Vol. 6(5), pp. 36-45, August 2020
DOI: 10.5897/JODA2019.0036
Article Number: 0EF6C0564423
ISSN 2476-8650

http://www.academicjournals.org/JODA

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Journal of Dryland Agriculture

Full Length Research Paper

Acclimatization and performance evaluations of sweetpotato (*Ipomoea batatas* L. Lam) on yield and yield components in different agro-ecologies of Northern Ethiopia

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Received 12 December, 2019; Accepted 6 February, 2020

The study is aimed at evaluating the genotype by environment interactions (GEI) on acclimatization of sweetpotato genotypes to the farmers' field conditions. A field evaluation was done on six sweetpotato genotypes planted in RCBD, three replications in three different agro-ecologies. These genotypes were previously (2012, 2014) tested for yield performance in the same environment. Data collected were subjected to ANOVA. Genetic merit and GEI for total storage root tuber yield (TSRTY) was tested using BLUPs and GGE biplot, respectively. Clustering of genotypes was done using Ward's linkage method in the Squared Euclidean distance. Breeding significance and distance among clusters was determined using Mahalanobis's distance. Environment played significant (P<0.01) role in determining the genotypes' maturity days; and genotypes in lowland matured earlier than those on higher altitudes. TSRTY ranged from 7.5 to 59.5 t/ha, and total fresh biomass (TFB) 21.6 to 36.0 t/ha. Genotypes with high harvest index produced high TSRTY, TFB and NNPP hence well acclimatized. GEI was responsible for the genotypes acclimatization in the studied agro-ecologies; Tulla and Kulfo demonstrated wide acclimatization while Berkume was specific. Cluster II with very high dry matter content may be explored for crossbreeding cluster I and III to produce OFSP transgressive segregants for Ethiopia.

Key words: Sweetpotato genotypes acclimatisation, agro-ecologies, yield and yield components, environment.

INTRODUCTION

Sweetpotato (*Ipomoea batatas* L. Lam), belongs to the family *Convolvulaceae*, genus *Ipomoea,* sub genus *eriospermum*, section *eriospermum* and series *batatas* (Pursegove, 1968). It is the 3rd most important root crop in the world and Ethiopia is the 7th producer (FAOSTAT, 2013). In Ethiopia, it is a major staple food in Gama Gofa and Wolayta zone, and Oromia Regional State (Fekadu. et al., 2015). The various uses of the crop include health due its high antioxidant property, food and nutritional security, animal feeds, income, bio-fuel, and industrial production of syrups, flour, colorants, starch and juice (Islam, 2006; Zhu et al., 2010; USDA, 2017). The purple

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colored sweetpotato leaves was discovered to be more superior to spinach or strawberries in nutritional quality thus was adopted as a very important green vegetable in countries like Uganda, Tanzania, Nigeria, Ghana (Tewe et al., 2003; Islam, 2006; Zhu et al., 2010). Despite all these benefits of the crop, sweetpotato is still produced in Ethiopia in small scale mainly for animal feeds especially in the Tigray region and little is marketed locally in boiled form (Belehu, 2003; CSA, 2013; Fekadu et al., 2015). Tigray region has dynamic agro-ecologies with various soils and climatic types which influences crop performances (Abdissa et al., 2011). This comes with need to test the general performance of each crop before release to farmers for production. In attempt to combat malnutrition using sweetpotato, most released sweetpotato varieties failed in the farmers' fields after distributions by the research centers (CIP, 2000; Assefa et al., 2007). Environment was found to affect sweetpotato storage root tuber yield and dry matter content (Shumbusha et al., 2010; Vimala and Hariprakash, 2011). This therefore, makes it very vital to investigate much on the growth parameters of the quality sweetpotato genotypes in circulations among the farmers to determine their acclimatization to the farmers' field conditions in the different agro-ecologies of the Northern Ethiopia to improve on the general production, consumptions and marketability of the crop for industrial, community's food, nutritional and economic security needs with better vines and storage root tuber yield returns using minimum input resources.

MATERIALS AND METHODS

Description of the experimental sites

The three experimental agro-ecological sites were; Endayesus (dry highland) found at an altitude of 2223 m above sea-level (masl), characterized by silty clay soil, minimum and maximum temperature of 12.5 and 26.0°C, and an average annual rainfall of 450 mm. Fachagama (dry lowland) characterized by silty clay loam soil, minimum and maximum temperature of 22.0 and 31.0°C, located at an altitude of 1585 masl, with an average annual rainfall of 350 mm. Rarhe (moist lowland) characterized by sandy clay loam soil, with average annual mean rainfall of 733 mm, minimum and maximum temperature of 15.0 and 30.9°C located at an altitude of 1460 masl.

Planting materials and experimental procedures

The study consisted of 1620 plants of the six sweetpotato genotypes; Kulfo, Vitae, Kabode and Tulla (orange fleshed), Awassa-83 and Berkume (white fleshed). For each genotype, 30 cm long cuttings with at least six nodes were planted in the main rainy season (July 2016 and harvested in January 2017). Planting was done on the ridges at a spacing of 0.3 m x 0.6 m in a 3.0 m x 2.4 m randomized complete block design (RCBD) in three replications. The spacing between each replication block was 1 m. Each replication plot received 30 cuttings of each of the genotype free from virus, diseases and pests sourced from Awassa Research Station in Ethiopia. The experimental plots were ploughed using an ox-plough twice. Supplementary irrigation was done using furrow application once a week (September to November) to raise the soil moisture level to field capacity. The soil received nutrient treatment twice, one with DAP (100%) and Urea (50%) (split application) at planting, then later after a month top dressed with Urea (50%) totaling to a rate of 100 kg/ha. Mechanical weeding was done four times using hand hoe.

Data collection

Data were collected on the following phenological and morphological parameters and were used in determining yield, yield components and acclimatization of the genotypes across the agro-ecological zones; vine length (VL) (cm), days to maturity (DTM), internodes' length (INL) (cm), total fresh biomass weight (TFB) in tons per hectare (t/ha), number of nodes per plant (NNPP), total number of storage root tuber per plant (TNRTP), Girth of the storage root tuber (RTG) (cm), number of unmarketable storage root tubers per plot (NUTP), number of marketable storage root tubers per plot (NMTP), total unmarketable storage root tuber yield in tons per hectare (TUSRTY) (t/ha), and total marketable storage root tuber yield (TMSRTY) (t/ha). The total storage root tuber yield (TSRTY) (t/ha) was calculated as a ratio of the summation of marketable yield and unmarketable yield to the net plot area (m^2) using the formula;

$$\text{TSRTY} = \frac{TMSRTY + TUSRTY}{\text{Total Net Area } (M^2)} X\ 10 \quad (1)$$

Where; TSRTY= total storage root tuber yield; TMSRTY= total marketable total storage root tuber yield; TUSRTY= total unmarketable storage root tuber yield; t/ha= tons per hectare; M^2= meters square (Grüneberg et al., 2005).

The dry matter content (DMC) was determined using morphological direct screening method where 200 g of fresh storage root tubers (TFWT) from each genotype were taken, put in paper bag and oven dried at 65 for 72 h till constant weight. The samples' dry weight (TDWT) was recorded instantly upon removal from the oven. The dry matter content was then calculated according to the formula:

$$\text{DMC} = \frac{TDWT}{\text{TFWT}} X\ 100 \quad (2)$$

Where; DMC= dry matter content; TDWT= total dry weight; TFWT= Total fresh weight (Benesi et al., 2004).

Harvest index was determined using the using the formula:

$$\text{HI} = \frac{\text{TSRTY (t/ha)}}{\text{TSRTY (t/ha)} + \text{TFB (t/ha)}} \quad (3)$$

Where; HI= Harvest Index; TSRTY = Total storage root tuber yield; TFB= Total Fresh Biomass (Vine yield); t/ha= tons per hectare (Bhagsari and Doyle, 1990).

Data analysis

In this study trial, all data collected were subjected to the Analysis of Variance (ANOVA). The genotypes were treated as fixed effects while replications and sites were the random effects. The variance components of the trait means and ranges of the random effects were obtained by subjecting the data to Residual Maximum Likelihood (REML) of Genstat 14th edition. The model used for analysis was: Yij = μ + ti +rj + eij (i = 1, 2, ..., t; j = 1, 2, ... r). Where; Yij = random variable observation from the i^{th} genotype in j^{th}

Table 1. ANOVA to test the significance in performance for Genotypes x Environment interactions.

Trait	Estimates of variance				
	Genotype	Environment	G x E	Residual	%CV
df	5	2	10	38	
DTM	14595.50**	2515.50**	1034.50**	17.60	3.10
INL	9.45**	31.24**	4.18**	0.09	9.20
TSRTY	747.12**	1579.87**	418.65**	46.71	25.20
VL	3683.50**	42953.10**	873.10*	396.50	17.60
TUSRTY	2.81**	4.16^{ns}	1.72**	0.36	25.80
TNRTP	4.24**	0.13^{ns}	3.93**	0.11	11.90
TFB	100.18**	5095.19**	168.78*	76.37	12.57
TMSRTY	7.88**	16.12**	4.60**	0.49	23.30
DMC	259.27**	0.616**	27.87**	2.16	5.20
RTL	49.02**	37.36ns	57.43**	13.09	18.40
RTG	226.60**	438.37**	35.13**	9.31	16.60
NNPP	132.87**	1463.82**	321.63**	15.57	11.11
HI	23.34**	142.27**	17.09**	0.68	1.80

df= Degree of Freedom; DTM= Days to Maturity; INL Internodes length; TSRTY=Total storage root Tuber Yield; VL= Vine length; TUSRTY=Total Unmarketable storage root tuber yield; TNRTP=Total number of storage root tuber per plant; TFB=Total fresh biomass; TMSRTY= Total Marketable storage root tuber yield; DMC= Dry matter content; RTL= Storage root tuber length; RTG= Storage Root tuber girth; NNPP=Number of nodes per plant; HI= Harvest Index; ** = highly significant at probability (P<0.01), * = significant at probability (P<0.05); ns = not significant

replication; μ, ti and rj = general mean effect of the i^{th} genotype and effect of the j^{th} replication. The i^{th} genotype effects is fixed variable; eij = the error component of environment, replication and location. The effects of the random variable were normally and independently distributed. The means were separated by Fisher Least Significant difference (LSD) (P<0.05) probability. The analysis of G x E interactions for storage root tuber yield was done using the GGE Biplot of GenStat 14^{th} version (Payne et al., 2011). The environment was considered to be the source of variation upon which the genotypic performance was tested. Meanwhile, the genotypes were considered as a fixed factor to be tested by the different environments. The cumulative interaction percentage of the environment and genotypes as well as the percentage contributions of the environment and that of the genotypes registered by the GGE Biplot were recorded as described by Yan and Tinker (2006). Clustering of genotypes to determine their relationships in line with the studied traits was done using Genstat 14^{th} version (Payne et al., 2011). The Ward's linkage, method in the Squared Euclidean distance was then used to appraise the relationship among the clusters as it quantifies and rank genotypes according to their yield adaptability (Ward, 1963). The distance between the clusters was determined using the Mahalanobis's distance (D^2). The Mahalanobis's distance measures the differences among the group centroids and estimates the breeding significance among the clusters members (Mahalanobis, 1963). The genetic merit of the genotypes was determined using best linear unbiased predictors (BLUP) (Robinson, 1991).

RESULTS

Evaluation of general performance of the genotypes across environments for the studied traits

Generally, the genotypes performed differently for the different traits across environments and were significantly different at different probability levels. Genotypes' main effect was highly significant (P<0.01) for all traits, environments' main effect was highly significant (P<0.01) for all traits except TUSRTY, RTL, and TNRTP which were not significant. This study also demonstrated a highly significant G x E (P<0.01) for all the traits except TFB and VL which were significant at probability (P<0.05). The observed coefficient of variation (CV) for the traits studied ranged between1.8 to 25.8 (Table 1).

Evaluating the effects of the environment on the genotypes using Best Linear Unbiased Predictors (BLUP)

In general, genotypes registered high performance for almost all the measured traits including TSRTY and TFB in environment Rarhe, and Fachagama was least. Each genotype performed differently in the three environments; for instance, genotype Berkume the best producer of TSRTY in Rarhe (59.5 t/ha) was the worst yielder in Fachagama (7.9 t/ha) and fourth best in Endayesus (16.5 t/ha). Vine length also varied in the same genotypes across environments. Similarly, Harvest index (HI) varied in genotypes across environments; Kulfo exhibited HI 57.0, 62.4 and 51.5 at Endayesus, Fachagama, and Rarhe respectively (Table 2).

Evaluation of genotypes' main effects, genotype by environment interactions using GGE biplot

The GGE Biplot analysis that combines genotypes main

Table 2. BLUP means for the studied traits.

Envt	Genotypes	DTM	INL	TSRTY	VL	TUSRTY	TNRTP	TFB	TMSRTY	DMC	RTL	RTG	NUTP	NMTP	NNPP	HI
End	Awassa-83	186	2.5	13.4	43.2	2.7	4	25.5	10.7	27	18.9	10.4	19	14	23	34.4
End	Berkume	150	3.7	16.5	90.2	2.8	2	23.1	13.7	21.3	17.2	13.1	15	13	27	40.3
End	Kabode	150	1	21.1	32.2	6.8	2	20.8	14.4	35.7	23.3	12	22	17	28	50.5
End	Kulfo	120	1.1	30.6	39.2	5.3	4	24.5	25.3	26	13.8	19.1	13	36	28	57.0
End	Tulla	120	1.1	29.4	43	7.8	3	19.3	21.7	22.8	13.5	20	10	18	27	60.4
End	Vitae	150	0.9	13.3	27.7	1.6	1	20.4	11.7	36	21.5	15	10	13	28	39.4
Fac	Awassa-83	140	2.9	9	35.7	2.3	1	18.6	6.8	28.7	12.8	10.4	5	2	34	32.7
Fac	Berkume	140	6.7	7.9	74.3	2.5	4	11.9	5.4	21.5	19.9	19.2	6	5	24	39.7
Fac	Kabode	129	2.8	18.2	29.9	3	3	13.2	15.2	37.3	28.8	12.7	14	7	36	58
Fac	Kulfo	123	3.3	19.7	42.9	6.8	2	12.1	12.8	24.5	20.4	21.1	14	8	40	62.4
Fac	Tulla	110	2.7	24.5	36.9	8.8	4	15.2	15.7	22.8	18.8	20.4	17	10	36	61.8
Fac	Vitae	150	3	14.7	32.7	2.5	3	10.1	12.1	36	23.1	12.8	21	8	41	59.2
Rarhe	Awassa-83	125	3.8	21.9	163	5.2	1	29.6	16.7	28.2	23.9	21.6	9	8	54	42.5
Rarhe	Berkume	120	7.4	59.5	155	21.3	4	37.4	38.2	28.2	18.8	30.5	3	12	59	51.2
Rarhe	Kabode	115	3.8	7.5	78.5	3.5	2	54.2	4	36.7	15.2	11.4	13	2	27	12.2
Rarhe	Kulfo	90	3.5	39.7	103	2.7	3	56.6	37	27.2	20.5	29.6	32	8	27	51.5
Rarhe	Tulla	90	3.7	54.3	136	21.3	4	56.7	33	23.7	20.1	31.3	2	14	58	48.9
Rarhe	Vitae	116	3.6	20	137	5.7	2	41.6	14.3	36.4	24	19.5	13	4	44	32.5

End= Endayesus; Fac= Fachagama; Envt= Environment; DTM= Days to Maturity; INL Internodes length; TSRTY=Total storage root Tuber Yield; VL= Vain length; TUSRTY=Total Unmarketable storage root tuber yield; TNRTP=Total number of storage root tuber per plant; TFB=Total fresh biomass; TMSRTY= Total Marketable storage root tuber yield; DMC= Dry matter content; RTL= Storage root tuber length; RTG= Storage Root tuber girth; NNPP=Number of nodes per plant; NUTP= number of unmarketable storage root tubers per plot; NMTP= Number of marketable storage root tubers per plot; HI= Harvest Index.

effects and genotypes by environment interactions clearly showed the relationship between the genotypes and the environments. Genotypes were scattered within the quadrate from the high yielding region (top right and bottom right), to the low yielding region (top left and bottom left). Genotypes Tulla and Kulfo were grouped by GGE Biplot in the top right quadrant, Berkume in the bottom right; showing they are the three superior genotypes for TSRTY. Genotype Kabode in the top left, Awassa-83 and Vitae in the bottom left performed below the vertical line showing that they are inferior for TSRTY (Figure, 1). The principle component 1 (PC1) and the second principle component (PC2) extracted from the GGE Biplot accounted for 82.83% and 16.16 (total 98.99%) of the variance respectively (Figure 1). The environments were ranked based on the relative performance of genotypes for TSRTY. The axis for the environment line was drawn that passes through the centroid (biplot origin) and the environment to test for specific acclimatization of genotypes in that environment. In Endayesus, genotypes Kulfo and Tulla were highly acclimatized and Vitae, Awassa and Berkume were inferior below the vertical line (Figure, 2-A). In Fachagama, genotypes Tulla and Kulfo had higher than average yield performance that is above the vertical line and was selected as best performers while Berkume, Awassa-83 and Vitae were inferior. Kabode showed near-average yield (Figure 2-B). In Rarhe, genotypes Berkume Kulfo and Tulla were more acclimatized than Kabode, Vitae and Awassa-83 (inferior) (Figure 2-C).

Evaluating the distance and divergence among the six genotypes based on TSRTY

The BLUPs values for TSRTY were used for

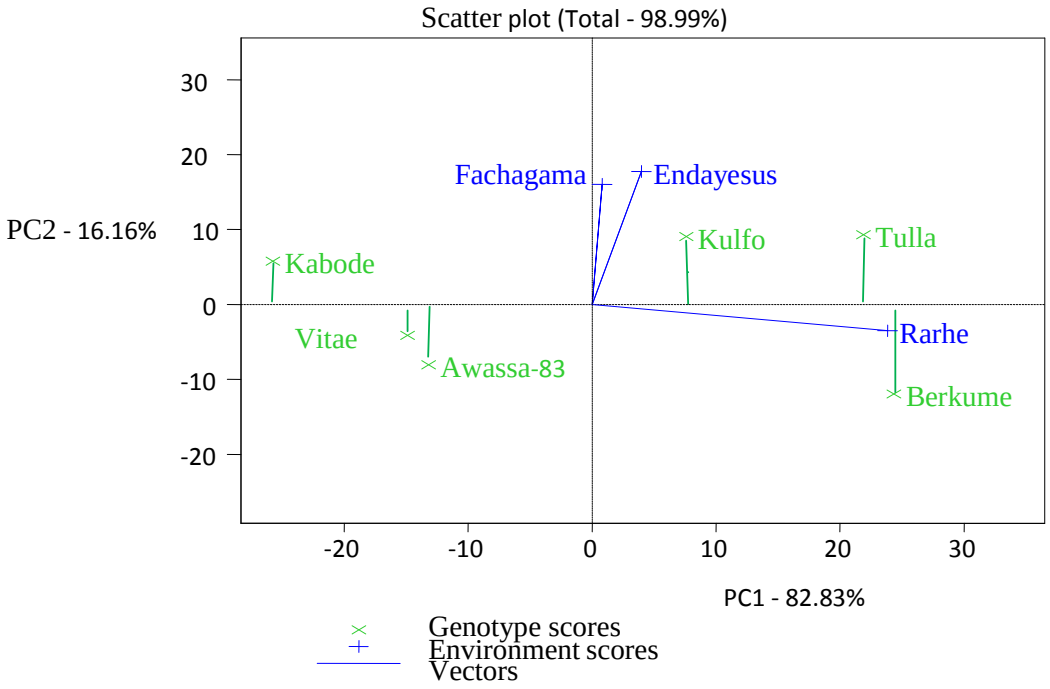

Figure 1. GGE biplot showing genotypes adaptability in the testing environments.

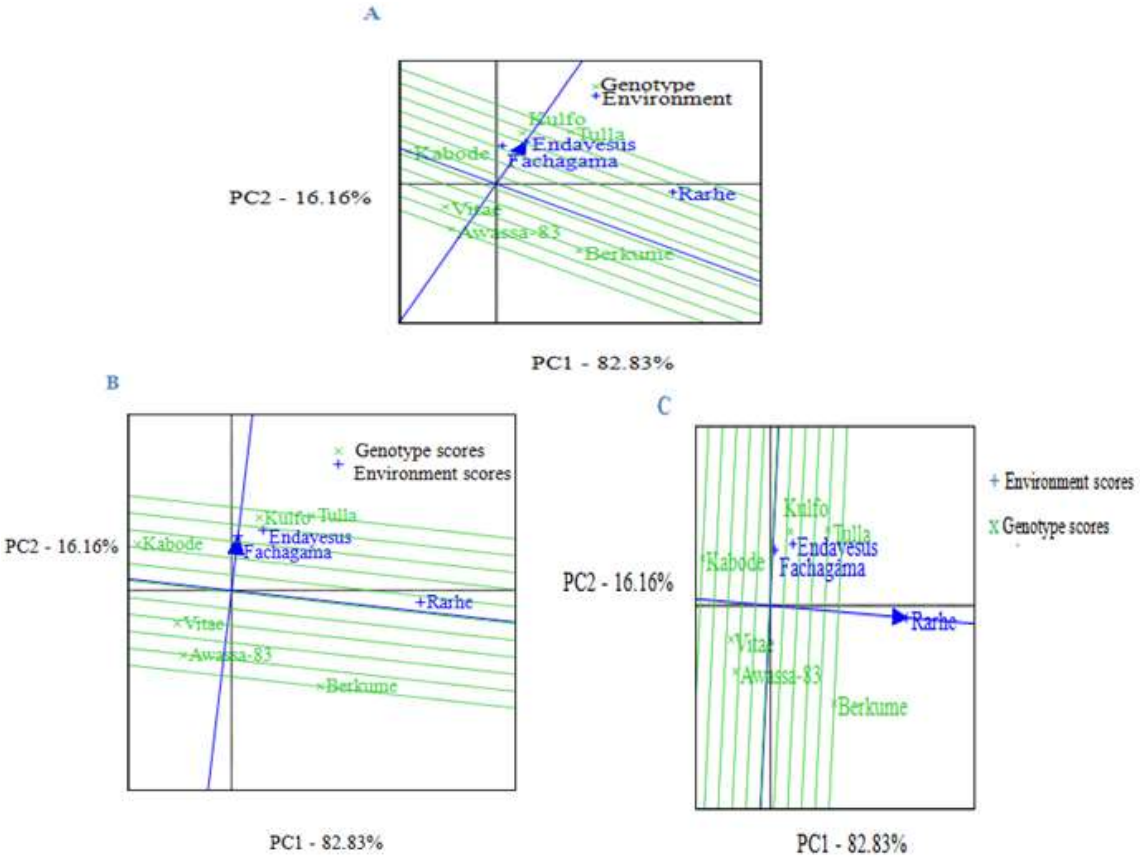

Figure 2. The GGE biplot showing ranking of genotypes in the different agro-ecological environments for TSRTY specific adaptability. A: Ranking of genotypes in environment Endayesus; B: Ranking of genotypes in environment Fachagama; C: Ranking of genotypes in environment Rarhe.

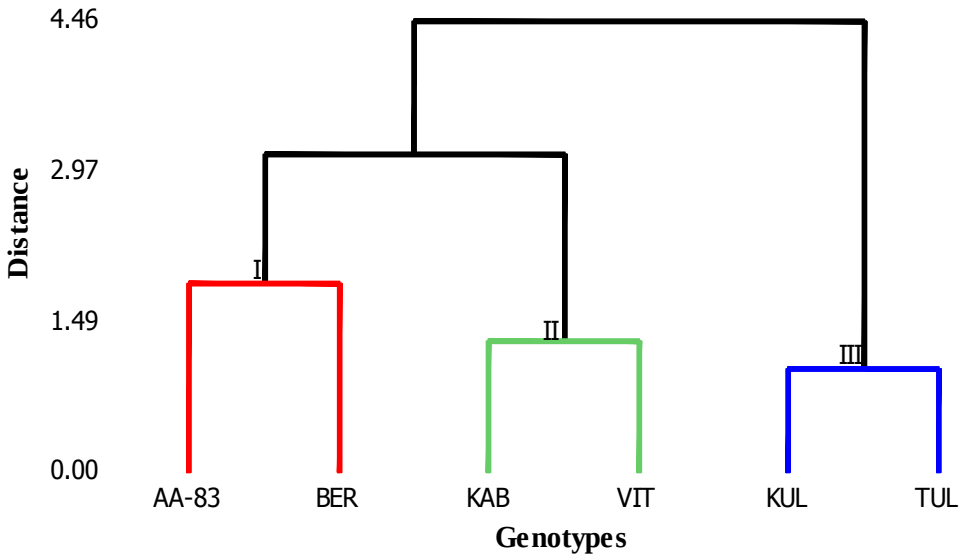

Figure 3. Dendrogram showing Wards linkage using a squared Euclidean distance among the six studied genotypes: AA-83=Awassa-83; BER=Berkume; KAB=Kabode; VIT=Vitae; KUL=Kulfo; TUL=Tulla; I, II, III are clusters' number.

Table 3. Mahalanobis's distance between clusters.

Cluster	I	II	III
I	-	740.68	2291.71
II	740.68	-	583.60
III	2291.71	583.60	-

clustering the genotypes. The Wards linkage strategy using a squared Euclidean distance partitioned the genotypes into three interlinked groups (clusters I, II, III). Genotype Tulla and Kulfo linked up closely to form cluster III, Kabode and Vitae formed cluster II at a very close range meanwhile, Awassa-83 is closely linked to Berkume form cluster I but distantly linked with Vitae and Kabode (Figure 3). The Mahalanobis's distance (D^2) was estimated to investigate divergence among clusters. There was a great distance between clusters I and cluster III (D^2=2291.71) followed by cluster I and cluster II (D^2=740.68). The minimum distance was observed between cluster II and cluster III (D^2=583.60) (Table 3).

DISCUSSION

Evaluating the contributions of the environments main effects, genotypes main effects, and genotype by environment interactions to the formation of the studied traits

The high significant variations (P<0.01) for traits TFB, TSRTY, DTM, INL, VL, RTG, NNPP, DMC, TUSRTY, RTL, TNRTP and HI showed that the formation of these traits are predominantly controlled by the genotypes' main effect, environment main effect and the interactions between the genotypes and the environment in which they were grown. It may also signify that genotypes performed differently across the different environments. These variations may be as a result of the individual genotypes' varied response to the different environmental conditions like temperature, rainfall, soil aeration as well as differences in the genetic components of the individual genotype. The significant difference in the GxE (P<0.01, P<0.05) component for all the studied traits, showed the positive responsiveness of the genotypes to the different environmental conditions in the three agro-ecological zones. Meanwhile, the exceptionally non-significant variation response in the TNRTP and RTL for the environment may indicate that the trait is predominantly controlled by the genotype and the G x E interactions; also, the environment has very negligible influence on genotypes for the formation of these traits (Table 1). This result is in agreement with the findings of Zebider (2015) on six sweetpotato cultivars yield and yield component study in Northern Ethiopia where she observed a non-significant response of storage root tuber length to environment.

The variations in HI may signify how efficient the

selections of sweetpotato genotypes for TSRTY based on HI would be. These differences may be as a result of differences in the genotypes source-sinks relationships and their ability to partition assimilates well to the vital economic parts (Bhagsari and Doyle, 1990). Genotype with high ability to produce carbohydrates and other useful organic compounds and store them in the storage root tubers results in high TSRTY (Table 2). Similar results in the variations of sweetpotato HI (29.0 to 51.4%) was reported by Oriba (2016). Additionally, Bhagsari and Doyle (1990) reported a HI range of 31 to 77% for sweetpotato. Genotypes with high HI and high TSRTY signify the genotype's high ability of assimilate conversion into storage root tubers and efficient storage within the storage root tubers (sinks). Hence, for sweetpotato storage root tuber production for marketing or consumption, genotypes Kulfo and Tulla may be well suited. Meanwhile, for Vine yield production particularly for green vegetables or for animals' feeds, genotypes Tulla, Kulfo and Kabode may be selected. Genotypes with high harvest index had correspondingly high TSRTY (Table 2).

TSRTY is generally affected by the storage root tuber size, and the number of storage root tubers per plant which is influenced by the genetic makeup of the genotype and the environmental factors as well as how the genotypes respond to the environment (Chipungu et al., 1999). Kareem (2013) reported close linkage between TSRTY and VL where he found out that those genotypes with averagely short VL produced high TSRTY. In this study, genotypes Tulla, Kulfo and Berkume had the widest mean storage root tuber girth (RTG) accompanied with the highest number of storage root tubers per plant. These attributes made them best producers of TSRTY in this study, however, their VL were moderately long except for Berkume which was longest, thus contradicting the findings of Kareem (2013) (Table 2). Additionally, lengths of growing periods (LGP) may influence the TSRTY production of a genotype; genotypes with longer days to maturity (DTM) could not perform well enough in environment of shorter LGP as their life reproductive cycle would be cut short while those with correspondingly shorter DTM were able to finish their reproductive cycles before the end of the short growing periods. Rarhe with low mean DTM is where genotypes matured much earlier than their counterparts in Fachagama or Endayesus. Endayesus with the largest DTM signifies late maturity average for all the six studied genotypes. The variations in DTM of the genotypes within and across environments may be as a result of genotype differences in response to specific environmental conditions (Table 2). According to Osiru et al. (2009), maturity days of sweetpotato are longer at high altitude environments than at lower altitudes. In agreement with this finding, genotypes in Endayesus (highland) had relatively longer maturity days compared to their counter parts in Rarhe (lowland) (Table 2). The same observation of delayed maturity for sweetpotato cultivars at higher altitudes was reported by Zebider (2015). Our study showed that genotypes with averagely higher number of DTM (Awassa-83, Vitae, and Kabode) had lower TSRTY and those with low number of DTM (Tulla and Kulfo) had relatively higher TSRTY. This may depict the longer duration the genotypes with high mean DTM take in vegetative growth at the expense of storage root tuber yield production. Meanwhile, those with shorter DTM take shorter period in vegetative growth phase thus are able to accumulate dry matter in the economic storage root tubers resulting into high TSRTY (Table 2). Variations in environmental factors especially rainfall was reported by Hagenimana et al. (1999) to have serious influence on yield formations. Optimum rainfall received during the root initiations and storage root formation in sweetpotato result in high TSRTY. Environment Fachagama had no rain for the first three weeks after planting and also the annual average rainfall received was comparatively lower than Endayesus or Rarhe; this might have led to the corresponding low average TSRTY in this site (Table 2).

The DMC of the genotypes tested were significantly ($P<0.01$) influenced by the genotypes main effects, environment's main effect and the way G x E interacts (Table 1). This agrees with several reports (Shumbusha et al., 2010; Vimala and Hariprakash, 2011; Birhanu, 2013; Zebider, 2015), who recorded variations in the DMC among sweetpotato genotypes and attributed the variations to difference in the growth environmental biotic and abiotic stress, genetic makeup of the genotypes as well as the agronomic practices. Genotypes with high DMC greater than 25% are highly desirable (Mwanga et al., 2009; Rukundo et al., 2013). A DMC range of 18-35% was recommended acceptable for desserts and industrial uses (Belehu, 2003). This study registered all genotypes had desirable DMC range (21.3 to 36.7%) with DMC of genotypes Kabode and Vitae higher than those reported in the previous studies for variety check release for East Africa (Mwanga et al., 2009; Kapinga et al., 2010) (Table 2).

The high TUSRTY in genotypes Tulla, Kulfo and Kabode at Endayesus was due to destructions by the wild animals. This might be because of their ability to mature a bit earlier than the rest of the genotypes or attractiveness of their orange storage root tuber colours or apealingness of the tastes to the animals. Kulfo and Tulla had the highest quantity of TUSRTY in Fachagama due to rotting of the storage root tubers. Most of their large storage root tubers were severely damaged by weevils (Table 2). This severity in damage might have been aggravated by high temperature accompanied by low soil moisture, as well as low resistance in the genotypes to avoid or resist attacks caused by environmental biotic and abiotic stress. Tulla and Berkume in Rarhe had the highest TUSTRY due to overweight that is to say most of the tubers weighed above 2 kg. Poor handling during harvesting caused

mechanical damages like cuts or breakages on the storage root tubers which lowered their market values (Table 2). Similarly, Zebider (2015) reported very high quantity of total unmarketable root yield in sweetpotato genotypes planted in Fachagama and attributed it to extremely high soil temperature. The significant variations in the VL and INL across the environments are also consistent with these reports (Rahman et al., 2013; Zebider, 2015). These differences may be due to the differences in the genotypes and environment and G x E interactions (Table 2).

Acclimatization of the genotypes to the three agro-ecological environments

From the agronomic point of view, genotype's individual differences to acclimatize to the different environmental conditions within the required shortest time possible to produce optimum yield and yield components are contributors to the variations in yield and yield components performances within as well as among the genotypes in the different environments (Tables 1 and 2). Crops perform better in environment where they are acclimatized to and this may be wide or specific acclimatization. A specific acclimatization occurs when a genotype is able to give a high mean yield at a definite environment(s) or some environments but not another. The wide acclimatization is characterized by a genotype producing high mean yield in multi-environment of varying soils and environmental factors (Grüneberg et al., 2005; Yan and Tinker, 2006; Adebola et al., 2013). Relative to these, genotypes in this study exhibited both wide and specific acclimatization (Table 2, Figure 1). Tulla and Kulfo depicted wide acclimatization for TSTRY and other yield component traits while Berkume showed a specific acclimatization to environment Rarhe. This is because Berkume was able to exhibit high (above average) TSRTY in Rarhe only and below average TSRTY performance in Endayesus and Fachagama. Meanwhile, Tulla and Kulfo consistently maintained an above average TSRTY performance in all environments (Table 2 and Figure 2-A, B and C). Similar findings on sweetpotato genotypes variant yield and yield component traits performance were reported by Birhanu (2013) and Zebider (2015). This may show that genotypes Tulla and Kulfo can be grown in variant agro-ecological conditions and because they have moderately low maturity days, it can be grown three times a year as insurance against both deep and hidden hunger. Meanwhile, Berkume can be grown at moist lowlands once or twice a year (Table 2). Generally, Environment Rarhe had the highest mean TSRTY for the genotypes and Fachagama tailed meaning that Rarhe was the most suitable site for sweetpotato production for both storage root tubers and vines. This could be due to the suitable environmental attributes of Rarhe in comparison to other sites (Table 2). This finding is in agreement with findings of Zebider (2015), however, the study contradicted Birhanu's findings where Rarhe was the least performer in storage tuber root yields (Birhanu, 2013), showing how change in seasons could influence on the environments potential for sweetpotato production. Genotype Vitae (16.6 t/ha) and Kabode (16.9 t/ha) were able to maintain low yield across all the growing environments (Table 2 and Figures 1 and 2). However, their average yield recorded in this study is within the variety release check range for East Africa (Mwanga et al., 2009; Kapinga et al., 2010). This could be because these genotypes have long DTM and the environment used for testing them have short LGP and may produce better TSRTY when augmented with supplementary irrigation. Genotypes which exhibited luxuriant vegetative growth showed their ability to acclimatize to the growing environmental conditions and were able to put on optimum branches, leaves, number of nodes, internode lengths and vine length which collectively gave rise to the TFB yield recorded in this study. It may also signify the genotype's ability to mobilize assimilates for vegetative growth which is greatly affected by the genetic make-up of each genotype and how each genotype interacted with the environment (Table 2). Genotype Awassa-83 had the highest mean TFB in both Endayesus and Fachagama which proved its ability to convert assimilates into vegetative parts at the expense of storage root tuber bulking, thus can be bred for vines harvestable for green vegetables, feeding livestock or marketing (Tewe et al., 2003; Islam, 2006; Ahmed et al., 2012). Meanwhile, genotype Tulla and Berkume registered high TFB yield in environment Rarhe showing a striking balance in apportioning assimilates between vegetative and storage root tuber production and at the same time may depict their high acclimatization to Rarhe. Thus, Tulla showed wide acclimatization and Berkume was specific acclimatized to environment (Table 2 and Figures 1, 2-A, B and C). However, the best three overall TFB production was recorded in genotypes Kulfo (31.1 t/ha), Tulla (30.4 t/ha) and Kabode (29.4 t/ha) (Table 2). Because these three genotypes (Kulfo, Tulla and Kabode) have purple leaf colorations, it may symbolize their richness in anthocyanin and polyphenolic compounds (Zhao et al., 2007; Zhu et al., 2010). Both the soft leaves and storage root tubers can be consumed as food base approach to fight malnutrition and other oxidative health disorders (Zhao et al., 2007; Yada et al., 2010; Zhu et al., 2010).

The clustering of genotypes is useful in determining how related they are for breeding program. The distance among clusters attested to the distinctness of the sweetpotato genotypes grouped into different clusters. The maximum distance between Cluster I and III may signify the proof of variations among the genotypes studied. In the dry high/lowlands with short LGP and terminal drought, Cluster III members will be good genotypes since they are early maturing with high TSRTY.

Crossing Cluster II with either Cluster I or III members would give rise to transgressive segregants for most of the desired important sweetpotato traits. This may increase the superior genotypes having high TSRTY, DMC and other yield component traits (Figure 3 and Tables 2 and 3).

Conclusions

The results obtained in this study show significant variations in the TFB, TUSRTY, TMSRTY, TSRTY, DMC, DTM, INL, VL, RTG, RTL, and NNPP, HI, which influenced acclimatization of the genotypes in the trial environments. Genotypes with high HI were superior producers of TSRTY, TFB, with high NNPP thus well acclimatized to the farmers field conditions in the studied agro-ecologies and vice versa. Genotypes Tulla and Kulfo have highly wide acclimatization to the trial environments, as opposed to Berkume which showed specific acclimatization to Rarhe only. This study also observed high significant difference in the environments' main effect in the formation of yield and yield components traits in sweetpotato which brought about variations in number of days to maturity of the genotypes in the different agro-ecologies. Sweetpotato genotypes at lower altitudes matured earlier than those at higher altitudes. G x E interactions also contributed much in determining genotypes adaptability proved by the GGE biplot. Crossbreeding Cluster II (Kabode and Vitae) which have higher than check variety release range DMC and within range TSRTY with Cluster III or Cluster I genotypes may be explored to produce transgressive segregants rich in desired orange fleshed sweetpotato yield and yield component traits for Ethiopia as proved by Mahalanobis's distance algorism. Genotypes Kulfo, Tulla and Kabode were promising producers of TFB with wide acclimatization for vine yield across environments that can be utilized by farmers for the dual production of storage root tubers and vines for green vegetables, marketing or feeding livestock.

CONFLICT OF INTERESTS

The author has not declared any conflict of interests.

ACKNOWLEDGEMENT

The author appreciates the financial support from the NORHED sweetpotato project and INTRA-ACP CSAA Project.

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