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GENETIC VARIABILITY STUDIES IN SOME LOCAL AND IMPROVED SWEET POTATO (*Ipomoea batatas* (L.) LAM.) VARIETIES IN OWERRI, IMO STATE, NIGERIA.

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ABSTRACT:

The present study was undertaken to estimate the genetic variability, heritability and genetic advancement for growth and yield parameters among some local and improved sweet potato (*Ipomoea batatas*(L.) Lam.] varieties obtained from four different locations in Nigeria. The experiment was laid in a randomized complete block design with three replications between the end of May – the end of September 2024 at the Federal University of Technology Owerri Research Farm. Analysis of variance revealed highly significant differences ($p<0.05$) among the genotypes for both the growth and yield parameters. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits. High (>20 %) genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were observed for number of marketable root per hectare, weight of top biomass per hectare, number of unmarketable root per hectare, sprout count and number of leaves. It indicated the existence of broad genetic gain, which would be amenable for further selection. High heritability (>60 %) were recorded for the following characters: weight of top biomass, sprout count, petiole length, root diameter, leaf width, number of leaves, plant girth, vine length, leaf length, number of unmarketable root, root length and number of marketable root (60%). High genetic advance as percentage over mean GAM% (>20 %) were recorded for the characters namely: Weight of top biomass, number of unmarketable root, sprout count, number of marketable root, number of leaves and root diameter. Traits with high heritability and GAM% value are governed by additive genes and selection would be efficient for further crop improvement. It is therefore recommended, that more accessions can be utilized in assembling varieties especially for characters which have a broad GCV value.

keywords: *Variability, Heritability, Genotypic coefficient, Phenotypic coefficient of variation*

1. Introduction

Sweet potato (*Ipomoea batatas* [L.] Lam)) is a tuberous rooted perennial crop that is usually grown as annual crop. It originated from Central America (Ecocrop, 2010) and is widely grown as an important staple food in most parts of the world. There are over 403 varieties of sweet potato of which the flesh can be white, yellow, red, purple, pink, violet and orange or brown while the skin colour varies among yellow, red, orange and brown. Many parts of the plant including the leaves, roots and vines are edible. Sweet potato is one of the major staple crops and the most important food security promoting root crops in the world, especially in sub- Saharan Africa (Low et al., 2009). Well adapted to the tropical and subtropical regions, sweet potato has nutritional advantage for the rural and urban dwellers (Ingabire and Hilda, 2011). Sweet potato is an excellent source of energy (438 kJ/100 g edible portion) and can produce more edible energy per hectare per day than cereals, such as wheat and rice and has other advantages, such as versatility, high yield, hardiness, and wide ecological adaptability (Laurie et al., 2012)

Breeding programs will succeed if supported by information of economic value, wide diversity, and high inheritance of the character to be corrected. Therefore, understanding the diversity of sweet potato genotypes based on agronomic traits is very important in planning sweet potato breeding programs and determining effective selection criteria (Ngailo et al., 2016; Selaocoe et al., 2019). Selection in breeding programs is the basis of all improvements to get new superior varieties. Efficient selection will be obtained by using several genetic parameters and heritability as considerations. According to Palumbo et al., (2019) and Irwan et al., (2019), wide genetic diversity is one of the conditions for an effective selection program, and selection for a desired character will be more meaningful if the character is easily inherited. Another important component that determines the success of a variety assembly program is information about inheritance (heritability values) and characters that are positively correlated with root yields. Breeders need this information to determine their selection strategies and criteria. Studies on parameters genetic and heritability has been done by researchers. Shaumi et al., (2012); Madawal et al., (2015); Rahajeng and Rahayuningsih (2016); EL-Sharkawy (2019) reported that jumlah dan bobot umbi serta hasil umbi adalah. The characters with the high and moderate heritability and genetic advance can be considered for direct selection for sweet potato improvement.

The amount of variability that exists in the germplasm collections of any crop is of utmost importance towards breeding for better varieties. Particularly, genetic variability for a given character is a basic prerequisite for its improvement by systematic breeding. Sweet potato is a highly heterozygous and cross-pollinated crop in which many of the traits show continuous variation. Since it is highly heterozygous, there is extensive variability within the species, which is available for exploitation by plant breeders (Jones et al.,1986). Hence, consideration of quantitative approaches for exploitation of the extensive genetic variability available in sweet potato is of utmost importance, which in turn is dependent on good estimates of the genetic parameters. Estimates of genetic parameters serve as a base for selection and hybridization as the degree of variability for a given character is a basic prerequisite for its improvement.

Sweet potato is a cross-pollinated and highly heterozygous crop resulting in large variability. Presence of variability is prerequisite to the plant breeder for planning an effective breeding programme. This is useful for selecting, identifying promising variants for developing hybrids or varieties directly or through recombinant breeding. Genetic analysis reveals the genetic nature of the inheritance of tuber yield and yield components which is required to design efficient sweet

potato improvement breeding strategy. Therefore, this research was conducted with the objective to assess the extent and nature of genetic variability and heritability among the sweet potato genotypes.

Aim:

To assess the amount of variability and heritability present in the sweet potato varieties collected.

Materials and Methods

Description of the Study Area:

The study was conducted in the Teaching and Research Farm of the School of Agriculture and Agricultural Technology, Federal University of Technology Owerri, Imo State. Owerri lies at latitude 05° 27°N and longitude 07° 02°E at an elevation of 55 meters above sea level and is in the tropical rainforest region of southeastern Nigeria. The area has a bimodal pattern of rainfall with peaks in July and September. It has minimum and maximum annual temperature of 20°C and 32°C respectively and mean annual rainfall of 2500 mm and relative humidity of 85-89% (Nwosu and Adeniyi, 1980)

Treatments:

The treatments comprised 12 sweet potato varieties (Table 1). The sweet potato varieties were obtained from four different locations namely: 6 improved varieties from National Root Crop Research Institute (NRCRI), Umudike, 2 local varieties from Abia State, 2 local varieties from Imo State and 2 local varieties from Nasarawa State respectively.

Table 1: List of sweet potato varieties and their locations used for the study

Sweet Potato Varieties	Designation	Location
King J (Umuspo 1)	KINRC	NRCRI
Ex-Igbariam	EXNRC	NRCRI
Solo Gold	SONRC	NRCRI
Mothers Delight (Umuspo 3)	MONRC	NRCRI
TIS 87/0087	TINRC 1	NRCRI
TIS 8164	TINRC 2	NRCRI
Bende 1	BELNR 1	Abia
Bende 2	BELNR 2	Abia
Bota Akpulu	BOLNR	Imo
IgbariamAkpulu	IGLNR	Imo
ApiDuglu	APLNR	Nasarawa

SokuwaDuglu	SOLNR	Nasarawa

2. Land Preparation and Experimental Design.

The experimental field was cleared using a cutlass. The area was measured using tape and ropes and ridges were made using a shovel. Each variety was planted in a 3m × 3m($9m^2$) plot and at a planting distance of 1.0m × 0.3m. The experimental design was randomized complete block design. Each block contained 12 plots and was replicated 3 times and separated from each other at a space of 1m. The planting material was approximately 20cm length with at least three leaf nodes. The total land area for the experiment was 13m × 41m ($533m^2$) with a total of 72 ridges (Each plot contained two ridges with 9 plants per ridge giving a total of 18 plants per plot and 54 plants per variety and a sum total of 648 plants for the entire experiment (approx.12, 158plants/ha)

3. Statistical Analysis:

All the data were subjected to Analysis of Variance (ANOVA) test using Genstat software (edition 4) while mean separation was done using Least Significant Difference (LSD) at 5% level of probability using the procedure by Obi (2002).

Genetic parameters were estimated by the formula given by Singh and Chaudhary (1985), Werf (2009) and Malek et al., (2014). These parameters include the following:

i. σ^2_G (or V_A which is an estimated of genotypic variance) = $(MS_G – MS_E)/r$, where MS_G is an estimate of mean square of tested accession, MS_E is an estimate of mean square of error and r refers to the number of replications.
ii. σ^2_P (or V_P which is an estimate of phenotypic variance) = $\sigma^2 G + (MS_E/ r)$
iii. H^2 (an estimate of Broad sense heritability) = $V_A/ V_P \times 100$
iv. GCV (Genotypic coefficient of variation) = $\sqrt{\sigma^2_G} / \bar{x} \times 100$, where σ^2_G is the genotypic component of variance and $\bar{x}$ is the mean of the trait.
v. PCV (Phenotypic coefficient of variation) = $\sqrt{\sigma^2_P} / \bar{x} \times 100$, where σ^2_P is the phenotypic component of variance and $\bar{x}$ is the mean of the trait.
vi. GAM (Genetic advance, which is taken as percentage of the mean assuming selection of the superior 5% of the varieties) = $K \times \sqrt{\sigma^2_P} / \bar{x} \times h^2 \times 100$, where K (the standard selection intensity) = 2.06 (at 5% selection intensity), σ^2_P is the phenotypic component of variance, h^2 is the heritability in narrow sense and $\bar{x}$ refers to the mean of the trait being evaluated. Genetic advance was estimated as per the formula proposed by Johnson et al., (1955). The range of genetic advance as per cent of mean was classified as low (Less than 10%), moderate (10 - 20%) and high (more than 20%) as suggested by Johnson et al., (1955).

4. Results and Discussion

The examination of readily available variability in the germplasm of the given varieties is also an important avenue available for the breeder. The first step in plant breeding programme is to determine the extent of variability for the traits under improvement and to divide this variability into genetic and environmental components.

Analysis of Variance

The analysis of variance (ANOVA) showed highly significant differences ($p<0.05$) among the genotypes for all the growth and most of the yield component traits namely: sprout count, number of leaves, vine length, leaf length, leaf with, petiole length, plant girth, root diameter, root length, number of marketable root, number of unmarketable root, weight of unmarketable root and weight of top biomass. However, only root number and weight of marketable root showed no significant difference (Table 2 and 3). The highly significant differences among the varieties studied indicated the existence of broad genetic base, which would be consider for further selection. These findings are in line with earlier reports of Basavaraj et al., (2005) in potato, Engida et al., (2006), Shashikanthet al., (2008) and Sharavatiet al., (2018) in sweet potato.

5. Phenotypic and Genotypic Coefficient of Variation

Higher magnitude of PCV (phenotypic coefficient of variation) and GCV (genotypic coefficient of variation) (> 20%) were observed for number of marketable root per hectare (67.36 and 52.39%), weight of top biomass per hectare (65.27 and 61.72%), number of unmarketable root per hectare (62.53 and 51.70%), sprout count (47.26 and 43.79%), number of leaves (43.72 and 39.30%), root diameter (39.74 and 36.17%),petiole length (30.13 and 27.78%), vine length (28.93 and 24.94%), root length (28.66 and 22.49%), leaf width (27.66 and 25.10%), plant girth (23.92 and 20.87%). But high PCV was observed for leaf length (22.58%). While moderate magnitude of GCV (10-20%) were observe for root number and leaf length (13.53 and 19.3%). The PCV of both the root number and leaf length was observed to be high (36.64 and 22.58%). Therefore, additive component is predominant here. This reveals that influence of the environment for these traits is negligible and the role of the genotypic performance in the full expression of the phenotype. Whereas, the low magnitude of PCV and GCV (<10%) wereobserved for weight of marketable root (4.32 and 3.20%) and weight of unmarketable root (7.17 and 3.08%) (Table 4 and 5). These results are in accordance with the findings of Sharma (2004) in sweet potato, Basavaraj et al., (2005) in potato, Engida et al., (2006) in sweet potato and Sharavatiet al., (2018) in sweet potato.

6. Heritability

With the genotypic coefficient of variation alone, it is difficult to determine the relative amount of heritable and non-heritable components of variations present in the population. Estimates of heritability and genetic advance would supplement this parameter. Estimate of heritability was recorded high (>60%) for the traits namely: weight of top biomass per hectare (89.00%), sprout count (86.00%), petiole length (85.00%), root diameter (83.00%), leaf width (82.00%), number of leaves (81.00%), plant girth (76.00%), vine length (74.00%), leaf length (73.00%), number of unmarketable root per hectare (68.00%) and root length (61.00%). The moderate heritability was observed for weight of marketable root per hectare (55.00%) and number of marketable root (60.00%). Whereas the low heritability was observed for root number (14.00%) and weight of unmarketable root (18.00%) (Table 4 and 5).

The high and moderate heritability recorded for the traits in this study indicated that these characters were less influenced by environmental factors and governed by the additive gene effects that are substantially contributing towards the expression of these traits. Hence, selection for these traits will lead to accumulation of more desirable genotypes. However, rest of the traits seems to be influenced by non-additive gene effects. The present findings on heritability are in

accordance with findings reported by the various researchers namely; Sahu (2003), Teshomeet al., (2004), Engida et al., (2006), Shashikanth et al., (2008) and Sharavatiet al., (2018) in sweet potato.

Table 2: Analysis of Variance for Growth Parameters in Sweet Potato Genotype at 9WAP

Sources of variation /Characters	Replication	Treatments	Error		
Degree of Freedom	2	11	22		
	SSG	SSE	MSG	MSE	p-value
Sprout count	795.22	225.28	72.29	10.24	<.001
Number of leaves	260001	99998	23636	4545	<.001
Vine length	120662	61941	10969	2816	<.003
Leaf length	217.448	116.880	19.768	5.313	0.004
Leaf width	316.141	111.761	28.740	5.080	<.001
Petiole length	742.74	221.98	67.52	10.09	<.001
Plant girth	14.0338	6.6661	1.2758	0.3030	0.002

Table 3: Analysis of Variance for Yield Parameters in Sweet Potato Genotype at harvest.

Sources of variation /Characters	Replication	Treatments	Error		
Degree of Freedom	2	11	22		
	SSG	SSE	MSG	MSE	p-value
Root Diameter per plot1	518.29	522.28	138.03	23.74	<.001
Root length per plot	941.96	726.95	85.63	33.04	0.028
Root number per plot	7.5177	12.7281	0.6834	0.5786	0.354
No. of Marketable root per ha	347.64	276.61	31.60	12.57	0.032
No. of Unmarketable root per ha	872.22	549.78	79.29	24.99	0.010
Weight of Marketable root per ha	36.660	32.893	3.333	1.495	0.053
Weight of Unmarketable root per ha	3.30083	2.05500	0.30008	0.09341	0.010
Weight of top biomass per ha	270556	57463	24596	2612	0.001

Keys: SSG- Sum of square Group, SSE- Sum of square Error, MSG- Mean square Group, MSE- Mean square Error, WAP- Weeks After Planting

Table 4: Estimation of Genetic for Growth Parameters of sweet potato at 9WAP

Traits	Genotypic variance (V_A)	Phenotypic variance (V_P)	Heritability (%)	GCV (%)	PCV (%)	GAM (%)
Sprout Count	20.68	24.09	86.00	43.79	47.26	83.27
Number of Leaves	6,363.67	7,878.67	81.00	39.30	43.72	73.42
Vine Length	2,717.67	3,656.34	74.00	24.94	28.93	44.21
Leaf Length	4.82	6.60	73.00	19.33	22.58	34.59
Leaf Width	7.89	9.58	82.00	25.10	27.66	47.30
Petiole Length	19.14	22.50	85.00	27.78	30.13	52.53
Plant Girth	0.32	0.42	76.00	20.87	23.92	37.57

Table 5: Estimation of Genetic for yield Parameters of sweet potato at harvest.

Traits	Genotypic variance (V_A)	Phenotypic variance (V_P)	Heritability (%)	GCV (%)	PCV (%)	GAM (%)
Root Diameter	38.10	46.01	83.00	36.17	39.74	68.39
Root Length	17.53	28.54	61.00	22.49	28.66	36.44
Root Number	0.03	0.22	14.00	13.53	36.64	10.67
NMRT	6.34	10.53	60.00	52.39	67.36	82.81
NUMRT	18.10	26.43	68.00	51.70	62.53	88.25
WTMRT	0.61	1.11	55.00	3.20	4.32	4.52
WTUMRT	0.07	0.38	18.00	3.08	7.17	2.60
WTBM	7328	8198.67	89.00	61.72	65.27	119.17

Keys: GCV- Genotypic coefficient of variation; **NMRT**- Number of Marketable Root**; PCV**- Phenotypic coefficient of variation; **NUMRT**- Number of Unmarketable Root; **GA**- Genetic Advance; **WTMRT**- Weight of Marketable Root; **WTUMRT**- Weight of Unmarketable Root; **WTBM**- Weight of Biomass.

7. Genetic Advance as Percentage Over Mean

Genetic advance is important to find out the genetic gains likely to be achieved in the next generation. These are classified as high (> 20%), medium (10 to 20 %) and low (< 10 %). The success of genetic advance under selection mainly depends upon genetic variability, heritability and selection intensity. In the present study, highest estimates of genetic advance as percentage of mean were obtained for characters namely: weight of top biomass per hectare (119.17%), number of unmarketable root per hectare (88.25%), sprout count (83.27%), number of marketable root (82.81%), number of leaves (73.42%), root diameter (68.39%), petiole length (52.53%), leaf width (47.30%), vine length (44.21%), plant girth (37.57%), root length (36.44%) and leaf length (34.59%). The moderate estimate of genetic advance as percentage of mean was observed for only root number (10.67%). Whereas, the low estimate of genetic advance as percentage of mean were observed for the characters namely: weight of marketable root (4.52%) and weight of unmarketable root (2.60%) respectively (Table 4 and 5).

Very often, heritability in broad sense is not the true indicator of inheritance of traits, since only additive component of genetic variance is transferred from generation to generation. Therefore, heritability in broad sense may mislead in judging the effectiveness of selection for the trait. Considering heritability in broad sense along with genetic advance over mean may reveal the prevalence of specific components (additive or non-additive) for the trait more accurately.

In the present study, high heritability coupled with high genetic advance as percentage over mean was recorded for the characters namely: sprout count, number of leaves, vine length, leaf length, leaf width, petiole length, plant girth, root diameter, root length, number of unmarketable root per hectare, weight of top biomass per hectare. Whereas, moderate heritability coupled with moderate genetic advance as percentage over mean was recorded for characters: weight of marketable root per hectare, weight of unmarketable root per hectare.

The above findings indicated that the characters with the high and moderate heritability and genetic advance can be considered for direct selection for improvement. These results are in agreement with the results of Engida et al., (2006), Shashikanth et al., (2008) Madawal et al., (2015), Demelie and Aragao (2016), Badu et al., (2017) and Sharavatiet al., (2018) in sweet potato.

8. Conclusions:

The results of ANOVA showed the significant difference among the tested genotypes in almost all traits observed except on root number per plot and weight of marketable root per hectare. PCV estimation was higher than GCV estimation for all the observed characters. The number of marketable root per hectare, number of unmarketable root per hectare, and the weight of top biomass per hectare showed a wide range of PCV and GCV as well as high broad sense heritability that indicated these traits to have additive gene effect and more reliable for effective selection. The broad GCV in a population is effective for selection to obtain superior variety. The result in this present study, is in agreement with that reported by Rahajeng et al., (2020) on Genetic Parameters of Agronomic Traits in Sweet potato Accessions, a research carried out in Indonesia. Traits with high heritability (H^2>60%) and genetic advance as percentage over mean (GAM%>20%) value are governed by additive genes and selection would be efficient for further crop improvement in breeding programme. It is therefore recommended that more accessions can be utilized in assembling varieties especially for characters which have a broad GCV value.

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