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# Yield Performance and Genotype × Environment Interaction of White-Fleshed Sweetpotato Genotypes across Different Agro-Ecologies in Ethiopia

BILILIGN MEKONNEN WUBE[1]*, MELESE LEMA TESEMA[2],
KANKO CHUNTALE CHULDA[3]

[1,2] Sidama Region Agricultural Research Institute, Hawassa Agricultural Research Center, Hawassa, Ethiopia
[3] South Ethiopia Agricultural Research Institute (SEARI), Arbaminch Agricultural Research Center,
Arbaminch, Ethiopia

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The white-fleshed sweetpotato (WFSP) remains vital to household food security in Ethiopia, where its adoption is limited by vulnerability to sweetpotato virus disease (SPVD) and low dry matter content (DMC). We assessed 10 WFSP genotypes (nine advanced lines and the standard check 'Awassa-83') across six environments (Halaba, Arbaminch, Werer; 2024 – 2025 main seasons) using a randomised complete block design with three replications. The analysis of variance was computed, and the results detected significant genotypic differences ($p < 0.05$) for storage root yield, DMC, and SPVD response. Genotype G2 (Ininda-1-20) achieved the highest mean yield (28.1 t/ha), a 32.3% advantage over the check, high DMC (~33%), and low SPVD severity (mean ≈1.5). The notable G × E interaction was observed for all traits recorded, including SPVD, vine length (VL), number of roots per plant (NRPP), above-ground fresh biomass weight (AGFW), storage root yield, and DMC, with variable magnitudes such as SPVD=21.3%, VL=6.7 %, storage root yield=8.9%, NRPP=8.7%, AGFW=3.2%, and DMC=7.6%. This demonstrates that the tested genotypes are sensitive to G × E interaction, warranting further stability analysis. GGE biplots (mean versus stability and the 'which-won-where' approach) indicated that G2 combined superior performance with acceptable stability across environments. Most genotypes scored less than 3.0 for SPVD, indicating resistance/or tolerance under the test conditions. We recommend on-farm participatory trials for G2 towards potential release in similar agro-ecologies. The results highlight the feasibility of selecting WFSP genotypes that simultaneously meet productivity, quality (DMC), and SPVD resistance requirements in Ethiopia's diverse environments.

Keywords: dry matter content, environment, food security, storage root yield, sweetpotato virus disease, stability

Sweetpotato (*Ipomoea batatas* (L.) Lam; 2n=6×=90) is cultivated across tropical and subtropical regions and is vital for food security and income generation (Low *et al.* 2020). While possessing a perennial growth habit, sweetpotato is commercially managed as an annual crop due to economic factors. Its classification places it within the Convolvulaceae family, genus *Ipomoea*, and section *Batatas*, a group comprising around 800 species (Truong *et al.* 2018; Wood *et al.* 2020). Genetically, sweetpotato exhibits a high chromosome number of 90 (Jones 1965; Bassett 1986; Lebot 2010). Uniquely within the genus

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Bililign Mekonnen Wube (*Corresponding author), Melese Lema Tesema, Sidama Region Agricultural Research Institute, Hawassa Agricultural Research Center, Hawassa, Ethiopia. E-mail: bililign.m@gmail.com; meleselema72@gmail.com
Kanko Chuntale Chulda, South Ethiopia Agricultural Research Institute (SEARI), Arbaminch Agricultural Research Center, Arbaminch, Ethiopia. E-mail: kankochuntale@gmail.com

Ipomoea, *I. batatas* is the only domesticated species (Austin & Huáman 1996) and is widely cultivated in warm temperate, tropical, and subtropical regions of over 120 countries (Luo *et al.* 2023).

The production of sweetpotato surpassed 93 million metric tons, ranking as the seventh most important food crop globally (FAOSTAT 2023). In 2023, the leading countries in sweetpotato production were China, Malawi, Tanzania, and Nigeria, with outputs of 51.4, 8.05, 4.51, and 4.08 million tons, respectively (FAOSTAT 2023). China was the dominant producer, contributing approximately 51 million tons-about 55% of the global total, followed by African countries such as Malawi and Tanzania. Sweetpotato plays a vital role in food security, income generation, and employment, particularly in Asia and Africa (FAOSTAT 2023; George *et al.* 2024; MoA-FDRE 2024). From a nutritional point of view, it is a rich source of dietary fibre, vitamins A and C, manganese, and antioxidants, which support immune function, promote healthy vision, and help mitigate risks of chronic diseases (Wang *et al.* 2016; Amagloh *et al.* 2021; Noreen *et al.* 2024).

Industrially, sweetpotato is increasingly processed into products such as chips, flour, starch, alcohol, animal feed, and biofuel, reflecting its growing importance in food processing and agro-industries (MoA-EDRE 2024; Wu 2024). The storage roots are notable for their diverse nutritional pigments, and the crop's drought tolerance, short growth cycle, and ability to grow in marginal soils make it essential for enhancing global food security and advancing climate change adaptation strategies (Fuglie 2007; Alam 2021; Meng *et al.* 2024). In Ethiopia, officially released sweetpotato varieties are grouped by their root flesh colour, with orange-fleshed (OFSP) and white-fleshed (WFSP) types (Mekonnen *et al.* 2024). Over the past two decades, WFSP genotypes have remained more popular among farmers and consumers primarily due to their superior mealiness compared to OFSP genotypes (Balcha 2015; Gurmu 2019). In Ethiopia, WFSP types remain widely preferred for their mealy texture, yet several popular varieties, particularly 'Awassa-83', are ageing and increasingly vulnerable to sweetpotato virus disease (SPVD), while some candidate replacements fail to meet consumer-preferred DMC ≥ 29 – 35% thresholds. Consequently, breeding priorities include improving storage root yield alongside DMC and SPVD resistance. The DMC is one of the critical quality attributes in sweetpotato genotypes, which is closely linked to desirable cooked root texture, which in turn impacts consumer preferences and accelerates the adoption of new varieties, particularly in East African countries, including Ethiopia (Tairo *et al.* 2008; Tumwegamire *et al.* 2011; Gurmu 2017; Lindqvist-Kreuze *et al.* 2023). DMC in sweetpotato genotypes is categorised into four classes based on computed percentage values: low (<25%), medium (25 – 28%), high (29 – 35%), and very high (>35%) (Loebenstein & Thottappilly 2009; Cervantes-Flores *et al.* 2010; Tumwegamire *et al.* 2011; Mourtala *et al.* 2023). Moreover, Tumwegamire *et al.* (2011) and Gurmu (2017) reported that genotypes with high dry matter content are most in demand, as this trait gives a mealy texture when cooked, which is preferred by most consumers across Sub-Saharan Africa, including Ethiopia. SPVD is a major bottleneck among biotic constraints in sweetpotato production, with over 20 known virus types infecting cultivated sweetpotato globally (Fuglie 2017). In sub-Saharan Africa and Asia, more than 15 different viruses have been identified as challenges to sweetpotato production (Gutiérrez *et al.* 2003; Ndunguru *et al.* 2009; Reynolds *et al.* 2015), and about seven virus types are predominantly distributed and infect sweetpotato either alone or synergistically in major growing areas of southern Ethiopia (Adane 2011; Mekonen *et al.* 2017). However, co-infection with sweetpotato feathery mottle virus (SPFMV) and sweetpotato chlorotic stunt virus (SPCSV), which leads to sweetpotato virus disease (SPVD), remains the most devastating disease of sweetpotato worldwide (Fuglie 2007; Ndunguru & Kapinga 2007; Ngailo *et al.* 2019; Abebe *et al.* 2023). During multi-location trials, selecting sweetpotato genotypes that combine better resistance to SPVD with high root yield potential is crucial for recommending genotypes that support sustainable production to meet consumers' food demands (Ngailo *et al.* 2015; Gurmu *et al.* 2017b).

Sweetpotato genotypes exhibit sensitivity to genotype-by-environment (G × E) interactions for various yield and quality traits, including resistance to virus diseases, when evaluated across diverse environments over multiple years (Yan & Tinker 2006;

Moussa *et al.* 2011; Kathabwalika *et al*. 2016; Gurmu *et al*. 2017). Multi-environment trials (METs) enable selection of broadly adapted and/or specifically adapted genotypes by quantifying genotype × environment interaction (G × E) (Yan & Tinker 2006; Moussa *et al.* 2011; Kathabwalika *et al*. 2016; Gurmu *et al*. 2017b). A Genotype plus genotype by environment interaction (GGE) biplot analysis (Yan *et al.* 2001; Yan 2002; Yan & Kang 2003) is widely used to visualise mean performance and stability, supporting actionable recommendations for candidate varietal release. Therefore, this study evaluated advanced WFSP genotypes across three contrasting locations over two main seasons to (i) quantify variation for yield, DMC, and SPVD response; (ii) assess G×E and stability using GGE biplots; and (iii) identify genotype(s) for advancement to on-farm testing and potential release.

## MATERIAL AND METHODS

### *Experimental Sites*

Trials were conducted during the 2024 and 2025 rainy seasons at Halaba (Central Ethiopia), Arbaminch (South Ethiopia), and Werer (Afar), representing diverse rainfall and temperature regimes (see Table 1 for coordinates and site descriptors). All sites were rainfed except Werer, where supplementary irrigation supported establishment.

### *Plant Materials and Seedling Establishment*

Five polycross families (Ininda, MUSG014001-3, MUSG014012-76, MUSG014012-26, MUSG014046-20) from CIP-Mozambique were used as source populations. Seeds (n=500) were scarified with concentrated $H_2SO_4$ (98%) to break dormancy; 334 germinated seedlings were raised and subsequently advanced via clonal cuttings. After preliminary screening for agronomic traits and disease response, nine promising genotypes plus the check 'Awassa-83' were selected for MET evaluation (Table 2).

### *Experimental Design and Crop Management*

A randomised complete block design (RCBD) with three replications was implemented at each environment. Spacing was 0.60 m between rows and 0.30 m within rows (plot size: 120 plants). Planting occurred from July to August and harvest from November to December, following national recommendations (HwARC 2015). No fertiliser was applied; standard weeding, cultivation, and ridging were performed.

### *Data Collection*

From the two central rows per plot (end plants discarded), we recorded: – Storage root yield [t/ha] and above-ground fresh biomass [t/ha] at harvest; – SPVD severity on a 1 – 9 scale (1 = immune; 9 = susceptible); – Vine length [cm] and number of roots per plant (count) from three sampled plants per row; – dry matter content (DMC) from 200 g root subsamples oven-dried at 70°C for 72 h and expressed as % (dry/fresh × 100) following data recording procedures for various traits in sweetpotato (IPGR 1991; Tairo *et al*. 2008; Grüneberg *et al.* 2019).

### *Statistical Analysis*

Homogeneity of error variances across environments was evaluated prior to combining analyses using GenStat (Payne *et al.* 2015). ANOVA followed Gomez & Gomez (1984); mean separation used *LSD* ($\alpha = 0.05$). The combined model was:

[Y_{ijkl} = + G_i + L_j + Y_k + (GL)*{ij} + (GY)*{ik} + (LY)*{jk} + (GLY)*{ijk} + B_{l(jk)} + _{ijkl}]

where: *i* – indexes genotypes (G), *j* – locations (L), *k* – years (Y), and *l* –blocks within location-year.

G × E and genotype stability were assessed using GGE biplots based on singular value decomposition of environment-centred data, displaying mean vs. stability and which-won-where views.

The GGE biplot model is based on the singular value decomposition (SVD) of the principal components, which was:

$$\overline{Y}_{ij} - \mu_i - \beta_j = \sum\nolimits_{k=1}^{t} \lambda_k \alpha_k \gamma_{jk} + \varepsilon_j$$

where: $Y_{ij}$ is the performance of genotype *i* in environment *j*, $\mu$ is the grand mean, $\beta_j$ is the main effect of environment *j*, *k* is the number of principal components (PC); $\lambda_k$ is the singular value of the $k^{\text{th}}$ PC; and are the scores of $i^{\text{th}}$ genotype and $j^{\text{th}}$ environment, respectively for PC$_k$; $\varepsilon_{ij}$ is the residual associated with genotype *i* in environment.

## RESULTS

*Storage Root Yield*

Genotypes differed significantly for yield across environments (Table 3). G2 (Ininda-1-20) recorded the highest overall mean 28.1 t/ha, followed by G3 (24.5) and G7 (23.1), outperforming the check ‘Awassa-83’ (21.3) by 32.3%, 15.1%, and 8.7%, respectively. Yield variation reflected both genetic differences and contrasting site conditions. GGE biplots (Figures 1 – 2) ranked genotypes along the average environment coordinate (AEC), with G2 closest to the “ideal” genotype-high mean and acceptable stability, indicating broad adaptation across test environments.

*Dry Matter Content (DMC)*

DMC varied significantly among genotypes (Table 4). G2 (~33%), G10/check (~32%), G6 (~30%), and G9 (~30%) met the high-DMC consumer preference range (≈29 – 35%). G5 (~24%) was the lowest. The GGE biplot for DMC (Figure 3) placed G2 nearest the ideal genotype, combining high level and stability across environments.

*Response to SPVD*

SPVD severity differed by genotype, location, and year (Table 5). Most genotypes had mean scores <3.0 (resistant/tolerant). GGE analysis for SPVD (Figure 4) indicated G2, G5 and G6 with negative PC1 scores (more resistant), while G1 and G4 showed higher susceptibility at specific sites/years.

Table 1

Description of the experimental sites

| Location |  | Altitude [masl]* | Coordinates | Annual R.F [mm] | Mean temperature [°C] |  | RH [%] |
|---|---|---|---|---|---|---|---|
| Name | Code |  |  |  | Min | Max |  |
| Halaba | HAL | 1,772.00 | 07°18’38”N,<br>38°05’38’E | 928.80 | 14.60 | 28.60 | 58.30 |
| Arbaminch | AMC | 1,220.00 | 6°6’55”N,<br>37o35’51”E | 1,050.00 | 17.40 | 30.60 | 55.90 |
| Werer | WER | 740.00 | 09°16’55”N,<br>40°09’23”E | 571.30 | 19.10 | 34.30 | – |

Note: *masl – meter above sea level; RF – rainfall; RH – relative humidity.

Table 2

Description of genotypes used in the trial

| Code | Genotype | Source of genotype | Root flesh colour | Year of release* |
|---|---|---|---|---|
| G1 | Ininda-1-12 | CIP-Mozambique | White | Not yet released |
| G2 | Ininda-1-20 | CIP-Mozambique | White | Not yet released |
| G3 | Ininda-1-23 | CIP-Mozambique | White | Not yet released |
| G4 | Ininda-1-52 | CIP-Mozambique | White | Not yet released |
| G5 | Ininda-1-40 | CIP-Mozambique | White | Not yet released |
| G6 | Ininda-1-25 | CIP-Mozambique | White | Not yet released |
| G7 | MUSG014012-26-4-10 | CIP-Mozambique | White | Not yet released |
| G8 | MUSG014012-76-3-3 | CIP-Mozambique | White | Not yet released |
| G9 | MUSG014012-76-3-35 | CIP-Mozambique | White | Not yet released |
| G10 | Check (Awassa-83) | Ethiopia | White | Released in 1983 |

Note: CIP – International Potato Centre, based in Mozambique;* National root crops research program, Hawassa Agricultural Research Centre, 2025.

### *Vine Growth, Biomass and Root Number*

Significant differences were observed for vine length, above-ground biomass, and number of roots per plant (Table 6). G7 had the highest biomass (38.0 t/ha), while G2 combined desirable biomass (37.3 t/ha) with high root number (6.78), supporting both food and potential fodder uses.

### *G×E and Stability Analysis in GGE Biplot*

In this study, the significant G × E interaction was observed for all traits recorded, such as SPVD, VL, NRRP, AGFW, root yield and DMC, with variable magnitude for SPVD = 21.3%, Vl = 6.7%, root yield = 8.9%, NRPP = 8.7%, AGFW = 3.2%, DMC = 7.6%. This study showed that the tested genotypes were sensitive to G × E interaction, which demands further stability analysis.

### *Storage Root Yield*

The GGE biplot analysis in Figures 1 and 2 illustrates the ranking and stability of genotypes for root yield performance. GGE biplot analysis is a powerful tool for ranking genotypes based on their positions along the average environment coordinates (AEC). The AEC abscissa represents the mean yield across environments. In this study, the GGE biplot ranked the genotypes as follows: G2>G3>G10>G9>G7>G6>G1>G4>G8, from highest mean performance (closest to the ideal genotype) to lowest (farthest from the ideal). This ranking reflects both yield and stability, with G2 identified as the top-performing genotype for recommendation (Figure 1). The mean yield versus stability biplot was depicted using ten WFSP genotypes evaluated across six diverse environments (Figure 2). Genotype G2 is situated farthest along the positive AEC abscissas, representing the highest mean storage root yield across environments, though it shows moderate stability due to its moderate projection from the AEC ordinate. In contrast, genotypes G6, G4 and G1 are located closer to the AEC ordinate, reflecting greater stability but lower mean yields.

Table 3

Storage root yield [t/ha] performance of sweetpotato genotypes as per cent of the check in the trial

| Genotype | | Storage root yield [t/ha] | | | | | | | | Overall mean | Yield advantage over the standard check [%] |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Code | Name | Year 1 (2024) | | | | Year 2 (2025) | | | | | |
| | | HAL | AMC | WER | Mean | HAL | AMC | WER | Mean | | |
| G1 | Ininda-1-12 | 20.40 | 25.30 | 6.10 | 17.30 | 11.20 | 36.00 | 5.70 | 17.70 | 17.50 | –17.80 |
| G2 | Ininda-1-20 | 29.40 | 52.10 | 6.60 | 29.40 | 28.80 | 36.00 | 15.80 | 26.90 | 28.10 | 32.30 |
| G3 | Ininda-1-23 | 27.80 | 44.70 | 7.90 | 26.80 | 17.50 | 38.00 | 10.70 | 22.10 | 24.50 | 15.10 |
| G4 | Ininda-1-52 | 15.50 | 30.80 | 8.10 | 18.10 | 9.10 | 30.10 | 3.60 | 14.20 | 16.20 | –23.80 |
| G5 | Ininda-1-40 | 21.40 | 32.70 | 7.70 | 20.60 | 12.20 | 46.80 | 3.50 | 20.80 | 20.70 | –20.50 |
| G6 | Ininda-1-25 | 20.80 | 32.80 | 8.40 | 20.70 | 15.80 | 33.30 | 3.90 | 17.70 | 19.20 | –9.90 |
| G7 | MUSG014012-26-4-10 | 13.80 | 40.50 | 18.80 | 24.40 | 8.90 | 43.60 | 2.80 | 21.80 | 23.10 | 8.70 |
| G8 | MUSG014012-76-3-3 | 19.00 | 14.70 | 13.80 | 15.90 | 10.70 | 21.50 | 3.60 | 12.00 | 13.90 | –34.60 |
| G9 | MUSG014012-76-3-35 | 21.20 | 40.60 | 4.80 | 22.20 | 16.00 | 34.90 | 3.00 | 18.00 | 20.10 | –5.50 |
| G10 | Check (Awassa-83) | 18.60 | 34.90 | 9.50 | 21.00 | 17.20 | 38.80 | 8.40 | 21.50 | 21.30 | – |
| Mean | | 20.80 | 34.90 | 9.20 | 21.60 | 14.70 | 35.90 | 6.10 | 19.80 | 20.70 | – |
| *LSD* (0.05) | | 3.20 | 8.10 | 3.40 | 4.90 | 4.90 | 6.60 | 3.50 | 5.00 | 5.00 | – |
| *CV* [%] | | 9.10 | 13.60 | 21.70 | 14.80 | 19.70 | 10.10 | 31.00 | 20.30 | 17.50 | – |

Where: HAL – Halaba; AMC – Arbaminch; WER – Werer; *LSD* – least significant difference; *CV* – coefficient of variation. Yield advantage over the standard check [%] refers to the percentage increase in yield of a genotype compared to the standard check variety, calculated as (genotype mean – standard check mean) / standard check mean × 100%.

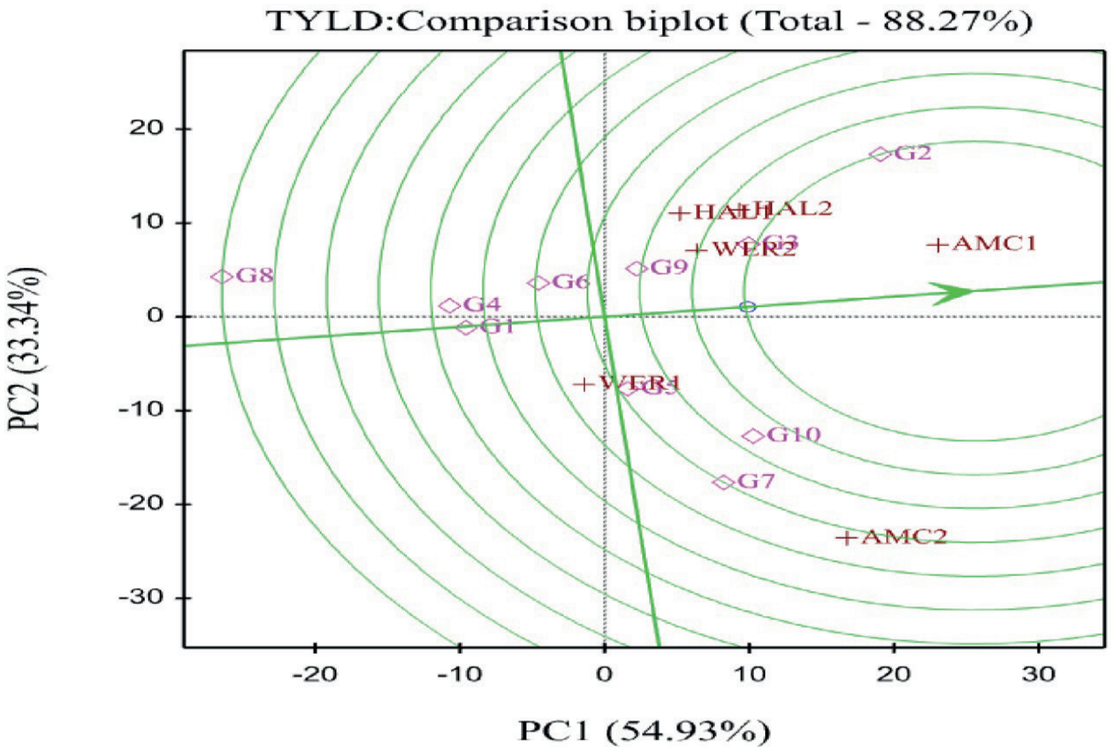

Figure 1. A GGE-biplot demonstrating the storage root yield [t/ha] performance of 10 WFSP genotypes in six environments.
Note: GGE – genotype main effect plus genotype-by-environment interaction; WFSP – white-fleshed sweetpotato; TYLD – total storage root yield.

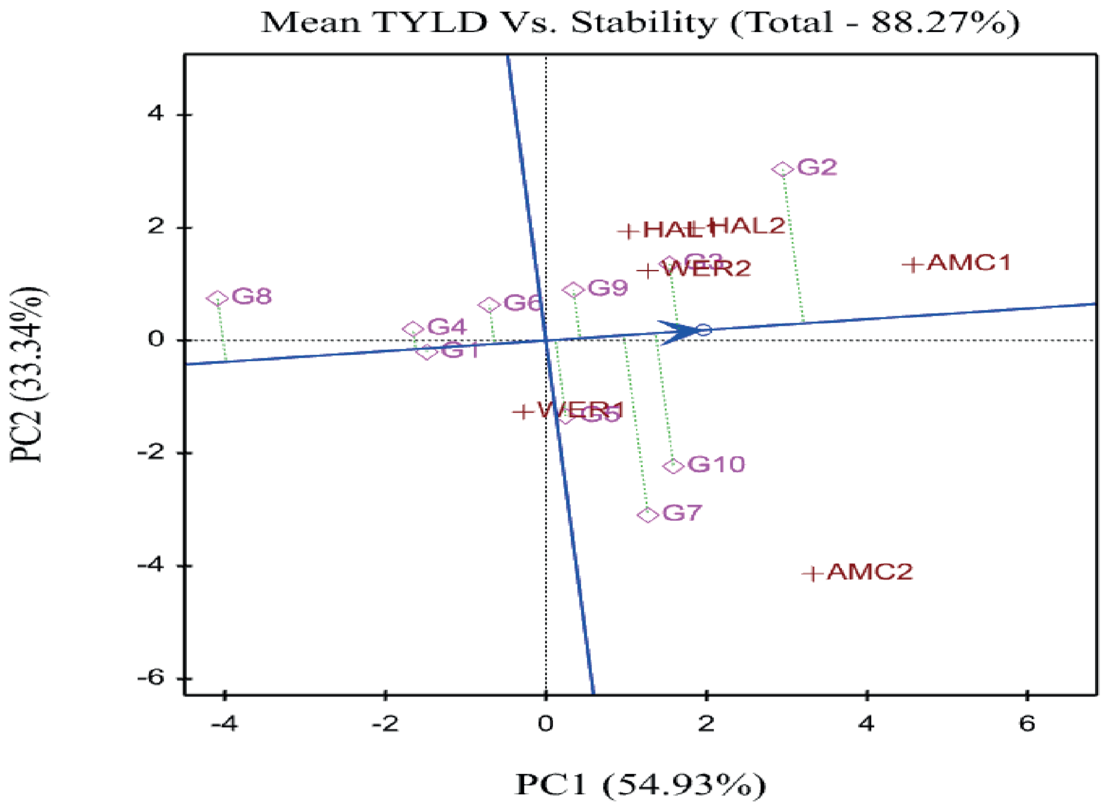

Figure 2. The mean storage root yield performance and stability of 10 white-fleshed sweetpotato genotypes evaluated in six environments.
Note: TYLD – total storage root yield.

Table 4

Mean performance of genotypes‘ dry matter content [%] across locations and over years

| Code | Genotype | Dry matter content [%] | | | | | | | | Overall mean | Yield advantage over the standard check [%] |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Year 1 (2024) | | | | Year 2 (2025) | | | | | |
| | | HAL | AMC | WER | Mean | HAL | AMC | WER | Mean | | |
| G1 | Ininda-1-12 | 0.30 | 0.27 | 0.31 | 0.29 | 0.31 | 0.31 | 0.26 | 0.29 | 0.29 | –9.40 |
| G2 | Ininda-1-20 | 0.35 | 0.32 | 0.32 | 0.33 | 0.36 | 0.32 | 0.30 | 0.33 | 0.33 | 3.13 |
| G3 | Ininda-1-23 | 0.28 | 0.27 | 0.33 | 0.29 | 0.29 | 0.27 | 0.31 | 0.29 | 0.29 | –9.40 |
| G4 | Ininda-1-52 | 0.28 | 0.27 | 0.30 | 0.28 | 0.29 | 0.25 | 0.27 | 0.27 | 0.28 | –12.50 |
| G5 | Ininda-1-40 | 0.26 | 0.17 | 0.25 | 0.23 | 0.27 | 0.23 | 0.26 | 0.25 | 0.24 | –25.00 |
| G6 | Ininda-1-25 | 0.28 | 0.30 | 0.33 | 0.30 | 0.29 | 0.32 | 0.28 | 0.30 | 0.30 | –6.30 |
| G7 | MUSG014012-26-4-10 | 0.29 | 0.29 | 0.28 | 0.29 | 0.30 | 0.26 | 0.22 | 0.26 | 0.27 | –15.63 |
| G8 | MUSG014012-76-3-3 | 0.25 | 0.23 | 0.31 | 0.26 | 0.26 | 0.25 | 0.30 | 0.27 | 0.27 | –15.63 |
| G9 | MUSG014012-76-3-35 | 0.30 | 0.30 | 0.26 | 0.29 | 0.31 | 0.31 | 0.31 | 0.31 | 0.30 | –6.30 |
| G10 | Check (Awassa-83) | 0.32 | 0.30 | 0.31 | 0.31 | 0.33 | 0.32 | 0.32 | 0.32 | 0.32 | – |
| Mean | | 0.29 | 0.27 | 0.30 | 0.29 | 0.30 | 0.28 | 0.28 | 0.29 | 0.29 | – |
| *LSD* (0.05) | | 0.01 | 0.02 | 0.08 | 0.04 | 0.02 | 0.08 | 0.07 | 0.02 | 0.02 | – |
| *CV* [%] | | 9.99 | 11.23 | 15.60 | 12.27 | 10.00 | 16.60 | 15.30 | 0.28 | 6.14 | – |

Where: HAL – Halaba; AMC – Arbaminch; WER – Werer; *LSD* – least significant difference; *CV* – coefficient of variation. Yield advantage over the standard check [%] refers to the percentage increase in yield of a genotype compared to the standard check variety, calculated as (genotype mean – standard check mean) / standard check mean × 100%.

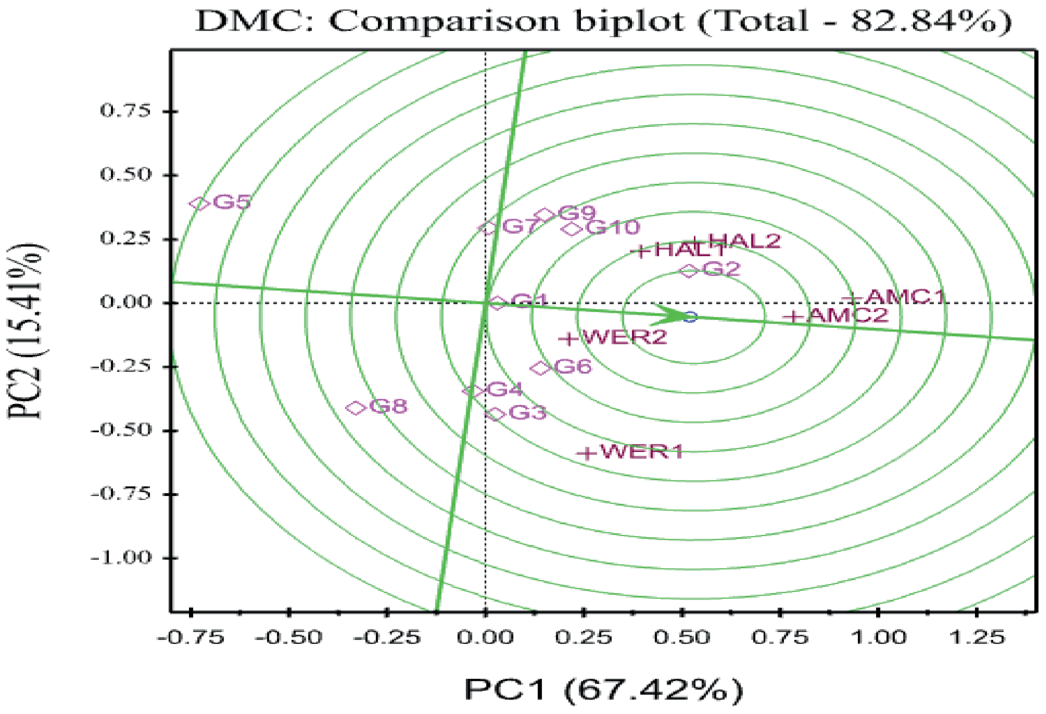

Figure 3. GGE biplot showing average DMC performance for 10 WFSP genotypes evaluated across six environments.
Note: GGE – genotype main effect plus genotype-by-environment interaction; WFSP – white-fleshed sweetpotato; TYLD – total storage root yield; DMC – dry matter content.

*Dry Matter Content (DMC)*

The GGE biplot analysis in Figure 3 demonstrates the DMC performance of genotypes across six environments (three locations over two years). Principal components (PCs) 1 and 2 accounted for 67.42% and 15.41% of the variation, respectively, a total (PC1and PC2) of 82.84%, which indicates adequately captured the variation in the data and met the criteria for applying GGE biplot analysis. Based on GGE biplot analysis, genotypes were ranked from the best performer (shortest distance to the ideal genotype to the least performer (farthest distance from the ideal genotype as G2>G6>G10>G1>G9>G3>G4>G7>G8>G5 (Figure 3). Accordingly, G2 is the desirable genotype (best genotype) as it falls the shortest distance to the ideal, G5 is identified as the least desirable genotype as it is found farther from the ideal genotype.

*Response to SPVD*

The GGE biplot, as depicted in Figure 4, shows the environment and the performance of the respective genotypes in response to SPVD. PC1 and PC2 accounted for 94.41% of the total variation for the performance of genotypes in response to SPVD, which sufficiently explained the reliability of GGE (Figure 4). Based on GGE biplot analysis, genotypes with high and positive PC1 scores are considered most desirable, while those with negative PC1 scores are considered poor performers. However, in terms of SPVD response, the pattern is reversed: genotypes with high and positive PC1 scores are the most susceptible, while those with negative PC1 scores are the most resistant. Accordingly, in this study, three G2, G5 and G6 were identified with negative PC1 scores, whereas G1 and G4 had high positive PC1 scores.

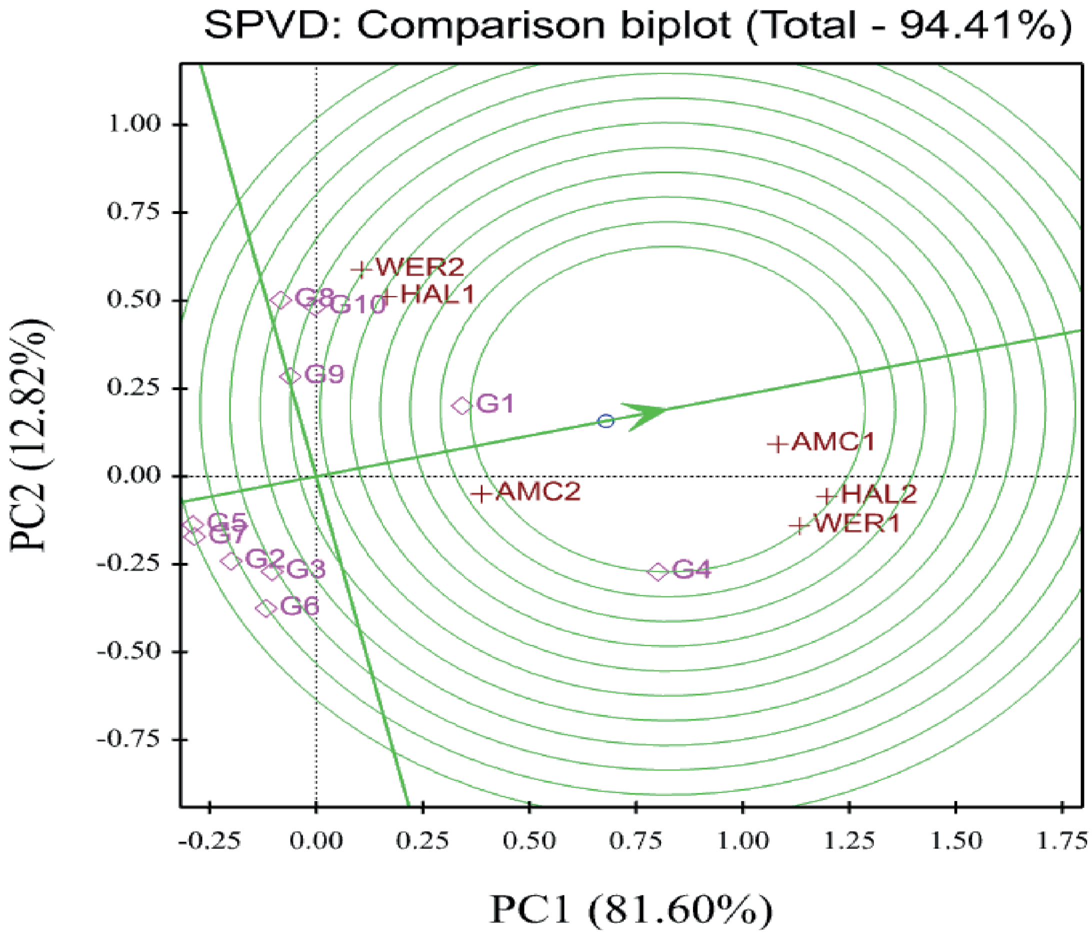

Figure 4. GGE biplot showing the SPVD performance for 10 WFSP genotypes evaluated across six environments.
Note: SPVD – sweetpotato virus disease; GGE – genotype main effect plus genotype-by-environment interaction; WFSP – white-fleshed sweetpotato.

## DISCUSSION

Genotypic performance varied significantly due to the cause of inherent genetic differences among the evaluated genotypes and the influence of the diverse environmental conditions under which they were grown. The significant genotype-by-environment (G × E) interaction indicates differential genotype performance across diverse environments, highlighting the challenge of identifying a single genotype with consistently superior performance across all locations (Gurmu *et al*. 2017). Highly significant differences ($p < 0.01$) were observed among genotypes for storage root yield. In this study, genotypes G2, G3 and G7 demonstrated relatively high storage root yields, with the yield increment over the check variety by 32.3%, 15.1% and 8.7%, respectively. In contrast, G8, G4 and G1 recorded significantly lower storage root yields of 13.9, 16.2 and 17.5 t/ha, respectively, highlighting the strong influence of both genotypic and environmental factors on yield performance (Gurmu *et al*. 2017a; Mbusa *et al.* 2018; Gurmu *et al.* 2024). The highest storage root yield, 52.1 t/ha, was recorded for G2 at the Arbaminch location in year 1 (2024), followed by G3 with 44.7 t/ha. In the same year, G2 gave 29.4 t/ha at the Halaba location. In year 2 (2025), G5 achieved the highest storage root yield of 46.8 t/ha, but its performance was inconsistent across locations and years. Genotype G2 produced 28.8 t/ha at the Halaba location in the second year (2025). Over both years, Arbaminch and Halaba were the most productive locations. In contrast, Werer was the least productive site, with maximum storage root yields of 18.8 t/ha and 15.8 t/ha recorded from G7 (year 1) and G2 (year 2), respectively. These results illustrated shifts in genotype rankings across locations and years, highlighting the need for further stability analyses to identify genotypes with consistent performance (Yan & Tinker 2006; Moussa *et al.* 2011; Kathabwalika *et al.* 2016; Gurmu *et al.* 2017b). Accordingly, G × E interaction was further

Table 5

Mean sweetpotato virus disease severity score (1 – 9 rating scale) of genotypes evaluated in NVT across locations from 2024 – 2025

| Code | Genotype | Sweetpotato virus disease (1 – 9) | | | | | | | | Overall mean |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Year 1 (2024) | | | | Year 2 (2025) | | | | |
| | | HA1 | AM1 | WER | Mean | HAL | AMC | WER | Mean | |
| G1 | Ininda-1-12 | 2.33 | 3.33 | 4.00 | 3.22 | 4.33 | 2.33 | 2.33 | 3.00 | 3.11 |
| G2 | Ininda-1-20 | 1.50 | 1.00 | 2.33 | 1.61 | 2.00 | 1.33 | 1.00 | 1.44 | 1.53 |
| G3 | Ininda-1-23 | 1.50 | 1.33 | 2.67 | 1.83 | 2.33 | 2.00 | 1.00 | 1.78 | 1.81 |
| G4 | Ininda-1-52 | 2.00 | 5.00 | 6.33 | 4.44 | 6.00 | 3.33 | 1.33 | 3.55 | 4.00 |
| G5 | Ininda-1-40 | 1.00 | 1.00 | 1.67 | 1.22 | 1.33 | 2.00 | 1.67 | 1.67 | 1.45 |
| G6 | Ininda-1-25 | 1.00 | 1.33 | 2.67 | 1.67 | 2.33 | 1.67 | 1.00 | 1.67 | 1.67 |
| G7 | MUSG014012-26-4-10 | 2.00 | 1.00 | 1.67 | 1.56 | 1.33 | 2.00 | 1.00 | 1.44 | 1.50 |
| G8 | MUSG014012-76-3-3 | 3.00 | 1.33 | 2.67 | 2.33 | 2.33 | 1.67 | 2.67 | 2.22 | 2.28 |
| G9 | MUSG014012-76-3-35 | 2.00 | 1.67 | 2.67 | 2.11 | 2.33 | 2.00 | 2.67 | 2.33 | 2.22 |
| G10 | Check (Awassa-83) | 3.00 | 3.00 | 2.80 | 2.93 | 3.00 | 3.00 | 3.33 | 3.11 | 3.02 |
| Mean | | 1.93 | 1.93 | 2.00 | 2.95 | 2.29 | 2.73 | 2.13 | 1.80 | 2.22 |
| *LSD* (0.05) | | 0.49 | 1.07 | – | 0.78 | 1.28 | 0.84 | 0.53 | 0.88 | 0.83 |
| *CV* [%] | | 14.50 | 30.10 | 21.80 | 22.13 | 28.30 | 25.40 | 31.00 | 28.23 | 25.18 |

Note: 1 – 9 scale (1 = immune, 9 = susceptible, hence, 1 – 3 = resistant, 4 – 6=medium and 7 – 9 = susceptible); *LSD* – least significant difference; *CV* – coefficient of variation; HAL – Halaba; AMC – Arbaminch; WER – Werer year.

explored using GGE biplot analysis, which identified G2 as the best performer, displaying both high storage root yield and relative stability. The GGE biplot ranked the performance of genotypes as follows: G2>G3>G10>G9>G7>G6>G1>G4>G8 from highest mean performance (closest to the ideal genotype) to lowest (farthest from the ideal).

The mean yield versus stability biplot, based on the position along the along the average environment coordinates (AEC) abscissa for storage root yield and stability as the distance from the AEC ordinate, identified genotype G2 as the high yielder across environments (location vs. year), positioned farthest along the positive AEC abscissa with moderate stability indicated by its moderate projection from the AEC ordinate. In contrast, genotypes G6, G4 and G1 were located closer to the AEC ordinate, reflecting greater stability, but had lower mean storage root yields. Consistent with previous interpretations of stability using GGE biplot analyses (Yan 2001; Yan & Tinker 2006; Gurmu 2017; Ebem *et al*. 2021), selection of a genotype that accompanied both high yield with relative stability would be rewarding in the selection process for a breeding program. Accordingly, G2 was identified as effectively balanced with relative stability. Significant differences ($p < 0.05$) were detected among genotypes for SPVD reaction across six environments (three locations over two years), demonstrating the sensitivity of genotypes to genotype-by-environment (G × E) interactions. Genotype G4 exhibited the highest SPVD severity scores of 6.33 and 6.00 at Werer and Halaba in years 1 and 2, respectively. Symptoms observed were leaf stunting, chlorosis, mottling, and growth abnormalities of the plant, indicating susceptibility to SPVD, which is consistent with findings reported by Ngailo *et al.* (2019) and Abebe *et al.* (2023). Moreover, Gruneberg *et al.* (2019) classified sweetpotato genotypes using a 1 – 9 rating scale, defining genotypes with mean severity scores greater than 3.0 as susceptible, while those with scores below 3.0 were considered resistant or tolerant under field conditions. This study also corroborates earlier reports by Gibson *et al.* (1998) and Gutierrez *et al.* (2003), which describe SPVD-infected sweetpotato as exhibiting stunted growth, leaf deformation, and distinctive chlorotic and mottled patterns- which signal genotype susceptibility (Gasura & Mukasa

Table 6

Mean performance of genotypes for agronomic traits in NVT at three locations over two years

| Genotype | | Agronomic traits | | |
|---|---|---|---|---|
| Code | Name | Vine length [cm] | Above-ground biomass yield [t/ha] | Number of roots per plant (no.) |
| G1 | Ininda-1-12 | 111.60 | 27.40 | 5.15 |
| G2 | Ininda-1-20 | 116.40 | 37.30 | 6.78 |
| G3 | Ininda-1-23 | 147.70 | 28.40 | 4.80 |
| G4 | Ininda-1-52 | 153.00 | 30.10 | 3.91 |
| G5 | Ininda-1-40 | 116.10 | 29.40 | 4.80 |
| G6 | Ininda-1-25 | 146.20 | 34.70 | 5.00 |
| G7 | MUSG014012-26-4-10 | 141.50 | 38.00 | 4.23 |
| G8 | MUSG014012-76-3-3 | 98.80 | 30.60 | 2.93 |
| G9 | MUSG014012-76-3-35 | 135.30 | 27.30 | 4.08 |
| G10 | Check (Awassa-83) | 109.30 | 31.30 | 3.90 |
| Mean | | 127.60 | 31.40 | 4.55 |
| *LSD* (0.05) | | 24.76 | 6.43 | 0.89 |
| *CV* [%] | | 38.32 | 31.10 | 26.21 |

Note: *LSD* – least significant difference; *CV* – coefficient of variation; NVT – national variety trial.

2011; Ngailo *et al.* 2019; Abebe *et al*. 2023). These authors also explained that high susceptibility is evident when SPVD is present, while non-significant differences were observed where the virus was absent or genotypes responded similarly regardless of disease presence. This may result from environments unsuitable for virus proliferation, genotypic resistance, or lack of vectors near experimental sites. The PC1 and PC2 of the GGE biplot explained 94.41% of total variation in SPVD response, with PC1 accounting for 81.60% and PC2 for 12.82%. Typically, genotypes with high positive PC1 scores are deemed desirable, whereas those with negative scores are less (Yan & Tinker 2006). However, for SPVD response, this pattern is reversed: high positive PC1 scores indicate greater susceptibility, whereas negative PC1 scores correspond to resistance or tolerance (Ngailo *et al.* 2019). Accordingly, genotypes G2, G5 and G6 exhibited negative PC1 scores, indicating SPVD resistance/tolerance, while G1 and G4 had high positive PC1 scores, reflecting susceptibility to SPVD. This aligns with the interpretation that genotypes on the right side of the biplot are more susceptible, and those on the left are more resistant (Ngailo *et al*. 2019).

In this study, the dry matter content (DMC) of genotypes varied significantly ($p < 0.05$) across evaluated environments. Four genotypes exhibited the highest mean DMC percentages: G2 (33%), G6 (30%), G9 (30%), and G10 (32%). Among the evaluated genotypes, G2 demonstrated the presence of an increment over the check by 3.13%. Conversely, genotype G5 recorded the lowest overall DMC at 24%, which is not an acceptable level for consumers. Most of these genotypes fell within the medium to high DMC range, a critical threshold for the acceptance and adoption of new sweetpotato varieties across various consumer markets (Tairo *et al*. 2008; Loebenstein & Thottappilly 2009; Cervantes-Flores *et al*. 2010; Tumwegamire *et al.* 2011; Gurmu 2017; Lindqvist-Kreuze *et al*. 2023; Mourtala *et al*. 2023). Genotypes with low DMC tend to be watery and less preferred, thereby limiting their market acceptance and adoption. Moreover, the GGE biplot explained approximately 82.84% of the total variation (PC1 = 67.42%, PC2 = 15.41%) in DMC among genotypes, effectively capturing the variation using the GGE biplot (Yan 2001; Yan & Tinker 2006). In the GGE biplot analysis, the concept of an ideal genotype integrates both high yield and stability, represented by a position at the centre of concentric circles on the biplot (Yan 2001; Yan & Tinker 2006). In this study, the performances of genotypes were ranked most desirable to least desirable as follows: G2>G6>G10>G1>G9>G3>G4>G7>G8>G5. Accordingly, G2 was closest to the ideal genotype, demonstrating its best performance across environments, whereas G5 was the least performer (undesirable). The ranking inconsistency among genotypes reflects significant G × E interactions, underscoring the complexity of identifying genotypes with both high and stable performance for this trait across diverse conditions (Gurmu *et al.* 2017b; Mekonnen & Gurmu 2024). In due course, the most suitable genotype is one that balances stability with relatively high yield performance across different environments (Gemechu *et al.* 2022).

The performance of genotypes for vine length (VL) was highly significant ($p < 0.01$). The longest VL of 153.0 cm was obtained from G4, followed by G3 with 147.7 cm, while the shortest VL of 98.8 cm was obtained from G8. Genotypes with optimal vine length are preferred by seed multipliers, as they provide sufficient planting material, especially for varieties in high demand within seed production systems. Sweetpotato vines form a functional part of the aboveground biomass and serve as valuable livestock feed in land-constrained areas. This aligns with previous reports by Kebede *et al*. (2008) and Nigussie *et al*. (2012), which highlight that sweetpotato vines are rich in protein and minerals, making them suitable for ruminant feed. Significant differences ($p < 0.05$) were observed among genotypes for aboveground fresh weight (AGFW) across locations and years. The highest AGFW of 38.0 t/ha was recorded for G7, followed by G2 with 37.3 t/ha, whereas G9 produced the lowest AGFW at 27.3 t/ha. Genotypes exhibiting both high storage root yield and optimum aboveground biomass yield can offer dual-purpose benefits: their roots serve as a staple food for human consumption, whereas the biomass provides valuable animal fodder. This trait is particularly advantageous in land-limited farming systems, enabling maximised productivity and efficient use of resources per unit area (Shumbusha *et al*. 2014). Significant variation ($p < 0.05$) was also detected for the number of roots per plant (NRPP), ranging from 6.78 for G4 to 2.93 for G8. These differences likely reflect genotypic variability affecting root yield components independently of root size (Ngailo *et al.* 2019). The number of roots per plant (NRPP) is a key trait that can play a significant role in determining and contributing to the overall yield of a given genotype. Earlier studies on sweetpotato have shown strong positive correlations between NRPP and total root yield, with root size and weight per root further influencing the yield potential of a given genotype (Shumbusha *et al.* 2014; Gurmu *et al.* 2017a; Mwanga *et al.* 2017). Therefore, selecting genotypes with an optimal number of roots per plant is an effective breeding strategy to improve storage root yield of sweetpotato. Overall, genotype G2 (Ininda-1-20) consistently outperformed others, combining high storage root yield, relative stability, high dry matter content (DMC), tolerance to SPVD, strong root set, and adequate biomass production-traits highly valued by farmers and consumers alike. Accordingly, G2 has been selected for the next stage of on-farm participatory evaluation and recommendation.

## CONCLUSIONS

Ten white-fleshed sweetpotato (WFSP) genotypes were tested across six environments for root yield, dry matter content (DMC), SPVD response, root number, biomass, and vine length. Genotype G2 (Ininda-1-20) consistently outperformed others, pairing high, stable yield with favourable DMC, SPVD tolerance, strong root set, and adequate biomass traits valued by farmers and consumers. SPVD severity was predominantly <3.0, indicating effective resistance and/or low pressure, though site- and year-specific susceptibility (e.g., G1, G4) underscores the need for continued multi-location, multi-season evaluation. Given its broad adaptation and stable performance across diverse environments, genotype G2 is recommended for participatory on-farm trials and potential release in similar agro-ecologies, particularly in areas facing production constraints due to irregular rainfall. Its deployment is expected to enhance productivity, improve product quality, and strengthen local food-system resilience.

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***Data Availability:*** Data supporting the findings are available from the corresponding author upon reasonable request.

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