

Original Research Article

Genetic Diversity Studies in 29 Accessions of Okra (*Abelmoschus* spp L.) using 13 Quantitative Traits.

ABSTRACT

Aims: Twenty nine (29) local and exotic lines (accessions), of okra (*Abelmoschus* spp L.) were evaluated for variation in phenotypic traits.

Study design: They were laid out in a Randomised Complete Block Design (RCBD) with four replications and evaluated based on 13 quantitative characters.

Place and Duration of Study: Research farm of the Biotechnology and Nuclear Agriculture Research Institute (BNARI), Ghana Atomic Energy Commission (GAEC), Department of Nuclear Agriculture and Radiation Processing, Graduate School of Nuclear and Allied Sciences, University of Ghana, between June 2011 and July 2012.

Methodology: The accessions were grown in the field, each on a subplot measuring 3.5 m x 2.5 m, with seeds sown at a spacing of 0.70 m x 0.50 m. Data were collected using the International Plant Genetic Resources Institute (IPGRI) Descriptor List for okra.

Results: The accessions exhibited significant variation in all quantitative traits studied. Block coefficients of variation were extremely low, implying that results obtained are reliable and repeatable over replications. Cluster analysis based on Canberra, Furthest Neighbour Similarity Matrix grouped the accessions into two major clusters and subsequently into four sub-clusters, with no duplications, based on the characters studied. Seven pairs of quantitative traits were positive and significantly correlated ($P \leq 0.05$) while three were highly significantly associated ($P \leq 0.01$). The highest correlation ($r = 0.95$) was between number of days to 50% flowering (NDF_f) and number of days to 50% fruiting (NDF_r).

Conclusion: The pattern of clustering showed some degree of association between quantitative characters and geographic origin of the collections. Five Principal Components (PCs) accounted for 78.51% of the total variance, with PC₁ recording 32.44%. Different traits contributed differently to total genetic variance.

Keywords: Okra, accessions, phenotypic characterisation, variation, factor score, coefficients

1. INTRODUCTION

Production and consumption of okra (*Abelmoschus* spp L. Moench) is widespread across West Africa (Ahiakpa et al., 2014; Oppong-Sekyere et al., 2012; Siemonsma and Kouame, 2004) where all vegetative and reproductive parts as well as the fresh fruits are used variously for food preparation (Osawaru et al., 2013; Oppong-Sekyere et al., 2012). Minor applications are found in folk medicine and industry (Kumar et al., 2010; Siemonsma and Kouame, 2004).

21 In Ghana, the vegetable is accepted for consumption in all regions. It is cultivated as a
22 garden or commercial crop (Norman, 1992). Intense cultivation is found in peri-urban areas to
23 meet an ever-growing urban population, with targeted exports from elite farmers. Selection of
24 varieties for cultivation is, therefore, based on end-user preference and adaptation to local
25 agro-ecology.

26 Currently, genotypes available include many locally adapted landraces as well as some
27 exotic lines selected to meet specifications of export destinations in Europe and America. On-
28 going breeding work in okra is limited (Ahiakpa, et al., 2013; Oppong-Sekyere et al., 2012).
29 Hence, characterisation of these genotypes is incomplete.

30 Characterisation based on phenotypic traits is not easily reproducible particularly, since these
31 traits are influenced largely by environmental variations (Staub et al., 1996). In addition, it
32 requires a large tract of land and/or greenhouse space in which to grow large populations of
33 plants, making it labour intensive and difficult to manage (Ahiakpa, et al., 2013; Vogel et al.,
34 1996). However, the tool has remained useful as a necessary first step prior to more in-depth
35 biochemical or molecular studies in okra germplasm studies (Smith and Smith, 1992).

36 By and large, the potential value of germplasm is hugely dependent on the efficiency of
37 techniques designed to facilitate detailed study of individual traits and to differentiate among
38 accessions (De Vicente et al., 2005; Engels and Visser, 2003; Rubenstein and Heisey, 2003).
39 Hence, characters recorded on individual accessions can serve as diagnostic descriptors for
40 those accessions (Rubenstein and Heisey, 2003); to help breeders as well as genebank
41 curators keep track of such accessions and check for genetic integrity over a number of years
42 of conservation. The objective of the study was to assess variability in quantitative
43 characteristics of some accessions of okra collected across eight out of ten geographic
44 regions of Ghana.

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47 **2. MATERIALS AND METHODS**

48 Twenty-nine (29) accessions of Okra (*Abelmoschus* spp L.) were assembled from eight
49 geographic regions of Ghana using IPGRI (1991) passport data as indicated in Table 1.

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55 **Table 1: Identities and Collection Sites of Accessions of Okra used in the Study**

No. of Accessions	Region	Accession
6	Ashanti	Agric short fruit, Agric type I, Asante type II, Asontem-ASR, Debo, Kortebortor-ASR
5	Brong Ahafo	Asontem-BAR, Asontem-NV., Kortebortor-BAR, Nkran Nkuruma, Yeji-Local
1	Central	Cape
3	Eastern	Amanfrom, DKA, Asontem-ER
8	Greater Accra	Asontem-GAR, Atomic, Clemson spineless, Cs-Legon, Labadi, Legon fingers, Volta, Indiana
3	Upper East	Mamolega, Mapelega, Wune mana
1	Western	Juaboso
2	Volta	Akrave', Kpeve'

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 57 The study was conducted at the Nuclear Agricultural Research Centre (NARC) of the
 58 Biotechnology and Nuclear Agriculture Research Institute (BNARI), Ghana Atomic Energy
 59 Commission (GAEC). The soil at the site is the Nyigbenya-Haatso series, which is a typically
 60 well-drained Savannah Ochrosol (Ferric Acrisol) derived from quartzite Schist
 61 (FAO/UNESCO, 1994).

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63 **2.1 Experimental Design and Field Layout**

64 A total land area of 60 m x 32 m was cleared, ploughed and harrowed to a fine tilth for
 65 planting. The Randomised Complete Block Design (RCBD) was used with four replications;
 66 each replicate measured 30 m x 12.5 m, separated by a distance of 2 m and consisted of 30
 67 subplots (within the block). Each subplot had a dimension of 3.5 m x 2.5 m and spaced by a
 68 distance of 1 m.

69 Field cultivation was done from July 2011 to February 2012. Seeds were sown at a depth of 2
 70 cm, at a spacing of 0.70 m x 0.50 m within and between rows with three to four seeds per hill
 71 and later thinned to two after germination. No fertiliser was applied, but weeds were
 72 controlled fortnightly and water was supplied during the dry season using watering can.

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74 **2.1.1 Data Collection**

75 Data were collected on five randomly selected and tagged plants within the central rows,
 76 using the International Plant Genetic Resources Institute, (IPGRI, 1991) Descriptor List for
 77 okra. Characters on which data were taken include:

78 First flowering node (FFN),

79 First fruit-producing node (FFPN),
80 Maximum number of internodes (MNI),
81 Maximum plant height (cm) (MPH),
82 Number of days to 50% germination (NDG),
83 Number of days to 50% flowering (NDF_f),
84 Number of days to 50% fruiting (NDF_r),
85 Number of fresh fruits per plant per harvest (NFPH),
86 Number of seeds per fruit (NSPF),
87 Stem diameter at the base (mm) (STB),
88 Total number of leaves per plant (TNLP),
89 Total number of fruits per plant (TNFP),
90 1000-seed weight (g), (TSW).

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92 **2.1.2 Data Analysis**

93 Mean values of data collected were used for Analysis of Variance (ANOVA) and Duncan's
94 Multiple Range Test (DMRT) for mean separation. Correlation analysis was used to
95 determine the degree of association among the traits. Further, the Principal Component
96 Analysis was employed to assess percentage contribution of each trait to total genetic
97 variability among the accessions. Cluster analysis based on Canberra, Furthest Neighbour
98 Similarity Matrix was also employed to obtain a dendrogram depicting the deduced genetic
99 relationships among the accessions based on evaluation of the 13 characters. Genstat
100 Statistical Software Programme (Payne et al., 2007), Microsoft Excel Software, and
101 Statgraphics Plus XV.I Software (2010) were used for all the data analyses.

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103 **3. RESULTS AND DISCUSSION**

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105 **3.1 Variability in Quantitative Traits**

106 Table 2 shows phenotypic variability in 13 quantitative traits among the 29 accessions of
107 okra. The accessions exhibited significant variation with respect to all thirteen quantitative
108 characters. DKA recorded the highest number of days to 50% germination (NDG), number
109 of days to 50% flowering (NDF_f) and number of days 50% fruiting (NDF_r). Similarly, Nkran
110 Nkuruma recorded the highest maximum plant height (MPH), maximum number of
111 internodes (MNI) and first fruit-producing node (FFPN).

112 In the same vein, Yeji-Local recorded the highest total number of leaves per plant (TNLP)
113 and number of seeds per fruit (NSPF) as did Kortebortor-BAR for stem diameter at the base

114 (STB), and total number of fruits per plant (TNFP). Four other accessions, Asontem NV,
115 Akrave, Amanfrom and Legon fingers recorded the highest values for maximum number of
116 internodes (MNI), first fruit-producing node (FFPN), total number of fruits per plant (TNFP)
117 and 1000-seed weight (TSW), respectively.

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123 Table 2: Variability in Quantitative Traits among 29 Accessions of Okra.

ACCESSION	MPH	MNI	FFN	TNLP	STB	NDG	FFPN	NDF _i	NDF _r	TNFP	NFPH	NSPF	TSW
Agric short fruit	59.00 ^{opqr}	17.00 ^e	6.00 ^o	13.75 ^{kl}	7.80 ^{jk}	52.50 ^{kl}	7.00 ^{ijk}	46.50 ^h	12.00 ^c	8.00 ^{ghi}	27.00 ^{hi}	23.75 ^o	48.12 ^q
Agric type I	76.05 ^{jk}	18.00 ^c	9.00 ^l	11.0 ^{mn}	8.10 ^{hi}	54.25 ^{fg}	10.25 ^{bcd}	47.00 ^g	12.00 ^c	10.00 ^{ghi}	42.25 ^d	27.75 ^{mn}	58.98 ^g
Akrave'	47.05 ^{rs}	19.00 ^a	9.00 ^l	27.00 ^c	9.30 ^e	89.75 ^c	7.50 ^{hijk}	80.00 ^c	10.00 ^f	15.00 ^{de}	21.75 ^{lm}	31.75 ^{ij}	48.63 ^p
Amanfrom	82.85 ^{ghij}	17.87 ^c	13.00 ^g	26.00 ^c	10.53 ^b	89.00 ^c	13.50 ^a	71.50 ^d	10.50 ^e	21.50 ^{bc}	30.50 ^g	51.00 ^b	56.02 ⁱ
Asante type II	116.33 ^{bc}	18.00 ^c	9.00 ^l	16.00 ^{hij}	8.15 ^{gh}	53.00 ^{ijk}	9.25 ^{cdefg}	47.00 ^g	9.50 ^g	16.25 ^{de}	21.50 ^{lm}	22.75 ^{op}	50.81 ⁿ
Asontem NV.	83.70 ^{ghij}	17.00 ^e	17.00 ^d	21.00 ^d	7.55 ^k	51.25 ^{mn}	7.0 ^{ijk}	41.00 ^m	12.00 ^c	23.25 ^{ab}	58.25 ^a	46.00 ^c	63.54 ^e
Asontem-ASR	89.75 ^{fghi}	15.87 ^g	9.00 ^l	13.75 ^{kl}	5.25 ^q	55.00 ^f	8.00 ^{fghij}	42.00 ^l	8.00 ⁱ	15.50 ^{de}	15.75 ⁿ	33.00 ^h	41.32 ^w
Asontem-BAR	128.53 ^b	18.00 ^c	13.00 ^g	14.50 ^{jk}	9.85 ^c	51.25 ^{mn}	11.75 ^{ab}	47.00 ^g	8.00 ⁱ	17.50 ^{de}	11.00 ^o	21.25 ^{pq}	53.92 ^j
Asontem-ER	90.08 ^{fghi}	13.67 ^j	10.25 ^j	17.00 ^{tgh}	6.38 ^{lm}	51.00 ^{mn}	7.75 ^{ghij}	44.00 ^k	12.00 ^c	17.00 ^{de}	26.00 ^{ij}	37.00 ^f	52.45 ^l
Asontem-GAR	113.40 ^{cd}	18.00 ^c	16.00 ^e	12.50 ^{lm}	9.00 ^f	52.00 ^{klm}	8.0 ^{fghij}	39.00 ^o	8.00 ⁱ	14.25 ^{ef}	22.00 ^l	41.25 ^e	64.41 ^d
Atomic	48.40 ^{qrs}	16.00 ^g	15.00 ^f	16.00 ^{hij}	6.25 ^{mn}	53.75 ^{gh}	5.50 ^{kl}	49.00 ^f	9.00 ^h	16.50 ^{de}	24.25 ^k	27.25 ⁿ	45.50 ^s
Cape	102.53 ^{def}	15.02 ^h	11.75 ^h	13.75 ^{kl}	5.93 ^{op}	53.75 ^{gh}	9.5 ^{cdefg}	38.50 ^p	11.75 ^{cd}	18.25 ^{cd}	52.50 ^b	43.00 ^d	59.03 ^g
Clemson Spineless	44.38 ^s	15.00 ^h	8.00 ^m	10.25 ⁿ	5.75 ^p	42.75 ^q	8.50 ^{efghij}	37.00 ^q	8.00 ⁱ	14.75 ^{def}	16.50 ⁿ	18.25 ^r	43.24 ^v
Cs-Legon	64.75 ^{lmno}	14.37 ⁱ	7.00 ⁿ	20.75 ^d	8.40 ^g	51.5 ^{lmn}	7.00 ^{ijk}	40.00 ⁿ	10.00 ^f	17.00 ^{de}	21.50 ^{lm}	37.00 ^f	56.33 ^{hi}
Debo'	77.7 ^{ijkl}	18.93 ^a	7.00 ⁿ	18.75 ^{ef}	5.93 ^{op}	51.25 ^{mn}	6.50 ^{jk}	47.00 ^g	11.50 ^d	15.25 ^{de}	28.00 ^h	31.75 ^{hi}	53.24 ^k
LoS	**	**	**	**	**	**	**	**	**	**	**	**	**
BE	ns	ns	ns	ns	**	ns	**	**	ns	ns	ns	ns	ns
TCV (%)	11.9	1.1	1.5	6.1	2.6	2.1	16.7	16.7	1.3	18.0	18.0	3.6	0.5
BCV (%)	1.3	0.3	0.3	1.7	1.0	0.2	6.3	6.3	0.3	2.9	2.9	0.5	0.1

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125 *ns* indicates non significance at the $p \leq 0.05$ level, * indicates significance at the $p \leq 0.05$ level and ** indicates high significance at $p \leq 0.01$
126 level. LoS = level of significance, BE = block efficiency, TCV = treatment co-efficient of variation, BCV = block co-efficient of variation and
127 Mean represent average of the individual characters measured for all accessions under consideration. MPH = Maximum plant height, MNI =
128 Maximum number of internodes, FFN = First flowering node, TNLP = Total Number of Leaves per Plant, NSPF = Number of Seeds per
129 Fruit, STB = Stem Diameter at Base, TNFP = Total Number of Fruits per Plant, NDG = Number of Days to 50% Germination, FFPN = First
130 Fruit Producing Node, NDF_i = Number of Days to 50% Flowering, NDF_r = Number of Days to 50% Fruiting, TSW = 1000 seed weight, NFPH
131 = Number of fresh Fruits per Plant per Harvest.

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Table 2 (Cont'd):

ACCESSION	MPH	MNI	FFN	TNLP	STB	NDG	FFPN	NDF _f	NDF _r	TNFP	NFPH	NSPF	TSW
DKA	60.70 ^{hnpq}	2.00 ^m	17.00 ⁿ	21.50 ^d	8.90 ^t	<u>125.00^a</u>	7.50 ^{hijk}	115.00 ^a	<u>15.00^a</u>	10.25 ^{gh}	52.50 ^b	31.50 ^{ijk}	43.73 ^u
Indiana	71.0 ^{ijklmn}	17.00 ^e	10.00 ^k	12.50 ^{lm}	7.85 ^{ij}	39.25 ^r	8.80 ^{defghi}	32.00 ^r	10.00 ^f	16.25 ^{de}	21.50 ^{lm}	29.00 ^{lm}	51.87 ^m
Juaboso	94.75 ^{etg}	17.50 ^d	18.00 ^c	26.75 ^c	8.10 ^{hi}	53.30 ^{hij}	8.00 ^{tghij}	47.00 ^g	10.25 ^{et}	14.50 ^{et}	44.50 ^c	46.25 ^c	46.71 ^r
Kortebortor-ASR	48.50 ^{qrs}	11.23 ⁿ	7.00 ⁿ	16.50 ^{ghi}	9.80 ^{cd}	50.75 ⁿ	8.00 ^{tghij}	42.00 ⁱ	12.00 ^c	6.70 ^{hi}	22.50 ⁱ	30.00 ^{kl}	52.75 ⁱ
Kortebortor-BAR	99.28 ^{ef}	18.50 ^b	19.00 ^b	13.75 ^{kl}	<u>11.03^a</u>	92.00 ^b	9.75 ^{bcdef}	82.00 ^b	8.00 ⁱ	25.25 ^a	57.50 ^a	28.5 ^{lmn}	53.83 ^j
Kpeve'	56.68 ^{pqrs}	12.32 ⁱ	8.00 ^m	17.25 ^{fghi}	7.55 ^k	55.00 ^f	9.00 ^{defghi}	36.75 ^q	12.00 ^c	11.25 ^{fg}	15.00 ⁿ	35.00 ^g	44.86 ^t
Labadi	92.55 ^{etgh}	18.00 ^c	11.00 ⁱ	18.50 ^{et}	8.78 ^t	51.00 ^{mn}	7.75 ^{ghij}	40.00 ⁿ	13.00 ^b	7.50 ^{hi}	28.25 ^h	37.00 ^t	46.71 ^r
Legon Fingers	72.63 ^{ijklm}	16.00 ^g	11.00 ⁱ	29.00 ^b	6.35 ^{lmn}	51.00 ^{mn}	8.80 ^{defghi}	45.00 ^j	10.00 ^f	17.75 ^{de}	25.00 ^{jk}	37.50 ^f	<u>74.95^a</u>
Mamolega	62.13 ^{nop}	16.46 ^t	7.00 ⁿ	12.75 ⁱ	6.15 ^{mno}	49.00 ^o	8.80 ^{defghi}	45.00 ^j	10.00 ^f	8.25 ^{ghi}	12.00 ^o	20.00 ^q	67.37 ^c
Mapelega	62.40 ^{nop}	13.16 ^k	10.25 ^j	18.00 ^{fg}	6.08 ^{no}	47.25 ^p	8.00 ^{tghij}	32.00 ^r	10.00 ^f	6.50 ⁱ	20.25 ^m	38.00 ^f	56.41 ⁿ
Nkran Nkuruma	<u>170.78^a</u>	<u>19.00^a</u>	<u>23.00^a</u>	20.00 ^{de}	9.98 ^c	53.50 ^{ghi}	10.75 ^{bc}	50.00 ^e	6.00 ^j	23.50 ^{ab}	40.50 ^e	18.25 ^r	69.43 ^b
Volta	79.5 ^{hijk}	17.00 ^e	11.00 ⁱ	15.75 ^{ij}	6.55 ⁱ	53.00 ^{ijk}	10.00 ^{bcde}	47.00 ^g	12.00 ^c	17.50 ^{de}	51.50 ^b	31.25 ^{jk}	33.92 ^x
Wune mana	62.13 ^{nop}	13.00 ^k	6.00 ^o	16.75 ^{ghi}	6.30 ^{lmn}	59.00 ^e	4.25 ⁱ	49.00 ^t	10.00 ^f	6.50 ⁱ	7.00 ^p	12.25 ^s	50.23 ^o
Yeji-Local	103.95 ^{cde}	16.78 ^e	8.00 ^m	<u>34.00^a</u>	9.55 ^{de}	78.00 ^d	8.25 ^{tghij}	39.00 ^o	10.00 ^f	18.25 ^{cd}	37.25 ^f	<u>63.00^a</u>	62.14 ⁱ
LoS	**	**	**	**	**	**	**	**	**	**	**	**	**
BE	ns	ns	ns	ns	**	ns	**	**	ns	ns	ns	ns	ns
TCV (%)	11.9	1.1	1.5	6.1	2.6	2.1	16.7	16.7	1.3	18.0	18.0	3.6	0.5
BCV (%)	1.3	0.3	0.3	1.7	1.0	0.2	6.3	6.3	0.3	2.9	2.9	0.5	0.1

139 *ns* indicates non significance at the $p \leq 0.05$ level, * indicates significance at the $p \leq 0.05$ level and ** indicates high significance at $p \leq 0.01$
 140 level. LoS = level of significance, BE = block efficiency, TCV = treatment co-efficient of variation, BCV = block co-efficient of variation and
 141 Mean represent average of the individual characters measured for all accessions under consideration. MPH = Maximum plant height, MNI =
 142 Maximum number of internodes, FFN = First flowering node, TNLP = Total Number of Leaves per Plant, NSPF = Number of Seeds per
 143 Fruit, STB = Stem Diameter at Base, TNFP = Total Number of Fruits per Plant, NDG = Number of Days to 50% Germination, FFPN = First
 144 Fruit Producing Node, NDF_f = Number of Days to 50% Flowering, NDF_r = Number of Days to 50% Fruiting, TSW = 1000 seed weight, NFPH
 145 = Number of fresh Fruits per Plant per Harvest.

149 **3.1.1 Cluster Analysis based on 13 Quantitative Traits**

150 Genetic relationships among the 29 accessions of okra, based on 13 quantitative traits are
151 displayed in the form of dendrogram (Figure 1), generated using the coefficient of Canberra,
152 Furthest Neighbour Similarity Matrix. Two clusters were formed at (67.90%) similarity, each
153 re-grouping into two sub-clusters, making a total of four sub-clusters at 76.30% genetic
154 similarity. The four sub-clusters comprised 10, 5, 10 and 4 accessions, respectively (Table
155 4). Clustering pattern revealed in the dendrogram indicates some degree of convergence
156 with geographical origin of accessions. Summary statistics of the 13 quantitative traits (Table
157 3) also shows great diversity among the accessions.

158 The first and last sub-clusters exhibited the highest inter-cluster distance and may be useful
159 as sources of variable genes in future okra improvement programmes through hybridisation.
160 The accessions Cs-Legon and Nkran Nkuruma, were the most divergent, and accordingly
161 could be utilised for obtaining heterobeltiosis (Ahiakpa et al., 2013; Irwin et al., 1998). Cs-
162 Legon, Legon fingers, Atomic, Indiana, Clemson spineless; and Yeji-Local, Kortebortor-BAR
163 and Nkran Nkuruma were placed in sub-clusters 1 and 4, respectively, coinciding with their
164 geographical origins of collection, a reflection of adaptation to similar environmental
165 conditions or related ancestry. This is in consonance with reports of Belete, (2011) and Hien
166 et al. (2007).

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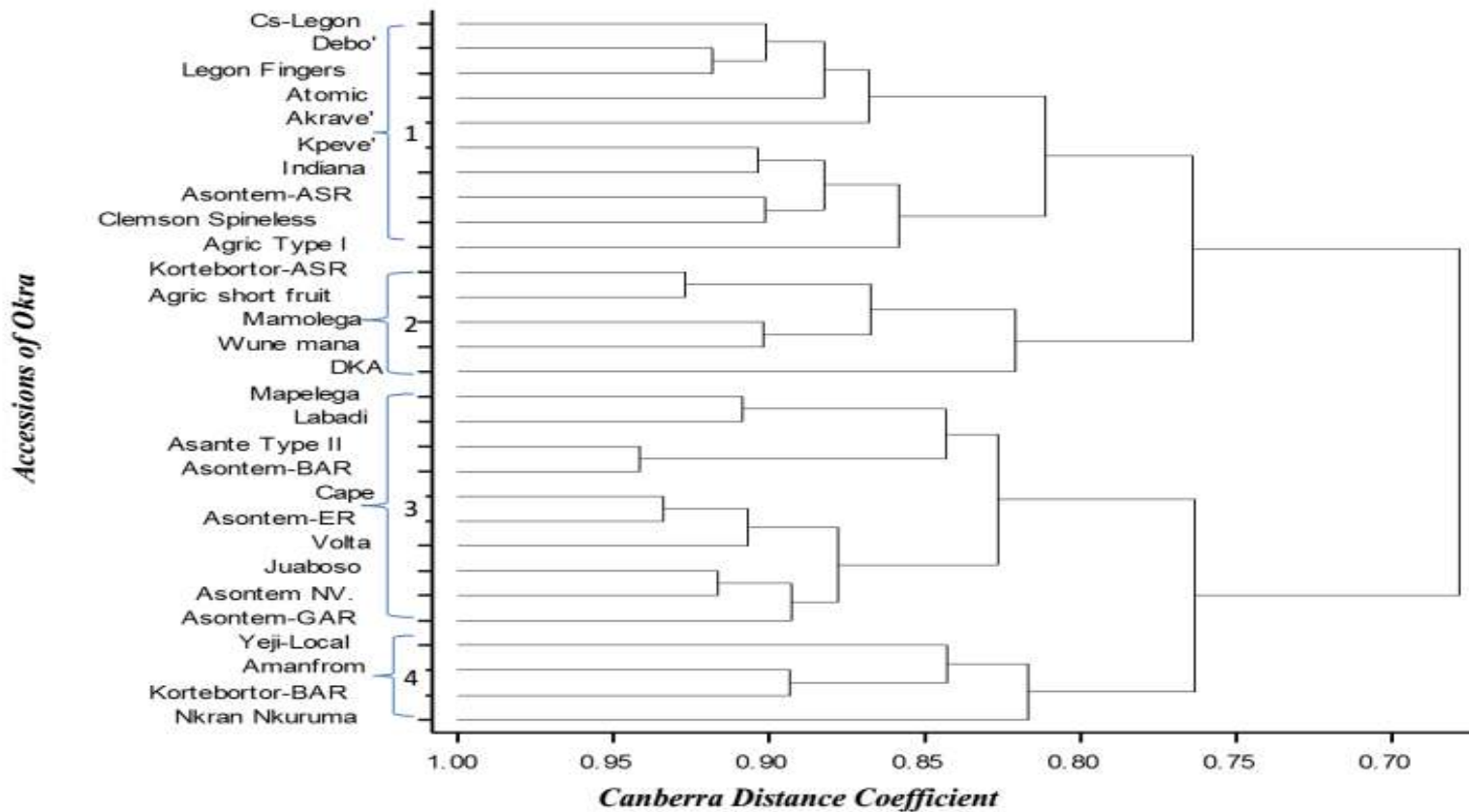


Figure 1: A Dendrogram Showing Genetic Relationships among 29 Accessions of Okra based on Quantitative Traits using Coefficient of Canberra, Furthest Neighbour Similarity Matrix.

178 **Table 3: Summary Statistics of 13 Phenotypic Characters of *Abelmoschus* spp L.**

Character	Mean	Median	Range	SD	CV
Number of Fruits per plant	27.97	12	7-59	13.89	49.66
Number of Seeds per Plant	32.79	20	12-63	10.81	32.97
First Flowering Node	8.31	8	5-14	1.68	20.22
First Fruit-Producing Node	10.89	11	6-23	4.23	38.84
Maximum Number of Internode	16.03	16	11-19	2.28	14.22
Maximum Plant Height (cm)	78.5	60.55	41.43-162.93	26.16	33.32
Number of Days to 50% Flowering	49.34	47	32-115	16.94	34.33
Number of Days to 50% Fruiting	59.21	53	39-125	17.9	30.23
Number of Days to 50% Germination	10.31	10	6-15	2.19	21.24
Total Number of Leaves per Plant	18.31	13	11-34	5.55	30.31
Total Number of fresh Fruits per Harvest	14.93	8	7-25	5.09	34.09
Stem diameter at Base (cm)	7.86	6.2	5.3-11.10	1.59	20.23
Thousand Seed Weight (g)	53.47	67.38	33.93-74.96	8.95	16.74

179 SD = Standard deviation (population); CV = Coefficient of variation.

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184 **Table 4: Distribution of 29 Accessions of Okra in Clusters**

Cluster Number	Number of Accessions	Accessions of Okra
1	10	Cs-Legon, Debo, Legon fingers, Atomic, Akrave', Kpeve', Indiana, Asontem-ASR, Clemson spineless, Agric type I
2	5	Kortebortor-ASR, Agric short fruit, Mamolega, Wune mana, DKA
3	10	Mapelega, Labadi, Asante type II, Asontem-BAR, Cape, Asontem-ER, Volta, Juaboso, Asontem NV., Asontem-GAR
4	4	Yeji-Local, Amanfrom, Kortebortor-BAR, Nkran Nkuruma

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193 **3.2 Correlations among 13 Quantitative Traits of *Abelmoschus* spp L.**

194 Table 5 shows the associations among thirteen quantitative traits of the various okra
195 accessions. NDG was negatively correlated to all other traits except NFPH to which it was
196 positive, but poorly correlated. Similarly, NDF_i and NDF_r showed negative correlation with
197 50.00 % and 41.67 % respectively, of the other traits. NDF_r was positive and significantly
198 associated with TNLP and STB as did MPH with FFN. MNI was positive and significantly
199 correlated with FFN as did also TNLP with NSPF as well as NSPF with NFPH and NFPH
200 with TNFP. FFN was also positive and highly significantly correlated with both NFPH and
201 TNFP. The highest positive and significant correlation ($r = 0.95$) was between NDF_i and
202 NDF_r . This corroborates findings of several researchers (Oppong-Sekyere et al., 2012;
203 Moukoubi et al., 2011; Nwangburuka et al., 2011; Hazra and Basu, 2000) and suggests
204 that component breeding would be very effective when there is positive association of major
205 yield characters (Ahiakpa et al., 2013) as found in this study.

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215 Table 5: Pearson's Correlations among 13 Quantitative Traits of *Abelmoschus* spp L.

<i>TRAIT</i>	<i>NDG</i>	<i>NDF_l</i>	<i>NDF_r</i>	<i>MPH</i>	<i>MNI</i>	<i>FFN</i>	<i>TNLP</i>	<i>TSW</i>	<i>NSPF</i>	<i>STB</i>	<i>NFPH</i>	<i>TNFP</i>	<i>FFPN</i>
NDG													
NDF_l	-0.24												
NDF_r	-0.19	0.95**											
MPH	-0.03	-0.05	-0.03										
MNI	-0.08	0.05	-0.03	0.42									
FFN	-0.13	0.05	0.01	0.62*	0.53*								
TNLP	-0.22	0.43	0.57*	0.12	0.12	0.15							
TSW	-0.07	-0.17	-0.13	0.39	0.18	0.30	0.29						
NSPF	-0.03	-0.13	0.08	0.34	0.14	0.36	0.57*	0.30					
STB	-0.03	0.44	0.50*	0.36	0.33	0.37	0.46	0.16	0.24				
NFPH	0.11	-0.10	-0.05	0.45	0.42	0.71**	0.26	0.21	0.60*	0.22			
TNFP	-0.28	0.14	0.14	0.44	0.47	0.68**	0.41	0.24	0.46	0.29	0.64*		
FFPN	-0.02	-0.05	0.01	0.14	0.27	0.20	0.00	-0.06	0.29	0.14	0.10	0.30	

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217 P ≤ 0.05.

218 * Significant

219 ** Highly significant

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230 3.3 Principal Components Analysis for Quantitative Traits

231 Table 6 displays the results of principal components analysis (PCA) of the 13 quantitative
232 traits, showing the factor scores of each character among the 29 okra accessions, eigen
233 values and percentage total variance accounted for by five principal components (PCs). Five
234 PCs accounted for about 78.51% of total variance with the first principal component (PC₁)
235 recording the highest (32.44%). The second, third, fourth and fifth principal components
236 (PC₂, PC₃, PC₄ and PC₅) accounted for 19.78%, 9.68%, 8.45% and 8.15% of the total
237 genetic variation, respectively. The Eigen values show the relative discriminating power of
238 the principal axes which was relatively high for PC₁ (4.22), medium for PC₂ (2.57) and low
239 (1.26, 1.09 and 1.06) for PC₃, PC₄ and PC₅. PC₁, which accounted for the highest proportion
240 (32.44%) of total variation mostly correlated with first flowering node, maximum number of
241 internodes, maximum plant height, stem diameter at the base, number of fresh fruits per
242 plant per harvest, number of seeds per fruit, total number of fruits per plant, total number of
243 leaves per plant and 1000-seed weight.

244 This is in consonance with findings by Doku et al. (2013) and Ogunbayo et al. (2005), where
245 factor scores of nine and twelve characters for rice accounted for variance among
246 accessions and were mostly correlated with PC₁, PC₂, PC₃ and PC₄. The total contribution of
247 the five principal component axes (78.51%), in this study, was higher than observations
248 made by Nwangburuka et al. (2011); Moukoubi et al. (2011); Campos et al. (2005);
249 Ogunbayo et al. (2005) where the principal component axes contributed 64.32%, 66.37%,
250 76.62% and 64.5% to variation, respectively. In the current study, all the eigen values were
251 lower than those observed by Nwangburuka et al. (2011). First fruit-producing node and
252 total number of leaves per plant were found to have contributed positively and significantly to
253 total genetic variance in this study, confirming a similar observation by Nwangburuka et al.
254 (2011).

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Table 6: Principal components analysis showing factor scores of 13 quantitative characters among the 29 Okra accessions, Eigen values and Percentage total variance accounted for by five principal components*.

CHARACTER	PC ₁	PC ₂	PC ₃	PC ₄	PC ₅
1000-Seed weight	0.203819*	0.153724*	-0.44768	-0.41751	-0.02082
Number of days to 50% flowering	0.111969	-0.56337	0.184005*	-0.07344	-0.08673
Number of days to 50% fruiting	0.14188	-0.57211	0.02661	0.07007	-0.10149
Number of days to 50% germination	-0.09528	0.17753*	-0.05589	0.36608*	-0.78663
Number of fresh fruits per harvest	0.35933*	0.21348*	-0.05857	0.14673	-0.14057
Number of seeds per fruit	0.318568*	0.09009	-0.43818	0.41697*	0.11012
First flowering node	0.389668*	0.16413*	0.22046*	-0.16218	-0.04067
First fruit-producing node	0.14729	0.08145	0.34392*	0.59379*	0.27169*
Maximum number of internode	0.29276*	0.11885	0.41954*	-0.14524	-0.04057
Maximum plant height	0.32356*	0.1805*	0.08216	-0.26811	-0.20185
Total number of leaves per plant	0.28419*	-0.3141	-0.44695	0.11124	0.07890
Total number of fruits per plant	0.39654*	0.0471	0.09077	0.03341	0.26771*
Stem diameter at the base	0.29013*	-0.2554	0.09383	-0.02465	-0.36787
Eigen value	4.22	2.57	1.26	1.09	1.06
% Variance	32.44	19.78	9.68	8.45	8.15
Cumulative % Variance	32.44	52.23	61.90	70.35	78.51

* Values bolded and asterisked made substantial contribution to total variance in the respective axes. Maximum and least discriminating power (eigen value), maximum and least percentage variance and maximum cumulative percentage variance values are bolded.

4. Conclusion

The 29 accessions of okra (*Abelmoschus* spp L. Moench) exhibited great diversity in the 13 quantitative traits studied. Cluster analysis grouped the accessions into four sub-groups with a bearing on geographical origin. No duplicates were detected while the accessions Cs-Legon and Nkran Nkuruma were the most divergent, and may provide variable genes useful in future okra improvement programmes, through hybridisation. The highest character association ($r = 0.95$) was found between number of days to 50 % flowering (NDF_f) and number of days to 50 % fruiting (NDF_r), implying that selection for one trait will lead to a high positive response in the other. Five Principal Components (PCs) accounted for 78.51% of total variance. The first principal component (PC₁) which contributed 32.44% to the total

278 genetic variation was mostly correlated with number of fresh fruits per plant per harvest, first
279 flowering node, total number of fruits per plant, maximum plant height, total number of seeds
280 per fruit, maximum number of internode, stem diameter at the base, number of leaves per
281 plant and 1000-seed weight.

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284 **References**

285 Ahiakpa JK, Amoatey HM, Amenorpe G, Apatey J, Ayeh EA, Agbemavor WSK. Mucilage
286 Content of 21 Accessions of Okra (*Abelmoschus* spp L.). *Scientia Agriculturae*. 2014; 2(2):
287 96-101.

288 Ahiakpa JK, Kaledzi PD, Adi EB, Peprah S, Dapaah HK. Genetic diversity, correlation and
289 path analyses of okra (*Abelmoschus* spp. (L.) Moench) germplasm collected in Ghana,
290 *International Journal of Development and Sustainability*. 2013; 2(2):1396-1415.

291 Belete YS. Genetic variability, correlation and path analysis studies in Ethiopian mustard
292 (*Brassica carinata* A. Brun) Genotypes. *International Journal of Plant Breeding and*
293 *Genetics*. 2011; 5 (4): 328-338. <http://dx.doi.org/10.3923/ijpbq.2011.328.338>

294 Campos ET, Espinosa MAG, Warburton ML, Monter AV. Characterisation of mandarin
295 (*Citrus* spp) using morphological and AFLP markers. *Interciencia*. 2005; 30 (11): 1-14.

296 De Vicente MC, Guzmán FA, Engels J, Ramanatha RV. Genetic characterisation and its use
297 in decision making for the conservation of crop germplasm: The Role of Biotechnology; Villa
298 Gualino, Turin, Italy–5-7. March 2005. 2005; 57pp.

299 Doku HA, Danquah EY, Amoah AN, Nyalemegbe K, Amoatey HM. Genetic Diversity among
300 18 Accessions of African Rice (*Oryza glaberrima* Steud.) Using Simple Sequence Repeat
301 (SSR) Markers. *Agricultural Journal*. 2013; 8(2): 106-112.

302 Engels JMM, Visser L. (eds.). Economic Research Service. Global resources and
303 productivity: questions and answers. A Guide to Effective Management of Germplasm
304 Collections. Engels, CABI, IFPRI, IPGRI, SGRP.PUB=899. 174 pp; 2003.

305 FAO/UNESCO. FAO/UNESCO Soil map of the world, revised legend, world resources
306 report 60. FAO, Rome. pp.146. 1994.

307 Hazra P, Basu D. Genetic variability, correlation and path analysis in okra. *Annals of*
308 *Agricultural Research*. 2000; 21(3): 452-453.

309 Hien NL, Sarhadi WA, Oikawa Y, Yutaka H. Genetic diversity of morphological responses
310 and the relationships among Asia aromatic rice (*Oryza sativa* L.) cultivars. *Tropics*. 2007; 16
311 (4): 333-355. <http://dx.doi.org/10.3759/tropics.16.343>.

312 IPGRI. Okra Descriptor List. International Crop Network Series 5. International Board for
313 Plant Genetic Resources (IBPGR), Rome, Italy. 1991.

314 Irwin SV, Kaufusi P, Banks K, de la Pe-a R, Cho JJ. Molecular characterisation of taro
315 (*Colocasia esculenta*) using RAPD markers. *Euphytica*. 1998; 99: 183–189.
316 <http://dx.doi.org/10.1023/A:1018309417762>.

317 Kumar S, Dagnoko S, Haougui A, Ratnadass A, Pasternak D, Kouame C. Okra
318 (*Abelmoschus* spp L.) in West and Central Africa: Potential and Progress on its
319 improvement. A special review. *African Journal of Agricultural Research*. 2010; 5(25): 3590 –
320 3598.

321 Moukoubi YD, Sié M, Vodouhe R, N'dri B, Toulou B, Ogunbayo SA, Ahanchede A.
322 Assessing phenotypic diversity of interspecific rice varieties using agro-morphological
323 characterisation. *Journal of Plant Breeding and Crop Science*. 2011; 3(5): 74-86.

324 Norman JC. Tropical Vegetable Crops. Arthur H. Stockwell Ltd., Elms C. Francanbe, Devon.
325 252pp.1992.

326 Nwangburuka CC, Kehinde OB, Ojo DK, Denton OA, Popoola AR. Morphological
327 classification of genetic diversity in cultivated okra, *Abelmoschus esculentus* (L) Moench
328 using principal component analysis (PCA) and single linkage cluster analysis (SLCA).
329 *African Journal of Biotechnology*. 2011; 10(54): 11165-11172.

330 Ogunbayo SA, Ojo DK, Guei R, Oyelakin OO, Sanni KA. Phylogenetic diversity and
331 relationships among 40 rice accessions using morphological and RAPDs techniques. *African*
332 *Journal of Biotechnology*. 2005; 4 (11): 1234-1244.

333 Oppong-Sekyere D, Akromah R, Nyamah EY, Brenya E, Yeboah S. Evaluation of some okra
334 (*Abelmoschus* spp L.) germplasm in Ghana. *African Journal of Plant Science*. 2012; 6(5):
335 166-178, DOI: <http://dx.doi.org/10.5897/AJPS11.248>.

336 Osawaru ME, Ogu MC, Braimah L. Growth Responses of Two Cultivated Okra Species
337 (*Abelmoschus cailei* (A.Chev.) Stevels and *Abelmoschus esculentus* L. Moench) in Crude
338 Oil Contaminated Soil. *Nigerian Journal of Basic and Applied Science*. 2013; 21(3): 215–
339 226, DOI: <http://dx.doi.org/10.4314/njbas.v21i3.7ISSN 0794-5698>.

340 Payne RW, Harding SA, Murray DA, Soutar DM, Baird DB, Welham SJ, Kane AF, Gilmour
341 AR, Thompson R, Webster R, Tunnicliffe GW. Genstat Statistical Programme, Ninth Edition.
342 Lawes Agricultural Trust (Rothamsted Experimental Station), vers.9.2.0.152.PC/Windows,
343 VSN International Ltd, UK. 2007.

344 Rubenstein K, Heisey P. Plant Genetic Resources: New Rules for International Exchange,
345 Bioversity's Regional Office for the Americas, IPGRI. Villa Gualino, Turin, Italy. March 1-5,
346 63pp. 2003.

347 Siemonsma JS, Kouame C. Vegetable. Plant Resource of Tropical Africa 2. PROTA
348 Foundation, Wageningen, Netherlands. pp. 21-29. 2004.

349 Smith JSC. & Smith OS. Finger printing crop varieties. *Advance Agronomy*, (1992). 47: 85 –
350 140. [http://dx.doi.org/10.1016/S0065-2113\(08\)60489-7](http://dx.doi.org/10.1016/S0065-2113(08)60489-7).

351 Statgraphics. Statgraphics Centurion XVI, version 16.1.11, Windows-based statistical
352 software, (32-bit) © 2010 Statpoint Technologies, Inc. Multilingual, USA. 2010.

353 Staub JE, Serquen JC, Gupta M. Selection for multiple lateral determinate cucumber
354 genotypes. *Cucurbit Gen. Coop. Rpt*. 1996; 18: 5-6.

355 Vogel JM, Rafalski A, Powell W, Morgante M, Andre C, Hanafey M, Tingey S V. Application
356 of genetic diagnostics to plant genome analysis and plant breeding. *Hort Sci.*1996; 31: 165-
357 167