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PHENOTYPIC VARIABILITY AMONG AFRICAN YAM BEAN LANDRACE ACCESSIONS FROM DIFFERENT AGRO-ECOLOGIES OF NIGERIA

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Abstract
The aim of this research work was to estimate the genetic variability and magnitude of the genetic components of some phenotypic traits among twenty African yam bean landraces collected from three agro-ecological zones of Nigeria. The accessions constituted the treatment which was laid out in a Randomized Complete Block Design with three replications. Accession seven performed best across the three locations in terms of grain yield, while accession ten had the least performance in term of grain yield. Levels of accessions and locations were significantly different ($P<0.05$) from one another for the studied traits except hypocotyl length, while accession x location interaction differed significantly (though at different levels) in all the traits except hypocotyl length, number of leaves per plant and pod length. The results revealed that phenotypic coefficient of variation were higher than genotypic coefficient of variation for the traits studied. Broad sense heritability estimates were high in all the studied traits. Genetic advance as percentage values were moderate to high for all the traits. High heritability estimate values coupled with high genetic advance in the research work depicts that improvement can be made on the crop through simple selection. This study provides baseline information for improving African yam bean landrace.

Keywords: **African yam bean, Agro-ecological zones, Improvement, Landrace, Traits**

Introduction

African yam bean [*Sphenostylis stenocarpa* (Hoscht ex. Rich) Harms] is an annual grain (leguminous crop) belonging to the family Fabaceae. It is one of the most economically important species in the genus *Sphenostlyis* (Abdulkareem *et al*., 2015). It has a climbing growing pattern similar to other leguminous crops (Ameh, 2003). The edible seeds and tubers produced by the crop make it to be the most culturally and economically important of all seven species of the genus *Sphenostylis* (Potter and Doyle, 1992). African yam bean thrives optimally on a wide range of soil (Duke *et al*., 1977) and in diverse climatic conditions. It is a minor grain legume with less popularity compared to soybean and cowpea. It is an under-exploited species (Saka *et al*., 2004). It is usually grown as a companion crop with yam, cassava, maize, sorghum and other crops (Togun and Egunjobi, 1997). Sole cultivation of African yam bean is rare because of the less importance attached to it and its low yield.

The crop is a good source of food for man and feed for livestock. African yam bean as a diet can either be cooked or roasted. The crop is also advantageous in enriching the soil by fixing atmospheric nitrogen. If the crop is properly exploited and improved by plant breeders, it has a great potential to alleviate poverty and reduce food insecurity in developing or under-developed countries where this issue is a challenge. According to Uguru, and Madukaife (2001), the amino acid values in African yam bean grains are high compared to some other leguminous crops like cowpea, pigeon pea, and Bambara groundnut. Despite its great nutritional potentials, the crop has been neglected in most Nigerian homes due to its longer cooking period, undesirable taste and texture, and tedious manual removal of the skin coat (Thomas *et al.,* 2005). Other factors limiting its cultivation among the farmers include; low grain yield of the available varieties, longer period of maturity, pests and diseases attack, poor marketing and price, and lack of acceptability in the market. Improving these traits will enhance the adoption of the crop for production and consumption in Nigeria.

A good knowledge of genetic variability among genotypes is essential and is one of the crucial requirements for a successful crop improvement programme (Agbowuro *et al.,* 2021). Breeding achievement rests on the genetic variability present in the accessions of the particular crop (Ndukauba *et al*., 2015). Information on the nature and degree of genetic variability of African yam bean landraces available in Nigeria is not readily available. Improvement of any trait and selection of an appropriate breeding program for any cultivar relies on the level of genotypic and phenotypic variability that exist among the cultivars (Agbowuro *et al*., 2019). The availability of this information is important for African yam bean germplasm conservation and improvement. An understanding of components of variance and their effects, heritability and genetic advance of desired traits will help the plant breeders to make a proper decision on the appropriate breeding techniques to be adopted in improving the crop. Therefore, this study was conducted to evaluate the genetic variability existing among the African yam landrace collection in Nigeria for important traits, and estimate some genetic parameters of the various phenotypic traits in African yam bean landrace collection.

Materials and Methods

The research work was conducted in three locations (the Biological Garden of Elizade University, Ilara-Mokin, Ondo State; Oke-Ako farm settlement, Ekiti State; and Golf Farm, Otun- Ekiti, Ekiti State) between April and December, 2019. The experimental sites had been previously used for the cultivation of arable crops like cocoyam, maize, melon, amaranths for more than three years. The three research locations: Ilara-Mokin, Ondo State; Oke-Ako farm settlement, Ekiti State; and Golf Farm, Otun- Ekiti, Ekiti State lies on rainforest, derived savanna and southern guinea savanna agro-ecological zone respectively. The twenty African yam bean landraces that constitute the treatments in this study were sourced from different agro-ecological zones in Nigeria. The experiment was laid out in a Randomized Complete Block Design with three replications. The twenty accessions were randomized into row plots in the three replications. Plot size of 25m^2 was used with plant spacing of 1m x 1m according to Adewale and Odoh (2013) with two seeds sowed per hole and later thinned to one at two weeks after emergence to make 10,000 stands per hectare. The experimental sites were manually cleared with cutlass and packed. The sites were ridged manually with hoes a week after. First weeding was done manually with the aid of hoes and cutlasses four weeks after planting. The second and third weeding were done at 10 and 16 weeks after planting respectively. Split bamboo poles of about five meters height were used as staking materials. Staking and training of the seedling vines started four weeks after planting. Harvesting of the mature and dried pods began as soon as possible to avoid shattering the pods. Fifteen plants per plot were randomly selected and tagged for record purpose.

Data were collected based on African yam beam descriptors by Adewale and Dumet (2011). Analysis of Variance was carried out using Proc GLM procedure of SAS software (SAS, 2002). Components of genotypic and phenotypic variance from the analysis of variance were calculated from the analysis of variance table based on the methods suggested by Robinson *et al*. (1955). Formula by Singh and Chaudhury (1985) was used for the computation of phenotypic and genotypic coefficients of variation, and genetic advance, while heritability in the broad sense was estimated by adopting the method suggested by Falconer (1989).

Table 1: List of African yam bean accessions showing their source of collection

Accs Code	Place of Collection	Agro-Ecological Zone	Accs.	Place of Collection	Agro-Ecological Zone
Acc. 1	Zaria	NGS	Acc. 11	Akpoga	DS
Acc. 2	Kujama	NGS	Acc. 12	Ikare-Akoko	DS
Acc. 3	Randa	NGS	Acc. 13	Asaba	FZ
Acc. 4	Mokwa	SGS	Acc. 14	Irele	FZ
Acc. 5	Zungeru	SGS	Acc. 15	Ijegu	FZ
Acc. 6	Kosubosu	SGS	Acc. 16	Benin City	FZ
Acc. 7	Okenne	DS	Acc. 17	Igueben	FZ
Acc. 8	Makurdi	DS	Acc. 18	Aboh	FZ
Acc. 9	Otukpo	DS	Acc. 19	Okitipupa	FZ
Acc.10	Ikole-Ekiti	DS	Acc. 20	Sapele	FZ

Note: NGS: Northern Guinea Savanna; SGS: Southern Guinea Savanna; DS: Derived Savanna; FZ: Forest Zone

Table 2: List of descriptor traits studied on the African yam bean accessions

Abbreviations	Traits and units used	Abbreviations	Traits and units used
HL	Hypocotyl length (cm)	PL	Pod length (cm)
NL	Number of leaves/plant	PWt	Pod weight (g)
VL	Vine length (cm)	LP	Number of locules pod^{-1}
TLL	Terminal leaf length (m^2)	P.Ped	Number of pods peduncles^{-1}
TLW	Terminal leaf width (m^2)	SWPl	Seed weight plant^{-1} (g)
50% DF	Days to 50% flowering	GY	Grain yield (ton/ha)

Results and Discussion

The results from the combined analyses of variance for three locations of the study are presented in Table 3. The accessions were significantly different (<0.05) from each other for all the studied phenotypic traits except hypocotyl length. The level of significance is a pointer to the degree of genetic variability in the genetic materials which provide a good opportunity for varietal improvement of the crop (Akinyosoye *et. al*., 2017). This result is in agreement with the findings of Ibirinde *et al.* (2019)**.** Location exhibited significant (P<0.05) effects on the expression of all the traits except in hypocotyl length. This shows that location have effects on landrace accessions. The variability among the accessions across the locations could be as a result of the different agro ecological zones that each of the research stations lies. Each of the agro-ecological zones has its prevailing climatic variables. Also, effects of accession-by-location interaction was found to be significant (P<0.05 and P<0.01) for most of the studied traits, except in hypocotyl length, number of leaves and pod length. The level significance in accession by location effects observed in this study indicated that the accessions used in the evaluation were inconsistent in their performance across the locations. Inconsistency in the performance of accessions in different locations is a major problem stunting the efficiency of selection as a breeding method (Ajayi and Gbadamosi, 2020).

The mean performance for some landrace African yam bean traits studied across the three location is presented in Table 4. Accession 7 had the highest mean values for grain yield (3.211ton/ha), hypocotyl length (9.522cm), terminal leaf length (10.700m^2), terminal leaf width (4.233m^2), days to 50% flowering (93.777days), pod length (29.455cm), pod weight (10.822g), and number of pods per peduncles (3.155). These were followed by Accessions 19, 12, 8, 16 and 3 with grain yields of 3.188, 2.986, 2.940, 2.871 and 2.760t/ha respectively, while Accession 10 had the least grain yield (1.717t/ha). Accession seven that recorded the highest mean value for grain yield had the highest number days to 50% flowering. The grain yield could be as a result of longer flowering time or the genetic makeup of the accession. The plant tends to produce more flowers due to longer flowering period. In determining the degree of variation in yield and other agronomy components among various accessions, it should be recalled that overall genetic variation within a germplasm for any trait depends on heritable and non-heritable components (Al-Tabbal and Al-Fraihat, 2012). The degree of variability existing within a population could be measured by the coefficient of variation, while heritability and genetic advance estimates provides useful information in deciding the appropriate breeding program to adopt.

Table 5 presents the genetic parameters of the traits studied. Phenotypic variance was least in grain yield (0.1400) and highest in seed weight per plant (123.3734), while the least genotypic variance (0.1397) was also observed in grain yield and the highest (123.2570) also in seed weight per plant. Phenotypic variance values were higher than the genotypic variance values for all the traits studied. The genotypic coefficient variance (GCV) values ranged from 5.5300% for days to 50% flowering to 53.4603% for seeds weight per pod, while phenotypic coefficient variance (PCV) values ranged from 5.5389% for days to 50% flowering to 53.4856% for seeds weight per pod. The phenotypic and genotypic coefficient of variation values, according to Sivasubramaniah and Menon (1973), were categorized as low, moderate and high as follows: 0-10 % = Low, 10-20% = Moderate, >20% = High. The recorded genotypic and phenotypic coefficients of variation values for hypocotyl length and days to 50% flowering were below 10% which were considered low according to Sivasubbramaniah and Menon (1973), with other traits having moderate to high values.

Genotypic coefficient of variation is a pointer to the degree of genetic variability present in genotypes for various agronomic traits. However, this is not sufficient in determining the variation that is heritable. Genotypic coefficient of variation, coupled with heritability estimate, gives a reliable estimation of the degree of genetic advance to be expected through phenotypic variation (Burton, 1952 and Johnson *et al*., 1955). Heritability estimates in the broad sense were high for all the traits studied (Table 5), which is an indication of the high response to selection that is achievable these traits. The nature of gene action that is involved in the appearance of various polygenic traits is better understood through the determination of genetic advance. Johnson *et al.* (1955) categorized genetic advance (as per cent of mean) as low, moderate and high as follows: 0-10 % = Low, 10-20% = Moderate, 20% and above = High. Singh and Narayanan (1993) reported that high values of genetic advance are associated with additive gene action, while low values are associated with non-additive gene action. The expected genetic advance values for all the studied traits were presented in Table 5. In this study, high heritability estimates were recorded in all the studied traits coupled with moderate to high genetic advance as percent of the mean studied traits indicated that all these are simply inherited traits, and most likely the heritability is due to additive gene action and selection is effective for its improvement.

Table 3: Analysis of variance for agronomic traits of 20 African yam bean accessions grown under field conditions in three locations

Variables	Replication	Location	Accession	Accession * Location	Error
DF.	2	2	19	38	118
HL	0.2490	13.6270^{ns}	4.1160 ^{ns}	0.1240 ^{ns}	0.1270
NL	3.2500	85.3080*	242.859*	0.3770 ^{ns}	0.4720
VL	0.0006	0.5781*	3.7266*	0.0040**	0.0021
TLL	0.1987	22.4043*	7.6253*	0.1500**	0.1832
TLW	0.2867	1.0671*	1.7066*	0.0133**	0.0152
50% DF	3.2326	61.7551*	203.9837*	0.6535**	0.3626
PL	2.7071	51.9845*	101.6850*	0.2928 ^{ns}	0.3938
PWt	0.1760	2.9068*	23.0664*	0.0196**	0.0236
LP	0.6051	21.4291*	29.9773*	0.1895**	0.1814
P.Ped.	0.0033	0.7242*	4.1897*	0.0080**	0.0057
SWPl	1.3373	10.1793*	1110.3612*	1.0478*	0.9243
GY	3.0593	0.4610*	1.2603*	0.0030*	0.0164

, ** significant at 5% and 1% level respectively

Table 4: The mean performance for some landrace African yam beans traits studied

ACC.	HL	NL	VL	TLL	TLW	50% DF	PL	PWt	LP	P.Ped	SWPl	GY
ACC. 1	9.388^{a}	46.735^{c}	2.533^{l}	8.900^{de}	3.477^{f}	81.688^{l}	18.455^{l}	6.688^{c}	16.877^{bcd}	1.755^{f}	18.922^{f}	2.624^{def}
ACC. 2	8.555^{bcde}	44.333^{f}	3.055^{i}	10.260^{b}	3.022^{i}	80.100^{m}	19.088k	6.366^{e}	17.677^{a}	1.777^{ef}	17.066^{g}	2.442^{g}
ACC. 3	8.863^{a}	41.256^{i}	3.166^{g}	7.700^{de}	2.788^{j}	86.877^{g}	20.655^{j}	6.622^{c}	14.144^{g}	2.933^{b}	19.088^{f}	2.760^{cd}
ACC. 4	7.555 ^{h}	50.500^{b}	2.955^{j}	9.466^{c}	4.022^{b}	77.400^{n}	16.355^{m}	5.800^{h}	15.344^{e}	3.144^{a}	17.011^{g}	2.426^{g}
ACC. 5	8.033^{fg}	51.222^{a}	3.177^{g}	9.000^{d}	3.555^{ef}	89.466^{e}	25.677^{de}	3.588^{k}	12.911^{h}	1.9666^{d}	18.844^{f}	2.604^{ef}
ACC. 6	8.322^{def}	46.000^{d}	3.444^{f}	8.900^{de}	3.633^{de}	91.666^{c}	27.322^{b}	5.855^{h}	16.500^{d}	1.277^{i}	14.644^{h}	2.504^{fg}
ACC. 7	9.522^{a}	37.111^{l}	2.877^{k}	10.700^{a}	4.233^{a}	93.777^{a}	29.455^{a}	10.822a	17.166^{bc}	3.155^{a}	7.111^{k}	3.211^{a}
ACC. 8	8.688^{bcd}	41.566^{hi}	3.122^{h}	7.877^{f}	3.222^{gh}	77.677^{n}	23.466^{i}	5.633^{i}	14.566^{f}	1.966^{d}	20.444^{de}	2.940^{b}
ACC. 9	7.766^{gh}	40.556^{j}	2.866^{k}	7.611^{f}	2.855^{j}	85.5000^{f}	23.533^{c}	8.788^{b}	15.444^{e}	2.966^{b}	20.989^{d}	1.757^{h}
ACC. 10	8.322^{de}	45.222^{d}	1.933^{n}	8.833^{de}	3.777^{c}	85.777^{h}	25.488^{ef}	4.677^{j}	15.255^{e}	1.844^{e}	19.800^{ef}	1.717^{h}
ACC. 11	8.466^{cde}	41.833^{hi}	4.055^{b}	8.800^{de}	3.688^{cd}	89.333^{e}	26.566^{c}	6.666^{c}	14.255^{fg}	1.612^{g}	17.178^{g}	2.517^{fg}
ACC. 12	8.788^{bc}	40.333^{j}	3.900^{cd}	10.655^{ba}	3.18^{h}	89.466^{e}	27.433^{b}	6.455^{de}	16.900^{bcd}	3.177^{a}	59.077^{a}	2.986^{a}
ACC. 13	7.155^{i}	41.278^{i}	3.933^{c}	8.966^{de}	3.322^{g}	84.488^{j}	24.688^{gh}	5.633^{i}	13.866^{g}	2.222^{c}	32.966^{b}	2.688^{de}
ACC. 14	7.977^{ef}	42.111^{h}	3.877^{d}	8.844^{de}	3.566^{ef}	908.911^{d}	25.433^{ef}	3.544^{k}	12.677^{i}	1.988^{d}	13.055^{i}	2.691^{de}
ACC. 15	7.055^{i}	50.73^{ab}	3.933^{c}	9.066^{dc}	3.455^{f}	92.355^{a}	27.322^{b}	6.588^{cd}	16.722^{cd}	1.433^{h}	28.288^{c}	2.620^{ef}
ACC. 16	8.288^{ef}	41.255^{i}	3.866^{d}	9.166^{dc}	3.511^{ef}	85.111^{e}	26.244^{cd}	5.600^{i}	11.733^{i}	1.333^{i}	15.311^{h}	2.871^{bc}
ACC. 17	7.700^{hg}	44.333^{f}	4.144^{a}	8.511^{e}	3.288^{gh}	83.222^{k}	24.255^{h}	6.033^{g}	16.944^{bc}	1.811^{ef}	15.088^{h}	2.708^{de}
ACC. 18	7.511^{h}	32.411^{m}	3.944^{c}	10.383^{ab}	4.111^{b}	81.433^{l}	23.566^{i}	4.711^{j}	12.855^{h}	1.966^{d}	10.555^{j}	2.640^{def}
ACC. 19	8.644^{bcde}	38.388^{k}	3.655^{e}	10.766^{a}	4.300^{a}	84.333^{j}	25.822^{de}	8.788^{b}	17.266^{b}	3.133^{a}	33.155^{b}	3.188^{a}
ACC. 20	8.800^{bc}	32.444^{m}	2.222^{m}	9.205^{cd}	3.011^{i}	85.555^{hi}	25.000^{fg}	6.200^{f}	16.955^{bc}	2.933^{a}	16.755^{g}	2.606^{ef}

Means with the same letter (s) in each Column are not significantly different ($P<0.05$) according to Duncan's Multiple Range Test (DMRT)

Table 5: Genetic parameters of some African yam bean landrace traits evaluated in three locations under field conditions

	δ^2g	δ^2ph	GCV	PCV	H_s	GA	GAM
HL	0.4431	0.4573	8.0490	8.1770	96.8948	1.3497	16.3216
NL	26.9420	26.9843	12.2341	12.2437	99.8432	10.6841	25.1825
VL	0.4136	0.4140	19.2950	19.30047	99.9033	1.3241	39.729
TLL	0.8305	0.8472	9.4779	10.0473	98.0288	1.8587	20.2894
TLW	0.1881	0.1896	12.2341	12.2437	99.2088	0.8898	25.4181
50% DF	22.5922	22.6646	5.5300	5.5389	99.6796	9.7757	11.3736
PL	11.2658	11.2983	13.7328	13.7526	99.7123	6.9043	28.2490
PWt	2.5607	2.5629	26.2373	26..2473	99.9141	3.2950	54.0250
L/P	3.3097	3.3308	11.8882	11.9260	99.3665	3.7357	24.4120
P.Ped	0.4646	0.4655	30.8702	30.9001	99.8066	1.4027	63.5312
SWPl	123.2570	123.3734	53.4603	53.4856	99.9056	5.3868	25.939
GY	0.1397	0.1400	14.2386	14.2539	99.7857	0.7691	29.3001

δ^2g =genotypic variances, δ^2ph=phenotypic variances, H_{bs} = broad sense heritability, GCV =Genotypic coefficient variance, PCV=phenotypic coefficient variance, GA= genetic advance and GAM =genetic advance as percent of mean expression

Conclusion

The findings from this study showed the existence of genetic variability among the local African yam bean accessions which can be exploited for further crop improvement program. The high values for the genetic parameters recorded point to the fact that if a suitable breeding design is adopted, new varieties that can deliver high genetic gain in farmers' fields can be developed. The study will also assist germplasm curators in their decisions on how to select core genotypes for conservation.

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