	51.70 ^{ab(-1)}	68.93 ^{abc(-2)}	6.17 ^{a-d(2)}	5.50 ^{b-d(1)}	24.00 ^{a-d(2)}	7.40 ^{b(1)}	11.20 ^{b(3)}	13.73 ^{bc(1)}	326.1 ^{a-e(2)}	10
NGB00356	61.60 ^{a-d(-1)}	88.70 ^{c-f(1)}	73.07 ⁽¹⁾	47.37 ^{b(-1)}	63.33 ^{bc(-1)}	8.00 ^{ab(3)}	5.33 ^{cd(1)}	30.67 ^{ab(3)}	7.40 ^{b(1)}	9.27 ^{b(1)}	15.47 ^{a-c(2)}	462.5 ^{a-c(3)}	13
NGB00499	61.60 ^{a-d(-1)}	88.70 ^{c-f(1)}	92.22 ^{ab(2)}	52.00 ^{ab(-1)}	63.27 ^{bc(-1)}	4.83 ^{d(1)}	6.67 ^{a-d(2)}	25.67 ^{a-c(2)}	6.90 ^{b(1)}	11.53 ^{b(3)}	14.77 ^{a-c(2)}	378.2 ^{a-d(3)}	14
NGB00644	61.27 ^{a-d(-1)}	176.17 ^{a(3)}	68.57 ^{ab(1)}	54.67 ^{ab(-2)}	64.33 ^{a-c(-2)}	7.75 ^{a-c(3)}	8.33 ^{a-c(3)}	5.3 ^{e(1)}	8.33 ^{b(1)}	10.00 ^{b(2)}	17.57 ^{ab(3)}	91.8 ^{de(1)}	13
NGB00353	60.80 ^{a-d(-1)}	97.47 ^{c-f(1)}	70.97 ^{ab(1)}	52.50 ^{ab(-1)}	67.23 ^{a-c(-2)}	6.167 ^{a-d(2)}	6.33 ^{a-d(2)}	26.33 ^{a-c(2)}	6.90 ^{b(1)}	9.50 ^{b(2)}	18.90 ⁽³⁾	520.8 ⁽³⁾	13
NGB00412	60.33 ^{a-d(-1)}	72.77 ^{ef(1)}	49.99 ^{b(1)}	52.50 ^{ab(-1)}	62.57 ^{bc(-1)}	5.33 ^{cd(1)}	5.17 ^{d(1)}	24.367 ^{a-d(2)}	7.27 ^{b(1)}	9.33 ^{b(1)}	15.53 ^{a-c(2)}	478.3 ^{ab(3)}	10
NGB00477	59.43 ^{b-d(-1)}	93.37 ^{c-f(1)}	93.30 ^{ab(2)}	50.33 ^{ab(-1)}	61.57 ^{bc(-1)}	6.167 ^{a-d(2)}	6.00 ^{a-d(2)}	9.67 ^{c-e(1)}	29.67 ^{a(3)}	9.60 ^{b(2)}	15.40 ^{a-c(2)}	197.4 ^{b-e(1)}	13
NGB00396	56.63 ^{cd(-1)}	114.63 ^{cd(2)}	67.27 ^{ab(1)}	47.167 ^{b(-1)}	56.53 ^{c(-1)}	5.33 ^{cd(1)}	6.33 ^{abcd(1)}	39.00 ⁽²⁾	8.53 ^{b(1)}	9.10 ^{b(1)}	14.17 ^{bc(2)}	505.2 ^{a(3)}	11
NGB00355	56.00 ^{d(-1)}	158.73 ^{a(3)}	67.15 ^{ab(1)}	52.75 ^{ab(-1)}	58.15 ^{c(-1)}	6.167 ^{a-d(2)}	7.87 ^{a-c(3)}	15.50 ^{b-e(1)}	7.25 ^{b(1)}	9.70 ^{b(2)}	15.85 ^{c(-2)}	239.5 ^{a-e(2)}	14

Means with different letters are significantly different from one another at $p \leq 0.05$ using DMRT. Negative index score indicates preference for lower values for the corresponding traits

Table 4 Trait loading, eigen value, proportion of variance explained, and cumulative variance obtained from principal component analysis

Character	PC1	PC2	PC3	PC4
Days to 50% flowering	0.36	0.11	-0.38	0.08
Plant height	0.28	0.02	0.53	-0.34
Plant height at flowering	0.33	-0.03	-0.14	0.26
Days to budding	0.40	-0.02	-0.18	-0.08
Days to podding	0.25	0.39	-0.30	0.24
Number of branches	0.03	0.51	0.18	0.22
Internode spacing	0.38	-0.04	0.26	-0.27
Number of pods.plant ⁻¹	-0.37	0.21	-0.18	-0.15
Pod length	-0.04	-0.22	0.34	0.77
Pod width	0.18	0.38	0.02	-0.05
1000-seed weight	-0.06	0.52	0.40	0.06
Pod yield	-0.37	0.26	-0.14	-0.09
Eigenvalue	5.26	1.82	1.41	1.12
Proportion of variance explained	0.44	0.15	0.12	0.09
Cumulative variance	0.44	0.59	0.71	0.80

as a source of high-yielding genotypes. The superiority or desirability of a genotype is more reliably determined if considered across several traits rather than a single trait (Yan & Fregeau-Reid, 2018). In our study, the total index scores reflect the genotypic values of the accessions across all traits of interest. NGB00355 and NGB00499 had the joint highest index score and were jointly followed by NGB00477, NGB00353, NGB00356 and NGB00644. Among the accessions with top index scores NGB00353 and NGB00356 combined earliness to flowering with high-yield thus indicating the desirability of the genotypes among the evaluated accessions. Though the accessions with the highest index scores (NGB00355 and NGB00499) also flowered early, they only had low to moderate pod yield. This re-emphasized the need to allot appropriate weights to plant characters in the development of selection index. However, the accessions with the lowest total index scores NGB00302, NGB00387 and NGB00421 were medium- to late-maturing and had low yields. This underscored the relative ability of the technique to discriminate among accessions based on field performance. Number of pods.plant⁻¹ and that had the highest CVs were used as the X and Y coordinates in plotting the metroglyph (Fig. 1). NGB00380 and NGB00396 exhibited the largest divergence implying that the genetic differences between the genotypes could be explored for heterotic breeding (Ranpise et al., 2018). The metroglyph classified the accessions into four clusters and thus indicated that the technique captured the variations among the accessions (Khalid et al., 2018). Cluster I had nine members that were generally low-

yielding but an admixtures of tall and short accessions as well as genotypes. Two of the nine members of this group were among the accessions with top total index scores across all measured traits. The within group variations could be explored either by selection or by developing composites with improved attributes that could arise from transgressive segregation (Shujaat et al., 2014). Cluster II had one member that was tall, early-maturing and relatively than members of Cluster I. The four members of Cluster III were evenly divided between low- and medium-yielding as well as early- and medium-maturing genotypes. The within group variation could also be explored in okra improvement programme. Cluster IV had four members that were generally high-yielding, early-maturing and short genotypes. Members of this group were generally associated with high total index scores indicating their potential as sources of favourable alleles for the development of quality pure lines and elite populations. The differences between groups could also be explored to develop superior hybrids and composites that could be used to broaden the genetic base of adapted germplasm. The principal component analysis which detailed the trait contributions to the variation among the accessions was presented in Table 4. The first four principal components (PCs) had significant discriminatory powers based on the eigen values (>1) and accounted for 80% of the total variation. PC1 with the highest discriminatory power explained more than half of the total variation that was accounted for by the four PCs. The next components, PC2, PC3 and PC4, when combined explained less than

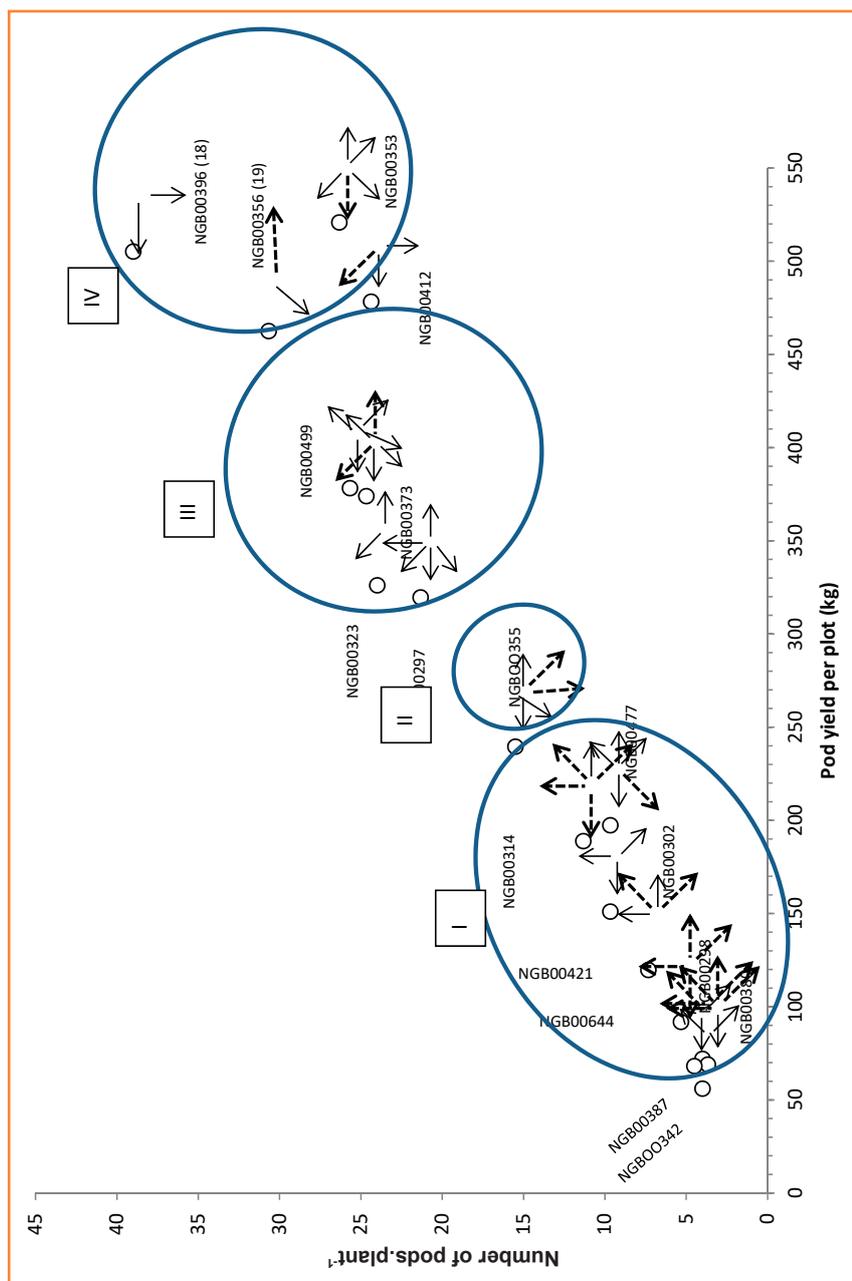


Figure 1 Scatter diagram from Metroglyph analysis showing the classification of the eighteen genotypes into four clusters

half of the total variation captured by the four components. This implies that loadings on the other three components must be considered with caution. PC1 was loaded with days to budding, internode length, pod yield.plot⁻¹ and the number of pods.plant⁻¹. This implied that these traits chiefly contributed to the variations observed among the accessions and therefore could be

targeted for developing selection index in okra breeding program.

4 Conclusion

There was substantial genetic variation among the eighteen accessions of okra for the measured characters. Some accessions combined earliness to maturity with high-yielding potential and would be valuable sources of favourable alleles

for okra improvement. Accessions classified into clusters based on phenotypic similarities and variation within and between clusters could be explored through selection or heterosis in okra breeding program. Four traits were identified to have contributed substantially to the observed variation among the genotypes and could be considered in the development of efficient selection index.

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