# Original Scientific paper 10.7251/AGRENG2001005L UDC 633.49(63) META-ANALYSES OF SWEETPOTATO (*IPOMOEA BATATAS L. LAM*) STABILITY PERFORMANCE IN DIFFERENT AGRO-ECOLOGIES OF THE TIGRAY REGION, ETHIOPIA

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#### ABSTRACT

The study aimed at evaluating the influence of environment on sweetpotato stability and identifying superior genotype(s) with high yield stability in the farmers' field conditions. Six sweetpotato genotypes were evaluated for two years in 'meher' season (July- December), 2014 and 2016; four of the six genotypes were assessed for three years in the 'meher' season, 2012, 2014, and 2016. Planting was done in three replications in RCBD in three unique agro-ecologies: Endayesus-dry highland, Fachagama-dry lowland, Rarhe-moist lowland. Genotypes genetic merits were predicted using BLUP. The AMMI and GGE were used to test the genotypes stability. The ANOVA for AMMI model showed high significant difference (P < 0.01) for genotypes, environments, seasons, and the interactions. Environment (41.67%) and the genotype main effect (35.71%) contributed largely to the cumulative variance for three years testing of four genotypes and two years testing of six genotypes, respectively. Berkume (42.44 t/ha), Tulla (33.92 t/ha) and Kulfo (33.67 t/ha) were superior for total storage root tuber yield (TTRY). Both the AMMI and GGE biplot predicted Tulla and Kulfo as ideal genotypes with dynamic stability; Berkume with static stability to Rarhe. The environment main effect had significant influence in determining how genotypes expressed their genetic potentials and stability as shown by the AMMI model and GGE biplot. The AMMI model partitioned the studied agro-ecologies of the Tigray region into two mega sweetpotato growing environments; the dry high/lowland in one environment and the moist lowland in another, completely different, but with high potentials for sweetpotato production.

Key words: Stability, Agro-ecologies, Yield, Sweetpotato, Superior.

### **INTRODUCTION**

Sweetpotato (Ipomoea batatas L. Lam) is the most important storage root tuber food security resilient crop in Sub Saharan Africa and Asia grown in diverse soils conditions with low input requirements (Low, 1995; FAOSTAT, 2013). The crop is widely adopted in Africa and Asia as an important root crop with tremendous nutritional, health, industrial and economic benefits (Islam, 2006; Kapinga et al., 2010; Zhu et al., 2010). However, in Ethiopia, it's newly introduced and its production, adoption and consumption are very low especially in the Tigray region (CSA, 2013). Sweetpotato is grown in small scale for livestock feeds majorly although in the Southern Nations Nationalities Peoples Region State, and Oromia, it forms a staple diet of the community (Fekadu et al., 2015). Tigray region prevails in malnutrition and deep hunger above the country's level with at least 42% of the total children's population (<5 years) malnourished. Both hidden and deep hunger intensifies with recurring drought in this region (CSA, 2015). Vitamin A supplementary high dose capsules reached only 79% leaving about 21% of the children's population uncovered at all (CSA, 2015; WHO, 2015). Sweetpotato can be use to answer the dire need of food and nutritional security in the Tigray region and Ethiopia at whole. Sweetpotato tops (soft stems and leaves) and storage root tubers (SRT) are edible and nutritious (Islam, 2006; Tewe et al., 2003). The  $\alpha$ xanthophylls and lutein in it protects the eyes against night blindness, meanwhile the Polyphenols, carotenoids, vitamins and minerals are strong anti-oxidants, antimutagens, anti inflammations, anti hypertension, anti diabetics, and reduces liver, kidney damage and cardiac arrest (Islam, 2006; Zhu et al., 2010; Matsui et al., 2004). Many attempts have been made to make sweetpotato familiar in the Tigray region through free distribution of quality high yielding cultivars to the farmers but the production and consumption coverage has not improved much (CIP, 2000; CSA, 2013). Even the highest yielding genotypes released to the farmers by the research centers were not giving high SRT yield in the farmers' fields (Assefa et al., 2007). Sweetpotato average yield in Tigray ranges between 0-4 t/ha in the farmers' field far below the mean yield range at research centers of between 9-31 t/ha (FAOSTAT, 2011). Thus there was urgent need to investigate much on the stability of the quality sweetpotato genotypes to the farmers' field conditions in the different agro-ecologies of the Tigray region to come-up with genotypes with high stability in multi environment with better yield returns.

### MATERIALS AND METHODS

Three unique agro-ecological sites were used for the experiment; Endayesus (dry highland) found at an altitude of 2223 meters above sea-level (masl), characterized by Silty Clay soil, minimum and maximum temperature of 12.5°C 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°C 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  $15.0^{\circ}$ C and  $30.9^{\circ}$ C located at an altitude of 1460 masl.

The study consisted of four orange fleshed (Tulla, Kulfo, Kabode and Vitae) and two white fleshed (Awassa-83 and Berkume) sweetpotato genotypes; two released check varieties (Tulla and Kulfo) and four germplasm sourced from Awassa Research center (AwARC), Ethiopia. Four of the genotypes were first planted in the "Meher" season (July- December) 2012. All the six genotypes were evaluated in the "meher season of 2014 and 2016 respectively. 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) with three replications having 1m in between each block. Each block received a treatment of each genotype, 30 vines cut at 30 cm long. All other basic agronomic practices were done timely including supplementary irrigation using furrow application once a week (September to November). At harvest, data were collected on SRT yield traits. The TTRY was calculated using the formula;  $TTRY = \frac{TMTY\left(\frac{r}{ha}\right) + TUTY\left(\frac{r}{ha}\right)}{TOTAT HET Area (m^2)}$  Where; TTRY= total storage root tuber

yield; TMTY= total marketable storage root tuber yield; TUTY= total unmarketable storage root tuber yield; t/ha= tons per hectare;  $m^2$ = meter square. The TTRY data were analysed using the general linear model of statistical analysis system (SAS) (SAS, 1995). The genotypes and environments' mean coefficient of variations, mean standard errors and mean least significance difference were accounted for. The environment, seasons and replication were considered as random factor source of variations, and the genotypes were considered as a fixed factor to be tested by the different environments and seasons. The genotypes genetic merit was estimated by BLUPs and the mean was subjected to the Additive Main effects and Multiplicative interactions (AMMI) to test the genotype by environment interactions effects, using Genstat 14<sup>th</sup> version (Payne et al., 2011). The AMMI model equation was:

Yij= $\mu$  + Gij + Ej + $\sum_{k=1}^{n} \lambda kaikyjk$  + eij. Where; Yij is the yield of the i<sup>th</sup>

genotype in the j<sup>th</sup> environment;  $\mu$  is the grand mean; Gi and Ej are the genotype and environment deviations from the grand mean, respectively;  $\lambda k$  is the singular value of the k<sup>th</sup> axis in the principle component analysis;  $\alpha i k$  and  $\gamma j k$  are the genotype and environment principal component scores for axis k; n is the number of principle components retained in the model; eij is the error term (Guach, 2008). Genotypes Main effects, Genotype by Environment Interactions (GGE) biplot were used to find which genotype won where. 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).

### **RESULTS AND DISCUSSION**

Combined Stability Analysis of Four Common Genotypes Performance for TTRY Trait across Environments in Three Years (2012, 2014, and 2016)

Generally, the environment grand mean yield of these genotypes (Kulfo, Tulla, Kabode, and vitae) showed great variations. The highest annual TTRY mean was obtained in the year 2014 (137.58 t/ha) followed distantly by 2016 (97.66 t/ha) and 2012 (80.89 t/ha) least. Fachagama (30.85 t/ha) and Rarhe (47.50 t/ha and 33.81t/ha) gave high annual TTRY in the year 2012, 2014 and 2016 respectively and the lowest mean TTRY was observed in Rarhe (13.53 t/ha), Endayesus (24.20 t/ha) and Fachagama (15.66 t/ha) in the year 2012, 2014, and 2016 respectively (Table 1). This may signify how change in seasons affected genotypes' TTRY performance and stability in multi-environments over time. This finding corresponded to similar studies done by Mcharo et al (2013). Vitae (16.40 t/ha) and Kabode (16.85 t/ha) persistently maintained low yield in all the environments in the three years (Table 1), however, their average yield recorded in this study is still within the Variety release check yield range (16.0 t/ha to 34 t/ha) reported (Kapinga et al., 2010; Mwanga et al., 2009). This could be because these genotypes comparatively have longer days to maturity and the testing environment had short growing periods.

The combined ANOVA for AMMI model, showed a highly significant variation (P<0.01) for genotypes, environment and seasons main effects as well as genotype x environment x seasons interactions. Environment (41.67%), contributed very highly to the cumulative variance, followed by interactions (39.94%) and genotypes main effects (17.97%) (Table 2). This may signify how environment dictated on the genotypes expressions of their genetic potentials which complicated the selection process of these genotypes. It also showed how change in seasons over time affected the SRT yield formation in sweetpotato in the same environment. The significant interactions effect may imply that genotype interact differently with seasons and environment which caused variations in the TTRY across environments over time. This is in agreement with similar studies (Adebola et al., 2013; Mcharo et al., 2013), who found variations in root yield stability of sweetpotato cultivars across environments. The model partitioned the interactions into three significant Interaction Principle Component Analysis axes (IPCA) in the order of their relevance that is IPCA1 explained 75.76%, IPCA2 18.86% and IPCA3 5.38% of the variance. The percentage contribution of each IPCA to the overall variance decreased with increase in the number of IPCA. All the IPCAs were statistically highly significant (P<0.01) (Table 2).

Total storage root tuber yield (t/ha)										
Seasons	2012			2014			2016			
Genotypes/E nvironment	Enday esus	Fachaga ma	Rarh e	Enday esus	Fachag ama	Rarhe	Enday esus	Facha gama	Rarhe	Mean
Kabode	7.00	18.83	5.43	16.53	20.39	36.68	21.13	18.17	7.53	16.03
Kulfo	24.44	43.49	13.71	34.09	65.68	63.21	30.58	19.69	39.74	33.67
Tulla	24.63	45.55	17.87	26.53	33.69	55.98	29.44	24.49	54.26	33.92
Vitae	9.08	15.54	17.09	13.56	15.57	30.83	13.29	14.65	20.00	16.40
Awassa-83				14.85	21.52	28.00	13.36	9.04	21.89	18.11
Berkume				39.63	60.82	70.32	16.49	7.93	59.46	42.44
Site means	16.29	30.85	13.53	24.20	36.28	47.50	20.72	15.66	33.81	26.76

# Table 1. The overall blups prediction of the TTRY for the six genotypes performance for three years

 Table 2. The AMMI analysis of TTRY for the four genotypes over three environments for three years production

			Total Variation	G x E	
SOV	df	SS	explained (%)	explained (%)	MS
Total	107	26083			243.8
Genotypes	3	4688	17.97		1562.7**
Environments	8	10869	41.67		452.9**
seasons	18	55	0.21		3.1**
Interactions	24	10417	39.94		1302.2**
IPCA1	10	9323		75.76	932.3**
IPCA2	8	1435		18.86	179.3**
IPCA3	6	111		5.38	18.5**
Error	72	109			1.5

SOV= Source of variations; df= Degree of Freedom; SS= Sum of Squares; MS= Mean Square; IPCA= Interaction Principle Component Analysis; \*\* highly significant at probability (P<0.01).

To identify the ideal genotype(s), the average–environment coordination (AEC) ordinate graph was plotted using the genotypes' and environments' mean scores. Tulla and Kulfo aligned themselves close to the centre of the concentric circles marked with AEC dot, considered to be a point of total stability in the positive direction (Figure 1). Thus Kulfo and Tulla were the most desired genotypes. This signified that Kulfo and Tulla maintained high stability and mean yield performance in all the tested agro-ecologies and seasons (Yan and Tinka, 2006).

## Evaluation of the Six Genotype Performance for TTRY Stability in the Year 2014 and 2016 using AMMI

The combined ANOVA for the AMMI model showed highly significant (P<0.01) difference among genotypes, environment, and genotype x environment x seasons interactions meanwhile, replication was statistically non significant for TTRY trait. The largest contribution to cumulative variance was genotypes (35.71%). The interactions were separated into two IPCA in their order of importance; both IPCA1 and IPCA2 were highly significant (P<0.01) and IPCA1 accounted for 92.10% meanwhile, IPCA2 contributed 7.90% of the total variations due to interactions sum of squares (Table 3). This may show that genotypes exhibited different stability response in the testing environment in the two years trials.



Figure 1. The AEC view to rank genotypes relative to an ideal genotype for the year 2012, 2014 and 2016.

Figure 2. The AMMI Biplot showing Mega Growing Environments

R-14=Rarhe 2014; R-16= Rarhe 2016; F-14=Fachagama 2014; F-16= Fachagama 2016; E-14=Endayesus 2014; E-16= Endayesus 2016.

			Total	Variation	G x E explained	
SOV	df	SS	explained (%)		(%)	MS
	5	1255				
Total	7	3				243.8 896.6*
Genotypes	5	4483	35.71			*
Environme	_					826.3*
nts	5	4132	32.92			*
Replication						193.6
S	6	1162	9.26			ns
Interaction	2					
S	5	2776	22.11			111**
						222.7*
IPCA1	9	2004			92.10	*
IPCA2	7	634			7.90	90.5**
Error	6	138				15.3

Table 3. ANOVA for AMMI model for genotypes interactions in the year 2014 and 2016

SOV= Source of variations; df= Degree of Freedom; SS= Sum of Squares; MS= Mean Square.

When the IPCA1 AMMI biplot graph of genotype against environment scores was plotted, genotypes main effect (PC1) and G x E interactions (PC2) accounted for 92.10% and 7.90 (total 98.00%) of the variance respectively (figure 2).AMMI model grouped the agro-ecological environments into two mega sweetpotato growing environments with Fachagama and Endayesus falling within one environment and Rarhe in another growing environment. The angle vertex between Fachagama and Endayesus was acute angle showing positive correlations between them. Nevertheless, the angle between either Fachagama/Endayesus with Rarhe was obtuse that implied their low correlations (Figure 2). This may also show that Rarhe comparatively had large G x E contribution to the cumulative variance (Yan and Tinka, 2006).

Ranking of the genotypes for TTRY comparative to the ideal genotype singled out Kulfo as the most desirable genotype followed by Tulla then Berkume surrounding the ideal genotype. Kabode, Vitae and Awassa-83 located below the vertical line and were the undesirable genotypes; they performed below the vertical line (Figure 3). This signified that Kabode, Vitae and Awassa-83 were very unstable in the testing environment (Yan and Tinka, 2006).





Figure 3. The AEC view to rank genotypes relative to an ideal genotype for the year 2014 and 2016

Figure 4. GGE Biplot showing the Genotype which Won where in TTRY Trait in Seasons 2014 and 2016

R-14=Rarhe 2014; R-16= Rarhe 2016; F-14=Fachagama 2014; F-16= Fachagama 2016; E-14=Endayesus 2014; E-16= Endayesus 2016.

Further analysis of the three high yielding genotypes (Kulfo, Tulla, and Berkume) specifically for TTRY was done using which-won-where function which explained 100% of the variations due to genotype main effect and G x E interactions effect. PC1 contributed 64.95% and PC2 contributed 35.05% (total 100%) cumulative variance. Kulfo won in Fachagama in 2014, 2016, and Endayesus in 2016. Meanwhile, Berkume won in Rarhe in the year 2014 and 2016, and Endayesus in 2014 respectively. Much as Tulla performed below Kulfo and Berkume in these testing environments, it showed more dynamic stability for TTRY (Figure 4). This finding is in agreement with findings from Yan and Tinka (2006).

### CONCLUSIONS

This study observed high significant difference in the environment's main effect, genotype's main effects, and genotypes by environment by season's interactions in the formation of storage root tuber yield stability in sweetpotato genotypes across the different agro-ecologies of the studied areas. Environment had a significant influence on sweetpotato genotypes stability and the way in which each genotype unleashed its genetic potentials in the different environments ultimately. The study also observed that the tested agro-ecologies of the Tigray region have two mega growing environments for sweetpotato production; the dry highlands/lowlands represented by Endayesus, and Fachagama in environment I and the moist lowlands represented by Rarhe in environment II which are completely different and thus need different genotypes for better TTRY production. The dry highlands/lowlands, preferably short maturing genotypes Tulla and Kulfo had dynamic stability and can be grown in any agro-ecology as opposed to Berkume which showed static stability to Rarhe (moist lowland) over time. There is hope that these

genotypes Kabode and Vitae when grown in environment with long growing period of at least 140 days may do well. Rarhe depicted high variability in the expression of TTRY trait making it more representative and discriminatory.

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