Journal of Experimental Agriculture International

42(2): 47-62, 2020; Article no.JEAI.51003
ISSN: 2457-0591
(Past name: American Journal of Experimental Agriculture, Past ISSN: 2231-0606)

Evaluation of Cassava Genotypes for Agronomic Performance, Correlation with CMD and CBSD Parameters and Stability across Alupe, Kakamega and Kibos in Western Kenya

L. N. Navangi[1,2*], S. M. Githiri[1], E. M. Ateka[1], E. Kanju[3], T. L. Munga[4], S. Tumwegamire[3], R. M. Otsyula[2], P. O. Kwena[2], V. W. Woyengo[2], J. Malinga[2] and L. O. Okitoi[2]

[1]Jomo Kenyatta University of Agriculture and Technology, P.O. Box 62000-00100, Nairobi, Kenya.
[2]Kenya Agricultural and Livestock Research Organization, P.O. Box 169-50100, Kakamega, Kenya.
[3]International Institute of Tropical Agriculture (IITA), P.O. Box 30441, Dar-es-Salaam, Tanzania.
[4]Kenya Agricultural and Livestock Research Organization, P.O. Box 16-80109, Mtwapa, Kenya.

Authors' contributions

This study was carried out in collaboration among all authors. Authors LNN, SMG, EMA and TLM designed the study, wrote the protocol and interpreted the data. Authors LNN, EK, TLM, RMO, POK, JM, LOO, VWW and ST anchored the field study, gathered the initial data and performed preliminary data analysis. While authors LNN and SMG managed the literature searches and produced the initial draft. Authors SMG and EK reviewed and refined the manuscript. All authors read and approved the final Manuscript.

Article Information

DOI: 10.9734/JEAI/2020/v42i230469
Editor(s):
(1) Dr. Biljana Bojovic, Institute of Biology and Ecology, University of Kragujevac, Serbia.
Reviewers:
(1) Oluwatoyin Sunday Osekita, Adekunle Ajasin University, Nigeria.
(2) R. Mahalakshmi, India.
(3) Bipinchandra B. Kalbande, Nabira Mahavidyalaya, India.
Complete Peer review History: http://www.sdiarticle4.com/review-history/51003

Original Research Article

Received 24 June 2019
Accepted 29 August 2019
Published 14 March 2020

ABSTRACT

Cassava (*Manihot esculenta* Crantz) production in sub-Saharan Africa (SSA) is constrained by the two biotic constraints namely, cassava mosaic disease (CMD) and cassava brown streak disease (CBSD). The aim of this study was to evaluate elite cassava genotypes for variation in agronomical traits, correlate them to CMD and CBSD parameters and identify stable genotypes in Alupe,

**Corresponding author: E-mail: lynet.nasiroli@gmail.com;*

Kakamega and Kibos in Western Kenya. Twenty three (23) elite cassava genotypes that had shown resistance to either one or both of CMD and CBSD in Eastern Africa were evaluated. The trial was conducted using an alpha lattice balanced design with twenty three (23) genotypes, replicated three times at Alupe, Kakamega and Kibos in Western Kenya for an extended cropping cycle between 2016 and 2017. Results showed significant differences ($P \leq 0.05$) between genotypes and location (or agro-ecology), but not interaction ($P \geq 0.05$), for all the agronomic performance parameters evaluated. All the 23 cassava genotypes evaluated across the three locations had mean cyanide potential levels ranging from of 3.00–6.00 and were therefore, sweet and not bitter. The significant but negative relationship between CMD and CBSD incidence and severity with agronomic performance implied that their relationship was inverse. Confirmation of stability for agronomic performance was achieved through AMMI analysis, using AMMI stability value (ASV). Stable genotypes based on AMMI stability values (ASV) for fresh root yield across Alupe, Kakamega and Kibos were KBH/2002/066, Kibandameno (a local standard check), NASE-18, Kizimbani and NASE-3. These genotypes need to be further evaluated in more environments to assess their wider adaptability and stability.

Keywords: Manihot esculenta; agronomic traits; AMMI; CMD; CBSD; correlation; stability.

1. INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a key food security crop in sub-Saharan Africa (SSA) and increasingly offers opportunities for income generation from the sale of fresh roots and diverse processed products [1-3]. World-wide, cassava is a staple food for more than 800 million people [4]. However, agronomic performance of cassava is increasingly constrained by the two principal biotic constraints, cassava mosaic disease (CMD), caused by cassava mosaic geminiviruses (CMGs) and cassava brown streak disease (CBSD), caused by cassava brown streak viruses (CBSVs) [3,5-7]. In Africa, yields are only 8-10 tonnes per hectare, on average approximately half of those achieved in Asia and Latin America [8].

Even though cassava is one of the most widely grown staple crops in Nyanza, Western and Coast regions of Kenya, cassava production losses in Kenya are estimated at over US$ 14 million per annum by CMD, and weight loss of produced roots of up to 70% by CBSD [9,10]. Whereas CMD is widely distributed wherever cassava is grown, CBSD has been endemic in the coastal region of Kenya and currently emergence has been reported in the Western region of Kenya [10,11]. Breeding for dual resistance is currently being pursued as the most cost-effective and sustainable way to manage the devastating effects of the viral diseases in ESA [3]. Continuous deployment of new resistant cultivars is necessary as CMGs are known to evolve producing virulent strains while different strains of CBSD are being reported [12]. Although high resistance for CMD has been found, only limited success has been documented for CBSD [1,3]. The desired goal of the breeding efforts is to identify stable genotypes that are high yielding and resistant to both viral diseases.

Identification of sources of virus resistance was achieved by screening germplasm by grafting or sap inoculation with the virus under greenhouse conditions or in the field under natural whitefly-mediated infection [12,13,14]. The work was undertaken in the early stages of the project "New Cassava varieties and Clean Seed to Combat CMD and CBSD (5CP)" and aimed at exchanging elite germ plasm among countries most affected by CMD and CBSD for adaptability breeding [3]. These collaborative efforts with different national cassava breeding programs have identified germplasm resistant or tolerant to CBSD/CMD [3]. However, these have been evaluated so far under a narrow range of conditions of environment, virus species/strains, and vector abundance [1]. These genotypes also need to be distinguished by agronomic performance traits such as plant height, height to first branching, time of maturity, biomass yield, fresh root yield, dry matter (DM), dry matter content (% DMC), Harvest Index (HI) and the cyanogenic glycosides content in the roots.

However, most of these important cassava agronomic traits have high genotype by environment interaction [2,3,15,16,17]. Suitable genotypes are those adapted to the target environment and requires breeding for both specific and broad/wider adaptation. Farmers, on the other hand, grow cassava under diverse

cropping systems, and therefore prefer genotypes that suit their cropping systems, are resistant to pests and diseases, especially CMD and CBSD, with resultant high yields. Therefore, multi-location trials are conducted for different crops throughout the world not only to identify disease tolerant/resistance and high yielding genotypes but also to identify sites that best represent the target environment for specific and wide adaptability [3,16,18,19].

Stable genotypes within and across environments can be determined using various methods, that range from parametric; such as environmental stability variance [20], regression slope [21], deviation from regression [22] and coefficient of determination [23]; and multivariate methods such as Additive Main effect and Multiplicative Interaction (AMMI) [24]. Therefore, the Eberhart and Russell [22] model and AMMI stability analysis could be the preferable tools to identify stable, high yielding and adaptable genotype (s) for wider or specific environments [7]. However, since analysis of variance (ANOVA), principal component analysis (PCA), and linear regression (LR) are sub-cases of the more complete AMMI model, then AMMI offers a more appropriate statistical analysis of agronomic performance trials that may have a GEI [25,26,27,28]. AMMI clarifies the GEI and summarizes patterns and relationships of genotypes and environments, to improve the accuracy of agronomic performance, including yield estimates [5,6,18,25,27,29,30]. The objectives of this study were to: (1) Assess the variation in agronomic performance of elite cassava genotypes in Alupe, Kakamega and Kibos in Western Kenya, and (2) correlate agronomic performance traits with CMD and CBSD parameters and identify stable genotypes at Alupe, Kakamega and Kibos.

2. MATERIALS AND METHODS

2.1 Experimental Materials

Twenty three (23) elite cassava genotypes that had shown great promise in terms of their resistance to both CMD and CBSD and were officially released or were in the final stages of official release in the New Cassava Varieties and Clean Seed to Combat CBSD and CMD (5CP) Project countries of Kenya, Malawi, Mozambique, Tanzania and Uganda [3], were evaluated in this study. Kibandameno from Kenya, a local landrace, not yet officially released, but with high susceptibility to both CMD and CBSD was included as a standard local check and infector plot.

2.2 Experimental Locations

The multi-location evaluation trials were conducted on-station, for an extended cropping season between 2016-2017, in three locations namely KALRO Kakamega, KALRO Kibos and KALRO Alupe, representing three agro-ecological zones: Upper Midlands zone 1 (UM1); Lower Midlands zone 2 (LM2) and Lower Midlands zone 1 (LM1) respectively [31]. These three sites were known CMD and CBSD hot spot areas [32].

2.3 Experimental Design and Planting Details

The trial at each location was laid out in a Balanced Alpha Lattice Design with twenty four (24) treatments (genotypes). Cassava genotype Mkumba was used twice to balance the experimental design, hence Mkumba-2 genotype. The trials were replicated three times in six (6) blocks with four (4) plots each. Healthy stem cuttings each 25 cm in length were horizontally planted in a flat seedbed at a spacing of 1 m×1 m within rows and 1 m x 1 m between rows giving a population density of 10,000 plants ha^{1}. Each plot measured 6 m × 7 m (42 m^2), comprising 6 rows of 7 plants each to give a total of 42 plants in each plot. The first and last rows and the first and last plant within the middle row of each plot were considered as border plants. The plots and blocks were separated by 2.0 m and 2.0 m alleys, to reduce inter-plot and inter-block plant competition, respectively. The trials were conducted without supplemental irrigation and weeded regularly.

2.4 Data Collection

Agronomic performance parameters of interest in this study are described in Table 1. At harvest time, 12 MAP, data on three agronomic traits, namely harvest index (HI), root dry matter content (DMC) and Cyanide content were computed. For estimating harvest index all harvested plants per genotype were partitioned into roots and biomass (stumps, stems and foliage). Thereafter, separate weights of roots and above-ground biomass were made and HI computed as the ratio of roots to the total biomass, expressed as a percentage (%). However, it's important to point out that the trials were carried out under open field conditions,

Table 1. Description of agronomic parameters of interest for elite cassava genotypes recorded in this study

Name of parameter	Description and estimation formula
Biomass Yield (t ha^{-1})	Total fresh weight of harvested foliage and stems in tonnes per hectare = Dry Matter Content (% DMC)|100*Fresh Biomass Weight, kg
Harvest Index (% HI)	Ratio of fresh root weight divided by total plant weight (biomass and fresh roots), expressed as percentage (%) = Fresh Root Weight, kg|100*Total Plant Weight, kg (Fresh Root Weight, kg + Fresh Biomass Weight, kg)
Root dry matter yield	Dry weight of harvested roots derived by multiplying fresh storage root yield by dry matter content expressed in tonnes per hectares = Fresh Root Weight, 250g - Dried Root Weight)|(Fresh Root Weight, 250g*100
Root dry matter content (% DMC)	Percentage dry matter content of storage roots. It is the ratio of dry root weight to the weight of 100 g fresh weight expressed in percentage = Dry Matter (DM)|250*100
Cyanogenic potential (CNP)	Cyanogenic potential of the fresh storage roots, determined by Picrate Concentration (PC) score method on a scale of 1-9
Fresh Root Yield (t ha^{-1})	Total fresh yield of storage roots harvested per plot measured in tonnes per hectare = Dry Matter Content (% DMC)|100*Fresh Root Weight, kg

hence leaf fall and all the roots were not accounted for in estimating HI. DMC was determined using the oven dry method, where fresh samples of each variety (250 g) were taken in triplicate and dried to constant weight in an oven maintained at 72°C for 48h. The difference between fresh and dry weights was then used to compute the percentage (%) dry matter content for each genotype. The Cyanogenic Potential (CNP) was carried out according to the procedure described by [33]. Cyanide content of fresh storage roots was determined by Picrate score (PC) method, characterized by colour change of the picrate on a 125 mm Whatman® filter paper strip as described by [33]. Colour change from pale green to dark brown was scored on a scale of 1 to 14 corresponding to a cyanide content of between <10ppm to>450ppm. Root sampling was standardized to account for known root variation in cyanide concentration and analysis was done within an hour after harvesting. Standardization was done with standard paper and a blank provided with the kit.

2.5 Data Analysis

Data was entered into MS Excel spreadsheet and analysis was carried out using Genstat statistical software Release 15.2 (Genstat procedure library release PL23.2, VSN International, 2015). Agronomic performance were subjected to analysis of variance (ANOVA) to establish whether or not significant differences existed among cassava genotypes with dual resistance to cassava mosaic and brown streak diseases. Further Pearson's correlations were carried out between: root and foliar incidence and severity; and root incidence and severity with DMC, HI, other agronomic traits, CMD and CBSD disease traits 12 MAP for associations. Combined analysis of variance across the environments (Alupe, Kakamega and Kibos) and variance components σ^2_G, σ^2_E, σ^2_{GxE} and σ^2_e were estimated based on the generalized mixed effect model, with genotype declared as fixed effects and location/environment as random effects using the following model:

$$Y_{ijkl} = \mu + G_i + E_j + GE_{ij} + R_{k(j)} + B_{l(k)} + \varepsilon_{ijkl}$$

Where: Y_{ijkl} is observed value of genotype i in block l and replication k of environment j, μ is grand mean, G_i is effect of genotype i, E_j is environment or location effect, GE_{ij} is the interaction effect of genotype i with environment j, $R_{k(j)}$ is the effect of replication k in environment j, $B_{l(k)}$ is the effect of block l in replication k, ϵ_{ijkl} is error (residual) effect of genotype i in block l and replication k of environment j.

2.6 AMMI Stability Analysis of Agronomic Performance Parameters

Similarities among test environments based on environmental main and GEI effects were evaluated using additive main effect and multiplicative interaction analyses. The method

uses a combination of ANOVA and principal components analysis (PCA) [34,35,18,24]. Therefore, while ANOVA partitioned the variance into three components: genotype, environment and G×E deviations from the grand mean, the PCA partitioned the G × E deviations into different interaction principal component axes (IPCA). These were tested for statistical significance using AMMI ANOVA. Since the AMMI model does not make provision for a quantitative stability measure, and as such a measure is essential in order to quantify and rank genotypes in terms of agronomic performance i.e. yield, biomass, etc., stability, the following measure as proposed by [24] was adopted for this study:

$$AMMI\ Stability\ Value\ (ASV) = \sqrt{\{\frac{IPCA\ 1\ Sum\ of\ squares}{IPCA\ 2\ Sum\ of\ Squares}\}(\text{IPCA1 Score})^2 + (\text{IPCA2 Score})^2}$$

Where, SSIPC1/SSIPC2 is the weight given to the IPC1 value by dividing the IPC1 sum of square on the IPC2 sum of square. The larger the IPCA (interaction principal component analysis) scores, either negative or positive, the more specifically adapted a genotype is to certain environments, smaller IPCA scores indicate a more stable genotype across environments. Therefore, genotypes with the highest ASV values are considered the most unstable in the test environments (specifically adapted to certain environments), while genotype with lowest ASV values close to zero (0) and one (1) are the most stable across environments [24,34].

3. RESULTS

3.1 ANOVA for Agronomic Performance Traits of Elite Cassava Genotypes across Alupe, Kakamega and Kibos

Analysis of variance (Table 2) on on agronomic performance traits of elite cassava genotypes with resistance to CMD and CBSD, evaluated across Alupe, Kakamega and Kibos, revealed that location alone had a highly significant influence ($P \leq 0.001$) on biomass yield (t ha^{-1}), fresh root yield (t ha^{-1}), dry matter (DM) yield (t ha^{-1}), harvest index (HI %) and dry matter content (% DMC). Analysis of variance (Table 2) further revealed that genotype alone had significant influence ($P \leq 0.001$) on cyanogenic potential (CNP). The interaction between genotype and location did not have any significant influence ($P \geq 0.05$) on all agronomic performance traits evaluated across Alupe, Kakamega and Kibos.

3.2 Fresh Root Yield (t ha^{-1})

The mean fresh root yield was 9.21 t ha^{-1}, 11.62 t ha^{-1} and 20.35 t ha^{-1} at Alupe, Kakamega and Kibos respectively and 13.73 t ha^{-1}, across the three locations. (Table 3). Kibos recorded the highest fresh root yield (Table 4) on genotypes TZ-130 (32.85 t ha^{-1}) and LM/2008/363 (28.66 t ha^{-1}) and least on Orera (13.71 t ha^{-1}) and Colicanana (15.22 t ha^{-1}). Kakamega recorded the highest fresh root yield (Table 4) on genotypes Mkumba-2 (24.48 t ha^{-1}) and Mkumba (18.57 t ha^{-1}), and least on Kalawe (2.13 t ha^{-1}) and KBH/2006/026 (2.82 t ha^{-1}). Alupe recorded the highest fresh root yield on genotypes Eyope (14.32 t ha^{-1}), KBH/2006/026 (13.58 t ha^{-1}) and NASE-14 (13.65 t ha^{-1}) and least on Kalawe (2.43 t ha^{-1}) and Sauti (4.80 t ha^{-1}). Cassava genotypes with the highest mean biomass yield across the three locations (Table 4) were TZ-130 (19.13 t ha^{-1}) and Mkumba-2 (17.92 t ha^{-1}), while the least was Kalawe (7.70 t ha^{-1}).

3.3 Dry Matter (DM) Yield (t ha^{-1})

The mean DM yield was 3.69 t ha^{-1}, 4.65 t ha^{-1} and 8.14 t ha^{-1} at Alupe, Kakamega and Kibos respectively, and 5.49 t ha^{-1} across the three locations (Table 3). As shown in Table 5, Alupe recorded the highest DM yield on genotypes KBH/2006/026 (7.43 t ha^{-1}), Eyope (5.73 t ha^{-1}) and TZ-130 (5.26 t ha^{-1}), and least on genotypes Kalawe (0.97 t ha^{-1}) and Sauti (1.92 t ha^{-1}). Kakamega recorded the lowest mean DM yield on genotypes Kalawe (0.85 t ha^{-1}) and KBH/2006/026 (1.13 t ha^{-1}) and the highest on genotypes Mkumba-2 (9.79 t ha^{-1}) and Mkumba (7.42 t ha^{-1}). Kibos, on the other hand, recorded the highest mean DM yield on genotypes TZ-130 (13.14 t ha^{-1}) and LM/2008/363 (11.46 t ha^{-1}), and the least on genotypes Orera (5.48 t ha^{-1}) and Yizaso (5.87 t ha^{-1}). Across the three locations (Table 3), the highest DM yield was recorded TZ-130 (7.65 t ha^{-1}) and the least on Kalawe (3.09 t ha^{-1}).

3.4 Biomass Yield (t ha^{-1})

The mean biomass yield was 3.72 t ha^{-1}, 7.98 t ha^{-1} and 9.50 t ha^{-1} at Alupe, Kakamega and Kibos respectively, and 7.07 t ha^{-1} across the three locations. Cassava genotypes TZ-130

(Table 4) recorded the highest biomass yield at Kakamega (12.03 t ha^{-1}) and Kibos (12.37 t ha^{-1}) and not at Alupe (3.04 t ha^{-1}). Alupe recorded the highest biomass yield (Table 4) on genotypes CH05-295 (6.63 t ha^{-1}) and Mkumba-2 (6.24 t ha^{-1}), and the least on Sauti (2.31 t ha^{-1}). Kakamega recorded the highest biomass yield (Table 4) on genotype Yizaso (12.22 t ha^{-1}), and the least on KBH/2002/066 (4.08 t ha^{-1}). While Kibos recorded the highest biomass yield (Table 4) on genotypes Kizimbani (13.94 t ha^{-1}) and Kibandameno (13.56 t ha^{-1}) and the least on Colicanana (4.82 t ha^{-1}). Cassava genotypes with the highest mean biomass yield across the three locations were CH05-203 (9.40 t ha^{-1}) and Sangoja (9.31 t ha^{-1}), while the least were NASE-1 (5.42 t ha^{-1}) and Colicanana (5.48 t ha^{-1}) as shown in Table 4.

3.5 Harvest Index (HI %)

The mean % harvest index was 48.29%, 34.79% and 46.79% at Alupe, Kakamega and Kibos respectively and 43.40% across the three locations (Table 4). Alupe recorded the highest HI on genotypes NASE-3 (60.67%) and KBH/2002/066 (59.97%), and the least HI on genotypes Kalawe (22.58%) and Sangoja (30.00%). Kakamega recorded the least HI on genotypes Kalawe (15.87%), TZ-130 (23.62) and Tajirika (25.31%) and the highest HI on genotypes Mkumba (43.89%) and Colicanana (43.64). Kibos recorded the least HI on genotypes Kizimbani (32.32%) and Orera (32.85%), and the highest HI on genotypes NASE-14 (60.48%) and LM/2008/363 (58.47%). Across the three locations (Table 4), HI for all cassava genotypes ranged from 28-50%, and was highest on genotypes Colicanana (49.59%) and NASE-3 (48.46%), and least on genotypes Sangoja (33.29%) and Kalawe (28.65%) as shown in Table 4.

3.6 Dry Matter Content (% DMC)

The mean % DMC was 36.30%, 44.20% and 42.80% at Alupe, Kakamega and Kibos, respectively, and 41.10% across the three locations (Table 6). Alupe recorded the highest DMC on genotypes NASE-14 (42.60%), NASE-3 (41.20%) and Pwani (41.80%) and the least DMC on genotypes Kibandameno (28.90%) and NASE-1 (26.40%). Kakamega recorded the highest DMC on genotypes CH05-203 (53.30%) and Colicanana (50.50%) and the least DMC on genotypes KBH/2006/026 (29.70%) and KBH/2002/066 (38.30%). Kibos recorded the highest DMC on genotype KBH/2002/066 (46.10%) and NASE-18 (45.90%) and the least DMC on genotypes NASE-14 (39.40%) and TZ-130 (39.90%). Across the three locations (Table 6), genotypes with the highest DMC were CH05-203 (44.69%), Kizimbani (43.71%) and Pwani (43.58%) and genotypes with least DMC were TZ-130 (37.47%) and KBH/2006/026 (36.27%).

3.7 Cyanogenic Potential (CNP)

All the 24 cassava genotypes across the three locations had mean CNP levels ranging from of 3.00–6.00 (Table 6), categorized as very low, low, moderately low and moderate CNP levels. As shown in Tables 5 and 6, the analysis revealed distinct genotypes for each picrate concentration (PC) category across the three locations. Hence, very low CNP (PC Score 3.00)

Table 2. ANOVA for agronomic performance of cassava genotypes 12 MAP at Alupe, Kakamega and Kibos

Agronomic traits	Location (L)			Genotype (G)			Interaction (G*L)		
	DF	Mean square	F-value	DF	Mean square	F-value	DF	Mean square	F-value
Fresh Root Yield, t ha^{-1}	2	2471.17	39.51***	23	47.85	0.77	46	62.71	1.00
Biomass Yield, tha^{-1}	2	640.61	49.56***	23	13.15	1.02	46	14.98	1.16
Dry Matter Yield, t ha^{-1}	2	395.39	39.51***	23	7.66	0.77	46	10.03	1.00
Harvest Index (%)	2	3752.35	15.39***	23	205.10	0.84	46	191.28	0.78
Dry Matter Content (%)	2	1243.56	35.07***	23	42.98	1.21	46	43.54	1.23
Cyanogenic Potential	2	0.12	0.88	23	11.12	79.51***	46	0.20	1.41

*DF = Degrees of Freedom; *** = Significance (P≤0.001)*

Table 3. Means and AMMI Stability Values (ASV) with ranks of fresh root and Dry Matter (DM) yield for elite cassava genotypes 12 MAP at Alupe, Kakamega and Kibos

Cassava genotypes	Fresh root yield, t ha^{-1}						Dry Matter (DM) yield, t ha^{-1}					
	Alupe	Kakamega	Kibos	Mean	ASV	Rank	Alupe	Kakamega	Kibos	Mean	ASV	Rank
CH05-203	11.98	9.52	23.49	15.00^{ab}	1.05	6	4.79	3.81	9.40	6.00^{ab}	0.42	6
Colicanana	9.22	16.67	15.22	13.70^{ab}	3.16	17	3.69	6.67	6.09	5.48^{ab}	1.27	17
Eyope	14.32	14.16	19.04	15.84^{ab}	1.28	7	5.73	5.66	7.61	6.33^{ab}	0.51	7
F10-30-R5	7.07	16.74	23.98	15.92^{ab}	1.80	10	2.83	6.70	9.59	6.37^{ab}	0.72	9
F19-NL	5.51	7.76	25.16	12.81^{ab}	3.01	15	2.20	3.11	10.06	5.12^{ab}	1.21	15
Kalawe	2.43	2.13	18.59	7.70^{a}	1.89	11	0.97	0.85	7.44	3.09^{a}	0.75	11
KBH/2002/066	9.34	9.52	18.18	12.35^{ab}	0.21	1	3.74	3.81	7.27	4.94^{ab}	0.08	1
KBH/2006/026	13.58	2.82	17.82	12.35^{ab}	5.31	23	5.43	1.13	7.13	4.94^{ab}	2.12	23
Kibandameno	7.15	11.22	21.93	13.43^{ab}	0.41	2	2.86	4.49	8.77	5.37^{ab}	0.16	2
Kizimbani	9.18	11.45	15.88	12.17^{ab}	0.77	4	3.67	4.58	6.35	4.87^{ab}	0.31	4
LM/2008/363	9.68	10.38	28.66	16.24^{ab}	3.17	18	3.87	4.15	11.46	6.49^{ab}	1.27	18
Mkumba	7.26	18.57	16.30	14.05^{ab}	4.16	21	2.91	7.43	6.52	5.62^{ab}	1.67	21
Mkumba-2	10.72	24.48	18.57	17.92^{b}	7.20	24	4.29	9.79	7.43	7.17^{b}	2.88	24
NASE-1	5.89	6.81	25.46	12.72^{ab}	3.50	20	2.36	2.73	10.18	5.09^{ab}	1.40	20
NASE-14	13.65	6.01	21.04	13.57^{ab}	3.16	16	5.46	2.40	8.42	5.43^{ab}	1.26	16
NASE-18	9.67	8.97	22.19	13.61^{ab}	0.65	3	3.87	3.59	8.88	5.44^{cd}	0.26	3
NASE-3	12.89	11.32	19.31	14.50^{ab}	0.79	5	5.15	4.53	7.72	5.80^{ab}	0.31	5
Orera	10.00	11.45	13.71	11.72^{ab}	1.99	13	4.00	4.58	5.48	4.69^{ab}	0.80	13
Pwani	10.11	16.35	17.13	14.53^{ab}	1.93	12	4.04	6.54	6.85	5.81^{ab}	0.77	12
Sangoja	5.42	15.22	20.49	13.71^{ab}	1.67	8	2.17	6.09	8.20	5.49^{ab}	0.67	8
Sauti	4.80	14.63	17.93	12.45^{ab}	1.80	9	1.92	5.85	7.17	4.98^{ab}	0.72	10
Tajirika	10.25	5.18	20.75	12.06^{ab}	2.11	14	4.10	2.07	8.30	4.82^{ab}	0.84	14
TZ-130	13.15	11.40	32.85	19.13^{ab}	5.14	22	5.26	4.56	13.14	7.65^{b}	2.06	22
Yizaso	7.83	16.23	14.67	12.91^{ab}	3.26	19	3.13	6.49	5.87	5.16^{ab}	1.30	19
Location Mean	9.21	11.62	20.35	13.70			3.69	4.65	8.14	5.49		

*ASV=AMMI Stability Value (Nduwumuremyi et al. 2017; Purchase, Hatting and Deventer 2013); $LSD_{0.05}$ = least significance difference at 5% (Fresh root yield, $LSD_{0.05}$ location = 7.34, $LSD_{0.05}$ variety = 2.61, $LSD_{0.05}$ loc*var = 12.77; Dry Mater (DM) yield - $LSD_{0.05}$ location = 2.95, $LSD_{0.05}$ variety = 1.04, $LSD_{0.05}$ loc*var = 5.11); CV_{rep} = % Coefficient of Variation; (Fresh root yield, CV% $_{rep}$ = 4.70; DM yield, CV% $_{rep}$ = 4.78); SE-Standard Error (Biomass yield, SE = 1.20; Fresh root yield, SE = 1.05); Means with different superscript letters were significantly different (P<0.05)*

Table 4. Means of biomass yield and harvest index for elite cassava genotypes 12 MAP at Alupe, Kakamega and Kibos

Cassava genotypes	Biomass yield, t ha^{-1}				Harvest index (%)			
	Alupe	Kakamega	Kibos	Mean	Alupe	Kakamega	Kibos	Mean
CH05-203	6.63	10.06	8.51	9.40^{a}	40.63	33.85	52.45	42.31^{ab}
Colicanana	3.12	8.49	4.82	5.48^{a}	49.01	43.64	56.13	49.59^{b}
Eyope	4.13	9.41	10.41	7.98^{a}	56.49	37.38	42.85	45.57^{ab}
F10-30-R5	2.92	10.63	11.38	8.31^{a}	50.62	37.57	47.23	45.14^{ab}
F19-NL	3.72	5.30	10.77	6.59^{a}	41.75	35.20	51.89	42.94^{ab}
Kalawe	2.68	4.56	9.41	5.55^{a}	22.58	15.87	47.51	28.65^{a}
KBH/2002/066	2.76	4.08	11.28	6.75^{a}	59.97	41.06	38.55	46.55^{ab}
KBH/2006/026	4.10	5.27	11.47	6.04^{a}	57.83	26.39	38.01	43.91^{ab}
Kibandameno	4.20	8.08	13.56	8.62^{a}	53.88	35.95	39.07	43.97^{ab}
Kizimbani	2.94	8.77	13.94	9.55^{a}	55.48	37.65	32.32	41.82^{ab}
LM/2008/363	4.16	6.34	8.14	6.21^{a}	47.97	37.51	58.47	47.98^{b}
Mkumba	3.07	9.75	7.40	6.74^{a}	40.74	43.89	46.83	43.82^{ab}
Mkumba-2	6.24	9.95	6.23	7.47^{a}	43.08	40.36	54.97	46.14^{ab}
NASE-1	2.45	5.49	8.31	5.42^{a}	49.59	31.62	55.60	45.60^{ab}
NASE-14	3.73	8.50	5.69	5.97^{a}	57.23	26.98	60.48	48.28^{b}
NASE-18	3.51	4.71	8.71	5.64^{a}	52.63	40.39	50.19	47.7^{4b}
NASE-3	3.27	5.48	8.74	5.83^{a}	60.67	37.41	47.29	48.46^{b}
Orera	4.03	5.35	11.87	7.08^{a}	49.77	39.15	32.85	40.59^{ab}
Pwani	4.88	11.30	6.69	7.62^{a}	45.66	36.73	50.11	44.17^{ab}
Sangoja	4.68	11.24	12.01	9.31^{a}	30.00	29.93	39.94	33.29^{ab}
Sauti	2.31	7.06	10.53	6.63^{a}	37.08	43.47	38.92	39.83^{ab}
Tajirika	4.17	7.36	9.12	6.68^{a}	46.39	25.31	45.10	38.93^{ab}
TZ-130	3.04	12.03	12.37	9.15^{a}	55.70	23.62	50.33	43.22ab
Yizaso	2.62	12.22	6.67	7.17^{a}	54.17	33.94	45.74	44.62^{ab}
Location Mean	3.72	7.98	9.50	7.07	48.29	34.79	46.79	43.40

*$LSD_{0.05}$ = least significance difference at 5% (Biomass yield - $LSD_{0.05}$ location = 2.95, $LSD_{0.05}$ variety = 1.04, $LSD_{0.05}$ loc*var = 5.11; Harvest Index - $LSD_{0.05}$ location = 14.23, $LSD_{0.05}$ variety = 5.03, $LSD_{0.05}$ loc*var=9.58); CV_{rep} = % Coefficient of Variation (Biomass yield, CV% $_{rep}$ = 4.70; Harvest Index - CV% $_{rep}$ = 8.50); SE-Standard Error (Biomass yield, SE = 2.63; Harvest Index, SE = 3.20); Means with different superscript letters were significantly different (P<0.05)*

Table 5. Means of dry matter content (% DMC) and Cyanogenic Potential (CNP) for elite cassava genotypes 12 MAP in Alupe, Kakamega and Kibos

Genotype	Dry matter content (% DMC)				Cyanogenic Potential (CNP)			
	Alupe	Kakamega	Kibos	Mean	Alupe	Kakamega	Kibos	Mean
CH05-203	39.30	53.30	41.50	44.69^{c}	6.00	6.00	6.00	6.00^{e}
Colicanana	34.30	50.50	40.60	41.82^{abc}	4.00	4.00	4.00	4.00^{b}
Eyope	37.40	44.50	42.50	41.47^{abc}	6.00	5.33	6.00	5.78^{e}
F10-30-R5	38.80	45.50	43.80	42.71^{abc}	4.00	3.67	4.00	3.89^{b}
F19-NL	35.90	44.10	43.70	41.24^{abc}	4.00	4.00	4.00	4.00^{b}
Kalawe	32.70	42.50	42.00	39.07^{abc}	5.00	5.00	5.00	5.00^{d}
KBH/2002/066	38.30	38.30	46.10	40.91^{abc}	3.00	3.00	3.00	3.00^{a}
KBH/2006/026	39.30	29.70	40.60	36.27^{a}	6.00	6.00	6.00	6.00^{e}
Kibandameno	28.90	45.00	43.70	39.22^{abc}	4.00	4.00	4.00	4.00^{b}
Kizimbani	39.80	45.70	45.60	43.71^{bc}	5.00	4.67	5.00	4.89^{cd}
LM/2008/363	36.50	41.40	40.10	39.31^{abc}	6.00	6.00	6.00	6.00^{e}
Mkumba	38.30	47.60	43.80	43.24^{bc}	3.00	4.00	3.00	3.33^{a}
Mkumba-2	37.90	47.10	44.40	43.10^{1abc}	3.00	3.00	3.00	3.00^{a}
NASE-1	26.40	45.90	42.90	38.40^{abc}	3.00	3.00	3.00	3.00^{a}
NASE-14	42.60	45.00	39.40	42.33^{abc}	5.00	4.00	5.00	4.67^{cd}
NASE-18	33.20	41.10	45.90	40.04^{abc}	3.00	3.00	3.00	3.00^{a}
NASE-3	41.20	42.90	44.90	43.00^{abc}	6.00	5.00	6.00	5.67^{e}
Orera	36.00	42.10	43.30	40.44^{abc}	4.00	4.00	4.00	4.00^{b}
Pwani	41.80	47.10	41.90	43.58^{bc}	6.00	6.00	6.00	6.00^{e}
Sangoja	38.90	45.70	41.70	42.11^{abc}	4.00	4.33	4.00	4.11^{b}
Sauti	30.50	43.90	45.20	39.87^{abc}	3.00	3.33	3.00	3.11^{a}
Tajirika	36.50	44.30	42.30	41.04^{abc}	5.00	5.00	5.00	5.00^{d}
TZ-130	30.30	42.10	39.90	37.47^{ab}	5.00	4.67	4.00	4.56^{c}
Yizaso	35.60	45.30	41.70	40.84^{abc}	6.00	6.00	6.00	6.00^{e}
Location Mean	36.30	44.20	42.80	41.10	4.54	4.46	4.50	4.50
Std. Error (SE)	2.00	2.00	2.00	2.00	0.22	0.22	0.22	0.22
$LSD_{0.05}$ Locat	5.53	5.53	5.53	5.53	0.12	0.12	0.12	0.12
$LSD_{0.05}$ Variety	1.96	1.96	1.96	1.96	0.35	0.35	0.35	0.35
$LSD_{0.05}$ L*V	9.58	9.58	9.58	9.58	0.61	0.61	0.61	0.61
CV% rep	2.80	2.80	2.80	2.80	0.30	0.30	0.30	0.30

$LSD_{0.05}$ = least significance difference at 5%; CV = % Coefficient of Variation; SE-Standard Error; Means with different superscript letters were significantly different (P<0.05)

Table 6. Cyanogenic Potential (CNP) for elite cassava genotypes at 12 MAP at Alupe, Kakamega and Kibos

Very low CNP (PC score 3.00)	Low CNP (PC score 4.00)	Moderately low CNP (PC score 5.00)	Moderate CNP (PC score 6.00)
KBH/2002/066 (3.00[a])	Colicanana (4.00[b])	Kalawe (5.00[d])	CH05-203 (6.00[e])
Mkumba (3.33[a])	F10-30-R5 (3.89[b])	Kizimbani (4.89[cd])	Eyope (5.78[e])
Mkumba-2 (3.00[a])	Kibandameno (4.00[b])	NASE-14 (4.67[cd])	KBH/2006/026 (6.00[e])
NASE-1 (3.00[a])	Orera (4.00[b])	Tajirika (5.00[d])	LM/2008/363 (6.00[e])
NASE-18 (3.00[a])	Sangoja (4.11[b])	TZ-130 (4.56[c])	NASE-3 (5.67[e])
Sauti (3.11[a])	F19-NL (4.00[b])		Pwani (6.00[e])
			Yizaso (6.00[e])

Values in brackets represents the actual mean cyanide levels for each genotype; *Means with different superscript letters were significantly different (P<0.05)*

Table 7. Confirmation of stable and unstable amongst elite cassava genotypes based on ASV and ranks for yield performance across Alupe, Kakamega and Kibos

Parameter	Rank 1	Rank 2	Rank 3	Rank 4	Rank 5
Stable genotypes across environments					
Fresh Root Yield	KBH/2002/066 (0.21)	Kibandameno (0.41)	NASE-18 (0.65)	Kizimbani (0.77)	NASE-3 (0.79)
Dry Matter Yield	KBH/2002/066 (0.08)	Kibandameno (0.16)	NASE-18 (0.26)	Kizimbani (0.31)	NASE-3 (0.31)
Combined Agronomic	KBH/2002/066 (0.15)	Kibandameno (0.29)	NASE-18 (0.46)	Kizimbani (0.54)	NASE-3 (0.55)
Unstable genotypes adapted more to specific environments					
	Rank 20	**Rank 21**	**Rank 22**	**Rank 23**	**Rank 24**
Fresh Root Yield	NASE-1 (3.50)	Mkumba (4.16)	TZ-130 (5.14)	KBH/2006/026 (5.31)	Mkumba-2 (7.20)
Dry Matter Yield	NASE-1 (1.40)	Mkumba (1.67)	TZ-130 (2.06)	KBH/2006/026 (2.12)	Mkumba-2 (2.88)
Combined Agronomic	NASE-1 (2.45)	Mkumba (2.92)	TZ-130 (3.60)	KBH/2006/026 (3.72)	Mkumba-2 (5.04)

genotypes comprised of KBH/2002/066 (3.00), Mkumba (3.33), Mkumba-2 (3.00), NASE-1 (3.00), NASE-18 (3.00) and Sauti (3.11). Low CNP (PC score 4.00) genotypes comprised Colicanana (4.00), F10-30-R5 (3.89), Kibandameno (4.00), NASE-14 (4.00), Orera (4.00), Sangoja (4.11) and F19-N (4.00).. Moderately low CNP (PC score 5.00) genotypes comprised Kalawe (5.00), Kizimbani (4.89), NASE-14 (4.67), Tajirika (5.00) and TZ-130 (4.46). Moderate CNP (PC score 6.00) genotypes comprised CH05-203 (6.00), Eyope (5.78), KBH/2006/026 (6.00), LM/2008/363 (6.00), NASE-3 (5.67), Pwani (6.00) and Yizaso (6.00).

3.8 Correlation among Disease Resistance and Agronomic Traits

As shown in Tables 3 and 5, DM yield was used to estimate the % DMC and hence the highly positive (1.000) significant relationship ($P = 0.001$) between them (Table 8). Therefore, the correlation coefficients and P - values of DM yield and % DMC with other agronomic and disease resistance parameters are the same (Table 8). The relationship of CNP with other agronomic parameters was positive and weak, but not significant ($P \geq 0.05$) as shown in Table 8. DM yield was significant ($P \leq 0.05$) and positively correlated with biomass yield, HI and fresh root yield. The relationship between HI and fresh root yield was positive and highly significant ($P = 0.001$). However, HI was highly negatively ($P = 0.001$) associated with biomass yield. Further, HI was negative but significantly associated with DM yield ($P = 0.01$) and % DMC ($P = 0.05$). The relationship between biomass yield, DM yield, % DMC and fresh root yield was positive and highly significant ($P = 0.001$). There was also a highly significant ($P = 0.001$) and positive relationship between fresh root yield and HI for the 24 cassava genotypes across the three locations (Table 8). However, the relationship

between fresh root yield, DM yield and % DMC was positively weak but significant (*P ≤ 0.05*). The correlation between disease resistance parameters (CMD and CBSD incidence and severity) 12 MAP across the three locations was positive and highly significant (*P ≤ 0.05*) as shown in Table 8. The relationship between biomass yield and disease resistance parameters was negative (inverse), but significant (*P ≤ 0.05*). While, the relationship between HCN and disease resistance parameters was inverse, but not significant (*P ≥ 0.05*). The relationship between DM yield, % DMC and disease resistance parameters was inverse, but highly significant (*P ≤ 0.001*). The association between HI with CBSD incidence, CBSD severity and CMD incidence was positive, but not significant (*P ≥ 0.05*), while CMD severity was inverse, but not significant (*P ≥ 0.05*). The relationship between fresh root yield and CBSD incidence was inverse, but not significant (*P ≥ 0.05*). However, as shown in Table 8, the relationship between fresh root yield with CBSD severity, CMD incidence and CMD severity was negative, bit significant (*P ≤ 0.05*).

3.9 Confirmation of Stability for Yield Performance amongst Cassava Genotypes

Confirmation of stability for yield performance (fresh root and dry matter yield) by the 24 cassava genotypes at Alupe, Kakamega and Kibos was achieved using AMMI analysis (Table 4). AMMI stability values and hence genotype ranks, showed that yield performance amongst cassava genotypes was variable across Alupe, Kakamega and Kibos. However, based on ASV, the top five genotypes with best possible yield performance, due to their very low ASV values hence high stability, are listed in Table 7. Dry matter (DM0 yield was derived from fresh root yield, hence genotype ASV between the two were the same (Tables 4 and 7). Therefore, stable genotypes for fresh root yield and DM yield, respectively, across Alupe, Kakamega and Kibos were KBH/2002/066 (0.21, 0.08), Kibandameno (0.41, 0.16), NASE-18 (0.65, 0.26), Kizimbani (0.77, 0.31) and NASE-3 (0.79, 0.31). AMMI analysis based on AMMI Stability Value (ASV) and genotype ranks identified unstable genotypes, with more specific adaptability, across Alupe, Kakamega and Kibos as shown in Table 4 and 7. Unstable genotypes for fresh root yield and DM yield, respectively, based on ASV were NASE-1 (3.50, 1.40), Mkumba (4.16, 1.67), TZ-130 (5.14, 2.06), KBH/2006/026 (5.31, 2.12) and Mkumba-2 (7.20, 2.88). Based on combined ASVs and ranking (Table 7), elite cassava genotypes that were stable for yield performance acoss Alupe, Kakamega and Kibos comprised NASE-18, F10-30-R5, NASE-3, Tajirika and Eyope. While, genotypes that were unstable, with specific adaptability across Alupe, Kakamega and Kibos comprised KBH/2006/026, TZ-130, NASE-14, Kalawe and Mkumba-2. It should be noted that Mkumba-2 was adopted from the remaining planting materials (left overs) of Mkumba to balance the Alpha lattice design. Hence, the quality of the planting materials could have been low, leading to poor performance compared to the original Mkumba.

4. DISCUSSION

The results from this study showed significant differences (*P ≤ 0.05*) between genotypes and location or agro-ecology, but not interaction *(P ≥ 0.05*), for all the agronomic performance parameters evaluated. This implies that the 24 elite cassava genotypes responded differently to agronomic performance at Alupe, Kakamega and Kibos. These findings were almost similar to what was reported by [36,37], who found out significant variation in agronomic traits among cassava genotypes evaluated in diverse locations and at different harvesting times and interactions. The same experiences on genotype by environment interaction were variously reported by [29,28,38,7,6,3].

Previous studies have shown cyanide potential (HCN) varies considerably with genotypes and across environment [38]. However, this study found significant difference (*P ≤ 0.05*) for CNP between cassava genotypes, but not location and genotype by location interaction, contrary to what has been reported in previous studies. Cyanide content of fresh storage roots was determined by Picrate acid concentration score (PC) method, characterized by colour change of the picrate on a 125 mm Whatman® filter paper strip as described by [33]. Colour change from pale green to dark brown was scored on a scale of 1 to 14 corresponding to a cyanide content of between < 10ppm to > 450ppm. According to [39,40,38], different varieties of cassava also have variations in their root's cyanogenic content, ranging from 10 to 450 mg HCN- .kg-1 fresh weight. Among the two main cassava groups, bitter cassava is characterized by its high contents of Cyanogenic Glycosides (15–450 mg HCN per kilogram of fresh weight of roots) while

Table 8. Correlations among agronomic performance and disease resistance traits for elite cassava genotypes 12 MAP at Alupe, Kakamega and Kibos

Agronomic and disease parameters	Biomass yield	CBSD incidence	CBSD severity	CMD incidence	CMD severity	HCN	DM yield	DM content	Harvest index
CBSD Incidence	-0.196*								
CBSD Severity	-0.133*	0.916***							
CMD Incidence	-0.184**	0.820***	0.779***						
CMD Severity	-0.202**	0.758***	0.747***	0.931***					
HCN	0.102	-0.063	-0.047	-0.061	-0.073				
DM Yield	0.332***	-0.384***	-0.363***	-0.468***	-0.537***	0.012			
DM Content	0.332***	-0.384***	-0.363***	-0.468***	-0.537***	0.012	1.000***		
Harvest Index (%)	-0.353***	0.027	0.005	0.013	-0.027	0.019	-0.153**	-0.153*	
Fresh Root Yield	0.410***	-0.168	-0.140*	-0.183***	-0.208**	0.068	0.134*	0.134*	0.587***

*Correlation Coefficients and level of significance test *=P<0.05, **=P<0.01, ***=P<0.001*

sweet cassava with low cyanide contents will typically contain approximately 10–150 mg HCN per kilogram of fresh weight of roots. All the 24 cassava genotypes evaluated across the three locations in this study had mean CNP levels ranging from of 3.00–6.00 (specifically, very low, low, moderately low and moderate CNP levels based on PC scale) and were therefore, sweet and not bitter.

Harvest index (HI) is used to determine the efficiency by which cassava converts the dry matter into the economic tuberous roots yield [36]. The shorter the variety the higher the index value. The more the value of the HI of a crop or a variety the more is the efficiency of the crop to convert the dry matter into the economic part, which is the tuberous root for cassava crop. Studies have shown that HI negatively correlates with plant biomass yield and positively correlates with tuberous roots yield. It is expected that an increase in plant biomass yield consequently reduces HI since it represents the ratio between tuberous root yields and total plant weight. On the other hand, increasing tuberous roots yield induces higher harvest indexes [28,41] This finding was consistent with the present study, where harvest index was average (mean 43.29%) for the 24 genotypes. Further, harvest index was negatively correlated to biomass yield, hence an increase in biomass yield would result into a decrease in HI and vice versa; but positively and significantly correlated to fresh root yield. As previously reported by [41], and similar to findings of this study, there was great variability among the data for agronomic performance of cassava genotypes, which was verified by the range of the results of the evaluated traits: mean tuberous fresh roots yield - 7.70 to 19.13 t ha^{-1}; mean dry matter (DM) yield - 3.09-7.65 t ha^{-1}; mean shoot biomass yield - 5.42 to 9.55 t ha^{-1}; mean harvest index – 28.65 to 49.59%; mean dry matter content – 36.27 to 44.69 and cyanogenic potential (CNP) – 3.00 to 6.00, with the respective means of 13.70 t ha^{-1}; 5.49 t ha^{-1}; 7.07 t ha^{-1}; 43.10%, 41.10% and 4.50.

Although CMD and CBSD incidence and severity correlated negatively in many cases with biomass yield, fresh root yield and harvest index, some of the 24 elite cassava genotypes had significant low fresh root yield, even with mild or no symptoms, indicating lack of a general correlation between symptom severity and yield loss. The presence of highly significant differences between the test environments for fresh root yield revealed that the 24 elite cassava genotypes performed differently across the three locations. The significance of environmental effects in evaluating cassava genotypes for agronomic performance was also manifested by the significant G x E interaction effects. The current result was supported by previous similar findings [28,42,36]. Correlation results, further, show that location level occurrences of CBSD and CMD were dependent of each other, due to positive correlation between them. Hence, infection with either disease seemed to affect the incidence and severity of the other. Similar observations on responses of the different varieties to the two diseases were reported previously [3,15,43]. The significant but negative relationship between CMD and CBSD incidence and severity with agronomic performance implied that their relationship was inverse. This was consistent with findings reported by several authors [5,6,37,43,45].

Confirmation of stability for agronomic performance was achieved through AMMI analysis. The AMMI model combines the analysis of variance for the genotype and environment main effects with principal components analysis of the GEI interaction effect. Stability (genotype-environment productivity and performance) was confirmed by the AMMI stability value (ASV), developed by (Purchase et al. 2013), based on the AMMI model's IPCA1 and IPCA2 (interaction principal components axes 1 and 2, respectively) scores for each genotype. The ASV is comparable with the joint regression methods of [22,20] to determine stability. Hence, genotypes with lower ASV values are considered more stable and genotypes with higher ASV are unstable. Based on ASV, this study was able to identify stable and unstable genotypes for yield performance across Alupe, Kibos and Kakamega. Stable genotypes for fresh root yield and DM yield, across Alupe, Kakamega and Kibos were KBH/2002/066, Kibandameno, NASE-18, Kizimbani and NASE-3. Unstable genotypes for fresh root yield and DM yield, based on ASV and ranks were NASE-1, Mkumba, TZ-130, KBH/2006/026 and Mkumba-2.

5. CONCLUSION

The relationship between CMD and CBSD incidence and severity and their combined influence on agronomic performance of elite cassava genotypes was variable across across Alupe, Kakamega and Kibos, verified by the

range of results of evaluated traits. Stability for high yield is the ultimate objective of cassava breeding programmes, as cassava is mainly grown for its storage roots. The study, using AMMI analysis, based on AMMI Stability Value (ASV) identified stable genotypes for yield performance (tuberous fresh root yield and dry matter (DM) yield), across Alupe, Kakamega and Kibos. These were KBH/2002/066, Kibandameno (a local standard check), NASE-18, Kizimbani and NASE-3. All the genotypes were sweet, with cyanogenic potential between 3.00 and 6.00. These superior genotypes needs to be further evaluated in more environments to assess their specific and wider adaptability and stability, including possible recommendation for release to farmers for cultivation.

DISCLAIMER

The materials/products used for this research are commonly and predominantly use materials/ products in our area of research and country. There is absolutely no conflict of interest between the authors and producers of the products because we do not intend to use these products as an avenue for any litigation but for the advancement of knowledge. Also, the research was not funded by the producing company rather it was funded by personal efforts of the authors.

FUNDING

This study was undertaken using a scholarship from the International Institute of Tropical Agriculture (IITA) through “The New Cassava Varieties and Clean Seed to Combat CBSD and CMD (5CP)” Project funded by the Bill & Melinda Gates Foundation.

ACKNOWLEDGEMENTS

The authors are greatly thankful to International Institute of Tropical Agriculture (IITA) and the Bill and Melinda Gates Foundation (BMGF) under the “The New Cassava Varieties and Clean Seed to Combat CBSD and CMD (5CP) Project, for the MSc scholarship and funding of the research. We thank the Director General, Kenya Agricultural and Livestock Research Organization (KALRO) for permission to undertake the studies, and the staff of KALRO-Kakamega, Embu, Kibos and Alupe for providing technical and logistical assistance during the study. We also thank Jomo Kenyatta University of Agriculture and Technology (JKUAT) for providing excellent institutional and professional support.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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