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GENETIC DIVERSITY STUDY IN OKRA (*ABELMOSCU SSPP*) ACCESSIONS

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ABSTRACT

Genetic variation is regarded as the basic material for selection and improvement of any crop breeding program.The present investigation was carried out to determine the genetic variability in pod yield and yield characters in 52 okra accessions. The accessions were grown in a Randomized Complete Block Design with three replications in the 2018 cropping season at the Teaching and Research Farm of the Federal University of Agriculture, Makurdi,(07^{0}41'N, 08^{0}37'E, 106.4m asl). Data were collected on growth, pod and seed characters and were subjected to Principal component and cluster analysis. The principal component analysis revealed that different characters contributed differently to the total variation. In the ten principal components, the result showed that the first five principal component were loaded by plant height, one hundred seed weight, pod weight, number of leaves/plant, number of branches/plant, number of seeds/pod, pod yield, days of flowering, Days to harvestable pods and pod girth. This means that these characters were largely responsible for the variation among the 52 okra accession studied. The dendrogram indicated that the accessions were grouped into 10 distinct clusters, suggesting the degree of resemblance within members of the same clusters and dissimilarity between members of different clusters.

Key words: Genetic diversity, accession, genetic variability, germplasm

INTRODUCTION

Okra (*Abelmoschu sspp*) belonging to the family malvaceae, is a widely cultivated vegetable which can be found in almost every market in Africa because the leaves, buds, pods, and flowers are consumed (Vineeta*eta*l, 2017). The two major cultivated okra types have been classified as *Abelmoschusesculentus* which originated from Asia and *Abelmoschus Callai* which originated from West Africa (Martin *etal*, 1981). The nutritive value of okra varies in different cultivars and depending upon the agro-climatic conditions. The development of improved varieties of crops involves the incorporation of specific genes governing desired traits, such as abiotic stress tolerance, pest and diseases resistance, stability in yield, adaptability to the environment, yield improvement among others. Thus the superiority of hybrids resulting from selection for desired traits depends to a large extent on the genetic diversity of the initial population (Germplasm) (Adekoya, 2008).

Genetic diversity represents the variability present among different genotypes of a species. It comes into play either as a result of geographical separation or due to genetic barriers to crossability (Singh, 2010). Genetic diversity plays an important role in plant breeding due to hybrids between lines of diverse origin which on a general note display a greater heterosis than those between closely related species.

In a self pollinated crop like okra, Germplasm often exist in the form of homozygous genotypes which could be released as varieties in the short run. However, for a long term improvement, diverse genotypes are needed as parental stock for the development of improved varieties. Thus, it is important to classify the range of variability among accessions to facilitate the maintenance and further acquisition of germplasm resources. Thus, information concerning the genetic diversity within crop species is essential for a rational use of genetic resources.

Genetic variability in pod yield and its components is quiet critical among okra accessions (Ariyo, 1990, Adekoya, 2008). It is therefore, important to determine the underlying sources of genetic variability in okra pod yield and yield component characters in newly collected accessions to estimate the variation inherent in the population of the okra germplasm to pave way for its selection and subsequent improvement.

Therefore, the objective of this study was to estimate the extent of genetic variability present among the okra accessions and classify them into various groups based on their performance.

MATERIALS AND METHODS

The present research took place at the Teaching and Research Farm of the University of Agriculture,Makurdi-Nigeria. ($07^0$41'N, $08^0$37'E, 106.4m asl) The experimental materials (Okra accessions) were collected from the National Centre for Genetic Resources and Biotechnology (NAGRAB) Ibadan and some local accessions from farmers in Benue, Nasarawa, Plateau, Kebbi and Borno States of Nigeria and were code named according to their locations of collection (Table 1).In all, fifty two (52) Okra accessions were used for the study. The treatments were laid out in a Randomized Complete Block Design (RCBD) with three replicates in the 2018 cropping season. A spacing of 60cm by 40cm was employed with a distance of O.5m and 1m between plots and blocks respectively. Two seeds were planted per hole and later thinned to one seedling per hole. Weeding was done manually and insect pests were controlled using cypermethrine at the rate of 4mls/litre of water. Data were recorded on five (5) plants randomly selected in the middle ridges in each plot. These includes plant height, number of branches per plant, number of leaves/plant, Days to first and fifty percent flowering, Days to harvestable pods, pod length, pod girth, fresh pod weight, number of seeds per pod and 100 seed weight.

Means of these data were computed and subjected to analysis of variance and significant treatment means were separated using least significant difference (LSD) (Obi, 2002). The data were also subjected to Principal Component analysis (PCA) to determine the pattern of variation and the major traits contributing to the delineation.Principal components with Eigen values above one were considered significant in determining the agro-morphological variability in the accessions and the component loadings greater than$\pm$ 0.30 were considered to be meaningful (Hair *et al*,1998).A cluster analysis was also carried out based on Euclidean distance matrix in a hierachial way to determine the diversity and similarity of the accessions from diverse background.

RESULT AND DISCUSSION

The analysis of variance for the accessions used for the study showed that the means for all the traits considered (Table 2) differed significantly ($p <$0.05).The result of the principal component analysis for the 52 okra accessions is presented in Table 3. Five (5) of the ten (10) principal components had variances of 32.00, 23.00, 12.00, 10.00 and 8.00 which accounted for the total variation that gave a cumulative percentage variance of 85.90%. The first principal component (PC1) was largely loaded by days to fifty percent flowering (0.455),days to harvestable pods (0.455), days to first flowering (0.447), plant height (0.215), PC2 was loaded by number of pods per plant (0.465), number of branches/plant(0.46) pod yield (0.436) and number of leaves/plant (0.38), PC3 was largely loaded by plant height (0.432), pod weight (0.412),pod girth (0.379), and pod length (0.337).Similarly, PC4 was loaded largely by pod girth (0.603), number of leaves/plant (0.364), number of seeds/plant (0.296) and number of branches/plant (0.247)while PC5 was loaded largely by pod girth (0.287), days to first flowering (1.52), days to harvestable pods (0.151) and days to fifty percent flowering (0.150) and days to harvestable pods (0.151).

Thus, the result of the principal component analysis revealed that different characters contributed differently to the total variation as indicated by their Eigen values as well as their weights and loadings on different principal axis. This confirmed the pattern of variation among the studied accessions of okra. The characters that contributed most to the variation within a group of entries were equally identified. It revealed that the first 5 PC accounted for 85.90% of the total variation. Findings from this study were in agreement with the report of Adekoya*etal*, (2011), who reported 79.93% variation accounted for by the first four principal components in their study on 20 okra accessions. Adebisi (2004) equally reported similar results in his work on sesame. Abubakar*etal*, (2018), reported 9 components from the thirty five pearl millet accessions/ land races collected from northern Nigeria.

Table 1: Common Features and Sources of Okra Accessions used in the Study.

Accessions' Name/Code	Source	Species	Height	Stem color	Leaf vein color	Pod color	Pod surface
293	NACGRAB	*A. caillei*	Tall	Pale green	Brown	Green	Hairy
297	″	*A. esculentus*	Short	Red	Red	Red	Smooth
298	″	*A. caillei*	Tall	Red	Red	Green	Hairy
301	″	*A. esculentus*	Sshort	Red	Red	Red	Smooth
302	″	*A. caillei*	Tall	Red	Red	Red	Hairy
303	″	*A. caillei*	Tall	Black	Black	Black	Hairy
304	″	*A. caillei*	Tall	Red	Red	Green	Smooth
322	″	*A. esculentus*	Short	Green	Green	Green	Smooth
326	″	*A. esculentus*	Short	Red	Red	Green	Smooth
328^{-B}	″	*A. caillei*	Tall	Red	Red	Green	Smooth
332	″	*A. caillei*	Tall	Red	Red	Green	Hairy
333	″	*A. caillei*	Tall	Green	Red	Light green	Smooth
335	″	*A.caillei*	Tall	Red	Red	Red	Smooth
342^{-A}	″	*A. esculentus*	Short				
342^{-B}	″	*A. caillei*	Tall	Pale green	Brown	Green	Smooth
343^{-A}	″	*A. caillei*	Tall	Red	Red	Green	Hairy
345	″	*A. caillei*	Tall	Red	Red	Red	Smooth
346^{-A}	″	*A. caillei*	Tall	Pale green	Brown	Green	Smooth
346^{-B}	″	*A. caillei*	Tall	Pale green	Brown	Green	Smooth
348	″	*A. caillei*	Tall	Red	Red	Green	Smooth
349	″	*A. esculentus*	Shot	Red	Red	Green	Smooth
350	″	*A. caillei*	Tall	Red	Red	Green	Hairy
356^{-A}	″	*A. esculentus*	Short	Pale green	Brown	Green	Smooth
356^{-B}	″			Red	Red	Green	Smooths
359	″	*A. caillei*	Tall	Red	Red	Red	Smooth
361	″	*A. esculentus*	Short	Pale green	Green	Green	Smooth
371	″	*A. caillei*	Tall	Pale green	Green		
372	″	*A. esculentus*	Short	Green	Red	Green	Hairy
376	″	*A. esculentus*	Short	Black	Black	Green	Smooth
380	″	*A. caillei*	Tall	Red	Red	Green	Hairy
394	″	*A. esculentus*	Short	Red	Red	Red	Hairy
396	″	*A. caillei*	Tall	Green	Green	Green	Smooth
452	″	*A. caillei*	Tall	Pale green	Brown	Green	Smooth
454	″	*A. esculentus*	Short	Red	Red	Green	Smooth
463	″		Tall	Red	Red	Green	Smooth
466	″	*A. esculentus*	Short	Green	Green	Green	Smooth
467	″	*A. esculentus*	Short	Red	Red	Red	Hairy
469	″	*A. esculentus*	Short	Red	Red	Red	Smooth
490	″	*A. caillei*	Tall	Green	Green	Green	Hairy
507	″	*A. caillei*	Tall	Red	Red	Green	Smooth
514	″	*A. caillei*	Tall	Brown	Brown	Green	Hairy
6502347		*A. caillei*	Tall	Pale green	Brown	Green	Smooth
ABJ	Abuja FCT	Local	Tall	Red	Red	Red	Smooth
AWE	Awe, Nassarawa State	Local	Short	Green	Green	Green	Smooth
BASS	Bassa, Plateau State	Local	Tall	Pale green	Green	Red	Smooth
BIU	Biu, Borno State	Local	Short	Red	Red	Green	Smooth
J.SOUTH	Jos south, plateau state	Local	Tall	Red	Red	Red	Smooth
LAF.	Lafia, Nassarawa state	Local	Short	Black	Black	Green	Smooth
MKD	Makurdi, Benue state	Local	Tall	Pale green	Green	Green	Hairy
OJU	Oju, Benue state	Local	Tall	Black	Black	Green	Hairy
YAW	Yawuri, Kebbi state	Local	Short	Red	Red	Green	Smooth
ZURu	Zuru, Kebbi state	Local	Short	Red	Red	Green	Hairy

Cluster Analysis

The variation among the 52 okra accessions were assessed based on 13 quantitative traits using cluster analysis as presented in Table 4. Based on their morphological similarities, the okra accessions were clustered into ten (10) groups. Cluster i,ii,iii, iv and v consist of 8,6,5,3 and 2 members respectively, while cluster vi,vii,viii,ix and x consist of 3,6,12,3 and 4 members, in that order. Based on thedendrgram grouping, the accessions that clustered into a particular group were highly similar with one another and quite distinct from those in other clusters (Figure 1). Thus, grouping of the accessions into ten clusters with each cluster containing accessions from different sources revealed that there was no association between pattern of clustering and sources of accessions used as the clustering pattern/membership of the accessions showed that clusters 1,2,3 and 6 consist of Okra accessions collected from NAGRAB only, while clusters 4,5,7,9,8 and 10 involves those collected form NAGRAB and farmers (Table 4). Thus, clustering of accessions into groups may be attributed to genetic and /or other factors. The inter cluster distances between the different clusters of okra accessions suggest wide genetic diversity among the okra accessions of different groups.Other researchers (Osawaru*eta,l* 2013, Shyam (2013) had reported six clusters from 53 okra accessions and four clusters from 34 Okra accessions respectively.The authors also posited that there were no correlation between ecological habitat and the diversity expressed among the accessions in their study.

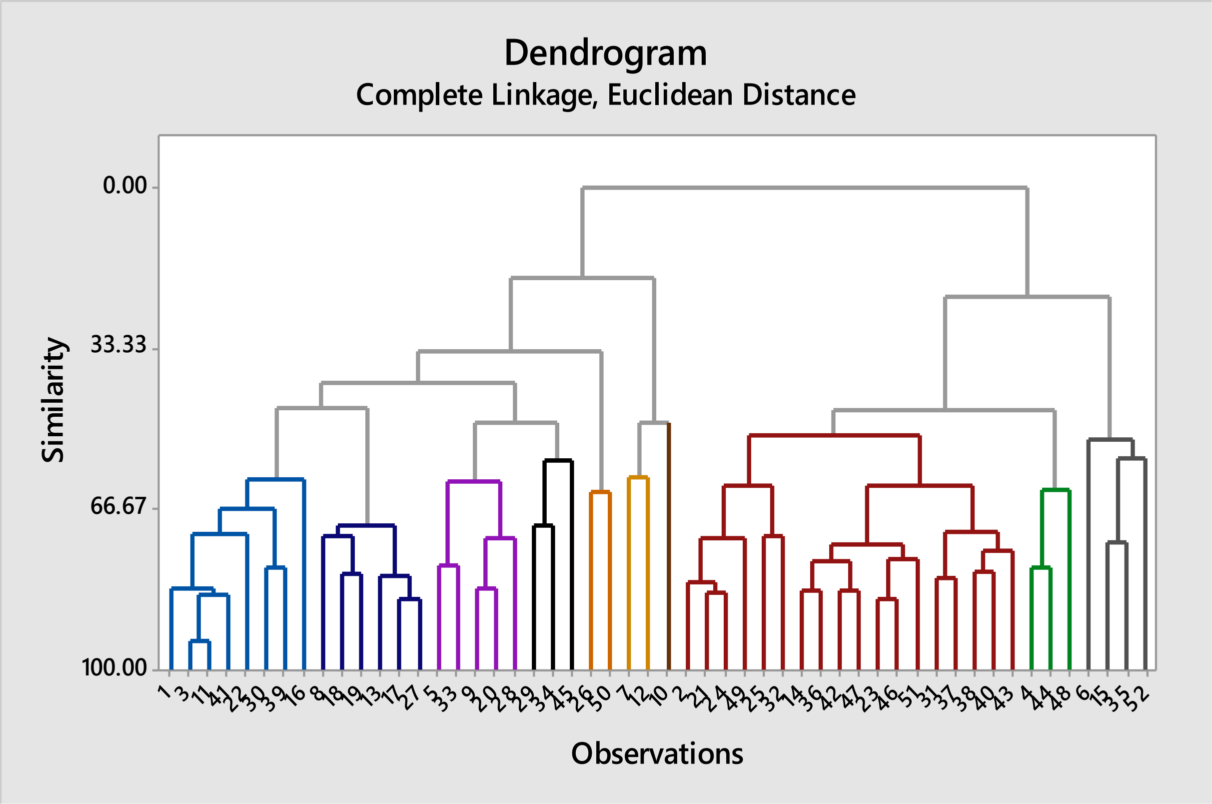

Figure 1:Dendrogram from Cluster Analysis of Fifty two Accessions of Okra

Table 2: Analysis of variance (ANOVA) for the 52 Okra Accessions

SOV	**DF**	**PHT(cm)**	**NOL/P**	**NOB/P**	**DFF**	**DTFF**	**DHP**	**NPP/P**	**PL(cm)**	**PG(cm)**	**PWT(g)**	**NSP/P**	**HSWT(g)**	**PY(g)**
ACC	51	10056.9**	292.69**	17.17**	1130.16**	992.39**	1144.54**	75.12**	7.16**	0.16**	184.73**	775.24**	0.86**	54927.80**
REP	2	5.33	10.74	1.86	3.56	6.74	12.03	0.18	0.33	0.27	10.26	1.26	0.23	301.19
ERROR	102.4	3.93	3.79	1.47	10.73	12.53	13.11	0.47	0.24	0.17	1.47	3.07	0.19	605.00

PHT=Plant height, NOL/p=number of leaves/plant, NOB/P=number of branches/plant, DFF=days to first flowering, DTFF=days to fifty percent flowering, DHP=days to harvestable pods, NPP/P=number of pods/plant, PL=Pod length, PG=Pod girth, PWT=Pod weight, NSP/P=number of seeds/pod, HSWT=hundred seed weight, PY=Pod Yield.

Table 3: Principal component Analysis showing contribution, Eigen values and percent total variance accounted for by the first 5 principal components axes of each character for the 52 Okra accessions:

Variable	PC1	PC2	PC3	PC4	PC5
PHT	0.215	-0.147	0.432	0.020	-0.272
NOL/P	0.132	0.380	-0.289	0.364	-0.307
NOB/P	0.056	0.460	-0.266	0.247	-0.295
DFF	0.447	0.093	0.153	-0.90	0.152
DTFF	0.455	0.080	0.157	-0.046	0.150
DHP	0.455	0.091	0.159	-0.077	0.151
NP/P	0.0362	0.465	0.140	-0.408	-0.148
PL	-0.362	0.044	0.337	-0.156	-0.148
PG	0.054	0.189	0.379	0.603	0.287
PWT	-0.346	0.108	0.412	0.279	0.013
NSP/P	0.095	-0.299	0.169	0.296	-0.411
HSWT	0.174	-0.232	0.115	-0.088	-0.608
PY	-0.158	0.436	0.311	-0.250	-0.171
Eigenvalues	4.00	2.90	1.55	1.33	1.12
Variance	32.00	23.00	12.00	10.00	8.00
Cumulative Variance	32.00	55.10	67.10	77.30	85.90

PHT=Plantheight,NOL/P=numberofleaves/plant,NOB/P=number of branches/plant,DFF=daystofirstflowering,DTFF=daystofiftypercent flowering,DHP=days to harvestable pods, NP/P=numberofpods/plant,PL=Podlength,PG=Podgirth,PWT=Pod weight, NSP/P=number of seeds/pod,HSWT=hundred seed weight,PY=Pod Yield.

Table 4: Clustering Pattern of 52 okra Accessions

Cluster	No. of members	Members
I	8	293, 298, 332, 514, 350, 380, 490, 343-A
II	6	322, 346,-A, 346-B, 335, 345, 371
III	5	302. 452, 326, 348, 372
IV	3	376, 454, Bassa
V	2	361, OJU
VI	3	304, 333, 328-B
VII	6	297, 349, 356-B, Makurdi, 359, 396
VIII	12	342-A, 466, 6502347, Jos, 356-A, Biu, Yawuri, 394, 467, 469, 507 Abuja
IX	3	301, Awe, Lafia.
X	4	303, 342-b, 463, Zuru

CONCLUSION

The classification of the okra accessions into distinct groups indicates that hybridization is possible between the accessions such that maximum heterosis could be achieved. Among the characters that had significant contribution to the total variation in the first 5 principal components included plant height at harvest, number branches/plant, number of leaves/plant, days of first and fifty percent flowering, pod weight, number of seeds/pod, one hundred seed weight and pod yield/ plant. These characters could be included in the okra improvement programme for pod yield and yield characters.

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