Orange-fleshed sweet potato [*Ipomoea batatas* (L.) Lam] genotype by environment interaction for yield and yield components and SPVD resistance under arid and semi-arid climate of northern Ethiopia

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ABSTRACT

Worldwide, sweet potato *(Ipomoea batatas* (L.) Lam) ranks the sixth most important crop valued for food security, income, and nutritious diet for poor farming communities. Despite its importance, there is lack of information and knowledge to introduce the crop to Afar region where malnourishment is high. Six orange-fleshed sweet potato genotypes (Amelia, Erica, Gloria,Ininda, Kulfo, and Melinda were evaluated for sweet potato viral disease (SPVD), yield and yield components in three contrasting locations, namely Aba'ala, Mekelle 1, and Mekelle 2 using a Randomized Complete Block Design to produce variance components. Joint regression, and additive main effects and multiplicative interactions were used to test the Genotype × Location Interactions (GEI). Means for significant traits were separated by Least Significant Difference ($p<0.05$). Results showed ample genetic variability for total tuberous yield (TTY), and SPVD resistance. Genotypes Ininda, Gloria, Amelia, and Kulfo were superior for TTY with high SPVD resistance. Aba'ala was a hotspot for SPVD, Mekelle 2 was with low SPVD and recorded a high mean TTY. Amelia and Kulfo exhibited static stability, Ininda and Gloria displayed dynamic stability, high harvest index, and fresh vine yield, and were recommended for further stability investigations. The information generated in this study may be useful as preliminary data however, the experiment has to be repeated for practical conclusions and recommendation of stable varieties for the studied agro-climatic zones.

Keywords: Orange-fleshed sweet potato genotypes; SPVD; Genotypes × environment interaction; Afar region; Arid and semi-arid agro-climate
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INTRODUCTION

Sweet potato (*Ipomoea batatas* L. Lam) ranked the world's third most important root crop after potato and cassava (FAOSTAT, 2018). The global production of sweet potato is dominated by Asian countries with China alone producing 53,009,000 metric tons (MT). In Africa, Malawi leads with 5,669,000 MT, followed by Nigeria (4,030,000 MT), Tanzania (3,744,000 MT), Uganda (1,956,000 MT), and Ethiopia (1,835,000 MT) (FAOSTAT, 2018). The Orange-fleshed sweet potato varieties are at its introductory stage in Ethiopia, the white-fleshed or cream-fleshed sweet potato cultivars are widely grown in Oromia regional state and Sidama, Gomo Gofa, and Wolayta. It is also grown on a very small scale mainly for food and animal feeds in Benishangul Gumuz, Gambella, Harari, and Tigray (Fekadu, 2019; CSA, 2018; CSA, 2011). The total land coverage under sweet potato production in Ethiopia is estimated to be 53,499 hectares with a production output of 33.4 tons per hectare in the farmers' field and up to 68 tons per hectare at the research centers (Fekadu, 2019; Zebyder, 2016).

Sweet potato is a rich edible carbohydrate crop, efficient in fighting malnutrition, and economic insecurity among the marginalized community in developing countries (Cai *et al*., 2004; Islam, 2006; Mwanga *et al*., 2009; Zhu *et al*., 2010). The crop also plays a role in improving the income of the producers. The root tubers are rich in β-carotene- a precursor of vitamin A, and its leaves are rich in proteins. The roots also contain vitamins C, B complex, and E as well as potassium, phosphorus, calcium, and iron. Sweet potato has a low glycemic index, this aids in controlling blood sugar levels. Additionally, the crop is known to control heart diseases, arthritis, stomach ulcers, bronchitis, vision impairments, skin diseases, asthma, and inflammations (Rios-Romero *et al*., 2021; Fekadu *et al*., 2017; Zhu *et al*., 2010). Despite all these important variant uses of sweet potato, the crop is still produced and consumed in a much lower scale in Sub Saharan Africa compared to China (FAOSTAT, 2018).

Sweet potato production and consumption in Sub Saharan Africa is constrained by pests and diseases among other factors. At least twenty viral diseases of sweet potatoes were confirmed and the most common of all being sweet potato virus disease (SPVD) and sweet potato chlorotic stunt virus (SPCSV) in Eastern Africa. Sweet potato blight is another disease that constrains sweet potato production (Gibson *et al*, 1998; Gibson & Aritua, 2002; Abraham, 2010). In Ethiopia, sweet potato production is limited by a poor extension system that doesn't encourage the production of root crops, market and postharvest handling problems, frequent drought in production areas, diseases and pests especially weevils and moths, and lack of knowledge on variant uses of sweet potatoes by the indigenous community (Fekadu, 2019; Fekadu *et al*., 2015). Tewodros *et al*. (2011), recorded high viral infection of sweet potato at lower altitudes in Southern Ethiopia. Sweet potato feathery mottle virus (SPFMV),

SPCSV, and sweet potato virus 2 (SPV2) were the most abundant with 100% viral incidence recorded in Wonde Genet and Hawassa in Ethiopia (Adane, 2010). Sweet potato virus infections cause a loss in both quality and quantity yield of storage tuberous roots and vines produced (Mwanga *et al*., 2001; Tefera *et al*., 2013). Sweet potato yield and yield components are important crop parameters in screening germplasm for adaptability and stability to an environment. Most of the orange-fleshed sweet potato genotypes have a very low resistance to drought, weevil, and diseases with low vine production which may leave the farmers with no planting materials after serious dry spells or infestations (Andrade *et al*., 2004). Identification of sweet potato cultivars with high adaptability and agronomical performance is essential in developing improved genotypes for better yield performance. Sweet potato variety improvement programs focus majorly on resistance to pests and diseases and high yield possibilities. Little attention is given to intermittent fluctuations over a range of marginal environments (Mwanga *et al*., 2001). SPVD and Alternaria blight have a negative correlation with yield traits; in this case selection for improved yield and high disease resistance is possible in one germplasm (Yada *et al*., 2011). Selection and breeding for resistance to virus remain the most affordable methods of viral diseases control and yield booster to small-scale farmers. However, its competence depends on clear knowledge of yield and yield component traits interactions (Ngailo *et al*., 2013). In Ethiopia, there is a dearth of information regarding on-spot orange-fleshed sweet potato genotypes by environment interactions or SPVD resistance. So far, there has been no sweet potato growth and production trials in the Afar region in Northern Ethiopia where drought, famine and malnutrition is high. Also, we couldn't find information regarding orange-fleshed sweet potato genotypes resistance to SPVD in Northern Ethiopia. The study, therefore, evaluated the orange-fleshed sweet potato germplasm for yield and yield component traits and SPVD resistance for varietal selections of superior genotypes in the farmers' field condition that can be used for the introduction of orange fleshed sweet potato in the arid agro-climatic zones (Afar region) and other parts of semi-arid agro-climatic zones of Tigray region where sweet potato is not in production. Also, these identified superior genotypes shall be used in human or animal diet to improve food security and reduce/minimize malnutrition in the arid and semi-arid areas in Northern Ethiopia. With achieved sweet potato adoption and sustainable nutrition and yield production, it shall be easier to influence the policymakers to adopt sweet potato as one of the major food and nutrition security crops in the arid and semi-arid agro-climatic regions of Northern Ethiopia.

MATERIALS AND METHODS

Description of the study sites

The study was done in three unique locations found in two different agro-climatic zones of Northern Ethiopia, namely Aba'ala (arid agro-climate), Mekelle-1 and mekelle-2 (semi-arid agro-climate). Aba'ala is located on lowland altitude whereas, Mekelle-1 and Mekelle-2 are located on a higher altitude. The topographic location and description of the study locations are shown in Figure 1, and Table 1.

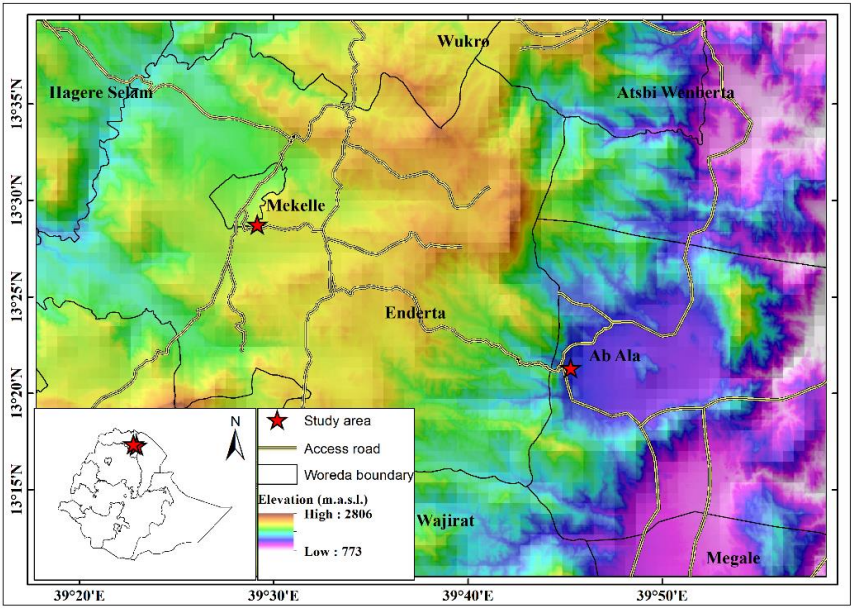

Figure 1. Study area locations

Table 1. Description of the study sites

Locations	Aba'ala	Mekelle 1	Mekelle 2
Latitude ^{o}N	13^{o} 21'19'	13^{o}28'46'	13^{o}28'46'
Longitude ^{o}E	39^{o} 45'17'	39^{o}29'09'	39^{o}29'09'
Altitude (m.a.s.l.)	1441	2223	2223
Annual rainfall (mm)	393.65	406.28	525.68
Minimum temperature (^{o}C)	18.6	13.09	12.17
Maximum temperature (^{o}C)	34.0	25.31	24.39
Climate type	Arid climate	Semi-arid	Semi-arid
Soil type	Silty loam	Silty clay	Silty clay

Description of experimental materials

The plant population used in this study consisted of six orange-fleshed sweet potato cultivars free from virus, diseases and pests; obtained from Tigray Agricultural Research Institute (TARI). These sweet potato genotypes were Melinda, Gloria, Erica, Ininda, Kulfo, and Amelia. Apart from Kulfo (standard-check), the rest of the genotypes were sourced from Mozambique by TARI for evaluations in Ethiopia (Table 2).

Table 2. The sweet potato genotypes used and their characteristics.

ID	Variety	Skin colour	Flesh colour	Status in Ethiopia
1	Amelia	Pale purple	Deep orange	Not yet released
2	Gloria	Cream	Deep orange	Not yet released
3	Ininda	Pink	Deep orange	Not yet released
4	Kulfo	Cream	Intermediate orange	Released in Awassa Research Center (ARC) (2005)
5	Melinda	Cream	Light orange	Not yet released
6	Erica	Pink	Orange	Not yet released

Source: Adapted from Tumwegamire *et al*., 2014; Birhanu, 2013.

Planting materials preparation and planting design

The planting sites were cultivated twice at an interval of three weeks using a disc plough for deep seedbed preparation. Ridging followed secondary tillage three weeks later. This was to allow for the complete decomposition of the organic materials. Planting materials were cut from the apical shoots at a length of 20 cm long with 6 to 10 nodes. Planting was done on the ridges at a spacing of 0.3 m x 1.0 m using a Randomized Complete Block Design (RCBD) with three replications. The space between each plot was 0.5 m, and 1 m in-between blocks. The total trial area in each location was approximately 225.5 m^2. The experiment was left to depend on the natural environmental conditions for disease infestations and moisture. However, supplementary irrigation was done twice a week from the very date of planting until the fourteenth day after planting to support the crop establishment in the arid agro-climatic location (Aba'ala). On the other hand, in the semi-arid locations, no supplementary irrigation was provided. Mechanical weed management using hand hoes was done promptly for three months before full sweet potato canopy cover the soil surface. The genotypes were evaluated for two years 2019 and 2020; however, the 2^{nd} year's total tuberous yield (TTY) harvest of arid agro-climate location was lost due to an escalated war.

Data collection

Data on sweet potato yield and yield components, and SPVD severity and incidences before and after harvest respectively were collected. This was done randomly from the middle part of each plot in each replication block, to avoid border effects. Five plants were randomly picked to form a study sample population from which all the yield (tuberous yield) and yield components such as tuberous length, tuberous width, vine length, fresh vine yield weight data were taken. However, for stand count establishment and SPVD incidences and severity all the plant stems alive in the whole plots were considered.

Evaluation of SPVD incidences and severity

Genotype SPVD resistance-scoring on the severity of damage was done using the observable disease symptoms on leaves, stems and branches of the sweet potato crop plants twice during the growing cycles. Physical eye observations were made 42 and 120 days after planting date. SPVD severity was then scored 1 to 9 as described by Grüneberg *et al*. (2010), where;

1 = no virus symptoms
2 = unclear virus symptoms
3 = clear virus symptoms in < 5 (%) of plants per plot
4= clear virus symptoms in 6 to 15 (%) of plants per plot
5 = clear virus symptoms in 16 to 33 (%) of plants per plot
6 = clear virus symptoms in 34 to 66 (%) of plants per plot (more than 1/3 less than 2/3)
7 = clear virus symptoms in 67 to 99 (%) of plants per plot (2/3 to almost all)
8 = clear virus symptoms in all plants per plot (not stunted)
9 = severe virus symptoms in all plants per plot (stunted).

The SPVD incidence was then expressed as a percentage of the diseased plant per plot to the total plant population per plot.

The above-ground yield

Stand counts: plant population was counted twice during this study trial. The first and the second stand count were made at 19 days (Sca19) and 120 days (ScaH) after planting date and before harvest respectively. The data collected were used to determine the total plant population per plot.

Days to maturity (MD): This was determined regularly using visual observations for the signs of maturity such as flowering, change in the stem colour from deep to pale colouration, and leaves yellowing at 60%. Pretests was done on the non-harvestable plots after observation of the maturity signs before harvest for tuberous root sizes and

exudates**.**

Fresh vine yield weight (FVWt): FVWT were taken from the sampled plants immediately upon harvest and weighed using the electronic balance in kilogram and then converted to tons/ hectare.

Below ground yield

Marketable tuberous yield (MTY): All clean, uninfected, undamaged tuberous roots weighed above 100 g were considered marketable. All the marketable tuberous roots, collected from the harvestable plots were weighed using a sensitive balance (kilograms per plant).
The unmarketable tuberous yield (UTY): All the tuberous roots weighed below 100g, mechanically damaged, infected, and rotten, from each sampled plant at harvest were separated and weighed and recorded as unmarketable tuberous yield per plant per plot.
The total tuberous yield (TTY): All the tuberous yield (marketable and unmarketable) from the harvestable plots were collected and weighed according to genotypes. The total tuberous yield in ton per hectare per genotype was then calculated using the equation:

$$\text{TTY} = \frac{\text{MTY + UTY}}{\text{Total net area}(m^2)} \text{ X } 10 \quad \text{..……...……...……..…..} \quad \text{Equation 1 (Grüneberge } \textit{et al.}\text{, 2010)}$$

Where; TTY= total tuberous yield; MTY= marketable tuberous yield; UTY= unmarketable tuberous yield; m^2= meters square.

Harvest Index (HI): HI was determined as a ratio of total tuberous yield to a combined fresh vine yield weight and total tuberous yield in tons per hectare using the equation:

$$\text{HI} = \frac{\text{TTY (t/ha)}}{\text{TTY (t/ha)+FVWt(t/ha)}} \text{…..Equation 2 (Grüneberge } \textit{et al.}\text{, 2005)}$$

Where; HI= Harvest index; TTY = Total tuberous yield; FVWt= Fresh vine yield weight; t/ha= tons per hectare.

Data analysis

Data collected from the studied traits were first compiled in the excel sheet, then imported to GenStat 18thedition (Payne *et al*., 2011). Homogeneity of variance tests was done using Bartlett's test before combining the three locations' data sets. Residual Error and Maximum Likelihood (REML) analysis was conducted to obtain the variance components (VComponent). The model used for analysis was:

$Yij = \mu + ti + rj + eij$ (i = 1, 2, ..., t; j = 1, 2, ... r) ……..…. Equation 3 (Gleeson & Cullis, 1987).

Where; Yij = random variable observation from the ith treatment in jth block; μ, ti and

rj = general mean effect of the i^{th} and r^{th} treatment and effect in the j^{th} block; eij = the error component which is a random variable.

These were assumed to be normally and independently distributed. The means were separated by Fisher's Least Significant Difference (LSD) ($P < 0.05$). The RELM variance components analyzed were used to compute the Best Linear Unbiased Predictors (BLUPs) for the studied traits used to test the genotypes' genetic merit over environment and time. Genotypes, location, and replication formed the random variable effects (Robinson, 1991). The linear model equation used here was: $y=X\beta +Zu + e$…….. Equation 4 (Robinson, 1991).

Where; y is the vector of n observable random variables effect; β is a vector of p unknown parameters having fixed values (fixed effects): X and Z are unknown matrices: u and e are vectors of n: Unobservable random variables (random effects). The BLUPs values were subjected to Finlay and Wilkinson joint regression analysis to test the sensitivity of the genotypes to the different locations' effects. The sensitivity of each genotype to the locations' effects was characterized by fitting a regression of the location means for each genotype on the grand average of the location. The model used was:

$yij= gi + bi \times ej + error$……Equation 5 (Finlay & Wilkinson, 1963).

Where: yij is the yield sensitivity of the i^{th} genotype in the j^{th} location; gi are genotype means, ej are location effects (with $\sum ej = 0$) and bi are the sensitivity parameters (with mean (bi) = 1).

The Additive main effects and multiplicative interactions (AMMI) biplot was used to test the genotypes' stability over the studied locations. The AMMI model first accounted for G x L interactions analyzed by the interaction principal component analysis (IPCA) which explained Variances and correlations in the data without compromising accuracy. The AMMI model equation used was:

$Yij = \mu + Gij + Ej + \sum_{k-1}^{n} \lambda kaikyjk + eij$……..... Equation 6 (Zobel *et al.*, 1988)

Where; Yij is the yield of the i^{th} genotype in the j^{th} location; μ is the grand mean; Gi and Ej are the genotype and location deviations from the grand mean, respectively; λk is the singular value of the k^{th} axis in the principal component analysis; αik and γjk are the genotype and location principal component and they are fixed; n is the number of principle components retained in the model; eij is the error term.

RESULTS

The performance of sweet potato genotypes in the study locations

Prediction of the genotypes' performance using Best Linear Unbiased Predictors (BLUPs)

The BLUPs used to test the genetic merits of the genotypes in the studied locations shows differences in the genotype's performance for the studied yield and yield component traits and SPVD resistance (Table 3):

Sweet potato viral disease (SPVD)

There was high SPVD severity and incidences in genotype Erica in all the studied locations with at least 92.11 %, 88.02%, and 83.67 % incidences on the study locations Aba'ala, Mekelle-1, and Mekelle-2 respectively. Meanwhile, the SPVD severity was visibly observed in all the stems, branches and leaves of the same genotype where the whole crop plants were stunted in all the studied locations. Genotypes Melinda and Ininda showed unclear symptoms of diseases with low incidences across locations. High site means SPVD incidence and severity was observed in Aba'ala location.

Total tuberous yield (TTY)

Genotypes Ininda and Gloria performed higher than the site average yield in all locations. Amelia gave a high yield in all locations although its performance was a little lower than Gloria and Ininda. Although Melinda and Kulfo performed below site grand mean, its performance was comparatively promising especially for locations Mekelle-1, and Mekelle-2. The overall site mean performance for this trait was high in location Mekelle-2.

Harvest index (HI) and marketable tuberous yield (MTY)

All genotypes had high HI in all locations except Erica which registered below-average HI in all locations. High performance in marketable tuberous yield was registered in genotypes Ininda and Gloria, and a moderate performance was observed in genotypes Amelia and Kulfo across locations. Comparatively, high marketable tuberous yield performance was recorded in location Mekelle-1, and Mekelle-2, respectively.

Unmarketable tuberous yield (UTY)

Genotypes Ininda and Erica had the highest weights of unmarketable tuberous yield record in location Aba'ala. Whereas, genotypes Ininda, Gloria, Melinda on Mekelle-1, and Amelia, Gloria, and Melinda at Mekelle-2 had the highest weight of unmarketable tuberous yield record.

Fresh vine yield weight (FVWt) and Vine Length (VL)

High fresh vine yield weight was recorded in genotypes Melinda and Ininda on location Aba'ala, Ininda, Amelia and Gloria on location Mekelle-1, and Ininda, Amelia, Kulfo, and Gloria on location Mekelle-2 respectively. Relatively, genotypes Gloria, Ininda, and Melinda had long vine lengths in all the studied locations. Short vine length was recorded in genotypes Erica in all the studied locations.

Maturity days (MD)

The genotypes' maturity days varied in all the locations. Genotypes Ininda (90-100 days) and Kulfo (114-120 days) were the earliest maturing genotypes in all locations. Meanwhile, genotypes Gloria (155-170 days) and Erica (160-185 days) were late maturing genotypes in all the studied locations.

Stand count at nineteen days after planting date (SCa19)

Genotypes Ininda (20.19, 19.50, 27.45), Gloria (20.29, 23.63, 28.61), Amelia (18.75,22.76,27.45) and Melinda (17.10, 19.29, 23.88) had a high number of stands counts at locations Aba'ala, Mekelle-1and Mekelle-2 respectively, meanwhile, Erica (11.86, 16.73, 22.73) and Kulfo (14.73, 20.28, 25.93) had a low number of stand counts for the same locations.

Stand count at harvest (SCaH)

There was an average reduction in the stand count numbers in all genotypes except for Kulfo (13.40, 20.53, 22.92), and Ininda (20.16, 18.00, 24.44) in all locations. Genotype Erica (4.31, 9.92, and 7.24) had the lowest stands count number in Aba'ala, Mekelle-1, and Mekelle-2, respectively.

Table 3. BLUPs values of the studies traits in the three locations.

Locations	Genotypes	**FVWt**	**HI**	**SPVD**	**VL**	**UTY**	**MTY**	**TTY**	**TL**	**TB**	**SCa19**	**SCaH**	**MD**
Aba'ala	Amelia	2.59	0.72	0.71	1.54	2.17	5.1	7.3	28.0	20.6	18.75	19.0	150.0
Aba'ala	Erica	2.32	0.18	92.11	0.47	2.76	0.3	3.0	12.4	19.0	11.86	4.3	160.0
Aba'ala	Gloria	2.60	0.83	0.83	2.94	2.64	10.5	13.1	26.3	13.4	20.29	19.9	155.0
Aba'ala	Ininda	6.88	0.82	5.06	1.84	3.71	28.2	32.0	26.7	25.0	20.19	20.2	90.0
Aba'ala	Kulfo	2.99	0.63	0.03	1.72	2.28	3.1	5.4	12.4	22.0	14.73	13.4	114.0
Aba'ala	Melinda	7.40	0.69	10.12	2.01	1.64	7.9	9.5	18.6	17.8	17.10	13.0	150.0
Mekelle 1	Amelia	3.94	0.79	0.89	0.42	2.06	12.3	14.3	19.7	20.2	22.76	23.7	120.0
Mekelle 1	Erica	1.46	0.75	88.02	0.13	1.45	2.8	4.2	11.4	23.0	16.73	9.9	170.0
Mekelle 1	Gloria	3.52	0.86	0.55	0.99	3.28	18.0	21.3	27.2	17.0	23.63	23.0	165.0
Mekelle 1	Ininda	8.80	0.80	6.25	0.55	3.57	31.2	34.8	20.3	23.8	19.50	18.0	95.0
Mekelle 1	Kulfo	2.09	0.83	0.15	0.51	1.15	8.6	9.77	11.2	24.8	20.3	20.5	120.0
Mekelle 1	Melinda	2.80	0.83	3.01	0.62	3.31	8.7	12.0	12.3	21.6	19.3	14.6	120.0
Mekelle 2	Amelia	4.14	0.85	2.78	0.63	4.95	17.4	22.4	17.5	34.6	27.5	24.4	130.0
Mekelle 2	Erica	2.74	0.67	83.67	0.28	2.04	4.4	6.5	12.0	26.0	22.8	7.2	185.0
Mekelle 2	Gloria	3.28	0.89	1.10	1.40	3.55	23.7	27.2	26.7	19.7	28.6	23.9	170.0
Mekelle 2	Ininda	7.25	0.85	8.73	0.65	1.56	40.9	42.5	23.0	29.4	27.3	24.4	100.0
Mekelle 2	Kulfo	4.63	0.80	0.14	0.57	0.53	18.6	19.2	14.2	34.9	25.9	22.9	120.0
Mekelle 2	Melinda	2.97	0.75	3.00	1.20	4.48	7.0	11.5	13.3	22.7	23.9	10.5	130.0

FVWt= Fresh vine yield weight; HI= Harvest index; SPVD= Sweet potato viral disease; VL= Vine length; UTY= Unmarketable tuberous yield; MTY= Marketable tuberous yield; TTY= Total tuberous yield; TL= Tuberous length; TB= Tuberous breadth; SCa19=Stand count at 19 days after planting date; SCaH= Stand count at harvest; MD= Maturity days

Evaluation of genotypes' vs locations' interactions

Regression analysis of genotypes by locations interactions

Generally, the genotypes performed differently for the different studied traits and were statistically significant at different statistical levels ($p< 0.01$, $p<0.05$). Almost all the traits were highly significant ($p<0.01$), *FVWt and ScaH were significant* ($p<0.05$) for genotypes' main effect except for UTY. For locations' main effects, there was a significant difference ($p<0.05$) in the abundance and distribution of rainfall in the studied locations, SPVD and TL. Most of the studied traits were highly significant ($p<0.01$) except FVWt, UTY, SCaH, and MD which were non-significant. The sensitivity reactions showed highly statistical differences ($p<0.01$) *for rainfall abundance and distribution response, and HI. Most traits were significant* ($p<0.05$) except FVWt, TL, TB, SCa19, SCaH, and MD which were statistically non-significant (Table 4).

Table 4. Genotypes joint regression analysis

Source	Genotypes	Locations	Sensitivities	Residual	Total
d.f.	5	2	5	5	17
Rainfall	6034.59**	884.66*	8917.06**	164.61	4550.04
FVWt	10.91*	0.62 ns	3.42 ns	1.30	4.67
HI	0.04**	0.05**	0.02**	0.0014	0.03
SPVD	3636.83**	5.27*	212.31*	1.438	1074.32
VL	0.72**	2.47**	0.15*	0.0182	0.56
UTY	1.70 ns	0.25 ns	2.49*	0.4442	1.39
MTY	348.61**	135.55**	20.87*	2.1909	125.26
TTY	368.34**	145.15**	16.75*	1.7078	130.84
TL	116.18**	23.15*	10.36 ns	2.3324	40.63
TB	46.15**	111.02**	12.23 ns	4.0553	31.42
SCa19	19.15*	119.85**	1.44 ns	1.87	20.71
SCaH	114.03**	27.06 ns	6.89 ns	6.47	40.65
MD	2422.89**	86.72 ns	207.24 ns	46.20	797.36

FVWt= Fresh vine yield weight; HI= Harvest index; SPVD= Sweet potato viral disease; VL= Vine length; UTY= Unmarketable tuberous yield; MTY= Marketable tuberous yield; TTY= Total tuberous yield; TL= Tuberous length; TB= Tuberous breadth; SCa19=Stand count at 19 days after planting; SCaH= Stand count at harvest; MD= Maturity days; ns= non-significant; *= Significant at $p<0.05$; **= Significant at $p<0.01$

Ranking of genotypes sensitivity estimated genotypes Amelia (1.54), Kulfo (1.42), Gloria (1.42), and Ininda (1.09) as highly sensitive genotypes, and Melinda (0.18) and Erica (0.35) less sensitive to the environment's interactions for TTY. For SPVD, genotypes Erica (4.15), ranked first followed by Melinda (3.88). High TTY mean and mean standard deviation (±) was recorded in genotypes Ininda (36.39 ± 1.96), Gloria (20.54 ± 3.01), moderate TTY was recorded in genotypes Amelia (14.65 ±

0.20), Kulfo (11.43 ± 1.57), and Melinda (10.97 ± 1.73), and Erica (4.56 ± 0.20) smallest amount. For SPVD, large mean was observed in genotypes Erica (87.93 ± 1.40), moderately low in genotypes Ininda (6.68 ± 0.97) and Melinda (5.37 ± 3.77). Meanwhile, genotype Kulfo (0.10 ± 0.00) and Gloria (0.82 ± 0.14) and Amelia (1.46 ± 0.91) registered very low mean SPVD incidences (Table 5).

Table 5. Genotypes performance sensitivity estimates for tuber yield production and SPVD in the studied locations.

Traits	Genotype	Mean	s.e.	Sensitivity	s.e.	Mean Square deviation	Rank
Total Tuberous Yield	Amelia	14.65	0.75	1.54	0.19	0.20	1
	Erica	4.56	0.75	0.35	0.19	0.07	5
	Gloria	20.54	0.75	1.42	0.19	3.01	3
	Ininda	36.39	0.75	1.09	0.19	1.96	4
	Kulfo	11.43	0.75	1.42	0.19	1.57	2
	Melinda	10.97	0.75	0.18	0.19	1.73	6
SPVD	Amelia	1.46	0.69	-0.93	0.85	0.91	5
	Erica	87.93	0.69	4.15	0.85	1.40	1
	Gloria	0.82	0.69	-0.09	0.85	0.14	4
	Ininda	6.68	0.69	-1.74	0.85	0.97	6
	Kulfo	0.10	0.69	-0.06	0.85	0.00	3
	Melinda	5.37	0.69	3.88	0.85	3.77	2

Comparative analysis of locations' sensitivity with genotypes' performance for SPVD, TTY, and rainfall responses ranked Aba'ala (1.09) as highly sensitive for SPDV. Meanwhile, Mekelle-2 had a huge effect on genotypes' response to rainfall (14.00), and TTY (5.13) production (Table 6).

Table 6. Sensitivity estimates of locations' performances relative to genotypes' performance for the studied traits.

Traits	Location	Effect	s.e	Mean	Rank
Sweet potato viral diseases	Aba'ala	1.09	0.16	18.15	1
	Mekelle 1	-0.21	0.16	16.85	2
	Mekelle 2	-0.88	0.16	16.19	3
Total tuberous yield	Aba'ala	-4.68	0.38	11.74	3
	Mekelle 1	-0.45	0.38	15.98	2
	Mekelle 2	5.13	0.38	21.55	1
Rainfall	Aba'ala	-7.74	0.84	65.91	3
	Mekelle 1	-6.26	0.84	67.38	2
	Mekelle 2	14.00	0.84	87.64	1

Ranking of the storage root tuber yield performance across locations using AMMI

The ANOVA for Additive main effects and multiplicative interactions (AMMI) model showed a highly significant ($p<0.01$) difference for genotypes, locations, and genotype by locations interactions for TTY trait. The largest contribution to variance was given by genotypes (75.65%). Genotypes by location interactions was separated into two interaction principal component analysis axes (IPCA) on their order of importance. Both IPCA 1 and IPCA 2 were statistically significant ($p<0.05$) and accounted for 78.95% and 21.05 % of the variations due to genotype by location interaction sum of squares. Genotypes by locations interactions accounted for 3.17 % of the cumulative variances. The location and replication contributed 16.32% and 0.91% respectively. The cumulative interactive sum of squares of errors was 324 and accounted for 3.94 % (Table 7).

The AMMI model ranked genotypes Ininda and Gloria first and second position respectively for TTY mean production in all locations with high grand mean performance. The mean TTY performance of Gloria and Ininda was higher than that of the released checked variety Kulfo in all location although Kulfo gave above locations average yield in Mekelle-2. Kulfo was the largest contributor of IPCA 1 variance meanwhile, Ininda's contribution to variance interactions was the least. Locations Mekelle 2 ranked first position for TTY performance, followed by Mekelle 1 and location Aba'ala least (Table 8).

Table 7. ANOVA table for AMMI model showing genotypes by locations' interactions.

Source	**d.f.**	**S.S.**	**Total variation explained (%)**	**G × L explained (%)**	**MS**
Total	53	8227			155.2
Genotypes	5	6224	75.65		1245**
Locations	2	1343	16.32		671.6**
Interactions	10	261	3.17		26.1*
IPCA 1	6	206		78.95	34.3*
IPCA 2	4	55		21.05	13.7*
Residuals	0	0	0		
Error	30	324	3.94		10.8

Table 8. AMMI Selection analysis of genotypes' root tuber yield and locations ranking.

Location	**Aba'ala**		**Mekelle 1**		**Mekelle 2**				
Genotypes	**Mean**	**Rank**	**Mean**	**Rank**	**Mean**	**Rank**	**Grand Mean**	**IPCAg1**	**IPCAg2**
Amelia	6.56	3	14.19	3	23.54	3	14.76	1.180	-0.337
Erica	0.19	6	3.77	6	5.91	6	3.29	-1.515	0.736
Gloria	12.49	2	21.59	2	28.07	2	20.72	0.607	-0.911
Ininda	32.18	1	34.67	1	43.07	1	36.64	0.081	1.31
Kulfo	2.96	5	8.94	5	19.54	4	10.48	1.264	0.239
Melinda	3.52	4	12.20	4	11.06	6	8.93	-1.618	-1.026
Location	**9.65**	**3**	**15.89**	**2**	**21.86**	**1**			
IPCAl 1	-1.340		-1.001		2.341				
IPCAl 2	1.387		-1.528		0.141				

To visualize the genotypes by locations' interactions (GEI), this data was plotted using AMMI biplot. Locations Aba'ala and Mekelle-1, formed a right angle at their axis while, the geometric angle between Aba'ala and Mekelle 2, Mekelle 1 and Mekelle 2 was obtuse angle (Figure 2).

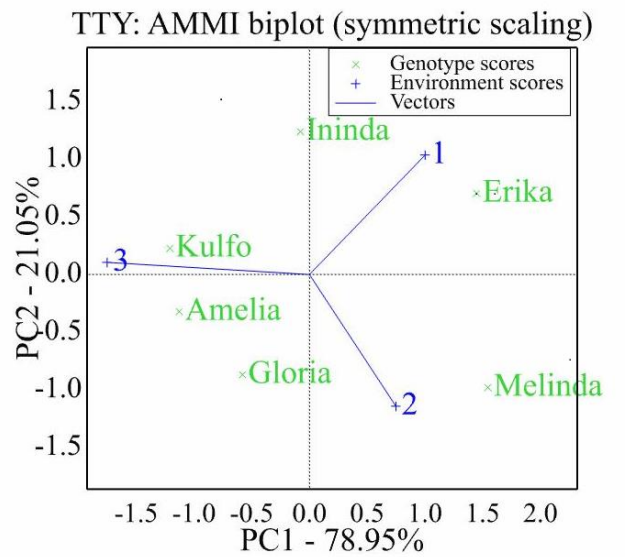

Figure 2. The AMMI Biplot showing genotypes performance in the studied locations (Location 1= Aba'ala, 2= Mekelle 1, 3= Mekelle 2).

The IPCA 1 scattered plotting shows genotypes scattered in all four quadrates: genotypes Ininda, Gloria Kulfo and Amelia, occupied the upper right and left quadrate while genotypes Melinda and Erica occupied the lower left quadrant. Genotypes Ininda aligned itself very close to the biplot origin followed by genotypes Gloria, Amelia and Kulfo (Figure 3).

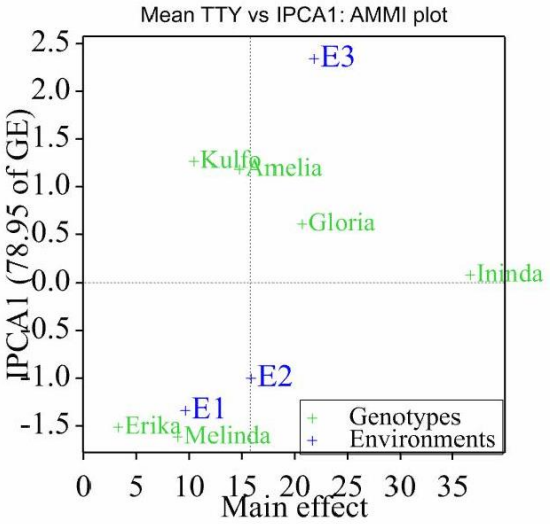

Figure 3. IPCA 1 Scattered plots showing genotypes interaction with locations for TTY trait (E1= Aba'ala, E2= Mekelle 1, E3= Mekelle 2).

DISCUSSIONS

Yield and yield components traits such as total tuberous yield, harvest index, and fresh vine yield were used to determine genotypes adaptability and stability in any given agro-ecology. Genotypes with well-established vines, high fresh vine yield weight, and total tuberous yield and harvest index signify the genotype's ability to partition nutrients and moisture well in all parts without compromising tuberous root yield. Genotypes with high HI are good producers of TTY (Oriba, 2017; Lamaro *et al*., 2020). In agreement with this, genotypes Ininda and Gloria, with high HI, TTY and FVWt, were suitable for production of tuberous roots and fresh vines useful for food and animal feed, respectively.

Sensitivity provides a way of assessing the stability of the genotypes to the environments. According to Eberhart & Russell (1966), genotypes with low sensitivity values are more stable than those with high sensitivity values relative to changes in environmental conditions. In addition, the means of the squared deviations of the observations about the line fitted for each genotype should be taken into consideration. Genotypes with large mean yield and smaller mean square deviations are giving more predictable responses on multi-locations. Selections of genotype(s) with large means and small sensitivities warrant a

reliable crop under variable conditions. In this study genotypes Ininda and Gloria are the most dynamically stable genotypes, and genotypes Erica and Melinda unstable for TTY in all locations (Table 5). The joint analysis of variance for studied traits showed highly significant differences among genotypes (G), Locations (L), and sensitivity. This showed that genotypes did not differ only genetically but also some of these unveiled disparity responses to different locations. The results indicated that the presence of abundant genetic variability for yield and yield component traits, SPVD resistance, and presence of genotype x location interaction. The genotypes Ininda, and Gloria, exhibited high TTY with high resistance to SPVD and was responsive to all locations. Moreover, genotype Melinda deviated significantly from linearity as mean square deviation > 0, and its TTY is below grand mean with low SPVD resistance. Although genotype Erica had <0 mean square deviation and its sensitivity <1 for TTY, with a high sensitivity for SPVD meaning it's highly susceptible to SPVD. This deviation from regression indicates that the genotypes were unstable and their performance was not stable across varied environmental conditions. The inability of genotype Kulfo (standard check) not to show any sign of SPVD even in location Aba'ala, may signify its ability to resist SPVD infections (Table 4). The ranking of location Aba'ala as 1st position for SPVD shows that this is a location where genotypes experience great effects for locations exposure to SPVD accompanied by low TTY comparatively (Table 6). This could be because the geographical position of Aba'ala having lower altitude and the unfavorable environmental conditions (Table 1). This finding is in agreement with a similar report from Tewodros *et al*. (2011), who observed high SPVD incidences on sweet potato planted on lower altitudes compared to their counterparts on higher altitudes in Southern Ethiopia. The TTY production was low in this location, however, some genotypes such as Ininda and Gloria produced more TTY higher than that reported by Fekadu (2015) (8 t/ha) at farmers field conditions. Location Mekelle-2 ranked 1st for its high mean TTY. This may be because of the high amount of rainfall received in Mekelle-2 which enhance high soil moisture content during the growing cycle compared to locations Mekelle-1 and/or Aba'ala (Tables 1 and 6).

The right-angle positioning of locations Aba'ala and Mekelle-1 indicates a non-correlation between these two locations, meanwhile, the obtuse angle between locations Aba'ala and Mekelle-2, locations Mekelle-1 and Mekelle-2 indicates negative correlations for total tuberous yield production (Figure 2). This could be because of the significant difference in the sum of rainfall received and other differences in the locations' growth factors during the study period (Table1). This finding agrees with previous studies on G × E interactions of sweet potato germplasms where the environment had negative correlations for root tuber yield traits analysis (Zebyder, 2016; Lamaro *et al*., 2020). The center of the AMMI biplot origin represents the grand mean phenotypic response to the environment for tuber yield production: the positioning of genotypes or locations relative to the

biplot origin provides an understanding of the G × L interaction for the TTY trait. Genotypes found close to the origin show their insensitivity to the locations interactions hence more broadly adapted to the studied locations (Yan and Tinka, 2006; Osiru *et al*., 2009). It also shows high and dynamic stability in all locations, thus genotype Ininda and Gloria exhibited wide adaptability with high dynamic stability. Genotypes found far away from the biplot origin shows they are sensitive to the location's interactions hence they have specific adaptability. It may also show static stability to the locations it aligned itself near to in the Biplot (Yan and Tinka, 2006; Osiru *et al*., 2009). For instance, Kulfo showed static stability to Mekelle-2. Genotypes found on the upper left or right quadrates signifies above-average yield for TTY, meanwhile, those aligned at the lower left or right quadrate shows below-average yield performance for TTY. Hence genotypes Ininda, Gloria, Amelia and Kulfo were the four superior genotypes for TTY production, and genotypes Erica and Melinda were inferior for TTY production in all the studied locations (Figure 3). This finding is in agreement with similar studies (Yan and Tinka, 2006; Adebola *et al*., 2013; Lamaro *et al*., 2020; Karuniawan *et al*., 2021), who found variations in genotypes' stability and adaptability over environment and time.

CONCLUSION AND RECOMMENDATION

Genotypes performed differently in the studied locations. The differences in performance are not attributed only to environmental differences but also to the differences in the genetic make-up of the individual genotypes appraised. Genotypes Ininda and Gloria were superior to the released variety Kulfo (standard check) for TTY with dynamic stability and high resistance to SPDV in all the studied locations.

Genotype Ininda and Kulfo have short gestation period which may suit the short length of growing period in the arid agro-climate represented by Aba'ala. In addition, more experimentation with these genotypes should be done for further multi-location stability trials to see if they can aid as parent stocks for future breeding of orange-fleshed sweet potatoes in Tigray and Afar region. Location Aba'ala representing the arid condition was highly sensitive to SPVD. Genotype Erica was the most affected by SPVD severity and incidences. The TTY production in Aba'ala was low although the yield production is still within the total sweet potato land productivity in Ethiopia making Aba'ala a new avenue for sweet potato production exploitation in Ethiopia. Location Mekelle 2 representing the semi-arid region was the most suitable location for sweet potato TTY production and the low SPVD mean incidence. Further study has to be done on the studied genotypes in the same locations to ascertain the stability and SPVD resistance demonstrated in this preliminary study.

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