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Adaptation of sweet potato [*Ipomoea batatas*] (L.) Lam] genotypes in various agro-ecological zones of Malawi

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Sweet potato [*Ipomoea batatas*] (L.) Lam] is grown by small holder farmers across a wide range of environments in Malawi. A multi-location trial of eight genotypes for three seasons at six research stations was undertaken using additive main effects and multiplicative interaction (AMMI) model analysis to determine the genotypes' stability and influence of genotype \times environment interactions (GEI) on storage root yield. ANOVA showed high significant differences in storage root yield of the genotypes among seasons and locations ($p \leq 0.01$). Genotype, environment and genotype \times environmental interaction significantly influenced storage root yield variation of the cultivars ($p \leq 0.01$). The variance in yield was mainly attributable to environment variability (62.86%) than genotypes variation (14.25%) and G \times E interactions (15.06%). Semusa was superior for storage root yield (27.77t/ha) and Lu96/334 was the most inferior (11.19 t/ha). AMMI stability analysis revealed that LU96/303 (24.72 t/ha) was the most stable genotype across sites. Biplot analysis showed that Chitedze and Baka were sites conducive for high yields hence can be used for preliminary yield evaluation to capture maximum genotypes' yield potential, while Lunyangwa was the lowest yields site; therefore useful for assessing the potential of worst performance of genotypes under unfavourable environmental conditions.

Key words: G \times E interactions, multi-locational trial, stability, sweet potato, genotypes, root yield.

INTRODUCTION

A better understanding of genotypes and environment interactions (GEI) is critical for any crop varieties improvement program (Singh et al., 2006; Osiru et al.,

2009; Andrade et al., 2016) as it helps breeders to identify superior genotypes and their best environments (Yan and Rajcan, 2002; Thiyaagu et al., 2013). GEI refers

Table 1. Sweet potato genotypes used for GEI study.

Clone/genotype	Source/origin
LU96/220	Lunyangwa 1996 selections
LU96/274	Lunyangwa 1996 selections
LU96/374	Lunyangwa 1996 selections
LU96/303	Lunyangwa 1996 selections
LU96/334	Lunyangwa 1996 selections
Mugande	CIP, Nairobi
Kenya (SPN/O)	Tanzania bred, came through Kenya
Semusa (Cemsa 74-288)	CIP, Nairobi

to differential sensitivity of genotype performance from one environment to another (Chalwe et al., 2017). While modern plant breeders work to improve various attributes of crops ranging from pest and disease resistance to biofortification, yield improvement has remained the main drive for most breeding programs (Yahaya et al., 2015). Yield is a complex quantitative trait that is determined by an interaction of various factors including external environment such as soil fertility, rainfall, pests and diseases (Dia et al., 2016). Sweet potato [*Ipomoea batatas*] (L.) Lam], like other crops suffers yield losses that are due to abiotic and biotics limitations (Tekalign, 2007; Kivuva et al., 2014; Chalwe et al., 2017) hence an understanding of the nature and magnitude of GEI among sweet potato genotypes is essential in both sweet potato breeding and variety release (Singh et al., 2006; Rukundo et al., 2013). From time in memorial, genotypic yield levels have been the focus of many sweet potato farmers but adaptation to environments and stability (consistency of yield) of the genotypes have always been the underpinning determinants of final yields (Eberhart and Russell, 1966; Bilbro and Ray, 1976; Rea and Vieira, 2002). Thus, a variety is considered more adaptive and stable if it has a high mean yield but a low degree of yield fluctuation in diverse environments (Kang, 2002; Osiru et al., 2009; Khamphas et al., 2015). Sweet potato [*I. batatas*] (L.) Lam] is grown under varying agro-ecological conditions in the tropical and subtropical regions (Thiyagu et al., 2013; Boney et al., 2014) and it is postulated that because of its high genetic diversity and expansive distribution, it exhibit large variability in genotypic expression in multi-environmental trials across regions (Grünerberg et al., 2005). Therefore, this study used the additive main effect and multiplicative interaction (AMMI) model to assess elite sweet potato genotypes in Malawi to determine their stability and influence of genotype \times environment interactions (GEI) on storage root yield in

order to identify superior cultivars.

MATERIALS AND METHODS

Table 1 presents eight genotypes of sweet potato used in this study. Materials included selections from open pollinated seeds in a crossing block that was established at Lunyangwa Research Station in 1995. Scarified (using sulphuric acid in 99 parts of water) true seeds were initially planted in a seedling nursery in 1996 where clonal selections were made, hence the coding of LU96. LU96 clones were combined with introductions from the International Potato Centre (CIP) and evaluated together in preliminary, advanced and uniform (multi-location) yield trials. Inferior clones in terms of pests and diseases, root yield, root shape, dry matter content, palatability, fiber content, etc. were dropped while the rest were maintained over the seasons. In the final entry, six genotypes were evaluated against Kenya (low yield check genotype) and Semusa (high yield check genotype) (Table 1) at six sites.

Evaluation sites and seasons

The multi-location trial was conducted during the 2002/2003, 2003/2004 and 2004/2005 seasons at Bvumbwe, Makoka, Chitedze, Chitala, Lunyangwa and Baka government agricultural research stations (Table 2). The testing sites represent sweet potato agro-ecological zones in Malawi. The sites differ by altitudes, soil texture, pH and climatic characteristics (rainfall and temperatures) as presented in Table 2 and Figures 1 and 2.

Trial design and field lay out

The clones were laid out in three replicates using a randomized complete block design (RCBD) at the six locations. The plots were planted and maintained following standard procedures with no fertilizer and herbicide application.

Collection of data

Harvesting was done five months after planting (5MAP) at all sites

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Table 2. Altitude and soil characteristics of the study sites (MoALD, 1995).

Location	Altitude (masl)	Soil texture	Soil pH
Bvumbwe (SR)	1164	Sandy clay loam	4.5-6.0
Makoka (ER)	1026	Sandy clay loam	5.2-5.7
Chitedze (CR)	1097	Sandy clay loam	5.5-6.7
Chitala (CR)	600	Sandy clay	6.1
Lunyangwa (NR)	1342	Clay to sandy clay	4.4-5.6
Baka (NR)	460	Sandy clay to sandy clay loam	6.0

SR = Southern region; ER = eastern region; CR = central region; NR = northern region.
Source, MOALD (1995).

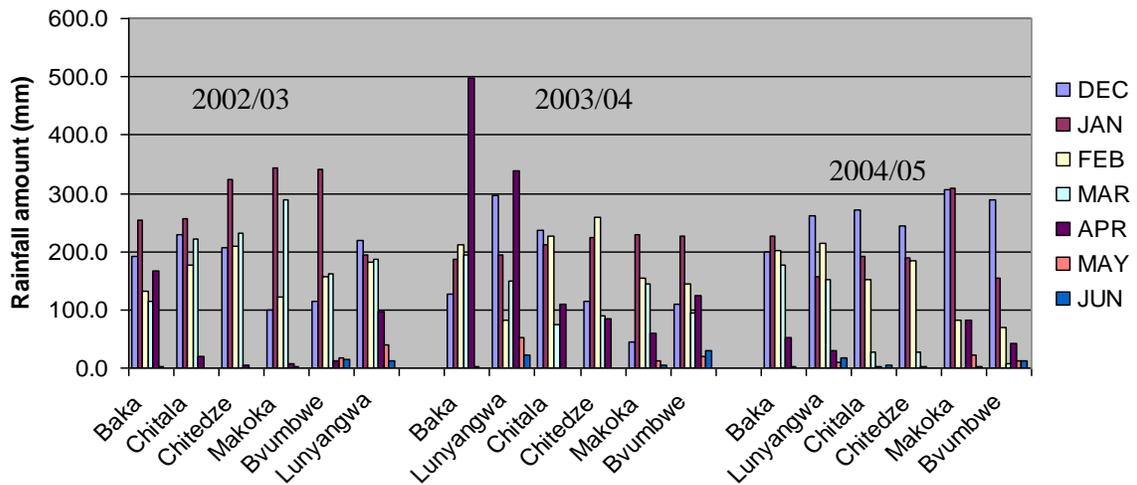


Figure 1. Rainfall amounts (mm) for testing sites over the study seasons (December to June).

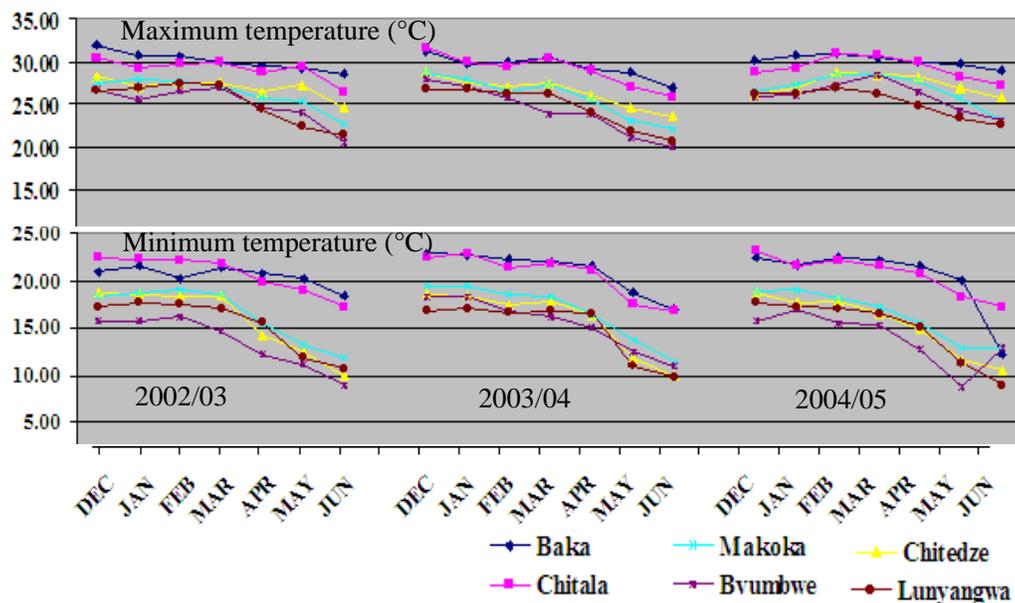


Figure 2. Maximum and minimum temperatures for six study sites and three seasons.

Table 3. Models of ANOVA used for analysis of interaction variance.

Source	DF	MS
Seasons (S)	(S-1)	
Locations (L)	(L-1)	
S × L	(S-1)(L-1)	
Reps (L and S)	LS(R-1)	
Genotypes (G)	(G-1)	$\sigma^2_e + r\sigma^2_{gls} + r/\sigma^2_{gs} + r\sigma^2_{gl} + r\sigma^2_g$
G × L	(G-1)(L-1)	$\sigma^2_e + r\sigma^2_{gls} + r\sigma^2_{gl}$
G × S	(G-1)(S-1)	$\sigma^2_e + r\sigma^2_{gls} + r/\sigma^2_{gs}$
G × L × S	(G-1)(L-1)(S-1)	$\sigma^2_e + r\sigma^2_{gls}$
Error	LS(G-1)(R-1)	σ^2_e

Table 4. Combined ANOVA for storage root yield (t/ha) over three seasons.

Source	Degrees of freedom	Sum of Squares	Mean squares	Contribution to total sum of squares (%)
Location (L)	5	17476.84	3495.37***	27.60
Seasons (S)	2	8523.73	4261.86***	13.46
L × S	10	13803.89	1380.39***	21.80
Genotype (G)	7	9020.83	1288.69***	14.25
G × L	35	5232.82	149.51***	8.26
G × S	14	1100.64	78.62***	1.74
G × L × S	70	3204.92	45.79***	5.06
REP (L × S)	36	964.55	26.79*	1.52
Error	252	3994.91	15.85	6.31
Total	431		63323.13	
		$r^2=0.94$		%CV=19.19

*= $p \leq 0.05$; ***= $p \leq 0.01$; r^2 =% repeatability.

and data on final stand count, representing final surviving plants in a net plot was recorded. Using a weighing scale, storage root yield (kg) per plot was determined with only marketable roots considered for analysis.

Data analyses

Analysis of variance

The effects of the genotype, location and season as well as their first and second order interactions were determined using analysis of variance (ANOVA) in Agrobase (1999) Agronomic Software 71. The effects of genotypes were assumed to be fixed, while those of seasons and location effects were considered to be random. Table 3 shows the models of the ANOVA used in the study. The ANOVA for estimating variance components is based on the model proposed by Allard (1960), and further developed by Comstock and Moll (1963) for the determination of interaction variance components. In the model, S, L, G and R are the number of seasons, locations, genotypes and replications, respectively. The σ^2_e and σ^2_g are components of variance of error and genotypes, respectively. Combinations of the subscript identify the components for the interactions.

AMMI stability analysis of root yield

Similarities among test environments based on environmental main and GEI effects were evaluated using additive main effect and multiplicative interaction (AMMI; Zobel et al., 1988) analyses (Agrobase, 1999). The method uses a combination of ANOVA and principal components analysis (PCA). While ANOVA partitioned the variance into three components: genotype, environment and G × E deviations from the grand mean, the PCA partitioned the G × E deviations into different interaction principal component axes (IPCA). These were tested for statistical significance using ANOVA.

RESULTS AND DISCUSSION

Genotypic variability for root yield

The analysis of variance (ANOVA) indicated high significant differences in storage root yield (t/ha) among genotypes at $p \leq 0.01$ within and among locations and seasons (Table 4). The variability in yield by different genotypes indicated their differing responses to diverse environments and seasons (Mulema et al., 2008). The

Table 5. Mean storage root yield (t/ha) across all locations, seasons and genotypes

Genotype	2002/03	2003/04	2004/05	Mean
Semusa	30.94	34.39	17.98	27.77
Lu96/303	26.17	28.33	19.65	24.72
Lu96/220	26.20	24.33	16.85	22.46
Lu96/374	22.50	26.11	13.80	20.80
Mugande	21.83	23.72	15.01	20.19
Kenya	21.11	24.28	13.10	19.50
Lu96/274	22.72	24.56	10.90	19.39
Lu96/334	10.56	13.56	9.47	11.19
Mean	22.75	24.91	14.60	20.75±2.36
LSD (genotypes)	2.34	2.77	1.79	
LSD (Location × Season)				1.89
Sig. (Location × Season)				***

*** $p \leq 0.01$; Sig. = significant; L = location; S = season; LSD = least significance difference.

difference in performance among the genotypes in a given environment is in part due to genetic variability which accounted for 14.25% of the total sum of squares (Table 4). The mean storage root yields of the genotypes (Table 5) ranged from 11.19 (LU96/334) to 28.33 t/ha (Semusa). The coefficient of variance (CV) was 19.19% which was reasonable and reflective of the study results reliability under field and rain fed conditions. The r^2 value = 0.94 represented a high (94%) repeatability (reproducing similar yields) of the trial. The relative yields of the eight genotypes (Table 5) showed that Semusa, the highest yielding reference was the most superior (27.77 t/ha) in two of the three seasons and six locations. The rest of the genotypes had different ranks in different seasons.

The selection criterion for early maturing and high yielding cultivars in Malawi is based on mean root yields of 20 t/ha at 5 months after planting (Chipungu et al., 1999). Such a selection criterion however, is a factor in stability in yield as illustrated by the yields of cultivars in 2005 which were below 20 t/ha. Breeders have always considered both yield levels and stability of performance, in order to present farmers with genotypes that are suitable (Farshadfar, 2008; Fikere et al., 2009). Considering the least significant difference (LSD), the root yield means were over 20 t/ha and above the lower yielding check, Kenya, except for Lu96/274 and LU96/334 (Table 5). Therefore, five of the six tested genotypes are good candidates for release in the national program assuming their performance is equally good in other traits such as tolerance/resistance to pests and diseases, palatability (dry matter content, colour, taste, texture, fiber content, etc.), root sizes and numbers.

Presence and magnitude of GEI on root yield

ANOVA (Table 4) showed significant effects of

genotypes, locations, seasons and their interactions ($P \leq 0.01$) on root yield. Similar results were shown by Mwololo et al. (2009) in their study on 17 genotypes, three sites and two seasons in Kenya. Khamphas et al. (2015) also found that location, genotypes and $G \times L$ interaction were significant for all characters of purple waxy maize genotypes. This underscores the importance of stability studies before recommendation of any crop genotypes for various locations.

In the present study, location which is a predictable environment had a variability of 27.60% (Table 4) of the total variation of yield and could be attributed to differences in soil type and pH and altitude (Table 2). The variability among seasons which is the unpredictable environment (13.46% contribution to total SS) may be attributed to seasonal rainfall and temperatures variations (Figures 1 and 2). When GEI is due to variation in predictable environmental factors, sweet potato breeders can either develop specific varieties for different environments (locations, soil types, management systems, etc.), or broadly adapted varieties that perform well under variable conditions (Farshadfar, 2008; Fikere et al., 2009). However, when GEI stems from variations in unpredictable environmental factors, such as year to year variation in rainfall distribution, as is the case in this study, stable varieties that can perform reasonably well under a range of conditions are needed. Such breeding strategies assist the farmers in risk avoidance. Fikere et al. (2008) indicated that farmers favor genotypes that yield constantly better across seasons and environments. In general, the environment accounted for 62.86% (27.60 + 13.46 + 21.80%) of the total variation in storage root yield. This finding is indicative of a high influence of the environment on root yield, further supporting the need for evaluation of candidate genotypes over multiple sites and seasons for accurate inference (Sial et al., 2001).

Table 6 shows that the best yield was from Semusa in

Table 6. Genotypes yield (t/ha) and performance rank (R) over three seasons and six sites.

Genotype	BK	R	MK	R	CH	R	BV	R	CZ	R	LU	R	OM	R
2002/2003 season														
Semusa	42.67	1	21.67	3	28.67	1	16.00	6	63.33	1	13.33	5	30.94	1
Mugande	32.33	3	13.00	7	14.67	7	16.33	5	39.67	5	15.00	2	26.20	2
LU96/220	38.21	2	21.00	4	24.67	2	19.00	4	42.33	4	12.00	6	26.17	3
Kenya	21.67	7	20.33	6	19.33	5	21.67	1	33.00	7	10.67	7	22.72	4
LU96/303	30.00	4	24.67	1	20.33	4	20.00	3	45.00	2	17.00	1	22.50	5
LU96/274	22.67	5	20.33	5	15.67	6	20.67	2	43.00	3	14.00	3	21.83	6
LU96/374	22.33	6	23.00	2	24.33	3	13.33	7	38.33	6	13.67	4	21.11	7
LU96/334	14.67	8	11.00	8	8.33	8	7.67	8	11.67	8	10.00	8	10.56	8
Mean	28.07		19.38		19.50		16.83		39.54		13.21		22.75	
2003/2004 season														
Semusa	39.33	1	18.33	4	25.67	1	34.67	1	62.33	1	25.67	1	34.39	1
Mugande	19.33	7	17.33	6	24.67	2	20.00	7	43.33	7	24.67	2	24.56	4
LU96/220	25.67	3	17.00	7	21.67	4	21.67	6	46.00	5	21.67	4	24.33	5
Kenya	20.33	5	18.33	5	17.67	7	27.33	3	46.33	4	17.67	7	23.72	7
LU96/303	32.00	2	22.00	1	24.33	3	23.00	4	44.67	6	24.33	3	28.33	2
LU96/274	19.67	6	20.00	3	19.67	5	22.33	5	48.00	3	19.67	5	24.28	6
LU96/374	22.00	4	20.33	2	18.00	6	33.33	2	49.67	2	18.00	6	26.11	3
LU96/334	10.67	8	11.33	8	16.67	8	13.33	8	19.67	8	16.67	8	13.56	8
Mean	23.63		18.08		21.04		24.46		45.00		21.04		24.91	
2004/2005 season														
Semusa	35.7	2	27.00	4	12.04	1	19.00	1	16.98	1	7.20	2	17.98	2
Mugande	19.44	4	24.67	7	8.38	3	17.67	3	12.69	3	7.20	1	13.80	4
Lu96/220	33.95	3	25.00	6	6.58	4	12.67	7	16.72	2	6.17	4	16.85	3
Kenya	14.61	7	26.67	5	5.25	6	16.67	4	10.91	5	4.53	8	10.90	7
LU96/303	36.01	1	28.33	1	9.77	2	17.67	2	10.65	6	5.45	6	19.65	1
Lu96/274	7.51	8	27.00	3	2.57	7	15.67	5	7.20	8	5.45	5	9.47	8
Lu96/374	16.46	5	28.33	2	5.97	5	14.67	6	12.34	4	5.04	7	15.01	5
Lu96/334	14.61	6	15.00	8	1.95	8	10.33	8	8.23	7	6.69	3	13.10	6
Mean	22.29		25.25		6.56		15.54		11.97		5.97		14.60	

BK=Baka; MK=Makoka; CH=Chitala; BV=Bvumbwe; CZ=Chitedze; LU=Lunyangwa; OM = overall mean.

2002/2003 and 2003/2004 seasons (30.94 and 34.39 t/ha, respectively) while LU96/303 had the highest yield (19.65 t/ha) in the 2004/2005 season. The most productive season was 2003/2004 (24.91 t/ha), while 2004/2005 (14.60 t/ha) was the worst season (Table 6). The seasonal difference was attributed to uneven distribution of rainfall amounts in 2004/2005 season (Figure 1). The season had recurrent dry spells between January and March. The seasons 2002/2003 and 2003/2004 were similar in terms of rainfall (Figure 1) amounts and distribution. However, all the three seasons were similar in terms of minimum and maximum temperatures (Figure 2). LU96/303 on average was second in yield after Semusa (Table 5) but highest in the drought season (19.65 t/ha) (2004/2005) attaining the

Malawian selection criterion (20 t/ha) (Chipungu et al., 1999). This implies that LU96/303 is an ideal cultivar because it combines both drought tolerance and high yield (Makunde et al., 2017). Drought is known to affect root yield negatively (Andrade et al., 2016)

The best site in terms of yield performance was Chitedze in 2002/2003 (39.54 t/ha) and 2003/2004 (45.00 t/ha) while in 2004/2005, Makoka was first (25.25 t/ha). Cultivar Semusa ranked first in five sites in 2003/2004, four sites in 2004/2005 and three sites in 2002/2003. LU96/303 was rated first in each season at Makoka, while LU96/334 was classified as last in each location in 2002/2003 and 2003/2004 seasons and in three sites in 2004/2005 season. The rest of the clones varied from positions 2 to 8 across sites over the seasons (Table 6),

Table 7. AMMI analysis of variance and %GEI explained for root yield.

Source	df	SS	MS	Explained (%)	Cumulative (%)
Environment (E)	17	39804.55	2341.44***	62.86	62.86
Genotype (G)	7	9020.78	1288.68***	14.25	77.11
Rep (G × E)	36	964.56	26.79***	1.52	78.63
G × E	119	9538.29	80.15***	15.06	93.69
Error	252	3994.91	15.85***	6.31	100.00
Total	431	63323.09			
IPCA 1	23	4919.65	4919.65***	51.58	51.58
IPCA 2	21	2545.50	2545.50***	26.69	78.27
IPCA 3	19	866.67	866.67***	9.09	87.35
IPCA 4	17	588.76	588.76***	6.17	93.52
IPCA 5	15	414.98	414.90*	4.35	97.87
IPCA 6	13	130.42	130.42ns	1.37	99.24
IPCA 2	11	72.31	72.31	0.76	100

*and ** *p \leq 0.05, and 0.01; ns = not significant; SS=sum of square; MS= mean square.

yet good cultivars must show high performance for yield and other essential agronomic traits over a wide range of environments (Becker and Leon, 1988).

Root yield additive main effect and multiplicative interaction (AMMI) for the genotypes across environments

The AMMI analysis of variance of root yield (kg/ha) of eight genotypes in 18 environments showed that genotype main effects, environmental main effects and their interactions were all highly significant for root yield ($p\leq 0.01$). This finding concurs with those of Chalwe et al. (2017) whose study on sweet potato genotypes in Zambia showed significant AMMI analysis variance of genotype, environment and their interactions on root yield and weevil damage. Gedif and Yigzaw (2014) and Daba et al. (2015) observed similar significant environment, genotype and genotype \times environment interactions influence on yield of potato (*S. tuberosum* L.) and sesame, respectively, in Ethiopia ($p\leq 0.01$).

A total of 62.86% of the total sum of square (SS) was attributable to environmental effects, 14.25% to genotypic effects, and 15.06% to GEI effects (Table 7). This means that G \times E interaction effects did not impact more on the resultant root yield than the variation in environments, suggesting that the environments (test sites) were highly diverse, hence causing most of the variation in root yield. Mitrović et al. (2012) also reported large portion (77.83%) of the total variation in maize yield as ascribed to the environment, while genotype and genotype \times environment accounted for 30% of the total variation. Contrary results which showed greater G \times E effects than environmental or genotypic effects were obtained by Andrade et al.

(2016) in their study on 58 sweet potato genotypes evaluated over three seasons at one research station. These findings could be due to use of a single site for testing genotypes. In the present study, the total percentage attributed to environment and G \times E interaction accounted for 77.92% of the disparity in storage root yield. Comparable results were found by Mwololo et al. (2009) in sweet potato (70%) and Ntawuruhunga et al. (2001) in cassava (50 to 90%).

The magnitude of the GEI (15.06%) sum of squares was above that of genotypes (14.25%), indicating that there were differences in genotypic response across environments (Table 7). Results of the AMMI analysis (Table 7) also showed that the first principal component axis (PCA 1) captured 51.58% of the interaction sum of squares. Similarly, the second principal component axis (PCA 2) explained a further 26.69% of the GEI sum of squares. The mean squares for the PCA 1 and PCA 2 were significant at $P\leq 0.01$ and cumulatively contributed to 78.27% of the total GEI. A F-test at $P\leq 0.01$ suggested that the two principal component axes of interaction were significant for the model with 44 degrees of freedom. Zobel et al. (1988) and Kaya et al. (2002) showed in their prediction assessment that AMMI with only two IPCA axes was the best model. Further interaction principal component axes capture mostly noise and therefore did not help to predict the interactions (Daba et al., 2015). Thus, the interaction of the eight genotypes with 18 environments in this study was best predicted by the first two principal components and the rest were less informative. Thiyagu et al. (2013) reported in their stability study that sweet potato accumulated contribution of IPCA1 and IPCA2 of 85.26%. Comparably, in studies on linseed yield by Adugna and Labuschagne (2002), the two IPCAs accounted for 69.5% of the total interaction

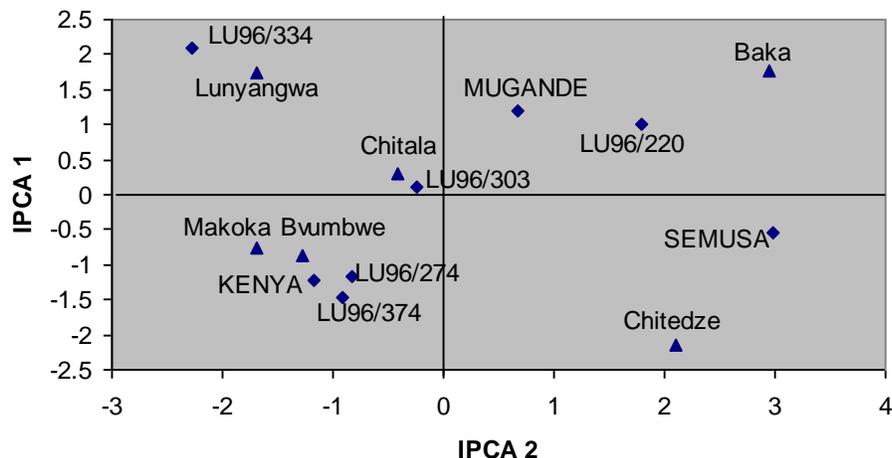


Figure 3. Biplot of eight genotypes and six locations for IPCA scores 1 and 2.

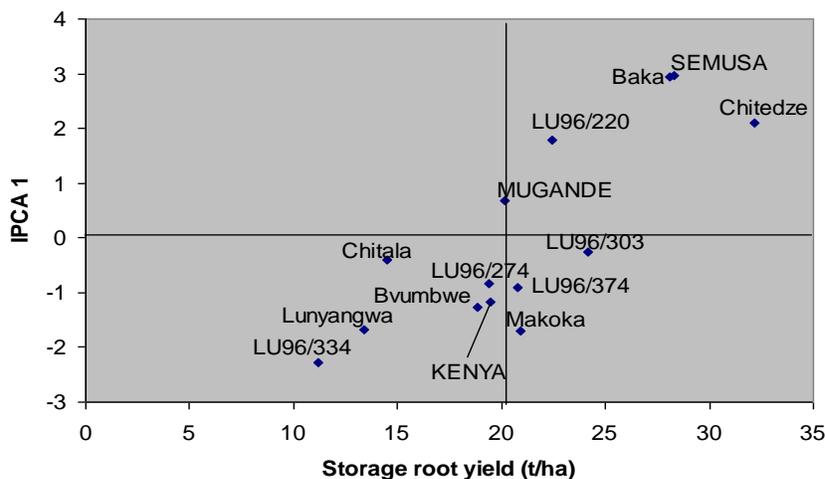


Figure 4. Biplot of eight genotypes and six locations for root yield and IPCA 1 scores.

and the remaining 30.5% was considered residual or noise not interpretable and was therefore discarded.

In order to identify genotypes adapted to specific test environments and their yield performance and stability, biplots were used (Yan, 2002). The biplot (Figure 3) was generated using genotypic and environmental scores of the first two PCA components as suggested by Vargas and Crossa (2000). Genotypes and location environments that appear almost on horizontal line (y axis) have a similar negative or positive interaction pattern for the IPCA 2 and equally those that fall along the x axis or close to it have similar interaction pattern along IPCA 1. Therefore, genotype LU96/334 is best for Lunyangwa while Kenya, LU96/274 and LU96/374 are best for Bvumbwe and Makoka and LU96/303 for Chitala.

LU96/303 is located near the plot origins of both IPCA1 and 2 and therefore less responsive than the vertex genotypes, hence more stable across the testing environments since its IPCA scores are closer to zero (Figure 3) (Mwololo et al., 2009; Osiru et al., 2009; Thiyagu et al., 2013). Such a stable performance is a desirable attribute of cultivars, particularly in Malawi where environmental variations especially the rainfall pattern are very high and unpredictable as shown in Figure 2.

Semusa was unstable (Figure 4) across the six sites when variation was explained by IPCA 1 but stabilised (Figure 3) when IPCA 2 was included. In contrast, LU96/334 is a non-adaptable genotype as indicated by its large IPCA 1 and IPCA 2 scores. Mugande and LU96/220

(high yielding) are moderately stable and are not closely associated with any site (Figure 3). Other genotypes of interest are LU96/274 and LU96/374 which are stable when explained by IPCA 2. Makoka and Bvumbwe are similar environments and Kenya, LU96/274 and LU96/374 exhibit similarity in interaction patterns (Figure 3).

Figure 4 is a biplot of average yield of a genotype at different sites and PCA 1 effects. Genotype Semusa had the highest average yield because it yielded the highest at sites Chitedze and Baka, and yielded above average at all other sites.

On the other hand, the average yield of genotype LU96/334 was the least while the yield of Mugande was average. LU96/220, LU96/303 and LU96/374 yielded above average. Piepho (1996) indicated that if cultivars are selected for varying environments, stability and mean yield across all environments are more important than yield for specific environments. This is even more important in view of climate change hence farmers would prefer widely adapted cultivars (Zhang et al., 2006; Fikere et al., 2009; Khamphas et al., 2015).

In this study therefore, LU96/303 is considered the most stable genotype (Figures 3 and 4) suitable for the variable production conditions under small holder farmers in the country. It is not uncommon for stability studies to recommend one or two genotypes from a test of many genotypes. Chalwe et al. (2017) and Makunde et al. (2017) both identified two out of eight and 48 genotypes respectively as most stable for root yield and weevil damage and root yield and drought tolerance, respectively. In a study done on winter wheat genotypes in Turkey, two were also reported as stable for all environments by Altay (2012).

Erratic rains in 2004/2005 season, which resulted in low root yields across sites for most of the genotypes, exemplified the variability of cropping seasons in Malawi. Makunde et al. (2017) showed that drought (water stress) reduced sweet potato storage root yield by as much as 35%. This observation indicates that though sweet potato generally grows in marginal areas characterized by poor soils and low rainfall, differential genotypic responses are registered in varying environmental conditions (Chalwe et al., 2017).

Chitedze and Baka were conducive for high yields (above average) and Makoka though close to Bvumbwe hence similar environments, Makoka yields were however above average (Figure 4), hence a better site of the two. Osiru et al. (2009) reported that high and positive PCA scores show that genotypes are likely to yield more in that environment and conversely high and negative PCA scores are indicative of lower yields in these environments. By implication, Figure 4 confirms that Semusa would yield highly at Baka and Chitedze and yields of Lu96/334 would be lower at Lunyangwa. These findings show that knowledge on GEI of a crop in a

country helps plant breeders reduce cost of extensive genotype evaluation by eliminating redundant testing sites (Shafii et al., 1992; Kang and Magari, 1996). The ultimate goal of any breeding program is to produce genotypes that consistently yield more in different environments (Khamphas et al., 2015).

Conclusions

Sweet potato [*I. batatas* (L.) Lam] cultivars in the study varied significantly in yield across locations and seasons as shown by combined analysis of variance ($p < 0.01$). The variance in yield was mainly attributable to environment variability (62.86%) than genotypes variation (14.25%) and $G \times E$ interactions (15.06%). Stability analysis (AMMI) revealed that LU96/303 (24.16 t/ha) was the most stable, while ANOVA identified Semusa as the highest yielding cultivar (28.33 t/ha). While Lunyangwa was a low yielding site, Chitedze was the highest; therefore Chitedze should be used to screen cultivars for maximum yield potential. In times of limited resources, Baka and Bvumbwe sites are not necessary for yield evaluation as they are similar to Chitedze and Makoka, respectively.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interest.

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