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Full Length Research Paper

Multivariate assessment of the agromorphological variability and yield components among sweetpotato (*Ipomoea batatas* (L.) Lam) landraces

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Understanding the nature and magnitude of variability existing among sweetpotato genetic materials for important traits is vital for the effective utilization of such materials for breeding purposes. Eighteen landraces from diverse origins, plus three released cultivars as checks, were evaluated in two contrasting locations, using nine agronomic and eight morphological traits of the crop, to estimate the nature and magnitude of the variability among the genetic materials, to determine the relationships among the traits, and to identify the important yield-related traits among the collections using multivariate tools. The principal component analysis identified number of marketable and unmarketable roots, total number of roots, weight of marketable and unmarketable roots, total root weights, incidence and severity of root *Cylas* spp, length of biggest, medium and smallest marketable roots, number of branches, as well as stand count at harvest as important traits that could be used to differentiate the landraces. The canonical variate analysis showed that the observed variation among the traits occurred mostly between-groups than within-groups, and that it was largely influenced by total root weight, weight of marketable roots, number of marketable roots, and total number of roots. Generally, all the traits, except stand count at harvest, exhibited positive and significant (P<0.01 and P<0.001) correlation with total root weight (yield) . Most of the traits also exhibited significant relationships among them. However, the use of forward selection multiple regression analysis revealed weight of marketable and unmarketable roots, as well as total number of roots as the most important yield component traits that could be used to improve sweetpotato. Thus, our work identified the existence of inherent variability in the local germplasm collections, and the traits that could be used to exploit the observed variability, eliciting important relationships among the traits in the process.

Key words: Sweetpotato, genetic variability, multivariate analyses, yield components.

INTRODUCTION

Sweetpotato (*Ipomoea batatas* (L). Lam) is a member of the *Convolvulaceae*, the morning-glory family.It belongs to the genus *Ipomoea*. The genus has four ploidy levels: the cultivated sweetpotato, *Ipomoea batatas* , a hexaploid (2n=6x=90); *Ipomoea tiliaceae*, very similar to *batatas*, a tetraploid (2n=4x=60); *I. cordatotriloba*, *I. lacunosa* and *I. triloba*, all diplods (2n=30) (Austin, 1988); and *I. trifida*, a wild species with different cytotypes such as diploids, tetraploids and hexaploids (Shiotani et al., 1991).

As one of the oldest vegetables known to mankind, having been in cultivation since about 10,000 years ago (Ugent and Peterson, 1988), the crop has evolved into many morpho-types, creating broad genetic diversity for most of the desirable agronomic traits.

In Nigeria, though long regarded as a minor root crop, sweetpotato is rapidly becoming more important due to its high yielding ability, its capacity to grow on relatively

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poor soils, and its high content of carbohydrates and vitamins, especially vitamin A. The crop has since ceased to be a backyard crop it was noted for. Survey reports in Nigeria show that production, marketing and utilization have expanded in the last decades beyond its traditional central and riverine areas (Agboola, 1979) to almost all ecological zones in the country (Tewe et al., 2003). Globally, Nigeria with 3.32 million metric tonnes (3.01% of total global production) (FAO, 2009) has become the second largest producer of sweetpotato, pushing Uganda (2.71 million metric tonnes) to the third position. China remains the leading sweetpotato producer with 85.21 million metric tonnes (FAO, 2009). The increased production can be attributed to increased area under sweetpotato cultivation rather than increased yield. According to Tewe et al. (2003), national sweetpotato average yield had declined from 13t/ha to 6.8t/ha, and going by the national production estimate of 3.32 million tonnes from 1.11 million hectares according to FAO (2009), average yield had further declined to an average of 3.0 t/ha. This necessitates a concerted effort to develop new varieties that can cope with the new environmental challenges militating against high productivity.

Genetic variability studies are important in the selection of parents for hybridization (Chaudhary and Singh, 1982) as sound crop improvement depends upon the magnitude of genetic variability in the base population (Adebisi et al., 2001). Once genetic variability has been ascertained in a crop, improvement is possible through the use of appropriate selection method. Planned plant introduction therefore becomes inevitable whenever the genetic base of a germplasm is narrow for important desirable traits. However, for the effective utilisation of the introductions, germplasm evaluation is an essential preliminary step.

Multivariate statistical tools have found extensive use in summarising and describing the inherent variation in the population of crop genotypes. Some of the tools that have found extensive application include principal component analysis (PCA), discriminant canonical analysis (DCA), and cluster analysis (CA). These techniques identify plant traits that characterise the distinctness among selected genotypes. They are often extended to the classification of a population into groups of distinct orders based on similarities in one or more characters, and thus guide in the choice of parents for hybridization (Ariyo, 1987; Nair et al., 1998). The PCA has been used to partition observed agronomic variations in genotypes of many crops such as rubber (Omokhafe and Alika, 2000), rice (Nassir, 2002), and sesame (Mponda et al., 1997). The canonical analysis is a tool used when it is of more interest to show differences between groups than between individuals (Labuschagne et al., 2002). Graybosch et al. (1993) used canonical correlation to ascertain the extent to which a set of biochemical measurements were related to a set of quality measurements of wheat. Osborne et al. (1993) also employed the tool to discriminate between the different quality properties of breeding materials where differences between groups were of more significance than individual lines. Correlation and regression analyses are multivariate tools that help to study the inter-relationships and inter-dependence among traits. While PCA and canonical variate analysis help to identify the traits with the highest variability, correlation and regression analyses help in the study of the relationships of the identified traits with yield and other traits, all in a bid to make the development of new varieties efficient and effective. Through correlation analysis, Islam et al. (2002) Tsegaye et al. (2007) showed that sweetpotato yield is related to many traits. Since only few traits can be improved at a time during a breeding cycle, it becomes necessary to select few traits among those that impact yield. Multiple regression analysis is a good tool to study the individual contribution of many traits (independent traits) to the performance of a trait (dependent trait). This was demonstrated by Stathers et al. (2003) who identified marketable and unmarketable root weight and total number of roots as good yield components that could be used to improve the genotypes they evaluated. Therefore, the objectives of this work were to determine the extent of agromorphological variability existing among sweetpotato landraces, to determine the relationships existing between yield and other traits so as to identify few traits that could serve as good yield components using multivariate tools to improve yield, and the heritability of the traits for the effective utilization of the landraces for breeding purposes.

MATERIALS AND METHODS

Experimental site

The study was carried out in two locations: Umudike, rain forest belt, and Otobi, guinea savannah ecology, in Nigeria, during the 2005 growing season under rainfed condition. The Umudike environment was characterized by very tall trees that formed canopies over very thick shrubs. The site of the experiment at Umudike was dominated by tall grasses where the forest had been opened, and the soil had been in use for a long time. Also, the Otobi experimental environment was predominated by very tall grasses and isolated short trees with thick bark characteristic of the wet guinea savannah of Nigeria. Umudike is located on 07°0331E and 05°0291N, at an elevation of 122 m above sea level. The soil is generally classified as an ultisol, and the location received an average of 2064.1 mm of rain during the growing season. Otobi is located on 08°0632E and 07°06966N with an elevation of 141 m above sea level. The soil of the location is classified as an alfisol. The average rainfall during the growing season was 914.3 mm.

Experimental materials, design and field management

Twenty-one genotypes comprising 18 landraces and three released cultivars (checks) were evaluated in a randomised complete block design with the genotypes replicated three times in two locations. The landraces were collected from different states across the

Table 1. List of the 21 sweetpotato genotypes evaluated in two the locations, including their source and origin.

S/No.	Cultivar names	Source
1	Digitate	Ibadan
2	Akoroda 3	Ibadan
3	Arrow Tip	Ibadan
4	WW Oduonu	Ibadan
5	Alphonso	Ibadan
6	TIS 4400-2	Ibadan
7	Caroline Lee	Ibadan
8	KB-Lobed	Ibadan
9	KB-Narrow	Ibadan
10	TIS XDB	Ibadan
11	Kayode	Ibadan
12	GR 325	Ibadan
13	TIS 80/0140	Ibadan
14	Ex-Igbariam*	NRCRI
15	Coconut	Ibadan
16	ML II	Ibadan
17	TIS 87/0087*	NRCRI
18	Shaba	Ibadan
19	TIS 8164*	NRCRI
20	Big Old	Ibadan
21	Akoroda 5	Ibadan

* = check varieties.

country in an impromptu fashion and maintained at the University of Ibadan Sweetpotato Conservation Unit (Table 1). The plot size used for the study was 15 m^2 containing 50 stands at a spacing of 1m X 0.3 m, with inter-plot spacing of 1m. Weeding was carried out at four weeks after planting (4WAP) supplemented by rouging at 8WAP. Fertilizer (NPK 15:15:15) was applied at the rate of 400 kg per hectare at 4WAP immediately after the first weeding. Nine agronomic data were measured on plot basis, including stand count at harvest, number of marketable (roots $\geq$ 100 g) roots, number of unmarketable roots (roots<100 g), total number of roots, weight of marketable roots, weight of unmarketable roots, and weight of total roots, as well as the incidence and severity (scale of 1 - 5 where 1 = 0%; 2 = 1 - 25%; 3 = 26 - 50%; 4 = 51 - 75%; and 5 = 76 - 100% root infestation according to Stathers et al., 2003) of root *Cylas* spp infestation. Eight morphological traits, which included biggest root length (length >15 cm taken from the proximal to the distal end of roots using a tread and a meter rule), medium root length (length 10-15 cm) and smallest root length (length < 10 cm), widest root girth (girth >15 cm taken from the widest part of the roots using a tread and a meter rule.), medium root girth (root girth 10 – 15 cm) and smallest root girth (< 10 cm root gorth), as well as number of vine branches and length of main vine were collected and analysed. The multivariate tools used for the analysis of the various data included principal component analysis (PCA), canonical variate analysis (CVA), phenotypic correlation and forward selection multiple linear regression analyses. The PCA and its biplot as well as the CVA were calculated using the PROC PRIN and PROC CAN commands of the SAS (1999) Version 8 software. The phenotypic correlation coefficients and the multiple linear regression analyses were derived through the PROC CORR and PROC REG commands of the SAS software.

RESULTS AND DISCUSSION

Principal component analyses

Only the first three principal component axes (PC1, PC2 and PC3) in the PCA analysis had eigen values up to 1.0, presenting cumulative variance of 76% (Table 2). Principal component one (PC1), with eigen value of 9.46, contributed 56% of the total variability, while PC2, with eigen value of 2.05, accounted for 12% of total variability observed among the 21 sweetpotato genotypes. PC3 had eigen value of 1.41 and contributed with 8% to the total observed variability. In PC1, the traits that accounted for most of the 56% observed variability among the 21 genotypes included number of marketable roots, with vector loading of 0.285, total number of roots (0.285), weight of marketable roots (0.246), weight of unmarketable roots (0.244), total root weight (0.255), roots incidence and severity of *Cylas* spp. (0.228 and 0.232, respectively), length of biggest (0.280), medium (0.271) and smallest roots (0.245), as well as diameter of biggest (0.282), medium (0.296) and smallest roots (0.279). PC2 and PC3, also identified stand count at harvest with a vector loading of 0.52, number of unmarketable roots with 0.34 vector loading, number of branches (vector = -0.31), and smallest marketable roots

Table 2. Principal component analysis of 17 agromorphological traits for 21 sweetpotato genotypes evaluated in Umudike and Otobi.

Traits	PCA 1	PCA 2	PCA 3
Stand count at harvest	0.004	0.520	0.206
Marketable root number	0.285	0.202	-0.118
Unmarketable root number	0.211	0.344	0.203
Total root number	0.285	0.294	0.0179
Marketable root weight	0.246	0.115	-0.363
Unmarketable root weight	0.244	0.298	0.029
Total root weight	0.255	0137	-0.343
Vine length (cm)	0.110	0.230	0.259
Numbers of branches	0.180	-0.199	-0.306
Cylas spp root incidence	0.228	0.082	-0.389
Cylas spp root severity	0.232	0.224	-0.224
Biggest root length	0.280	-0.126	0.239
Medium root length	0.271	-0.193	0.244
Smallest root length	0.245	-0.200	0.326
Biggest root diameter	0.284	-0.212	0.120
Medium root diameter	0.296	-0.191	0.105
Smallest root diameter	0.279	-0.198	0.185
Eigen value	9.46	2.05	1.41
%variance contribution	0.56	0.12	0.08
Cumulative variance contribution	0.56	0.68	0.76

length with vector loading of 0.33 as important traits that distinguished one genotype from the other.

PCA is a technique which identifies plant traits that contribute most to the observed variation within a group of genotypes. The tool has a practical application in the selection of parent lines for breeding purposes. The cumulative variance of 76% by the first three axes with eigen values of >1.0 indicates that the identified traits within these axes exhibited great influence on the phenotype of the landraces, and could effectively be used for selection among them. Afuape and Nwachukwu (2005), who reported a cumulative variance of 70.09% for the first three axes in the evaluation of nine sweetpotato genotypes, had found stand count, number of *Cylas* infested roots and degree of *Cylas* root infestation, leaf area, dry matter percent and starch content percent, weight of saleable roots, saleable and total root number, weight of total roots, weight of biomass, and biomass dry matter as the important traits that distinguished the elite materials they worked with. Tairo et al. (2008) also used PCA to study the variability among Tanzanian landraces, and found low genetic variability among them. This was evident in the cumulative variance of 52.5% got from the first five principal component axes. Our findings among Nigerian landraces were at variance with the findings of these authors as there was enough variability to aid selection among the genotypes.

However, the capability of PCA as a tool that can aid in the study of variability, hence selection of parents for breeding purpose was demonstrated by the authors and our work.

Principal component biplot

The clustering of the 21 landraces and the 17 traits were carried out to show the underlying relationships among the genotypes. The principal component biplot of PC 1 against PC 2 (Figure 1) shows the pooled performances of the landraces across the two locations. Genotypes 2 (Akoroda 3), 13 (TIS 80/0140), 15 (Coconut) and 21 (Akoroda 5) showed strong similarities among the landraces across traits, so also genotypes 4 (WW Oduonu) and 12 (GR 325). These landraces with close similarities could be duplicate genotypes. Thorough morphological and molecular characterization is needed to arrive at a good conclusion about their closeness whether they are the same materials with different names, or whether they shared the same parental background. The observed weak similarities between cultivar 10 (TIS XDB), 16 (ML II) and 20 (Big Old), and between 1 (Digitate), 4 (WW Oduonu) and 12 (GR 325), 6 (TIS 4400-2), 9 (KB Narrow) and 11 (Kayode) which is depicted by the relative distance among the genotypes, is a measure of the existence of exploitable variability existing among the genotypes, even though they have some traits in common. Cultivars 14 (Ex-Igbariam), 5 (Alphonso), 19 (TIS 8164), 18 (Shaba), 7 (Caroline Lee)

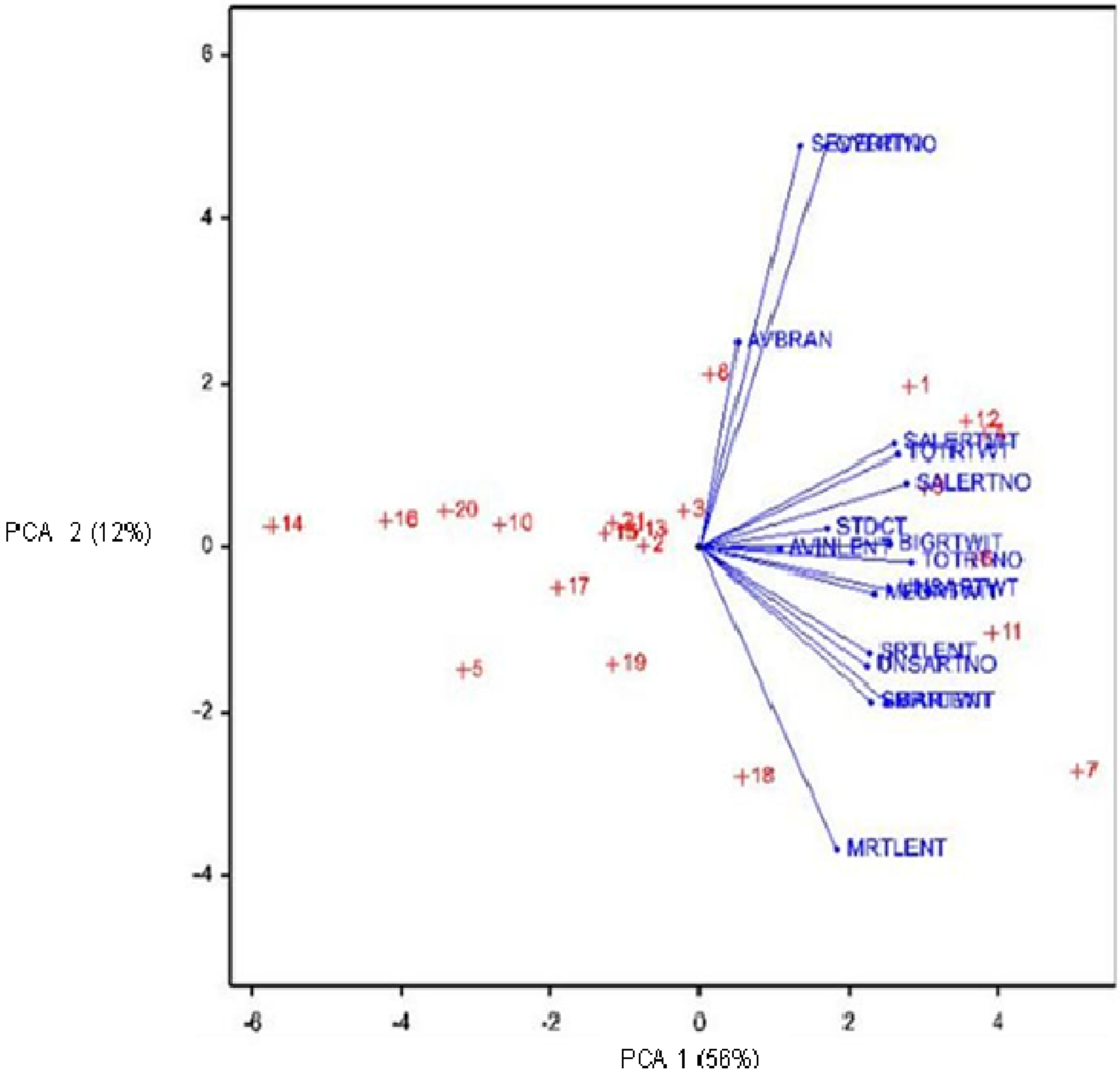

Figure 1. PCA biplot of principal component1 against principal component 2 showing the clustering of the 21 sweetpotato landraces and the 17 traits measured across two locations.

and 8 (KB Lobed) are completely distinct from others, while the three check materials (Ex-Igbariam, TIS 87/0087 and TIS 8164) were also totally distinct from the landraces. Such wide variability gives room for the exploitation of the benefits of heterosis after good parent selection. On the whole, the biplot showed wide variability between most of the landraces, though few genotypes exhibited strong similarities. For the traits, the smaller the angle between traits, the stronger the correlation between them. The principal component biplot shows that cultivars with high number of roots with *Cylas spp* infestation (CYLRTNO) also had *Cylas spp* severity (SEVERITY) . In the same vein, most cultivars with high number of marketable roots (SALERTNO) had high weight of marketable roots (SALERTWT) which resulted to high total root weight (TOTRTWT). Since width of biggest roots (BIGRTWT) and total root number (TOTRTNO) had close relationship, it means most of the landraces had most of their roots made of big roots. This is a good attribute in developing acceptable varieties for Nigerian

Table 3. Canonical discriminant coefficient showing the contribution of morphological traits to the expressions of the agronomic traits among the 21 sweetpotato genotypes evaluated.

Character	CV 1	CV 2	CV 3
Agronomic Traits			
Stand count at harvest	-0.2790	0.2459	-0.1399
Number of marketable roots	1.2126	-0.634	-2.7911
Number of unmarketable root	0.8329	-1.5634	-0.2968
Total number of roots	-0.9485	2.5999	3.6633
Weight of marketable roots	1.5333	-13.8961	7.8317
Weight of unmarketable roots	-0.0098	-0.7390	0.3239
Total root weight	-1.5380	14.3147	-8.2915
Roots *Cylas* spp incidence	-0.2232	-0.9060	0.0270
Roots *Cylas* spp severity	0.5170	-0.1545	-0.2599
Morphological Traits			
Vine length (cm)	0.1199	0.0703	0.5695
Number of branches	0.1720	-0.5719	0.0732
Biggest roots length	-0.0005	1.5602	-0.2500
Medium roots length	0.0257	-0.651	1.6937
Smallest roots length	-0.2061	0.2776	-0.4177
Biggest roots diameter	0.0958	-1.1530	-0.7787
Medium roots diameter	0.6916	0.2934	-1.0894
Smallest roots diameter	0.2493	0.1785	0.7094
Eigen Value	3.2710	0.4401	0.1977
% Variance Contribution	0.7916	0.1065	0.0478
Cumulative variance contribution	0.7916	0.8981	0.9459

consumers as big roots are preferable to small ones for fresh root consumers.

Canonical variate analysis (CVA)

Canonical variates (CV) are linear combinations of the original measurements and are thus given as vector loadings for the original measurements. It is a tool used when it is of more interest to show differences between groups than between individuals (Labuschagne et al., 2002). In our study, the 17 traits measured were made of nine agronomic traits and eight morphological traits. Of the 17 canonical variate (CV) axes generated by the 17 traits, only the first (CV1) had eigen (latent root) value greater than 1.0 (3.27) (Table 3). This identified CV1 as the only axis with traits that exhibited more between-groups variability than within-groups variability, while CV2 and CV3, with their axes having eigen value <1.0, had more of within-group variability. The canonical variate axis 1 (CV1) contributed a total of 79.16% to the total variability observed between the groups, while CV2 contributed 10.65%. The 79.16% variability observed in CV1 was a measure of the strength of the variability between the agronomic and the morphological traits. This between-groups variability was largely influenced by total root weight, with vector loading of -1.538, weight of marketable roots (1.533), number of marketable roots (1.212); and minimally impacted by total number of roots, with vector of -0.948, and number of unmarketable roots, with vector of 0.832. Morphological traits measured did not contribute much to the between-groups variability. Therefore, the agronomic traits serve as a better set of traits to focus in characterising and selecting lines from these genotypes for breeding purposes that include root yield and yield components. The 10.65% contribution of CV2 to the total variability was a measure of the amount of the within-group variability among the traits.. Among the agronomic traits in CV2, total root weight, with vector loading of 14.31, and weight of marketable roots, with vector value of -13.90, was largely responsible for the 10.65% variability observed. However, within the morphological traits group, length of biggest roots (1.56) and diameter of biggest roots (- 1.15) were also moderately important in studying the existing diversity among the genotypes for practical use. The contrasting signs mean very long roots had smaller girth, while rotund ones were shorter.

The application of canonical variate analysis in this study is to go a step beyond identifying the traits that most influenced the variability among the genotypes, but also to determine which group of the two traits were more responsible for the observed variability among the genotypes. This will help the breeder to know what group of traits to focus more in his crop improvement plan as only few traits can be considered during breeding. The use of canonical variate analysis as a tool in variability studies in root and tuber crops is scarce, more so in sweetpotato. Graybosch et al. (1993), in their work on wheat, used canonical correlation to ascertain the extent to which a set of biochemical measurements were related to a set of quality measurements of wheat. Osborne et al. (1993), also working on wheat, used the tool to discriminate between the different quality properties of the wheat materials where differences between groups were of more significance than individual lines. The identification of agronomic traits as important contributors to the variability observed among the sweetpotato cultivars was in agreement with the reports of Islam et al. (2002);Tsegaye et al. (2006), who observed wide variability for root weight and root number traits among the sweetpotato cultivars they evaluated. While we report length and diameter of the biggest roots as contributing moderately to the variability among the cultivars, both authors (Islam et al., 2002; Tsegaye et al., 2006) reported wide variability for length and diameter of storage roots among the cultivars evaluated.

Correlation studies

Correlation coefficients for the 17 traits are presented in Table 4. Generally, all the traits except stand count at harvest exhibited positive and significant ($P<0.01$ and $P<0.0001$) correlation with total roots weight (yield). Most of the traits also exhibited significant and positive association among themselves, except stand count at harvest against weight of marketable roots ($r = 0.14$) and total root weight ($r = 0.16$); stand count at harvest against root *Cylas* spp incidence ($r = -0.04$) and root *Cylas* spp. severity ($r = -0.16$); stand count at harvest against length of biggest, medium and smallest roots with r = 0.03, -0.10 and -0.02, respectively; and stand count at harvest against diameter of biggest, medium and smallest roots with r = -0.10, - 0.06 and -0.09, respectively. Vine length against number of vine branches, and vine length against root *Cylas* spp severity also exhibited no significant relationship, with r = 0.01 and 0.18, respectively. All the root size traits (length and diameter of biggest, medium and smallest roots) were positively and significantly correlated with one another, and with other traits.

According to Grafius (1959), increasing total yield would be made easier by selecting for components because components are more often easily inherited than total yield itself. Correlation studies enable the breeder to understand the mutual component characters on which selection can be based for genetic improvement. Many economically important traits of plants, usually, are related one to another in one or several ways. Various workers studied the relationships between different traits in different crops such as soybean (Adebisi et al., 2001), cassava (Varma and Rai, 1993), sweetpotato (Islam et al., 2002; Stathers et al, 2003; Afuape and Nwachukwu, 2005, Tsegaye et al., 2006). Islam et al. (2002) showed vine length, number of roots and root diameter to be positively and significantly correlated with root yield (total root weight) in sweetpotato, while Tsegaye et al. (2006) found positive and significant root girth among thirty sweetpotato genotypes. Alcoy (2007), in his work, reported a significant association between yield and marketable roots. Earlier, Lowe and Wilson (1975) had reported positive relationship between marketable root yield and the duo of root number and root weight. These findings corroborated the results of this study, and the significance of the results is that quite a number of these traits can be used to select indirectly for yield. However, the non-significant correlation found between yield and number of stems by Islam et al. (2002) was at variance with the significant correlation ($P<0.0001$) found between the two traits in this study. The genotypes used in our study were not the types that root at every node, which would have constituted another sink aside the main tuberous roots. Rather, the stems (branches) seem to serve as scavengers of nutrients which were partitioned to the tuberous roots. Stathers et al. (2003) reported positive association between *Cylas* infestation and the two traits of number of roots and root mean weight per plot, which was also found to be true in this study. This association is not a good one as number of roots and mean root weight are important agronomic traits. The positive and significant relationship between total root weight and other traits (except stand count at harvest) implies that total root weight is determined by the contribution of many genes (polygenic). Thus, the trait can be improved by simultaneous selection for other traits. However, the relationship between total root weight and *Cylas* incidence and severity is not a useful relationship in the context of breeding for increased yield. Increased incidence and severity will negatively affect yield through losses in quantity and quality. However, the incorporation of genes for resistance will moderate this relationship.

Forward selection multiple regression analysis

The results of the forward selection multiple regression analysis between total root weight (yield) and other traits are presented in Table 5. The traits that came into the model and left the model significant ($P<0.05$) after regression with the dependent trait (yield), starting from the most important trait, and followed by progressive addition of new traits in an iterative manner, will be retained by the model as important yield components. Only three traits - weight of marketable roots, unmarketable root weight and total root number - met the significant level entry criterion of $P<0.05$ into the model, using total root weight (yield) as the dependent variable.

Table 5. Forward selection multiple regression analysis between total roots weight and other significant ($P<0.05$) traits in the multiple regression model.

Variable entered	Number of variable	Partial R^2	Model R^2	F Value	Pr>F
Weight of marketable roots	1	0.9944	0.9944	20500.9	<0.0001
Weight of unmarketable root	2	0.0053	0.9997	1969.34	<0.0001
Total number of root	3	0.0000	0.9997	4.49	0.0363

*No other variable met the 0.05 significant probability level for entry into the model. The regression equation for the determination of the response of yield to selection using the three identified yield components is given as: $Y = 0.027 + 0.998 (X_1) + 0.900 (X_2) + 0.002 (X_3)$ Where: X_1 = Marketable root weight; X_2 = Unmarketable root weight; X_3 = Total number of roots.

Thus, only the three traits entered into the model and were retained. The traits that were retained in Table 5 were those that had significant contribution to root yield. Marketable roots weight accounted for 99.44% of the regression model of the traits against total root weight (yield). Unmarketable root weight contributed 0.53% to the model, pushing up the model R-square to 0.9997 fit (99.97%). Though total number of roots did not contribute to the model R-square due to its 0.000 partial R-square, its contribution to total root weight was still significant. It was the only trait among the rest that met the entry point criterion ($P<0.05$) and still left the model significant ($P < 0.036$) . Others could not meet the $P<0.05$ criterion of entering into the model and so could not be regressed against yield. For every 15m ^{2} of sweetpotato field using the cultivars (landraces) at the recommended experimental conditions, weight of marketable and unmarketable roots contributed approximately 1kg each to total yield, while total root number added 2g (ther egression equation is: $Y = 0.027 + 0.998 (X_1) + 0.900 (X_2) + 0.002 (X_3)$, where X_1 = Marketable root weight; X_2 = Unmarketable root weight; X_3 = Total number of roots).

All the traits measured, except stand count at harvest, had positive and significant correlation with total root weight. This gives rise to the need to identify few traits that have the highest influence on yield that could be used in fresh root yield improvement among the cultivars. The tool of forward selection multiple regression analysis used above identified only three traits, marketable and unmarketable root weight and total number of roots, as the most important contributors to total root weight. The use of stepwise multiple linear regression analysis in identifying important yield components had been demonstrated by Stathers et al. (2003), Adeniji and Peter (2005); Somasundaram and Mithra (2007). Stathers et al. (2003) identified marketable and unmarketable root weight and total number of roots as good yield components. This corroborated the findings of our work. The length of root identified by Somasundaram and Mithra (2007) as yield component was at variance with our findings where root length had no much influence on yield. The identification of these traits as important yield components will aid in the effective utilisation of the cultivars in breeding for higher yields using an indirect selection for yield through these identified yield components.

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