



Genetic Diversity of Sweet Potato (*Ipomoea Batatas* (L.) Lam) Accessions from Nigeria and Niger Based on Agro-Morphological

Josefina Ndamononghenda Abed*^{1,2}, Happiness Ogba Oselebe¹, Samuel Chibuike Chukwu² and Issa Zakari Mahaman Mourtala³

¹Department of Crop Production and Landscape Management, Faculty of Agriculture and Natural Resources Management, Ebonyi State University, Abakaliki, Nigeria.

²Department of Crop Production and Agricultural Technologies, Faculty of Agriculture, Engineering and Natural Science, University of Namibia, Namibia.

³Department of Natural Resources Management, National Institute of Agronomic Research of Niger, Niamey, Niger.

*Correspondence: Email: josefinandamononghenda@gmail.com

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Abstract— *Utmost tropical nations regard the sweet potato(Ipomoea batatas(L.) Lam.) as their most significant chief crop. It's substantially privileged for its capability to deter disaster, improvement, and produce with many inputs. A study was carried out during the 2020 and 2021 growing time seasons in a field trial conducted at the University of Ebonyi State – CAS , to determine variability among sweet potato accessions, and identify traits that are positively and significantly associated with yield and accessions with high yield. A randomized complete block design with three replications was used to determine variability among sweet potato accessions, The results of both years combined statistical analysis indicated that the types significantly varied in terms of all yield and yield- related traits. As a result, the Umu SPO 3 acquired had the topmost values of average root storage in both the 2020 (5.2 cm) and 2021 (2.4 cm) growing seasons. In both 2020 and 2021 growing seasons and over time combined analysis, the haughtiest average root yield (2.67 Kg), and total root yield(8.89 t/ ha) were recorded for Koudakou. PCV was advanced than GCV suggesting a major environmental influence on those characters. Low heritability coupled with high, moderate, and low inheritable advance in percent of mean was observed in all characters. Traits considered in the study revealed positive and significant correlations. The grouping of accessions into two main clusters highlights genetic relationships among them. Understanding these relationships can help breeders identify potential parent lines for cross-breeding, which can lead to the development of new varieties with desirable traits.*



Keywords— *heritability, correlation, yield-related traits, variability, breeding*

I. INTRODUCTION

Starchy root and tuber crops are a significant global source of carbohydrates, second only to cereals. They contribute a substantial portion of the world's food supply, as well as serving as an important animal feed and raw material for human and industrial products (Chandrasekara & Josheph, 2016). Storage roots like cassava and sweet potatoes, and edible rhizomes like canna and arrowroots, can all be

propagated using vegetative parts, including tubers (potatoes and yams), stem cuttings (cassava), vine cuttings (sweet potatoes), and side shoots, stolons, or corm heads (taro and cocoyam) (Chandrasekara & Josheph, 2016; Mohanty et al., 2016). The importance of tropical root and tuber crops to global food security cannot be overstated (Nanbol & Namo, 2019). Sweet potato is a dicotyledonous plant belonging to the Convolvulaceae family. It is an

herbaceous perennial vine with medium-sized, sympetalous flowers that are frequently pale violet in color and alternating leaves that can have lobes or not (Alfred et al., 2019). Sweet potatoes are storage roots with a sweet flavor that are largely utilized for human use (storage roots and leaves), with less of them being used as an industrial raw material and animal feed (Yan et al., 2022). Sweet potatoes are prized for their sweetness, high nutritional value, and short (3 to 4 month) growing period (Adepoju & Adejumo, 2015). One of the top seven foods consumed worldwide is sweet potatoes. Because of the quantity and quality of food it generates, it has the ability to ensure food security, particularly for low-income populations (Vargas et al., 2017). The concept of association can be effectively utilized to develop selection strategies for enhancing yield components by examining the correlation between quantitative and qualitative characteristics (Rahman, 2018). Breeders can choose the most desirable features for yield by using genetic indices such as heritability, genetic advance, genotypic, and phenotypic coefficients of variation (Narasimhamurthy et al., 2018).

Sweet potato cultivars, propagation material origin, environment, and soil conditions significantly influence storage root yields across and within plants (Hayati, & Anhar, 2020). Alves et al. (2017) showed that although sweet potatoes exhibit considerable genetic variation, genotypes with desirable traits have been lost due to changes in consumption habits and limited research. It is still necessary to create and introduce new, high-yielding varieties of sweet potatoes with high dry matter and beta-carotene content (Harriman et al., 2017). The major problem for low production output for sweet potato is inadequate supply of improved material for smallholder farmers (Chidozie, 2017; Nanbol & Namu, 2019). Sweet potato production in Nigeria has been low due to limited capital to boost production, use of improved planting materials amongst other factors (Tewe et al., 2003). The existence of genetic diversity in a crop population and proper knowledge on this divergence is of great importance

to breeders (Bassey, 2017; Hamidah et al., 2020; Njoku et al., 2017). Because of this, an effort has been undertaken to compile background data on the level of genetic variability present in sweet potato genotypes (Rahman, 2018). The study aims to identify the best accessions for sweet potato cultivation, focusing on storage root yield and nutritional value. This will allow small-scaled farmers to enhance their income by supplying enough tubers to the market and for household consumption. In addition, breeders can select the most promising accessions for future growth and dissemination. The aim of this study is to access genetic diversity across sweet potato accessions and identify traits that are positively related with yield, thus resulting in high agricultural production for small-scaled farmers.

II. MATERIALS AND METHODS

A field experiment was carried out at the University of Ebonyi State–CAS Campus, in southeast Nigeria, between latitude 60° 20'N and longitude 008° 06'E, during the 2020–2021 growth season. According to (Njoku et al., 2017) the average annual minimum rainfall is 1800 mm, the average annual maximum rainfall is 2000 mm, and the average annual minimum and maximum temperatures are 27°C and 31°C, respectively, and average annual minimum and maximum rainfall are 1800 mm and 2000 mm, respectively. Relative humidity peaks at 80% during the rainy season and falls to 60% during the dry season, particularly during the Harmattan era. A total of 20 accessions were accessed in the study, where five accessions were from Niger and 15 were from Nigeria (National Root Crops Research Institute Umudike, Abia State (Table 1). The experiment of the study was in a randomized complete block design (RCBD) in three replications. The experimental area was 330 m² (30 m long × 11 m wide). The size of individual plots was 3 m² (3 m long × 1 m wide) with a spacing of 0.30 m intra-row and 0.50 m inter-row, giving one row totaling a population of 10 plants per plot. The estimated total plant population for the experiment was 600 plants.

Table 1. Background information of the 20 sweet potatoes accessions assessed for genetic diversity

N°	Acc ID	Accession name	Collection country	Latitude	Longitude	Collection source	Status of sample
1	SP-PhD-2	BUTTER MILK	Nigeria	05°29'N	07°33'E	Field	Landrace
2	SP-PhD-4	NWA OYORIMA	Nigeria	05°29'N	07°33'E	Field	Improved
3	SP-PhD-12	DELVIA	Nigeria	05°29'N	07°33'E	Field	Improved
4	SP-PhD-15	Dan Bouza	Niger	13°18.260' N	002°20.253'E	Field	Landrace
5	SP-PhD-29	Dan Maradi	Niger	13°18.260' N	002°20.253'E	Field	Landrace
6	SP-PhD-20	Koudakou 3	Niger	13°18.260' N	002°20.253'E	Field	Landrace
7	SP-PhD-21	Koudakou 4	Niger	13°18.260' N	002°20.253'E	Field	Landrace

8	SP-PhD-22	Dan Maradi 2	Niger	13°47.013' N	002°59.102'E	Field	Landrace
9	SP-PhD-39	EBO/SP 2	Nigeria	5°28'26"N	007°32'19"E	Market	Landrace
10	SP-PhD-42	EBO/SP 5	Nigeria	5°28'26"N	007°32'19"E	Market	Landrace
11	SP-PhD-46	NSPO 2012-005	Nigeria	5°28'26' N	007°32'19"E	Field	Advanced Line
12	SP-PhD-34	NSPO 2012-022	Nigeria	5°28'26' N	007°32'19"E	Field	Advanced Line
13	SP-PhD-56	NSPW 2012-001	Nigeria	5°28'26' N	007°32'19"E	Field	Advanced Line
14	SP-PhD-52	NSPW 2012-018	Nigeria	5°28'26' N	007°32'19"E	Field	Advanced Line
15	SP-PhD-62	NASPOT 8	Nigeria	5°28'26' N	007°32'19"E	Field	Improved
16	SP-PhD-64	NASPOT 11	Nigeria	5°28'26' N	007°32'19"E	Field	Improved
17	SP-PhD-71	LOURDES	Nigeria	5°28'26' N	007°32'19"E	Field	Landrace
18	SP-PhD-72	Umu SPO 3	Nigeria	5°28'26' N	007°32'19"E	Field	Improved
19	SP-PhD-75	NKWO	Nigeria	5°28'26' N	007°32'19"E	Field	Landrace
20	SP-PhD-77	TIS-87/0087	Nigeria	5°28'26' N	007°32'19"E	Field	Improved

2.1. Data collection

Data on the following characters were acquired from each accession and replication during the experimentation. The data for the quantitative traits were collected as follows: vine length (VL, cm) on five plants per plot, vine internode length (VIL, cm) on five plants during harvesting per plot, mature leaf length (MLL, cm) on five leaves per five plants per plot, mature leaf width (MLW, cm) on five plants at harvest, petiole length (PL, cm) on five plants at harvest, number of branches (NBP) per five plants at harvest, number of roots (NRP) on five plants at harvest, root length (RL, cm) on five roots per plot, root girth (RG, cm) on Root yield (RYP, Kg) per plant during harvest, total root yield (TRY, t/ha) for the entire experiment, biomass (BM, Kg/m²) at harvest, one day after harvest. Data were collected on the following qualitative traits every three months for five plants: plant type, vine pigmentation, number of leaf lobes, leaf lobe type, abaxial leaf vein pigmentation, mature leaf color, petiole pigmentation, storage root shape, storage root skin color, and storage root flesh color. Both quantitative and qualitative data were obtained based on sweet potato descriptors (Huama'n, 1991).

2.2. Statistical analysis

Data were subjected to analysis of variance (ANOVA) using SAS software program version 9.0 (SAS, 2017) to determine the presence of significant variations between accessions. When significant differences were found, the means were separated using the least significant difference (LSD) test at a 5% level of significance. The qualitative data were generated using Excel. Multivariate analysis of agro-morphological data by principal component analysis (PCA) was used to discriminate between the genetic diversity of

the sweet potato accessions, and correlations between variables were found using correlation analysis (Sabri et al., 2020; Chukwu et al., 2015)

III. RESULTS AND DISCUSSION

3.1 Analysis of variance and mean performance of sweet potato accessions during 2020 and 2021 growing year

The analysis of variance (ANOVA) means square values of accessions during 2020 and 2021 growing seasons were is presented in Table 2 and supplementary material Table 2. Over the course of several years of growth. ANOVA revealed significant variations in accessions by year in 80% of variables, but no significant differences in biomass (supplementary material Table 2). Based on a combined-year analysis, Umu SPO 3 (300.15 cm), TIS-87/0087 (255.73 cm), NSPW 2012-001 (236.02 cm), and NSPO 2012-005 (207.06 cm) had the longest vine lengths. Whereas, UTY 2014-078 (37.40 cm) had the shortest vine length (see supplementary material Table 2). Umu SPO 3 had the longest vine internode (6.44 cm), followed by NSPW 2012-001 (5.69 cm), TIS-87/0087 (4.98 cm), and Dan Maradi 2 (4.78 cm); UTY 2014-078 had the shortest (1.10 cm). In the two- years combined analysis, Accession TIS-87/0087 (13.84 cm) had the longest average mature leaf length, followed by Umu SPO 3 (13.56 cm), Koudakou 3 (13.51 cm), and Butter Milk (13.33 cm), while UTY 2014-078 (3.76 cm) had the shortest over-year combined length. In the over-year combined study, accession Koudakou 4 (12.57 cm) had the highest mean root number per plot, followed by Koudakou 3 (12.00 cm), Dan Maradi (12.00 cm), and Dan Maradi 2 (9.40 cm), while the UTY 2014-078 (2.33 cm) and EBO/SP 5 (1.67 cm) accessions had the

lowest values. Koudakou 3 (2.7 Kg/m²) and Umu SPO 3 (2.4 Kg/m²) had the largest storage root output across the years, followed by Koudakou 4 (2.4 Kg/m²) and Koudakou 3 (1.9 Kg/m²). The lowest root yields were obtained for EBO/SP 5 (0.2 kg/m²) and UTY 2014-078 (0.0 kg/m²).

Furthermore, the results showed that Koudakou 3 (8.9 t/ha) had the highest total root yield, followed by Koudakou 4 (8.4 t/ha), Umu SPO 3 (8.0 t/ha), and Dan Maradi (5.5 t/ha). The lowest total root yield was seen in EBO/SP 5 (0.6 t/ha) and UTY 2014-078 (0.1 t/ha).

Table 2. Combined analysis of variance for agro-morphological characteristics of the sweet potato accessions in 2020 and 2021 growing seasons

	Replication (Season)	Year	Accession	Accession*Year	Error
DF	4	1	19	19	75
VL(cm)	5043.99ns	21427.76*	21661.028*	17859.045*	4373.03
VIL(cm)	1.022ns	0.47ns	10.028*	8.039*	1.39
MLL(cm)	15.23ns	88.92*	52.078*	48.58*	7.80
MLW(cm)	1.28ns	29.80*	21.17*	29.24*	3.57
PL(cm)	9.69ns	57.48*	55.96*	61.40*	11.40
NBP	12.31ns	85.92*	47.894*	24.16*	10.60
NRP	4.27ns	754.69*	52.68*	68.47*	21.058
RL(cm)	6.34ns	757.14ns	89.024*	72.22*	20.40
RG(cm)	7.29*	230.47*	5.65*	4.77*	1.25
RYP(Kg)	0.51ns	1.80ns	4.019*	3.021*	0.67
RYPP(Kg/m ²)	3.15ns	5.032ns	4.96ns	5.50*	3.16
TRY(t/ha)	6.061ns	10.38ns	45.99*	35.61*	7.54
BM(Kg)	4103.29*	483.29*	85.15ns	117.28ns	75.81

ns: no significant (p>0.05), *: significant (p<0.05),: **VL**: Vine length, **VIL**: Vine internode length, **MLL**: Mature leaf length, **MLLW**: Mature leaf width, **PL**: Petiole length, **NBP**: Number of branch per plant, **NRP**: Number of roots per plant, **RL**: Root length, **RG**: Root girth, **RYP**: Root yield per plant (Kg), **RYPP**: Root yield per plant (Kg/m²) **TRY**: Total root yield, **MB**: Biomass.

3.2 Genetic variability, heritability and genetic advance

The performance of the genotypes for each character is detailed below. The results of the study to determine the extent of genetic variation in relation to 17 characters are presented in Table 3 showing values for phenotypic variance (VP), genotypic variance (VG), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h²b), genetic advance (GA), genetic advance in percent of mean, and coefficient of variation (CV). The genotypic variance and phenotypic variance for vine length were 5762.67 and 26034.06, respectively (Table 3). The phenotypic variance for vine internode length (11.42) was higher than genotypic variance (2.88). GCV and PCV were high (36.45 and 73.42, respectively) (Table 3). The heritability estimates for this trait were low (22.14) and there were high genetic advances (73.57) and low genetic advances (32.05) as a percentage of the mean. The phenotypic and genotypic variances were

59.88 and 14.76, respectively (Table 3). PCV (73.42%) and GCV 36.45%) were high for mature leaf length. The results indicated (24.74 and 5.87) phenotypic and genotypic variance, PCV (57.91%) and GCV (28.20%) were high for mature leaf width. However, the genetic advance estimates were low for mature leaf length and mature leaf width (3.93 and 2.43, respectively), with a low and moderate genetic advance in percent of mean for mature leaf length and width (7.54 and 11.48%) and a less genetic advance in percent (7.54 and 11.48%). Furthermore, the majority of the parameters showed very high PCV values: vine length (97.07) and vine internode length (83.00); high for root girth (145.34), number of roots per plant (116.47), biomass (104.75), and total root yield (234.39). GCV was high, however, for the following: number of branches per plant (42.81), number of roots per plant (44.04), root length (42.95), biomass (14.56), root yield per plot (107.02), total root yield (114.70), root girth (66.97), petiole length (33.79). Consequently, petiole length, number of roots per plot, number of branches per plant, root length, root girth,

root yield per plot, total root yield, and biomass were shown to have low values for the heritability estimate in a broad sense. For root yield, genetic advance as a percentage of mean was high (26.43). Additionally, for root girth (20.35), mature leaf length (11.48), and vine internode length

(17.50), it was moderate; however, for petiole length (6.66), number of branches per plat (6.99), number of roots per plant (4.80), root length (5.06), total root yield (7.85), and biomass (0.59), the results showed very low genetic advance.

Table 3. Estimation of genetic parameters, heritability, and genetic advance for agro-morphological characters of the sweet potatoes

Characters	Mean	CV (%)	GMS	EMS	VG (δ2g)	VP (δ2p)	GCV (%)	PCV (%)	Heritability h ² bs (%)	GA	GA %
VL(cm)	166.23	39.78	21661.03	4373.03	5762.67	26034.06	45.67	97.07	22.14	73.57	0.34
VIL(cm)	4.07	28.97	10.03	1.39	2.88	11.42	41.68	83	25.21	1.76	17.5
MLL(cm)	10.54	26.5	52.08	7.8	14.76	59.88	36.45	73.42	24.65	3.93	7.54
MLW(cm)	8.59	21.99	21.17	3.57	5.87	24.74	28.2	57.91	23.72	2.43	11.48
PL(cm)	11.41	29.61	55.96	11.4	14.85	67.36	33.79	71.96	22.05	3.73	6.66
NBP	8.24	39.52	47.89	10.6	12.43	58.49	42.81	92.86	21.26	3.35	6.99
NRP	7.37	62.24	52.7	21.06	10.55	73.76	44.04	116.47	14.3	2.53	4.8
RL(cm)	11.13	40.56	89.02	20.4	22.87	109.42	42.95	93.95	20.9	4.5	5.06
RG(cm)	1.81	61.92	5.65	1.25	1.46	6.9	66.97	145.34	21.23	1.15	20.35
RYP(Kg)	0.99	83.09	4.01	0.67	1.11	4.68	107.02	219.47	23.78	1.06	26.43
RYPP(Kg/m ²)	0.49	365.4	4.96	3.16	0.6	8.12	158.96	585.52	7.37	0.43	8.73
TRY(t/ha)	3.12	87.95	45.99	7.54	12.82	53.53	114.7	234.39	23.95	3.61	7.85
BM(Kg)	12.11	71.89	85.15	75.81	3.11	160.96	14.56	104.75	1.93	0.51	0.59

Characters	Mean	CV (%)	GMS	EMS	VG (δ2g)	VP (δ2p)	GCV (%)	PCV (%)	Heritability h ² bs (%)
VL(cm)	166.23	39.78	21661.03	4373.03	5762.67	26034.06	45.67	97.07	22.14
VIL(cm)	4.07	28.97	10.03	1.39	2.88	11.42	41.68	83	25.21
MLL(cm)	10.54	26.5	52.08	7.8	14.76	59.88	36.45	73.42	24.65
MLW(cm)	8.59	21.99	21.17	3.57	5.87	24.74	28.2	57.91	23.72
PL(cm)	11.41	29.61	55.96	11.4	14.85	67.36	33.79	71.96	22.05
NBP	8.24	39.52	47.89	10.6	12.43	58.49	42.81	92.86	21.26
NRP	7.37	62.24	52.7	21.06	10.55	73.76	44.04	116.47	14.3
RL(cm)	11.13	40.56	89.02	20.4	22.87	109.42	42.95	93.95	20.9
RG(cm)	1.81	61.92	5.65	1.25	1.46	6.9	66.97	145.34	21.23
RYP(Kg)	0.99	83.09	4.01	0.67	1.11	4.68	107.02	219.47	23.78
RYPP(Kg/m ²)	0.49	365.4	4.96	3.16	0.6	8.12	158.96	585.52	7.37

TRY(t/ha)	3.12	87.95	45.99	7.54	12.82	53.53	114.7	234.39	23.95
BM(Kg)	12.11	71.89	85.15	75.81	3.11	160.96	14.56	104.75	1.93

CV: Coefficient of variation, **GMS:** Genotypic mean sum of squares, **EMS:** Error mean sum of squares, **VG:** Genotypic variance, **VP:** Phenotypic variance, **PCV:** Phenotypic coefficient variation, **GCV:** Genotypic coefficient variation, **h²_{bs}:** Heritability broad sense, **GA:** Genetic advance, **GA (%)**: Genetic advance as percentage of mean. **VL:** Vine length, **VIL:** Vine internode length, **MLL:** Mature leaf length, **MLLW:** Mature leaf width, **PL:** Petiole length, **NBP:** Number of branches per plant, **NRP:** Number of roots per plant, **RL:** Root length, **RG:** Root girth, **RYP:** Root yield per plant (Kg), **RYPP:** Root yield per plant (Kg/m²) **TRY:** Total root yield (t/ha), **MB:** Biomass (Kg/m²),

3.3 Pearson Correlation Coefficients

In the year combined analysis, the study found that there was a significant and positive correlation between vine length and the following variables: vine internode length (0.83), mature leaf length (0.67), mature leaf width (0.65), petiole length (0.49), number of branches per plant (0.38), number of roots per plot (0.21), root length (0.36), root yield per plot (0.34), total root yield (0.33). On the other hand, there was a positive non-significant correlation between vine length and root girth (0.12), and biomass (0.041). Mature leaf length (MLL) also showed a significant

correlation with mature leaf width (0.79), petiole length (0.61), number of branches per plant (0.55), number of roots per plant (0.28), root length (0.47), root yield per plot (0.36), total root yield (0.36) and biomass (0.29) in the two-year combined analysis. Nonetheless, MLL exhibited a non-significant positive association (-0.0069) and a negative correlation (0.17) with root girth and bloom width, respectively. Additionally, throughout the 2020 and 2021 growth seasons, there was a substantial positive association between the number of roots per plot and all morphological features.

Table 4. Pearson correlation coefficients of different morphological traits of the 20 sweet potato accessions during 2020 and 2021 growing years

Traits	VL	VIL	MLL	MLW	PL	NBP	NRP	RL	RG	RYP	RYPP	TRY	BM
VL	1	0.83*	0.67*	0.65*	0.49*	0.38*	0.21*	0.36*	0.12ns	0.34*	0.084ns	0.33*	0.041ns
VIL		1	0.71*	0.71*	0.57*	0.51*	0.36*	0.43*	0.25*	0.43*	0.12ns	0.41*	0.24*
MLL			1	0.79*	0.61*	0.55*	0.28*	0.47*	-0.0069ns	0.36*	0.095ns	0.36*	0.29*
MLW				1	0.79*	0.58*	0.41*	0.56*	0.23*	0.28*	0.12ns	0.27*	0.27*
PL					1	0.49*	0.32*	0.45*	0.21*	0.25*	0.11ns	0.24*	0.18*
NBP						1	0.46*	0.42*	0.32*	0.27*	0.55*	0.29*	0.28*
NRP							1	0.64*	0.59*	0.71*	0.33*	0.69*	0.27*
RL								1	0.49*	0.57*	0.060ns	0.53*	0.22*
RG									1	0.55*	0.30*	0.49*	0.071NS
RYP										1	0.29*	0.97*	0.19*
RYPP											1	0.35*	0.14NS
TRY												1	0.22*
BM													1

ns: not significant (p>0.05), *: significant (p<0.05); VL: Vine length, VIL: Vine internode length, MLL: Mature leaf length, MLLW: Mature leaf width, PL: Petiole length, NBP: Number of branch per plant, NRP: Number of roots per plant, RL: Root length (cm), RG: Root girth (cm), RYP: Root yield per plant (Kg), RYPP: Root yield per plant (Kg/m²) TRY: Total root yield (t/ha), BM: Biomass (Kg),

3.4 Multivariate analysis

3.4.1 Principal component analysis (CPA)

The study found that four major components with eigenvalues equal to or greater than one explained 83.03% of the variability. PC1 contributed 55.8% of total diversity,

representing individual variables. PC2 contributed 14.87%, representing two variables. PC3 contributed 6.77%, and PC4 contributed 5.59%, representing three individual variables. These components represent the equivalent of individual variables. Twenty accessions were

tested. (Table 5). The study found four major components, PC1, PC2, PC3, and PC4, accounting for 73.08% of variability.

Table 5. Principal component analysis of 20 sweet potato accessions

Traits	PC1	PC2	PC3
MLL(cm)	-0.28693	-0.08038	0.03593
MLW(cm)	-0.27612	-0.11509	-0.05132
NBP	-0.26595	0.1789	-0.2321
NRP	-0.25476	0.20967	-0.07919
PL(cm)	-0.24396	0.07868	-0.26208
RG(cm)	-0.20994	0.25859	0.10867
RL(cm)	-0.26595	-0.16855	0.20654
RYPP(Kg/m ²)	0.09656	0.21789	0.58393
RYP(Kg)	-0.16045	0.43399	0.29576
TRY(t/ha)	-0.12868	0.47411	0.20239
VIL(cm)	-0.28137	-0.00693	0.02524
VL(cm)	-0.22447	-0.09476	0.10727
BM(Kg)	-0.21298	-0.03746	0.05969
D50F	0.27428	-0.12245	0.01119
D50S	-0.27225	-0.16102	0.06469
D80M	-0.22983	-0.18865	-0.07801
FL(cm)	-0.19275	-0.15485	-0.05499
FW(cm)	-0.1401	0.39703	-0.42509
Eigenvalue	10.602	2.825	1.286
PV	55.8	14.87	6.77

VL: Vine length, VIL: Vine internode length, MLL: Mature leaf length, MLLW: Mature leaf width, PL: Petiole length, NBP: Number of branch per plant, NRP: Number of roots per plant, RL: Root length, RG: Root girth, RYP: Root yield per plant (Kg), RYPP: Root yield per plant (Kg/m²) TRY: Total root yield, MB: Biomass, FL: Flower length, FW: Flower width, D50S: Days to 50% sprouting, D50F: Days to 50% flowering, D80M: Days to 80% maturity. PV: Percentage variation

IV. DISCUSSION

4.1 Analysis of variance and mean performance of sweet potato accessions during 2020 and 2021 growing year

Accessions Umu SPO 3, TIS-87/0087 NSPW 2012-001 and NSPO 2012-005 were superior in vine length, vine internode length and mature leaf size. In his examination of five sweet potato varieties. Nazrul (2018) also noted a significant variance in the length of the sweet potato vine, which varied from 119 cm to 192.3 cm. Koudakou 3, Koudakou 4, Dan Maradi 2, and Umu SPO 3 demonstrated superior performance in root number, root yield, and total

yield, while EBO/SP 5 and NSPO 2012-005 showed insufficient results. Awel (2018) found variations in the average number of roots per plot, with Kulfo varieties having the lowest average root number per plot and local and Beletech varieties having the highest. Sora (2021) also noted a significant variation in the number of roots per plant. The study found that accession Dan Maradi, Koudakou 3, Umu SPO 3, NSPW 2012-001, and TIS-87/0087 had the longest and widest roots, while UTY 2014-078, Nwa Oyorima, and EBO/SP had the lowest value. In line with our results, Sora (2021) reported that root length

varied among the genotypes significantly and ranged from 8.9 cm to 24.8cm.

1.1 Genetic variability, heritability and genetic advance

High PCV values were observed for traits such as total root yield, root yield per plant, root girth, number of roots per plant, biomass, vine length, and vine internode length. GCV was high for root yield per plant, root yield per plot, total root yield, root girth, petiole length, and number of branches per plant, number of roots per plot, and root length. However, GCV moderate for biomass. Mohammed et al. (2015) The study found that vine length had a higher genetic advance percentage, while vine length had less heritability and a lower genetic advance mean. Alemu and Aragaw (2016) study on three sweet potato varieties and eight introductions revealed that genotypic coefficients of variation were smaller than phenotypic coefficients of variation.

1.2 Pearson Correlation Coefficients

The study found a positive correlation between root length, root girth, root yield, biomass (Table 4). The results showed a positive correlation with most traits, except for biomass, which showed a positive non-significant correlation (Table 4). The 2020 and 2021 growing seasons showed a positive correlation between total root yield, and biomass (Table 4). Total root output, biomass, all had positive correlations throughout the 2020 and 2021 growing seasons.

These outcomes concur with those attained by Ochieng, (2019) and Apon (2016) found a strong positive correlation between vine growth rate, mature leaf size, root yield, storage root diameter, and storage rootstalk length. However, vine internode length had a negative correlation with biomass. These outcomes concur with the conclusions of other researchers (Nwaigwe et al., 2016; Dash et al., 2015; Shrestha, 2016). Apon (2016) and Chukwu et al. (2022) also reported that number of roots per plot had positive direct effects on storage root yield. These results are in agreement with those reported by Mohanty et al., (2016) study found that stored root production per hectare is influenced by plant number, root length, root yield, and starch content, aiding breeders in selecting positive traits and reducing breeding costs and time.

1.3 Principal component analysis (CPA)

PC1 is well correlated with leaf characteristics, such as leaf general outline, and mature leaf length and leaf width while PC2 correlated with flowering rate, root maturity and total root production. These results are in line with those obtained by Placide et al. (2015) who employed PCA to examine the variation among 54 sweet potato genotypes and discovered that the first seven main component axes had a cumulative variance of 77.83%. There was sufficient

variation across the genotypes for our findings. The cluster analysis separated the 20 accessions into two clusters. Cluster 1 consisted of 12 accessions and cluster 2 consisted eight accessions. In a cluster, study of elite sweet potato genotypes from Tanzania for high dry matter content and resistance to the sweet potato viral diseases. Tairo et al. (2008) found two main groups with a low genetic similarity of 0.52. Both of the accession's genes could be utilized to create superior sweet potato varieties that are enhanced for high production potential. The 20 genotypes were grouped into two main groups demonstrating a genetic link between accessions. In contrast, cluster analysis of 116 genotypes in another study produced 12 groupings Mohammed et al., 2015; Chukwu et al 2015).

V. CONCLUSION

The study reveals significant differences in observed characteristics and variance results among 20 sweet potato accessions. It suggests Koudakou 3, Koudakou 4, Dan Maradi 2, TIS-87/0087, Butter Milk, and Dan Bouza as potential parents for genetic improvement and breeding for yield enhancement, based on their widely cultivated history. The majority of the investigated characters had low genetic progress as a percentage of mean, weak heritability, and greater phenotypic coefficients of variation than genotypic coefficients of variation, according to the study's findings. Additionally, accessions Koudakou 3, NSPO 2012-005, Dan Maradi, and Koudakou 4 are great choices for animal feed due to their superior vegetative growth performance.

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