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

Article in American Journal of Experimental Agriculture · October 2014
DOI: 10.9734/AJEA/2015/12306

CITATIONS
15

READS
569

7 authors, including:

Emmanuel Kwatei Quartey
Ghana Atomic Energy Commission (GAEC)
25 PUBLICATIONS  99 CITATIONS

Frederick Sossah
Jilin Agricultural University
26 PUBLICATIONS  52 CITATIONS

Kojo Ahiakpa
Research Desk Consulting Ltd
33 PUBLICATIONS  90 CITATIONS

Some of the authors of this publication are also working on these related projects:

- Pathogenomics and resistance to control diseases of edible fungi View project
- Excellence in higher education for Liberian development (EHELD) View project

All content following this page was uploaded by Kojo Ahiakpa on 21 November 2014.

The user has requested enhancement of the downloaded file.
Genetic Diversity Studies in 29 Accessions of Okra (Abelmoschus spp L.) Using 13 Quantitative Traits

HM Amoatey¹,², GYP Klu¹, EK Quartey², HA Doku³, FL Sossah², MM Segbefia⁴ and JK Ahiakpa¹*

¹Graduate School of Nuclear and Allied Sciences, Department of Nuclear Agriculture and Radiation Processing, University of Ghana, P.O. Box AE 1, Atomic-Accra, Ghana.
²Biotechnology and Nuclear Agriculture Research Institute, Ghana Atomic Energy Commission, P.O. Box LG 80, Legon, Ghana.
³Crops Research Institute, Council for Scientific and Industrial Research, P.O. Box 3785, Kumasi, Ghana.
⁴Bayer S. A. Representative Office West and Central Africa. 6, Motorway Extension, KA PMB 177, Airport-Accra, Ghana.

Authors’ contributions

This work was carried out in collaboration between all authors. Authors HMA and JKA designed the study, wrote the protocol and wrote the first draft of the manuscript. Author GYPK reviewed the experimental design and all drafts of the manuscript. Authors EKQ, HAD and FLS managed the analyses of the study. Author MMS identified the plants. Authors HMA and JKA performed the statistical analyses and did the literature search. All authors read and approved the final manuscript.

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

*Corresponding author: Email: jnckay@gmail.com;
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 ≤ 0.05) while three were highly significantly associated (P ≤ 0.01). The highest correlation (r = 0.95) was between number of days to 50% flowering (NDF) and number of days to 50% fruiting (NDFr).

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 characterization; variation; factor score; coefficients.

1. INTRODUCTION

Production and consumption of okra (Abelmoschus spp L. Moench) is widespread across West Africa [1,2,3], where all vegetative and reproductive parts as well as the fresh fruits are used variously for food preparation [2,4]. Minor applications are found in folk medicine and industry [3,5].

In Ghana, the vegetable is accepted for consumption in all regions. It is cultivated as a garden or commercial crop [6]. Intense cultivation is found in peri-urban areas to meet an ever-growing urban population, with targeted exports from elite farmers. Selection of varieties for cultivation is, therefore, based on end-user preference and adaptation to local agro-ecology.

Currently, genotypes available include many locally adapted landraces as well as some exotic lines selected to meet specifications of export destinations in Europe and America. On-going breeding work in okra is limited [7,2]. Hence, characterisation of these genotypes is incomplete.

Characterisation based on phenotypic traits is not easily reproducible particularly, since these traits are influenced largely by environmental variations [8]. In addition, it requires a large tract of land and/or greenhouse space in which to grow large populations of plants, making it labour intensive and difficult to manage [8,9]. However, the tool has remained useful as a necessary first step prior to more in-depth biochemical or molecular studies in okra germplasm exploitation[10].

By and large, the potential value of germplasm is hugely dependent on the efficiency of techniques designed to facilitate detailed study of individual traits and to differentiate among accessions [11,12,13]. Hence, characters recorded on individual accessions can serve as diagnostic descriptors for those accessions [13]; to help breeders as well as genebank curators keep track of such accessions and check for genetic integrity over a number of years of conservation. The objective of the study was to assess variability in quantitative characteristics of some accessions of okra collected across eight out of ten geographic regions of Ghana.

2. MATERIALS AND METHODS

Twenty-nine (29) accessions of Okra (Abelmoschus spp L.) were assembled from eight geographic regions of Ghana using [14] passport data as indicated in Table 1 below.

The study was conducted at the Nuclear Agricultural Research Centre (NARC) of the Biotechnology and Nuclear Agriculture Research Institute (BNARI), Ghana Atomic Energy Commission (GAEC). The soil at the site is the Nyigbenya-Haatso series, which is a typically well-drained Savannah Ochrosol (Ferric Acrisol) derived from quartzite Schist [15].
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’            |

2.1 Experimental Design and Field Layout

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

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

2.1.1 Data collection

Data were collected on five randomly selected and tagged plants within the central rows, using the International Plant Genetic Resources Institute, [14] Descriptor List for okra. Characters on which data were taken include:

- First flowering node (FFN),
- First fruit-producing node (FFPN),
- Maximum number of internodes (MNI),
- Maximum plant height (cm) (MPH),
- Number of days to 50% germination (NDG),
- Number of days to 50% flowering (NDF),
- Number of days to 50% fruiting (NDF),
- Number of fresh fruits per plant per harvest (NFPH),
- Number of seeds per fruit (NSPF),
- Stem diameter at the base (mm) (STB),
- Total number of leaves per plant (TNLP),
- Total number of fruits per plant (TNFP),
- 1000-seed weight (g), (TSW).

2.1.2 Data analysis

Mean values of data collected were used for Analysis of Variance (ANOVA) and Duncan’s Multiple Range Test (DMRT) for mean separation. Correlation analysis was used to determine the degree of association among the traits. Further, the Principal Component Analysis was employed to assess percentage contribution of each trait to total genetic variability among the accessions. Cluster analysis based on Canberra, Furthest Neighbour Similarity Matrix was also employed to obtain a dendrogram depicting the deduced genetic relationships among the accessions based on evaluation of the 13 characters. Genstat Statistical Software Programme [15], Microsoft Excel Software, and Statgraphics Plus XV.1 [17] were used for all the data analyses.

3. RESULTS AND DISCUSSION

3.1 Variability in Quantitative Traits

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

In the same vein, Yeji-Local recorded the highest total number of leaves per plant (TNLP) and number of seeds per fruit (NSPF) as did Kortebortor-BAR for stem diameter at the base (STB), and total number of fruits per plant (TNFP). Four other accessions, Asontem NV, Akrave, Amanfrom and Legon fingers recorded the highest values for maximum number of internodes (MNI), first fruit-producing node...
significant correlation (r = 0.95) was between both NFPH and TNFP. The highest positive and significantly correlated with NFPH and NFPH with TNFP. FFN was also positive and significantly correlated with FFN as did MPH with FFN. MNI was positive and significantly associated with TNLP and NSPF as well as NSPF with STB as did MPH with FFN. MNI was positive and significantly correlated with TNLP of okra, based on 13 quantitative traits are displayed in the form of dendrogram (Fig. 1), generated using the coefficient of Canberra, Furthest Neighbour Similarity Matrix. Two clusters were formed at (67.90%) similarity, each re-grouping into two sub-clusters, making a total of four sub-clusters at 76.30% genetic similarity. The four sub-clusters comprised 10, 5, 10 and 4 accessions, respectively (Table 4). Clustering pattern revealed in the dendrogram indicates some degree of convergence with geographical origin of accessions. Summary statistics of the 13 quantitative traits (Table 3) also shows great diversity among the accessions.

The first and last sub-clusters exhibited the highest inter-cluster distance and may be useful as sources of variable genes in future okra improvement programmes through hybridisation. The accessions Cs-Legon and Nkran Nkuruma, were the most divergent, and accordingly could be utilised for obtaining heterobeltiosis [7,18]. Cs-Legon, Legon fingers, Atomic, Indiana, Clemson spineless; and Yeji-Local, Kortebortor-BAR and Nkran Nkuruma were placed in sub-clusters 1 and 4, respectively, coinciding with their geographical origins of collection, a reflection of adaptation to similar environmental conditions or related ancestry. This is in consonance with reports of [19,20].

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

Table 5 shows the associations among thirteen quantitative traits of the various okra accessions. NDG was negatively correlated to all other traits except NFPH to which it was positive, but poorly correlated. Similarly, NF1 and NDF showed negative correlation with 50.00% and 41.67% respectively, of the other traits. NDF was positive and significantly associated with TNLP and STB as did MPH with FFN. MNI was positive and significantly correlated with FFN as did also TNLP with NSPF as well as NSPF with NFPH and NFPH with TNFP. FFN was also positive and highly significantly correlated with both NFPH and TNFP. The highest positive and significant correlation (r = 0.95) was between NDF and NDF. This corroborates findings of several researchers [2,21,22,23] and suggests that component breeding would be very effective when there is positive association of major yield characters [7] as found in this study.

3.3 Principal Components Analysis for Quantitative Traits

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

This is in consonance with findings by [24,25], where factor scores of nine and twelve characters for rice accounted for variance among accessions and were mostly correlated with PC1, PC2, PC3, PC4 and PC5. The total contribution of the five principal component axes (78.51%), in this study, was higher than observations made by [21,22,25,26] where the principal component axes contributed 64.32%, 66.37%, 76.62% and 64.5% to variation, respectively. In the current study, all the eigen values were lower than those observed by [22]. First fruit-producing node and total number of leaves per plant were found to have contributed positively and significantly to total genetic variance in this study, confirming a similar observation by [22].

4. CONCLUSION

The 29 accessions of okra (*Abelmoschus* spp L. Moench) exhibited great diversity in the 13 quantitative traits studied. Cluster analysis
| ACCESSION         | MPH  | MNI  | FFPN | TNLP | STB  | NDG  | FFPN | NDF₁ | NDF₂ | TNFP | NFPH | NSPF | TSW  |
|------------------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| Agric short fruit| 59.00| 17.00| 6.00 | 13.75| 7.80 | 52.50| 7.00 | 46.50| 12.00| 8.00 | 27.00| 23.75| 48.12|
| Afric type I     | 76.05| 18.00| 9.00 | 11.00| 8.10 | 54.25| 10.25| 47.00| 12.00| 10.00| 42.25| 27.75| 58.98|
| Akra             | 47.05| 19.00| 9.00 | 27.00| 9.30 | 89.75| 7.50 | 80.00| 10.00| 15.00| 21.75| 31.75| 48.63|
| Amanfrom         | 82.85| 17.87| 13.00| 26.00| 10.53| 89.00| 13.50| 71.50| 10.50| 21.50| 30.50| 51.00| 56.02|
| Asante type II   | 116.33| 18.00| 9.00 | 16.00| 8.15 | 53.00| 9.25 | 47.00| 12.00| 16.25| 21.50| 22.75| 50.81|
| Asante-NV        | 83.70| 17.00| 17.00| 21.00| 7.55 | 51.25| 7.00 | 41.00| 12.00| 23.25| 58.25| 46.00| 63.54|
| Asante-ASR       | 89.75| 15.87| 9.00 | 13.75| 5.25 | 55.00| 8.00 | 42.00| 8.00 | 15.50| 15.75| 33.00| 41.32|
| Asontem-BAR      | 128.53| 18.00| 13.00| 14.50| 8.95 | 51.25| 11.75| 47.00| 8.00 | 17.50| 11.00| 21.25| 59.32|
| Asontem-ER       | 90.08| 13.67| 10.25| 17.00| 6.38 | 51.00| 7.97 | 44.00| 12.00| 17.00| 26.00| 37.00| 52.45|
| Asontem-GAR      | 113.40| 18.00| 16.00| 12.50| 9.00 | 52.00| 8.00 | 39.00| 8.00 | 14.25| 22.00| 41.25| 64.41|
| Atomic           | 48.40| 16.00| 15.00| 16.00| 6.25 | 53.75| 5.50 | 49.00| 9.00 | 16.50| 24.25| 27.25| 45.50|
| Cape             | 102.50| 15.00| 11.75| 13.75| 9.36 | 53.75| 9.50 | 38.50| 11.75| 18.25| 52.50| 43.00| 59.03|
| Ns indicates non significance at the p ≤ 0.05 level, * indicates significance at the p ≤ 0.05 level and ** indicates high significance at p ≤ 0.01 level. LoS = level of significance, BE = block efficiency, TCV = treatment co-efficient of variation, BCV = block co-efficient of variation and Mean represent average of the individual characters measured for all accessions under consideration. MPH = Maximum plant height, MNI = Maximum number of internodes, FFPN = First Flower Producing Node, NDG = Number of Days to 50% Germination, FFPN = First Fruit Producing Node, NDF₁ = Number of Days to 50% Flowering, NDF₂ = Number of Days to 50% Fruiting, TSW = 1000 seed weight, NFPH = Number of fresh Fruits per Plant, NSPF = Number of Seeds per Fruit, STB = Stem Diameter at Base, TNFP = Total Number of Fruits per Plant, NDG = Number of Days to 50% Germination, FFPN = First Fruit Producing Node, NDF₁ = Number of Days to 50% Flowering, NDF₂ = Number of Days to 50% Fruiting, TSW = 1000 seed weight, NFPH = Number of fresh Fruits per Plant, NSPF = Number of Seeds per Fruit.
Fig. 1. A dendrogram showing genetic relationships among 29 accessions of Okra based on quantitative traits using coefficient of Canberra, furthest neighbour similarity matrix.

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  | 49.6  |
| Number of Seeds per Plant         | 32.79  | 20     | 12-63          | 10.81  | 32.9  |
| 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  | 33.2  |
| 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 |

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

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, Akrope', 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                   |
Table 5. Pearson’s correlations among 13 quantitative traits of *Abelmoschus* spp L.

| TRAIT       | N DG | NDFₐ | NDFᵣ | MPH | MNI | FFN | TNLPGA (NDFₐ) | TSW | NSPF | STB | NFPH | TNFP | FFPN |
|------------|------|------|------|-----|-----|-----|---------------|-----|------|-----|------|------|------|
| N DG       | -0.24|      |      |     |     |     |               |     |      |     |      |      |      |
| NDFₐ       | -0.19| 0.95*|      |     |     |     |               |     |      |     |      |      |      |
| NDFᵣ       | 0.003| -0.05| -0.03|     |     |     |               |     |      |     |      |      |      |
| MPH        | -0.08| 0.05 | -0.03| 0.42|     |     |               |     |      |     |      |      |      |
| MNI        | -0.13| 0.05 | 0.01 | 0.62*| 0.53*|     |               |     |      |     |      |      |      |
| FFN        | 0.05| 0.95**|     |     |     |     |               |     |      |     |      |      |      |
| TNLPGA     | -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        | 0.04| 0.24 | 0.30 | 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       | 0.34| 0.21| 0.47 | 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|      |

*p ≤ 0.05; * Significant; ** Highly significant

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                          | PC1            | PC2            | PC3            | PC4            | PC5            |
|------------------------------------|----------------|----------------|----------------|----------------|----------------|
| 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*       | 0.02661        | 0.14673        | -0.14057       |
| Number of seeds per fruit          | 0.318568*      | 0.09009        | 0.09009        | 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*       | -0.31441       | -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

The accessions were grouped 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 (NDFₐ) and number of days to 50 % fruiting (NDFᵣ), 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 genetic variation was mostly correlated with number of fresh fruits per plant per harvest, first flowering node, total number of fruits per plant, maximum plant height, total number of seeds per fruit, maximum number of internode, stem diameter at the base, number of leaves per plant and 1000-seed weight.

ACKNOWLEDGEMENTS

The authors are grateful to all Technicians, especially Mr. Samson Laar, of the Nuclear Agricultural Research Centre of the Biotechnology and Nuclear Agriculture Research Institute, Ghana Atomic Energy Commission for their assistance with the field work.
COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Ahiakpa JK, Amoatey HM, Amenorpe G, Apatey J, Ayeh EA, Agbemavor WSK. Mucilage Content of 21 accessions of Okra (Abelmoschus spp L.). Scientia Agriculturae. 2014;2(2):96-101.
2. Oppong-Sekyere D, Akromah R, Nyamah EY, Brenya E, Yeboah S. Evaluation of some okra (Abelmoschus spp L.) germplasm in Ghana. African Journal of Plant Science. 2012;6(5):166-178. DOI: http://dx.doi.org/10.5897/AJPS11.248.
3. Siemonsma JS, Kouame C. Vegetable. Plant Resource of Tropical Africa 2. PROTA Foundation, Wageningen, Netherlands. 2004;21-29.
4. Osawaru ME, Ogu MC, Braimah L. Growth responses of two cultivated Okra species (Abelmoschus cailei (A. Chev.) Stevels and Abelmoschus esculentus L. Moench) in crude oil contaminated soil. Nigerian Journal of Basic and Applied Science. 2013;21(3):215–226. DOI: http://dx.doi.org/10.4314/njbas.v21i3.7ISS N 0794-5698.
5. Kumar S, Dagnoko S, Haougui A, Ratnadass A, Pasternak D, Kouame C. Okra (Abelmoschus spp L.) in West and Central Africa: Potential and progress on its improvement. A special review. African Journal of Agricultural Research. 2010;5(25):3590–3598.
6. Norman JC. Tropical vegetable crops. Arthur H. Stockwell Ltd., Elms C. Francanbe, Devon. 1992:252.
7. Ahiakpa JK, Kaledzi PD, Adi EB, Peprah S, Dapaah HK. Genetic diversity, correlation and path analyses of Okra (Abelmoschus spp. (L.) Moench) germplasm collected in Ghana. International Journal of Development and Sustainability. 2013;2(2):1396-1415.
8. Staub JE, Serquen JC, Gupta M. Selection for multiple lateral determinate cucumber genotypes. Cucurbit Gen. Coop. Rpt. 1996;18:5-6.
9. Vogel JM, Rafalski A, Powell W, Morgante M, Andre C, Hanafey M, Tinge SV. Application of genetic diagnostics to plant genome analysis and plant breeding. Hort Sc.1996;31:165-167.
10. Smith JSC, Smith OS. Finger printing crop varieties. Advance Agronomy. 1992;47:85–140. Available: http://dx.doi.org/10.1016/S0065-2113(08)60489-7.
11. De Vicente MC, Guzmán FA, Engels J, Ramanatha RV. Genetic characterisation and its use in decision making for the conservation of crop germplasm: The Role of Biotechnology. Villa Gualino, Turin, Italy—5-7. March 2005. 2005;57.
12. Engels JMM, Visser L. (eds.). Economic Research Service. Global resources and productivity: questions and answers. A guide to effective management of germplasm collections. Engels, CABI, IFPRI, IPGRI, SGRP.PUB=899. 2003;174.
13. Rubenstein K, Heisey P. Plant genetic resources: New rules for international exchange. Bioversity’s Regional Office for the Americas, IPGRI. Villa Gualino, Turin, Italy. March 1-5. 2003:63.
14. IPGRI. Okra Descriptor List. International Crop Network Series 5. International Board for Plant Genetic Resources (IBPGR), Rome, Italy; 1991.
15. FAO/UNESCO. FAO/UNESCO Soil map of the world, revised legend, world resources report 60. FAO, Rome. 1994;146.
16. Payne RW, Harding SA, Murray DA, Soutar DM, Baird DB, Welham SJ, Kane AF, Gilmour AR, Thompson R, Webster R, Tunnicliffe GW. Genstat Statistical Programme, Ninth Edition. Lawes Agricultural Trust (Rothamsted Experimental Station), vers.9.2.0.152.PC/Windows, VSN International Ltd, UK; 2007.
17. Statgraphics. Statgraphics Centurion XVI, version 16.1.11, Windows-based statistical software. (32-bit) © 2010 Statpoint Technologies, Inc. Multilingual, USA; 2010.
18. Irwin SV, Kaufusi P, Banks K, de la Pe-a R, Cho JJ. Molecular characterisation of taro (Colocasia esculenta) using RAPD markers. Euphytica. 1998;99:183–189. Available:http://dx.doi.org/10.1023/A:1018309417762.
19. Belete YS. Genetic variability, correlation and path analysis studies in Ethiopian mustard (Brassica carinata A. Brun) Genotypes. International Journal of Plant Breeding and Genetics. 2011;5(4):328-338. Available:http://dx.doi.org/10.3923/ijpbg.2011.328.338.
20. Hien NL, Sarhadi WA, Okawa Y, Yutaka H. Genetic diversity of morphological responses and the relationships among Asia aromatic rice (Oryza sativa L.) cultivars. Tropics. 2007;16(4):333-355. Available: http://dx.doi.org/10.3759/tropics.16.343.

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

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

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

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

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

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