

Original Article

The Analysis of Genetic Stability of Sweet potato varieties (*Ipomoea batatas*(Lam). L)propagated through Roots

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Abstract - An experiment was conducted between 2022 and 2023 in the South-South part of Nigeria to analyze the genetic stability of sweet potato varieties raised from the roots using their yield and yield components. The data collected were subjected to analysis of variance (ANOVA) using the Genstat Edition 3. Means were separated using the Least Significant Difference (LSD). From the result obtained in both years of the experiment, Nwaoyorima gave a very high mean value in terms of yield in tons per hectare (4.06). This was closely followed by kwara(4.87) and buttermilk (3.86). The result also showed that the varieties had good marketable root weight, marketable root number, total root number and total root weight across the year. The variety, kwara, gave the highest marketable root number (30.91), followed by Nwaoyorima (25.71). Also, the mean marketable root weight was highest in kwara (3.86). This was followed by Nwaoyorima(3.48). The result obtained from the experiment also showed significant relationships among the traits considered ($P < 0.05$). The table shows that the number of marketable roots had a very strong relationship with the number of unmarketable roots (0.550**), total root number (0.472**) and marketable root weight (0.481*). The table also showed a significant relationship between marketable root weight, total root number (0.364*) and total root weight (0.345*). The unmarketable root weight also had a highly significant relationship with total root weight (0.417*) but had no significant relationship with virus incident (-0.467) and virus severity (0.041). The result showed that sweet potato propagation using the root can also retain the genetic stability of a variety, as it does with those propagated with vines or nodes.

Keywords - Yield stability, Roots, Yield and yield components, Landraces, Sweet potato.

1. Introduction

Sweet potato is one of the major staple foods grown widely in Africa, especially in the western and Eastern parts of Africa [1, 2, 3]. Other parts are also helpful besides the roots, which serve as a major food. Many countries in Sub-Saharan Africa consume the leaves. Varieties such as Orange Flesh Sweetpotato (OFSP) have played a significant role in dietary balance as they supply vitamin A, thereby reducing Vitamin A deficiency, especially in Africa. This is a result of fortification of the variety (OFSP) b-carotene [4, 5]. Though sweet potato is being grown in many countries, studies have shown that its popularity has drastically declined due to the drop in the number of farmers who grow the crop [6]. Sweet potato is propagated asexually from vine cuttings or sexually from seeds, but breeding programs do the latter. Propagation of sweet potato is done using one of the following methods: sprouting of whole storage roots (sprouts are then used as planting materials) and stem or vine cuttings from plants used for production or from multiplication plots. In the latter method, green vines of approximately 30cm in length with at

least three leaf nodes are planted into the soil. Sweet potato is most commonly grown on mounds or ridges and occasionally on raised beds or flats. Deep cultivation enhances root growth and bulking of the sweet potato roots. Mounds and ridges promote adequate drainage and ease of harvesting. Often, plant breeders want to develop broadly-adapted genotypes for a wide range of environments. However, it is often impossible to identify genotypes superior in yield and yield components in all environments. Furthermore, the same genetic system may not control yield over diverse environments [7, 8] Simmonds, . Therefore, breeders often develop genotypes for a particular environment to take advantage of specific adaptations [9]. However, breeding for a specific adaptation is efficient if production areas are divided into mega-environments, each representing a target environment for breeding. Mega-environment is a portion (not necessarily contiguous) of the growing region of a crop species having a fairly homogenous environment and causes similar genotypes to perform best there. The success of any plant breeding program depends on many factors; one of the most important



factors is understanding and selecting suitable test locations [10]. An efficient test location discriminates so that differences among genotypes can be easily detected using few replications, and it is representative of the target environments for the cultivars to be released. The representation of the location for the target environment should be repeatable so that genotypes selected in each year will have superior performance in future years. For the purpose of breeding for a locally suited genotype, it is crucial to understand the target environment, which necessitates breaking the target locales down into mega-environments. Plant breeding strategies frequently include multiple-environment trials. The trials are used to categorize target regions into several mega-environments and to determine which genotypes are preferable. Segmenting an area used for crop growth into many mega-environments facilitates information sharing between breeding programs, target genotype distribution to suitable production areas, and resource allocation in breeding programs [11, 12]. Heritability increases in a comparatively well-defined and predictable environment when mega-environments are understood and identified.

Therefore, it improves the efficiency of the testing and breeding program by focusing on the most promising material. Many statistical techniques have been put forth to quantify the stability of genotypes across contexts. Nonetheless, according to [13] no single technique can fully account for cultivar performance in various settings. Two distinct theories of stability were proposed by [14]: dynamic (agronomic) and static (biological). According to the stability notion, a stable genotype will function similarly no matter how the environment changes. Both stability ideas are beneficial, but how they are applied depends on the characteristics under consideration. The idea of stability is helpful for qualitative attributes like stress tolerance or illness resistance. The dynamic concept of stability is helpful for quantitative features like yield [15]. Therefore, this research looks at the genetic stability in yield and yield components of sweet potato (*Ipomoea batatas* (Lam) L) propagated from sweet potato roots. This results from the many difficulties associated with using sweet potato vine for sweet potato propagation. Therefore, there is a need to develop genetically and economically viable alternatives to enhance productivity. The work tries to emphasize the use of sweet potato tubers as propagating material, which will reduce the cost and the bulkiness of carrying vines for planting as the sweet potato tubers can be sliced into pieces, germinated and planted out in the field and still maintain their genetic stability.

2. Related Literature

The adventitious sprouts from storage roots are used as propagules in sweet potatoes. This vegetative propagation theoretically ensures genetic fidelity. However, variability is still observed at the phenotypic level among propagules. Environmental interactions probably contribute to this

variability, wherein the expression of quantitative traits is conditioned by prevailing environmental factors [27-29]. Confounding effects arise due to phenotypic plasticity, e.g., several types of leaves occurring on individuals of most species [30] (Yen, 1974) and variable root yield among hills within a location [31] (Steinbauer et al., 1943). Even rigorously selected materials in foundation seed programs continue to exhibit qualitative changes such as root skin and flesh color anomalies [32] (Sloan, 1994).

[16] Researched sweet potato clones' growth and yield stability across four locations in east Nusa, Indonesia. The goal was to ascertain the development and yield of sweet potato clones throughout the locations and to clarify the impact of genotype by environment interaction on these traits. Their experiment's findings demonstrated high mean values and robust yield stability in the yield components of sweet potatoes and other plants. In the three agro-ecological zones of Malawi, [17] conducted a study on the plant development and yield stability of orange fleshed sweet potato genotypes. The study aimed to assess the genotypes of orange flesh sweet potatoes for yield stability. According to the data, there were notable variations in vine length across the genotypes and between the experimental sites. The longest vines across all sites were generated by the check variety Zondeni, with a cumulative mean of 146.0 cm.

The genotype's longest measures, 166.0 cm and 168.7 cm, were taken at the Maseya and Bunda locations, respectively. When stability analysis was done for genotypes and environments, the differences in root yield were mainly caused by genotypes, environments, and their interactions, which had highly significant impacts of 34.8%, 21.8%, and 43.4%, respectively. The findings demonstrated notable variations across genotypes in terms of vine length, growth rate, leaf area, and tuber production. Zondeni has the largest vine length on record, with LU06/0252 coming in second. This suggests that these two genotypes benefit tuber yield and are good sources of vines, particularly in situations where the production goal is to produce sweet potato vines. Because the vines are rich in proteins and minerals that are required in livestock feeds, ruminants can consume the vines as forage [18-21].

Crop production and growth result from the interplay between its genetic potential and surroundings. According to [22], crops thrive in surroundings to which they are acclimated. According to [23], genotype performance is limited in terms of broad and particular adaptation and yield stability. The broad adaptability is typically ascribed to genotypes that exhibit high mean yields in various settings and perform well over extensive areas. When a variety is among the genotypes with the highest yields at only a few places, it possesses a particular adaptability. A genotype's stability, which can be either static or dynamic, is its capacity to function reliably in various settings. Before a new variety is

released, it is crucial to understand the different genotypes by environment (GxE) interactions in order to determine whether they have broad or specialized adaptation, 2005; [24]. When many genotypes and locations are involved, it becomes more challenging to compare genotype performance across settings, and it frequently causes a delay in the breeding program's selection process [25]. Before a new variety is released, genotypes with high yield potential are assessed for multiple years and in several places to determine their yield stability and GxE interaction. Breeders, therefore, require reliable biometric techniques to analyze GxE interactions and assess phenotypic stability [26].

3. Methodology

The roots of Sweet potato landraces were obtained from the local farmers, and the check varieties were obtained from the National Root Crop Research Institute Umudike. The planting was done in an experimental Port Harcourt, Rivers State farm. The roots of the sweet potatoes were cut into sizes that carry the buds.

They were planted directly into the already prepared ridges. Three landraces were used, and a check variety was used for the experiment. The experiment was carried out in two replications. Each variety was planted on plots measuring 3m (2m x 1.5m). This corresponded to a total of 3333.33 sweet potato plants per hectare standard.

Below is the list of the varieties used for the research.

- Nwaoyorima.
- Buttermilk
- kwara
- Umuspo3 (Check Variety).

3.1. Data were Collected on the following

- Number of marketable roots
- Number of unmarketable roots
- Total number of roots
- Weight of marketable roots
- Weight of unmarketable roots
- Total weight of roots
- Virus incidence
- Virus severity

3.2. Experimental Design

The Randomized Block Design was used for the experiment because it was a field experiment

3.3. Data Analysis

The data collected were subjected to analysis of variance (ANOVA) using the Genstat Edition 3. Means were separated using the Least Significant Difference (LSD). Correlation Analysis (Step-Wise) was carried out to know the level of variations between the yield and yield components of the varieties.

4. Results and Discussion

The mean performance of the varieties in 2022 in terms of yield and yield components was recorded in Table 1. From the table, Nwaoyorima had the highest mean value (4.89) in yield (t/h). This was followed by kwara (4.87). Buttermilk also had a high mean value (3.86) but not as high as Nwaoyorima and kwara. Umuspo3 had the lowest yield in tons per hectare (1.35). The number of marketable roots followed the same trend. Kwara gave the highest marketable root number (30.91), closely followed by Nwaoyorima (25.71).

Buttermilk had the lowest mean value in terms of the number of marketable roots (14.26) among all the landraces considered. The number of unmarketable roots was highest in buttermilk (6.72), followed by Nwaoyorima (2.84). kwara had the lowest number of unmarketable roots. The mean marketable root weight was highest in kwara (3.86), followed by Nwaoyorima (3.48). Buttermilk and the check variety, Umuspos3, had the lowest marketable weight, respectively (2.97 and 0.81). Unmarketable root weight was highest in Nwaoyorima (1.49), followed by buttermilk (1.24). The lowest unmarketable root weight was recorded by Umuspos3 (0.55)

Table 2 presents the mean performance of the varieties in 2023. From the table, kwara had the highest yield in tons per hectare (4.01 t/h). This was followed by Nwaoyorima (3.88t/h). The number of marketable roots was highest in kwara (28.14). Nwaoyorima also had a high value for marketable root numbers (20.41), while Umuspos had the lowest number of marketable roots (16.25). Unmarketable roots were highest in Nwaoyorima (3.11) and lowest in kwara (0.64). The marketable root weight(kg) was highest in kwara (3.06), followed by Nwaoyorima (2.82) and butter mark (2.71).

The unmarketable root weight was highest in Nwaoyorima (0.89kg) and lowest in Umuspos3 (0.23kg). The root performance, virus incidence and virus severity among varieties in 2022 can be seen in Table 3. The variety kwara, had the highest yield in tons per hectare (4.87) but was highest in virus severity and also high in virus incidence. The virus incidence and severity also were (0.32) and (0.38), respectively, though high in total root number (16.32).

The highest virus incidence was recorded in Umuspos3 (0.84), but the lowest severity rate (0.20). Nwaoyorima also had a high virus incidence (0.46) with high virus severity (0.36) but not as high as kwara's in virus severity and Umuspos3 virus incidence. Table 4 presents the mean root performance, virus incidence and severity among the varieties in 2023. From the table, the virus severity was highest in Umuspos3 (0.86) also with the highest virus incidence also with the highest virus incidence level (1.02). Buttermilk had the lowest virus severity rate (0.13). Kwara with the highest yield in tons per hectare (4.01), high total root number (28.78),

total root weight (1.74) and high total root numbers (28.78), total root weight (1.74) and high member of marketable root (24.14) also had high virus incidence (0.34) and high virus severity (0.41)

Table 5 presents the correction of the agronomic traits of the varieties in 2022. From the observation, the number of marketable roots had a very strong positive correction with the number of unmarketable roots (0.556**), marketable roots weight (0.481) and total root number (0.472**). A significant association also existed between the number of marketable roots with total root weight (0.389*) and unmarketable root weight (0.387*). The number of marketable roots positively correlated with virus severity but was insignificant. Also, the relationship between the number of unmarketable roots and the total root number is significant (0.404*). However, the association between the unmarketable roots and virus incidence (-0.108) and the virus severity (0.261) were negative, non-significant, and positive but not significant, respectively. The table also reveals a positive relationship between marketable root weight and total root members. Though not significant, a significant relationship exists between the marketable root weight and total root weight. Also shown in the table is the relationship between the marketable root weight and virus incidence, which are positive but not significant.

The table also showed that the unmarketable root weight had a highly significant relationship with the total root (0.510**) and a significant relationship with the total root weight (0.416*). The unmarketable root weight also had a significant but negative relationship (-0.433*) with virus incidence. The table also showed that the association between the total root weight and the total root weight was highly significant (0.542**). Total root weight was also positively associated with virus incidence (0.167) and severity (0.20) but not significantly.

Table 6 presented the correlation coefficient of the varieties in 2023 using the agronomic traits. From the table, a highly significant relationship existed between the number of marketable roots, the number of unmarketable (0.487**) and

the unmarketable root weight (0.402**). The table also showed that unmarketable root weight (0.531*), total root number (0.381*) and total root weight (0.364*) all had positive and significant relationships with the number of unmarketable roots and total root weight (0.476**). The unmarketable root number also had a significant relationship with the unmarketable root weight (0.361*). While a non-significant relationship exists between the number of unmarketable roots and virus severity (0.201).

The table also showed a significant relationship between marketable root weight, total root number (0.364*) and total root weight (0.345*). The unmarketable root weight had a significant relationship with total root weight (0.417*), but there was no significant relationship between virus incident (-0.467) and virus severity (0.041). Finally, the table shows that the total root number had a significant relationship with the total root weight (0.431**)

5. Conclusion

Sweet potatoes are generally known to be propagated through vines. The method of propagation has ensured genetic stability across environments for years. The study showed that genetic stability across the years showed that using roots in the propagation of sweet potatoes can still maintain the stability of yield and yield components. The performance of varieties across the year showed that high yield in tons per hectare, high total root number, and high marketable weight all had a non-significant correlation with virus incidence and severity.

Varieties such as Nwaoyorima, Buttermark, and Kwara all performed well in terms of yield in tons per hectare, number of marketable roots, marketable root weight, total root member, and total root weight. The correlation analyses of the attributes had a highly significant relationship with one another. This suggests that selecting one attribute also means selecting other attributes based on the correlation analysis. The results from the study have shown that genetic stability can also be achieved through using roots in sweet potato propagation. It has also opened the doors for further genetic stability studies using sweet potato roots to propagate.

Table 1. Mean performance of the varieties in 2022

Varieties	Yield(t/h)	No. of marketable roots	No of unmarketable roots	Marketable root weight	Unmarketable weight
Nwaoyorima	4.06	25.71	2.84	3.48	1.49
Buttermilk	3.86	16.84	6.72	2.97	1.24
Kwara	4.87	30.91	1.74	3.86	0.91
Umuspos 3	1.35	14.26	2.27	0.81	0.55
LSD=5%	0.34	9.45	0.87	1.57	4.67

Table 2. Mean performance of varieties in 2023

varieties	Yield(t/h)	No. of marketable roots	No of unmarketable roots	Marketable root weight	Unmarketable weight
Nwaoyorima	3.88	20.41	3.11	2.82	0.89
Buttermilk	3.14	14.79	2.63	2.71	0.70
Kwara	4.01	28.14	0.64	3.06	0.42
Umuspos3	2.02	16.25	1.18	1.72	0.23
LSD=5%	0.78	15.73	1.04	0.09	0.52

Table 3. Mean root performance, virus incidence and severity among the varieties 2022

Varieties	Yield(t/h)	Total root	Total root weight(kg)	No. of marketable root	No. of unmarketable root	Virus incidence	Virus severity
Nwaoyorima	4.06	14.27	2.69	25.71	2.84	0.46	0.36
Buttermilk	3.86	11.78	2.10	16.84	6.72	0.21	0.28
Kwara	4.87	16.32	2.38	30.91	1.74	0.32	0.38
Umuspos3	1.35	8.26	0.68	14.26	2.27	0.87	0.20
LSD=5%	1.05	3.20	2.06	9.09	2.13	0.94	0.10

Table 4. Mean root performance, virus incidence and severity among the varieties 2023

Varieties	Yield(t/h)	Total root	Total root weight(kg)	No. of marketable root	No. of unmarketable root	Virus incidence	Virus severity
Nwaoyorima	3.88	11.76	1.85	20.41	3.11	0.24	0.14
Buttermilk	3.14	8.71	1.70	14.79	2.63	0.16	0.13
Kwara	4.01	28.78	1.74	28.14	0.64	0.34	0.41
Umuspos3	2.02	8.715	0.97	16.25	1.18	1.02	0.86
LSD=5%	1.56	4.69	1.98	11.09	1.67	1.05	1.00

Table 5. Correlation coefficient of the varieties in 2022 using the Agronomic characters

characters	No of unmarketable roots	Marketable root weight	Unmarketable root weight	Total root no.	Total root weight	Virus incidence	Virus severity
No of marketable roots	0.556**	0.481**	0.387*	0.472**	0.389*	-0.242*	0.181
No of unmarketable roots		0.261	0.542**	0.404*	0.410*	-0.108	0.261
Marketable root weight			0.271	0.211	0.376*	0.245	-0.286
UnmarketableRoot weight				0.510**	0.416*	-0.453*	0.192
Total root number					0.542**	-0.02	0.010
Total root weight						0.167	0.200
Virus incidence							0.171
Virus severity						

Table 6. Correlation coefficient of the varieties in 2023 using the Agronomic characters

Characters	No of unmarketable roots	Marketable root weight	Unmarketable root weight	Total root no.	Total root weight	Virus incidence	Virus severity
No of marketable roots	0.487**	0.531*	0.402**	0.381*	0.364*	0.002	0.011
No of unmarketable roots		0.210	0.361*	0.294	0.476**	-0.418	0.261
Marketable root weight			0.021	0.364*	0.345*	0.104	-0.041
Unmarketable root weight				0.547**	0.417**	-0.467	0.041
Total root number					0.431**	-0.002	0.101
Total root weight						0.167	0.20
Virus incidence							0.190
Virus severity							-----

*correlation is significant at 5%, **correlation is significant at 1%

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