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Genotype-by-Environment interaction for yam (*Dioscorea species)* mosaic virus resistance, dry matter content, and yields in Uganda

Emmanuel Amponsah Adjei[1,2,4,*], Williams Esuma[3], Titus Alicai[3], Emmanuel Boache Chamba[4], Richard Edema[1,2], Isaac Onziga Dramadri[1,2], Alfred Adebo Ozimati[3,6], Rolland Agaba[1,5] and Thomas Lapaka Odong[1]

[1]Department of Agricultural Production, College of Agricultural and Environmental Sciences, Makerere University, P.O. Box 7062, Kampala, Uganda

[2]Makerere University Regional Centre for Crop Improvement, Makerere University. P.O. Box 7062, Kampala, Uganda

[3]National Crops Resources Research Institute, National Agricultural Research Organization, P.O. Box 7084, Kampala, Uganda

[4]Council for Scientific and Industrial Research, Savanna Agricultural Research Institute, P.O. Box TL 52 Tamale, Ghana

[5]Kachwekano Zonal Agricultural Research and Development Institute, National Agricultural Research Organization, P.O. Box 421, Kabale Uganda

[6]College of Natural Science, School of Bioscience, Department of Plant Science, Microbiology and Biotechnology, Makerere University, P.O. Box 7062, Kampala, Uganda

* Correspondence: emmaadjei1@gmail.com; Tel.: +256771023078

Abstract: Often yam varieties grown in different agro-ecologies show differential responses across production environments, a term known as genotype-by-environment interaction. Genotype-by-environment interaction makes selecting the best genotypes under varied production environments more complex. This study tested twenty yam genotypes evaluated in six test environments to assess genotype, environment, and the interaction between genotypes and environmental effect for tuber yield, yam mosaic virus, and dry matter content. The experiments were conducted in two seasons across three locations in Uganda using a randomized complete block design with three replications. The results showed a significant effect ($p \leq 0.001$) for genotype (G), environment (E), and genotype by environment interaction for all the traits. Serere 2021 and Namulonge 2021 were identified as the most discriminating and representative environments for testing the yam mosaic virus, respectively. Serere 2021 was recognized as the most discriminating environment, whereas Arua 2021 was identified as the closest to an ideal environment for assessing yam tuber yields. The tested genotypes also exhibited high resistance to yam mosaic virus disease, high tuber yields, and high dry matter content. Genotypes UGY16020, UGY16034, UGY16042, and UGY16080 demonstrated great resistance to yam mosaic virus disease, high yielding, and considerable dry matter content and are thus potential parents for yam improvement. Further evaluation of the four genotypes should be done under farmers' production systems for selection, improvement, and release as new yam varieties for Uganda

Keywords: *Dioscorea*; yield stability; environments; genotype; dry matter; disease resistance; Uganda.

1. Introduction

Yam (*Dioscorea* spp.) is one of the strategic crops for sustainable food production in Africa, given its superior productivity compared to other crops [1]. It is an important tuber crop with major food, commercial and socio-cultural values. Globally, *Dioscorea alata* is the most widely cultivated species but it is second to *Dioscorea rotundata* in terms of the quantity produced in Africa [2]. The significance of yam in terms of volume and value of production cannot be over-emphasized in Africa and beyond. Africa accounts for over 95% of the world's annual production of about 49 million tons [3]. The yam belt region of West Africa, which includes Benin, Ghana, Ivory Coast, Nigeria, and Togo, produces nearly 96% of global production with Nigeria as the world's leading yam producer, accounting for more than 65% of worldwide production (72.6 million tonnes) [3]. Within the yam belt, over 60 million people are directly involved in yam production [4]. Yam is, therefore, an economically important part of the GDP of the top producers and exporters in West African countries. For instance, Ghana's yam exports between 2017 and 2018 increased by USD 5.4 million [5] from USD 3.4 million.

Yam cultivation is suited to humid and subhumid lowlands. In the yam belt, the most suitable agro-ecological zones for yam production (also called yam agroecology) are Deciduous Forest and Savannahs areas [4] as such, there is evidence of strong genotype and environment interaction effect [6]. Thus, multi-location trials are important in yam breeding programs to enable the identification of genotypes with desired performance for broad or particular adaptation [7]. Stable genotypes are those that show minimal genotype by environment interaction across environments [8,9].

There exists scanty information and data on yams in East Africa [10]. In Uganda, yams are grown on small-scale farms, often intercropped within banana fields with crops such as coffee, cassava, and cocoyam, or as individual plants grown against trees for support. It is also mono-cropped in a few areas such as Eastern Uganda where it has local importance [11]. The crop plays a vital role in local livelihood, particularly in densely populated areas of central, northern, and eastern parts of the country. Yams have become an important cash crop in most localities. Yams are also served during the traditional homes of Uganda which coincides with the lean season thus allowing farmers to earn profit from the market. It grows in the altitude range of 1140 to 2200 and in a wide range of soils mainly in clay, clay loam, sandy, and sandy loam types [12]. It is planted in March-April (in most parts of Uganda) and harvested in November and December (in most parts of the country)

Several studies have reported a strong genotype and environment interaction (GEI) in yam [13] [14]. A stability study of seven white yam genotypes in 13 environments in Ghana by Otoo et al. [15] showed that the genotypes accounted for 8.9%, environment 30.8%, and G x E 43.7% of the total variation. It was concluded that yam improvement, therefore, should be focused on multiple diseases and pest resistance, which would guarantee the stability of crop performance. With disease incidence, severity, and environmental effects, Pinnschmidt and Hovmøller [16] explain that one major problem frequently encountered in deploying resistant host plants for disease control is the plasticity of phenotypic expression of resistance across different environments due to the interaction between host genotypes and the environment. Earlier reports have attributed variation in yield performance of yam to inherent genotypic characteristics, as well as preferences for different environmental conditions [2,9]. Therefore, careful evaluation is critical in identifying the suitable genotypes that will give the highest possible yield in different environments [13]. High yield and stability of genotypes across different environments are very important attributes desired by plant breeders. As a result, breeding materials are tested in diverse environments to assess the consistency in genotypic performance in order to identify superior ones for wider or specific adaptation [17]. Genotypes whose G×E interaction effect remains insignificant from one environment to the other and across years are considered stable [18].

The principal aim of our study was to evaluate the effect of Genotype x Environment Interaction on yam mosaic virus disease, tuber yield, and dry matter content of Uganda yam genetic resources in six test environments. In addition, we examined the magnitude of genotype by environment interactions for traits studied and reported the performance of the crop in the different agro-ecologies.

2. Materials and Methods

2.1 Genetic materials

A total of twenty (20) yam genotypes comprising fourteen (14) landraces assembled at National Crops Resources Research Institute (NaCRRI), Uganda, and six (6) new introductions from West Africa were used for evaluation in this study (Table 1).

Table 1. Yam genotypes used for the study

S/N	Field Code	Status	Origin
1	UGY16001	Landrace	Uganda
2	UGY16012	Landrace	Uganda
3	UGY16020	Landrace	Uganda
4	UGY16080	Landrace	Uganda
5	UGY16085	Landrace	Uganda
6	UGY16003	Landrace	Uganda
7	UGY16013	Landrace	Uganda
8	UGY16022	Landrace	Uganda
9	UGY16034	Landrace	Uganda
10	UGY16039	Landrace	Uganda
11	UGY16042	Landrace	Uganda
12	UGY16064	Introduced	Nigeria
13	UGY16065	Introduced	Nigeria
14	UGY16066	Introduced	Nigeria
15	UGY16067	Introduced	Nigeria
16	UGY16069	Landrace	Uganda
17	UGY16070	Landrace	Uganda
18	UGY16071	Landrace	Uganda
19	UGY16073	Introduced	Nigeria

20	UGY16075	Introduced	Nigeria

2.2 Experimental sites and cropping seasons

The trials were established at three sites. ie. Arua in North-Western Uganda, Serere in eastern Uganda, and Namulonge in central Uganda. The trials were conducted in two cropping seasons between March 2020 and December 2021, with each cropping season lasting nine months. Each cropping season and location combination was considered an environment, giving a total of six environments (Table 2).

Table 2. Geographical characteristics of environments for the genotype by environment interaction study

E[a]	**Code**	**Location**	**Latitude**	**Longitude**	**Altitude (m)**	**Cropping season**
E_1	Namu_2020[b]	Namulonge	$1^0$31'47.6'' N	$33^0$27'24.7'' E	1,140	2020
E_2	Namu_2021	Namulonge	$0^0$31'39.3'' N	$32^0$37'20.7'' E	1,156	2021
E_3	Serere_2020[c]	Serere	$1^0$31'47.6'' N	$33^0$27'24.7'' E	1,125	2020
E_4	Serere_2021	Serere	$1^0$31'58.5'' N	$33^0$27'17.8'' E	1,121	2021
E_5	Arua_2020[d]	Arua	$3^0$4'44.4'' N	$30^0$56'43.8'' E	1,198	2020
E_6	Arua_2021	Arua	$3^0$4'39.9'' N	$30^0$56'50.0'' E	1,197	2021

[a] Environments in which GEI trials were conducted; [b] National Crops Resources Research Institute (NaCRRI), Namulongu; [c] National Semi-Arid Resource Research Institute, Serere, and [d] Abi Zonal Agricultural Research and Development Institute, Arua.

2.3 Experimental design and trial management

All trials were laid out in a randomized complete block design (RCBD) with three replications. In each replication, a plot comprised of eight plants (two-row with four mounds per row) was established at a spacing of 1.2 m x 1.2 m. Before planting, mounds were sprayed with preemergence herbicide to control weeds, and setts were pre-sprouted to ensure uniform sprouting times. All plants were tagged for ease of identification during data collection. No fertilizer was applied and weed control was done manually when necessary. Mounds were reshaped by covering them with topsoil to avoid exposure of tubers to air. Vines were tailed with rope and twines at eight (8) weeks after planting.

2.4 Data collection

Data were collected for yam mosaic virus severity, yam tuber yield expressed as kg/plot, and percent dry matter content (%). All measurements were done based on the standard operating protocol for the yam varietal performance evaluation trial [19] and the trait ontology dictionary described in YamBase (https://yambase.org/) (Table 3).

Table 3. Trait descriptors used for the evaluation of yam genotypes

Descriptor	Description	Period of collection
Yam virus disease severity	1 = No visible symptoms, 2 = Mosaic on most leaves, 3 = Mild symptoms, 4 = Severe Mosaic and 5 = Severe leaf distortion and stunting	Monthly (8 weeks after planting)
Tuber yield	Weight per plot	Between 1 to 14 days after harvesting
Dry matter content	Calculated using the oven method and presented in percentage: $= \frac{\text{weight of dry sample (g)}}{\text{weight of wet sample (g)}} \text{x } 100$	

Source: [19]; https://yambase.org/

2.5 Data analysis

Analysis of variance for the studied traits was done combined across environments using a linear model implemented in the R package [20]. Violations of assumptions of analysis variance were tested before making mean comparison and other downstream analyses. Means were separated using Fishers Protected least significant difference. The linear model used in the analysis is presented below;

$$Y_{ij} = \mu + \beta_i + G_i + E_j + GE_{ij} + \varepsilon_{ij}$$

Where: Y_{ij} = Trait value of genotype; μ = grand mean; β_i = i^{th} block effect; G_i = i^{th} treatment effect; E_j = j^{th} enironmental effect; GE_{ij} = ij^{th} genotype by environment effect; and ε_{ij} = treatment x block interaction, treated as error.

The means data obtained from analysis variance were later utilized in AMMI analysis [21] for the determination of stability of the different yam genotypes as implemented using the "*Metan*" Package in R software [22] using the model below;

$$Y_{ijk} = \mu + G_i + E_j + \sum_{K=1}^{M} \lambda_k * \propto_{ik} * \gamma_{jk} + \rho_{ij}$$

Where: Y_{ijk} = the yield of the i^{th} genotype in the j^{th} environment, G_i = the effect of the i^{th} genotype (genotype mean minus the grand mean), E_j = the effect of the j^{th} environment (environment mean minus the grand mean), λ_k = the square root of the eigenvalue of the k^{th} Interaction Principal Component (IPCA) axis, α_{ik} and γ_{jk} = the principal component scores for IPCA axis k of the i^{th} genotypes and the j^{th} environment respectively and ϱ_{ij} = the deviation of genotype i^{th} on environment j^{th} from the model.

To determine the mega-environments and visualize the "*which-won-where*" pattern, GGE analysis was performed using "*Metan*" package in R software [22]. The GGE biplot was based on singular value decomposition (SVD) of the principal components as described by [23] and the GGE model below was implemented:

$$Y_{ij} = \mu_i - \beta_j = \sum \lambda_k \propto_{ik} \gamma_{jk} + \varepsilon_{ij}$$

Where: y_{ij} is the performance of genotype i^{th} in environment j^{th}, μ is the grand mean, β_j is the main effect of j^{th} environment, k is the number of principal components (PC); λ_k

is the singular value of the k^{th} PC; and α_{ik} and γ_{jk} are the scores of i^{th} genotypes and j^{th} environment, respectively for PC; ε_{ij} is the residual associated with genotype i^{th} environment j^{th}.

For mega-environment delineation of the experimental site, the "*which-won-where*" scatter plot was constructed by a polygon drawn by symmetrical scaling by connecting genotypes that are very distant from the biplot such that the polygon contained all other genotypes. Then the polygon was dissected by perpendicular lines drawn to the polygon sides and running from the biplot origin [23]. The environment vectors were projected from the axis. The ranking plot based on mean versus stability was generated by symmetrical scaling using the concept of Average environment coordinate (AEC) to draw the average line and the arrow line which points to the direction of increasing yield mean performance [24]. The comparison plot of genotype ranking relative to ideal genotype was generated by symmetrical scaling using the same concept of AEC to draw an analogy between the genotypes and an ideal genotype.

3. Results

3.1 Performance of yam genotypes for studied traits across six environments

The analysis of variance (ANOVA) for yam mosaic virus, total yield of yams, and dry matter content revealed a significant difference ($p \leq 0.001$) effect of genotypes, environments, and genotypes x environment interactions (Table 4). For yam mosaic virus, the contribution of genotype, environment, and genotype x environment interactions were 49.7%, 41.4%, and 8.8%, respectively, whilst the percentage variation due of genotype, environment, and genotype x environment interactions for total tuber yield was 46.0%, 50.4%, and 3.6%, respectively. For dry matter content, environment contributed the largest proportion variation (72.4%), followed by genotype interaction (17.1%), while the least contributor to the observed phenotypic variation (10.5%) was due to genotype-by-environment interactions (Table 4).

Table 4: Analysis of variance of twenty yam genotypes evaluated for the YMV, TWY and DMC in six environments in Uganda

Source of variance	DF[a]	YMV[b]	TWY[c]	DMC[d]
Replication	2	0.09	8.52	5.41
Genotypes	19	1.74***	1037.22***	71.33***
Environment	5	1.45***	1135.69***	302.42***
Genotype x Environment	95	0.31***	80.71***	43.92***
Residuals	238	0.11	54.23	11.24

[a]Degrees of freedom; [b]Yam Mosaic Virus; [c]Total yield of yams; [d]Dry matter content (%)

Despite the study showing significant differences in disease severity between the genotypes across the six test environments, generally, there were low severity scores among the genotypes. The mean disease severity score ranged from 1.3 to 2.2 with an average of 1.8 across environments (Table 5). Genotypes with the most outstanding performance for yam mosaic virus disease tolerance were UGY16001, UGY16085, UGY16012, UGY16042, UGY16080, and UGY16034 with mean severity scores less than 2.0. The worst performing genotypes had severity scores above 2.0 which included genotypes UGY16064, UGY16065, UGY16067, UGY16070, UGY16073, and UGY16075. Based on the studied environments, the lowest yam mosaic virus severity scores were recorded at Namulonge 2020 (1.7) and Namulonge 2021 (1.6). On average genotypes scored slightly higher at Serere in both seasons 1.8 (2020) and 2.0 (2021) (Table 5).

Table 5. Mean performance of twenty yam genotypes for Yam Mosaic Virus assessed in six environments

Genotypes	**E_1[a]**	**E_2[b]**	**E_3[c]**	**E_4[d]**	**E_5[e]**	**E_6[f]**	**Mean**
UGY16001	1.8	1.9	1.2	1.2	1.8	1.9	1.6
UGY16003	2.0	1.7	1.7	2.0	2.4	2.0	2.0
UGY16012	1.4	1.4	1.1	1.7	1.2	1.8	1.5
UGY16013	1.8	1.6	1.7	1.7	2.5	2.0	1.9
UGY16020	1.3	1.4	1.1	1.3	1.3	1.9	1.4
UGY16022	1.8	1.5	1.6	2.1	2.3	2.0	1.9
UGY16034	1.4	1.4	1.3	1.0	1.4	1.3	1.3
UGY16039	1.9	1.7	2.0	1.5	2.4	2.0	1.9
UGY16042	1.5	1.4	1.1	1.0	1.8	1.6	1.4
UGY16064	1.9	1.4	2.7	2.6	2.1	2.0	2.1
UGY16065	1.6	1.5	2.7	2.5	2.5	2.0	2.1
UGY16066	1.5	1.4	2.2	2.7	2.1	2.0	2.0
UGY16067	2.0	2.0	2.7	2.5	1.9	2.0	2.2
UGY16069	1.9	1.4	2.0	2.4	2.2	2.0	2.0
UGY16070	1.9	1.4	2.1	2.6	2.5	2.0	2.1
UGY16071	1.9	1.7	1.8	2.0	1.6	2.0	1.8
UGY16073	1.9	1.5	2.5	2.9	2.1	2.0	2.2
UGY16075	2.4	1.6	2.2	2.9	2.3	1.8	2.2
UGY16080	1.5	1.4	1.3	1.1	1.3	1.7	1.4
UGY16085	1.5	1.6	1.2	1.5	1.7	1.7	1.5
Mean	1.7	1.6	1.8	2.0	2.0	1.9	1.8
LSD[g]	0.6	0.4	0.5	0.5	0.7	0.4	0.2
CV[h]	19.2	19.3	16.5	15	21.2	13.3	17.9

[a]Namulonge 2020; [b]Namulonge 2021; [c]Serere 2020; [d]Serere 2021; [e]Arua_2020; [f]Arua 2021; [g]Least significant difference; [h]Coefficeint of variation

The mean yield of yams ranged from 8.1 kg/plot to 31.9 kg/plot with an average of 18.4 kg/plot across test environments (Table 6). Genotypes UGY16034, UGY16085, UGY16012 and UGY16020 had the highest tuber weight with mean values of 31.9 kg/plot, 29.6 kg/plot, 29.0 kg/plot and 28.6 kg/plot respectively. The least performing genotype across the test environment was UGY16070 (8.1 kg/plot) followed by UGY16022 (9.2 kg/plot) and

UGY16003 (11.8 kg/plot). Serere 2020 had the highest mean total weight of yams of 22.6 kg/plot, this was followed by Namulonge 2021 and Arua 2021 with a mean total weight of yams of 22.0 kg/plot and 20.6 kg/plot respectively. The least performing environment was Arua 2021 with a mean total weight of yam of 11.5 kg/plot (Table 6).

Table 6. Mean performance of twenty yam genotypes for yield of yams in six environments

Genotypes	**E_1[a]**	**E_2[b]**	**E_3[c]**	**E_4[d]**	**E_5[e]**	**E_6[f]**	**Mean**
UGY16001	18.5	30.6	32.7	33.8	26.7	16.6	26.5
UGY16003	14.1	12.9	18.7	10.8	10.8	3.5	11.8
UGY16012	17.7	39.1	37.1	32.6	34.5	13.2	29.0
UGY16013	11.4	11.6	17.5	12.3	15.4	3.6	12.0
UGY16020	20.4	35.1	39.4	36.5	23.2	17.1	28.6
UGY16022	9.7	11.9	14.6	10.2	4.8	3.9	9.2
UGY16034	35.5	31.3	25.5	32.4	40.7	25.8	31.9
UGY16039	8.7	29.1	16.0	8.6	9.1	8.3	13.3
UGY16042	12.9	25.2	33.6	40.2	27.8	19.8	26.6
UGY16064	14.7	9.8	13.9	7.1	19.1	3.1	11.3
UGY16065	15.3	16.7	17.5	12.0	26.5	8.0	16.0
UGY16066	19.4	21.1	23.7	10.8	20.2	12.7	18.0
UGY16067	10.0	11.4	18.7	15.3	18.4	9.0	13.8
UGY16069	19.5	17.3	15.9	8.2	13.7	10.2	14.1
UGY16070	7.5	10.3	13.7	7.6	5.4	4.2	8.1
UGY16071	14.7	15.1	19.1	10.7	17.7	6.2	13.9
UGY16073	13.3	20.9	17.0	9.5	25.9	9.3	16.0
UGY16075	9.8	24.6	21.9	13.7	23.9	8.2	17.0
UGY16080	11.2	28.6	23.7	30.9	18.3	19.9	22.1
UGY16085	17.4	37.4	32.3	33.8	29.4	27.0	29.6
Mean	15.1	22.0	22.6	18.8	20.6	11.5	18.4
LSD[g]	10.4	13.4	11.7	11.9	15.2	8.1	4.8
CV[h]	41.6	36.9	31.3	38.3	44.8	42.8	39.9

[a]Namulonge 2020; [b]Namulonge 2021; [c]Serere 2020; [d]Serere 2021; [e]Arua 2020; [f]Arua 2021; [g]Least significant difference; [h]Coefficeint of variation

The mean of the dry matter content ranged from 25.1% to 33.5% with an average of 28.4% across test environments. The genotype with the least dry matter content cross environments was genotype UGY16069 (25.1%) while the highest dry matter content was UGY16064 (33.5%) (Table 7). Arua 2021 had the highest mean dry matter content of 31.6% followed by Namulonge 2020 with a mean dry matter content of 30%. The least performing environments were Serere 2020 and Serere 2021 with mean dry matter content of 25.1% and 27.2% respectively (Table 7).

Table 7. Mean performance of dry matter content of twenty yam genotypes evaluated in six environments

Genotypes	E_1[a]	E_2[b]	E_3[c]	E_4[d]	E_5[e]	E_6[f]	**Mean**
UGY16001	31.5	27.8	26.3	24.1	27.5	33.6	28.5
UGY16003	31.0	25.9	23.7	27.3	33.2	24.8	27.6
UGY16012	28.2	28.5	23.0	29.1	24.7	21.2	25.8
UGY16013	30.3	21.4	27.3	31.6	29.3	30.5	28.4
UGY16020	27.9	28.9	23.0	32.7	25.3	35.5	28.9
UGY16022	30.9	28.6	28.0	27.7	32.3	33.1	30.1
UGY16034	29.1	25.2	22.3	26.2	22.2	30.8	26.0
UGY16039	33.4	32.1	28.7	26.5	33.0	33.3	31.2
UGY16042	29.7	27.7	23.0	24.5	29.2	33.6	27.9
UGY16064	41.1	39.5	29.0	31.2	31.2	29.2	33.5
UGY16065	29.4	30.8	21.0	28.3	30.7	33.5	29.0
UGY16066	33.6	24.0	20.3	34.8	31.8	33.2	29.6
UGY16067	31.3	27.8	29.7	24.1	31.3	29.6	29.0
UGY16069	22.7	25.0	24.0	17.2	24.2	40.1	25.5
UGY16070	28.6	28.5	25.3	27.7	32.0	33.5	29.3
UGY16071	20.6	21.3	30.0	28.5	24.8	25.0	25.1
UGY16073	35.9	27.9	18.7	21.7	28.3	30.6	27.2
UGY16075	29.9	30.1	33.4	24.2	27.5	28.9	29.0
UGY16080	26.2	28.1	20.0	30.2	24.8	38.3	27.9
UGY16085	28.4	28.5	26.3	26.5	26.0	34.2	28.3
Mean	30.0	27.9	25.1	27.2	28.5	31.6	28.4
LSD[g]	5.7	8.4	6.5	0.9	6.0	0.7	2.2
CV[h]	11.5	18.3	15.7	2.1	12.8	1.4	11.8

[a]Namulonge 2020; [b]Namulonge 2021; [c]Serere 2020; [d]Serere 2021; [e]Arua 2020; [f]Arua 2021; [g]Least significant difference; [h]Coefficeint of variation

3.2 Additive main effect and multiplicative interaction (AMMI) results

AMMI analysis showed significant effect ($p<0.01$) of genotypes, environments and interaction between genotype and environment on the all traits. The first interaction principal component axis (IPCA 1) was significant ($p \leq 0.001$) for all studied traits. Meanwhile, only dry matter content and yam mosaic virus were highly significant ($p \leq 0.001$) for the second interaction principal component axis (IPCA 2) (Table 8). The first two IPCA (IPCA 1 and IPCA 2) accounted for more than 60% of the variability in GEI for all traits investigated (Table 8).

Table 8. AMMI analysis of 20 yam genotypes evaluated in six environments

SOV[a]	**Df**[b]	**DMC**[c]	**TWY**[d]	**YMV**[e]
Genotypes	19	71.3 ***	1037.2 ***	1.7 ***
Environments	5	302.4 ***	1135.7 ***	1.4 ***
Replication	12	9.75	75.3	0.2
Genotype x Environment	95	43.9***	80.7**	0.3 ***

IPCA 1	23	64.0 ***	167.4 ***	0.8 ***
IPCA 2	21	49.2 ***	71.2	0.2 **
IPCA 3	19	51.6	65.7	0.2
Error	228	11.3	52.7	0.1
Total	359	27.1	128.1	0.3

[a]Source of Variance; [b]Degrees of freedom; [c]Dry matter content; [d]Total weight of yam; [e]Yam Mosaic Virus

The AMMI biplots (Figure 1) depicted correlations between IPCA 1 and genotype means for the various traits studied. Genotype UGY16022 had the lowest absolute IPCA 1 (0.033) value for dry matter content and thus the most stable genotype throughout the six-test environment, followed by UGY16066 (0.09) and UGY16073 (0.18) (Table 9; Figure 1A). Based on the absolute score for IPAC 1 (2.717), UGY16069 showed the least stable dry matter response in the six environments. Except for genotypes UGY16022, UGY16066, and UGY16073, practically all of the genotypes in the dry matter content evaluation had absolute IPAC scores that were far from zero, indicating that the genotypes' performance was usually unstable for the trait (Table 9; Figure 1A).

The ideal environment identified for dry matter content was Namulonge 2021 with the lowest absolute IPAC 1 score of 0.41 with a mean of 27.880 (Table 9). In terms of total tuber yield, UGY1622, UGY16075, and UGY16070 with low IPAC 1 absolute scores (Table 9; Figure 1B) were the most stable in the test environment. The least stable genotypes were UGY16020 (2.10) and UGY16042 (2.42).

Analysis of the YMV disease incidence in the test environments revealed relatively high absolute IPAC 1 scores, compared to values obtained for dry matter content and total yield of yam. The top three most stable genotypes in response to yam mosaic virus were UGY16022, UGY16071, and UGY16003 (Table 9; Figure 1C). Yam mosaic virus had the highest IPAC 1 score of 1.030 for Serere 2021 and the lowest IPAC 1 score of 0.073 for Arua 2020 (Table 10).

Table 9. Genotypes mean for traits, stability index (IPCA 1) and ranking across six environments used in the study

Genotype	DMC[a]			TWY[b]			YMV[c]		
	Mean	IPCA1	Rank	Mean	IPCA1	Rank	Mean	IPCA1	Rank
UGY16001	28.48	-0.38	5	26.48	-1.43	8	1.64	0.61	20
UGY16003	27.62	1.45	12	11.79	0.56	5	1.97	0.09	1
UGY16012	25.77	1.74	14	29.04	-1.48	17	1.46	0.17	10
UGY16013	28.40	0.38	11	11.97	0.46	1	1.87	0.22	6

UGY16020	28.87	-0.85	10	28.61	-2.12	16	1.39	0.32	12
UGY16022	30.10	0.03	1	9.19	-0.01	6	1.90	0.01	2
UGY16034	25.96	-0.31	7	31.85	1.68	18	1.31	0.31	7
UGY16039	31.18	0.25	6	13.31	-0.35	19	1.92	0.27	11
UGY16042	27.93	-0.55	3	26.57	-2.42	20	1.39	0.45	13
UGY16064	33.53	1.83	18	11.28	1.75	12	2.10	-0.49	16
UGY16065	28.95	-0.38	8	15.98	1.39	10	2.13	-0.47	18
UGY16066	29.61	0.09	17	17.97	1.26	9	1.98	-0.48	15
UGY16067	28.99	0.62	9	13.81	0.19	4	2.20	-0.26	14
UGY16069	25.52	-2.72	20	14.14	1.58	14	1.99	-0.22	3
UGY16070	29.27	-0.29	2	8.10	0.15	3	2.07	-0.33	8
UGY16071	25.05	0.59	19	13.89	0.94	2	1.83	0.09	4
UGY16073	27.18	0.18	15	15.98	1.28	11	2.16	-0.55	19
UGY16075	28.99	0.72	13	17.00	0.03	7	2.21	-0.39	17
UGY16080	27.93	-1.72	16	22.12	-1.96	15	1.37	0.35	9
UGY16085	28.33	-0.65	4	29.58	-1.53	13	1.52	0.29	5

[a]Dry matter content, [b]Total weight of yams, [c]Yam Mosaic Virus

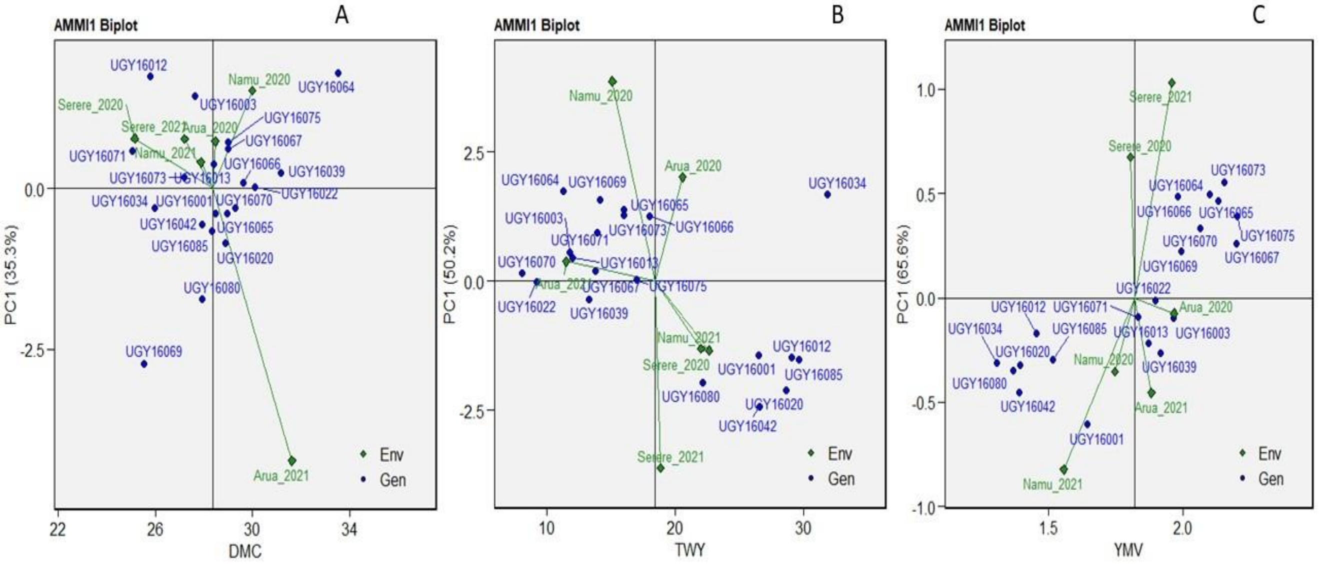

Figure 1. AMMI1 biplot for mean dry matter content (A), the total weight of tubers (B), yam mosaic virus (C), and their respective PC1 scores for twenty yam genotypes evaluated in six environments

Table 10. Environment means for traits and stability index (IPAC 1) scores evaluated in the study

Environment	DMC[a]		TWY[b]		YMV[c]	
	Mean	IPCA 1	Mean	IPCA 1	Mean	IPCA 1
Arua 2020[d]	28.47	0.74	20.57	2.01	1.97	0.07
Arua 2021	31.63	-4.23	11.48	0.38	1.88	0.46
Namulonge 2020[e]	29.98	1.53	15.08	3.88	1.75	0.35
Namulonge 2021	27.88	0.41	22.00	-1.31	1.56	0.82

Serere 2020[f]	25.15	0.78	22.63	-1.34	1.81	-0.67
Serere 2021	27.20	0.77	18.84	-3.62	1.96	-1.03

[a]Dry matter content (%); [b]Total weight of yams; [c]Yam Mosaic Virus; [d]Abi Zonal Agricultural Research and Development Institute, Arua; [e]National Crops Resources Research Institute (NaCRRI), Namulonge; [f]National Semi-Arid Resource Research Institute, Serere

3.3 Stability and "*which-won-where*" pattern of genotypes for traits studied

For GGE analysis, the first two PCs explained 87.38% (PC 1 (77.34%) and PC2 (10.04%) of the total interaction variations for yam mosaic virus severity. The "*which-won-where*" GGE biplot showed a visual representation of the genotype and genotype x environment interactions for yam mosaic virus (Figure 3A). The six environments were divided into three mega environments; i) Serere 2020 and Serere 2021 with genotype UGY16073 as the best performer; ii) Arua 2020 with genotype UGY16039 as the best performer, and; iii) Arua 2021, Namulonge 2020, and Namulonge 2021 with genotype UGY16003 as the best performer (Figure 3A). This was revealed by the long length of Serere 2021 vectors from the origin. Namulonge 2021 was the most discriminating of the test environments compared to the rest due to the average environment axis; a small angle (Figure 3B).

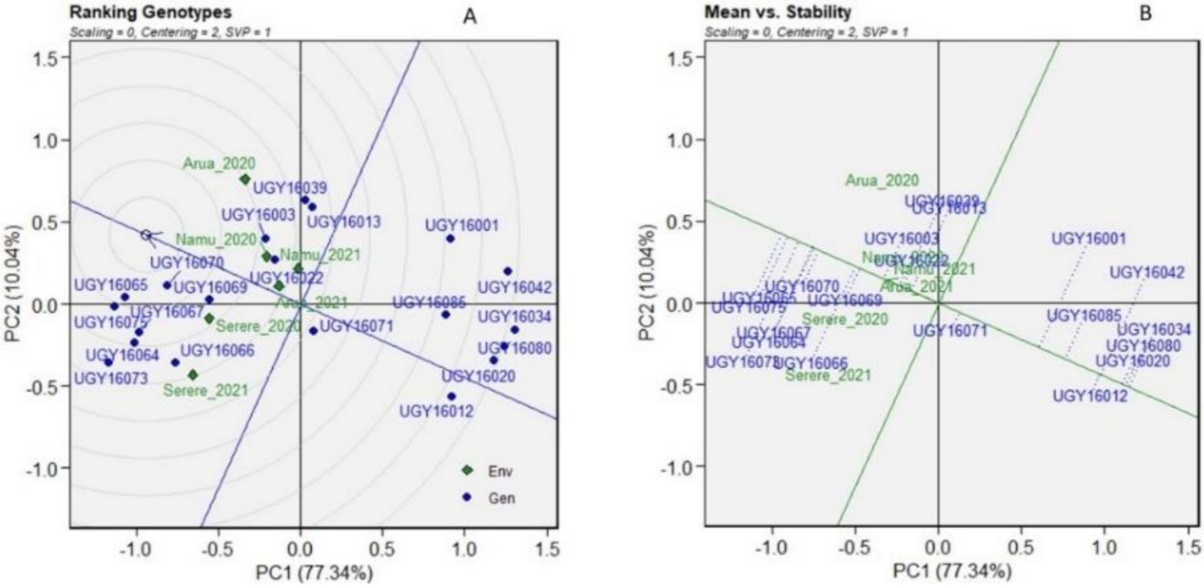

Figure 2: A GGE ranking biplot showing the mean performance (A) and stability (B) of twenty yam genotypes for yam mosaic virus evaluated in six environments.

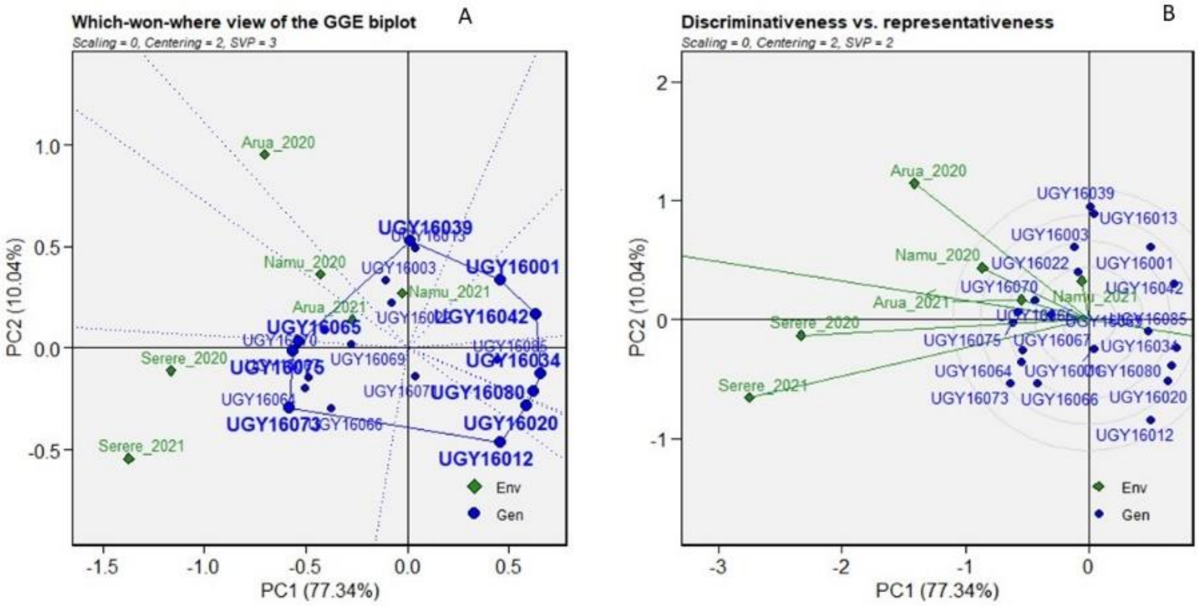

Figure 3. A GGE scatterplot based on symmetrical scaling for the "*which-won-where*" pattern (A) and the discriminating power and representativeness of test environments (B) involving the 20 yam genotypes for yam mosaic virus evaluated in six environments

The six test environments were grouped into three major mega environments for the total yield of yams. The first mega environment included Serere 2021 and Serere 2020 with the best genotype as UGY16020. The second mega environment included only one environment which was Namulonge 2021 with genotype UGY16085 as the best performer for the environment. The third mega environment consisted of three major environments which are Arua 2020, Namulonge 2020, and Arua2021. The mega environment has genotype UGY16034 as the best performer (Figure 5A). The best performing genotype in terms of yield was genotype UGY16034 and was observed to be the most unstable genotype among the rest. Other genotypes such as UGY16003, UGY16067, and UGY16075 were observed to be stable across the environment but with low yield, and performance compared to other studied genotypes (Figure 4A and 4B). The GGE polygon plot gave a visual assessment of the GEI. The GGE biplots explained 88.16% of the total variations, with 77.95% and 10.21% for PC1 and PC2 (Figure 5A). The GGE biplot showed that Serere 2021 was the most discriminating environment, whilst Arua 2021 was the least of the six text environments (Figure 5B). This was revealed by the long and short environment vectors of Serere 2021 and Arua 2021 respectively. Arua 2021 was the most representative of the mega environment of all the six test environments compared to the rest due to the small angle from the average environment axis (Figure 5B).

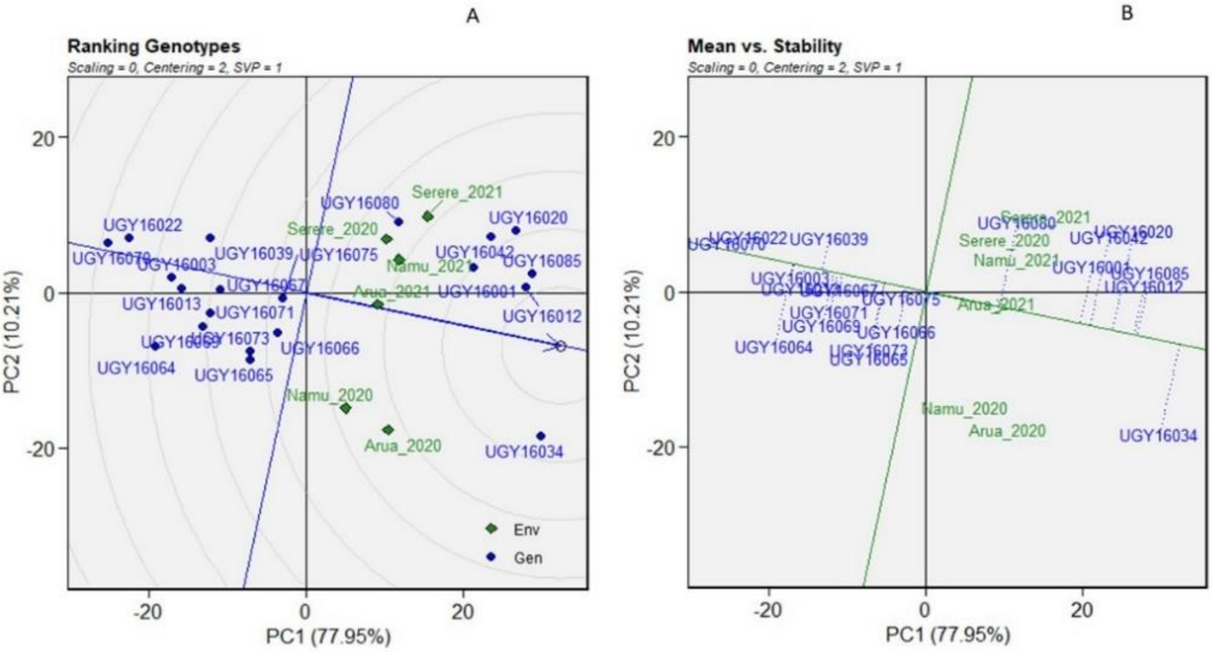

Figure 4. A GGE ranking biplot (A) showing the mean performance and stability (B) for the Total yield of yams (kg/plot) of twenty yam genotypes evaluated in six environments

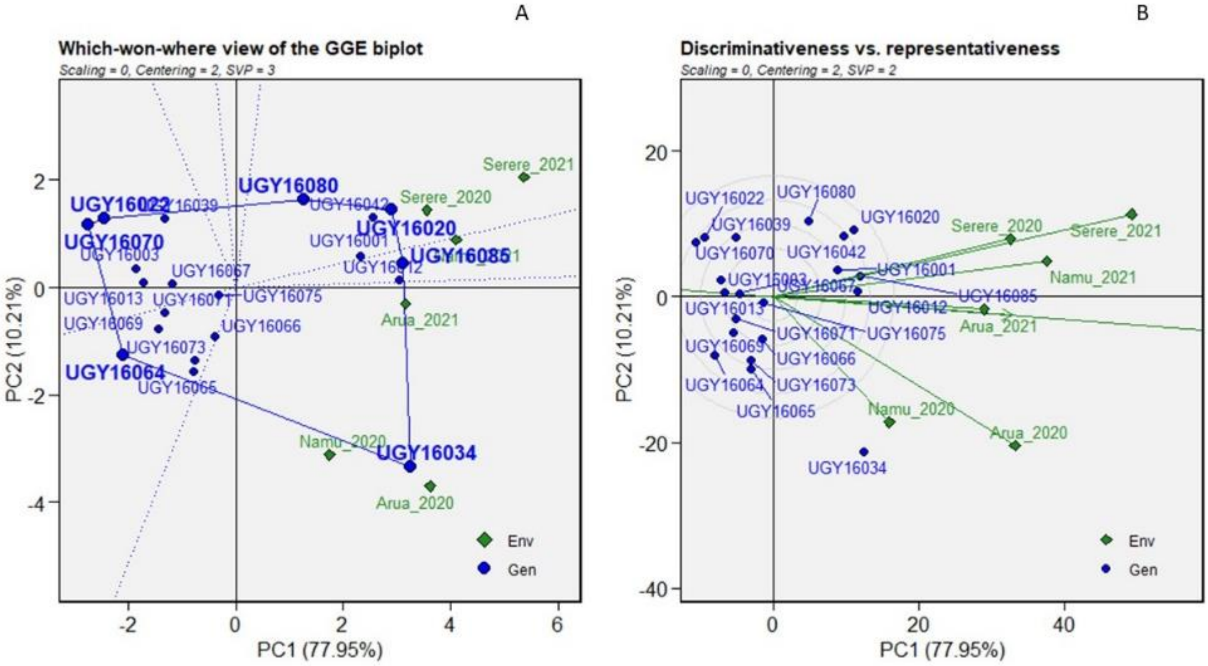

Figure 5. A GGE biplot based on symmetrical scaling for the "*which-won-where*" pattern (A) and the discriminating power and representativeness of test environments (B) involving 20 yam genotypes for total yield of yams (kg/plot) evaluated in six environments

The GGE polygon plot (Figure 7A) gave a good visual assessment of GGE with both PC1 and PC2 explaining about 58.33% of the total variation observed. The biplot indicated that the six test environments were grouped into three mega environments. The first mega environment included only Arua 2021 with the best genotype being UGY16069. The second mega environment comprised Namulonge 2020, Namulonge 2021, Arua 2020, and Serere 2021 with the best performing genotype being UGY16064 (Figure 7A). The third mega environment consisted of Serere 2020 with genotype UGY16003 as the best performer. The GGE biplot (Figure 7B) showed that Arua 2021 was the most discriminating environment, while Serere 2021 was the least of the six test environments. This was revealed by the long and short environment vectors of Arua 2021 and Serere 2021, respectively. Of all the six environments, Arua 2020 was the most representative of the mega environment than the rest due to the small angle from the average environment axis (Figure 7B).

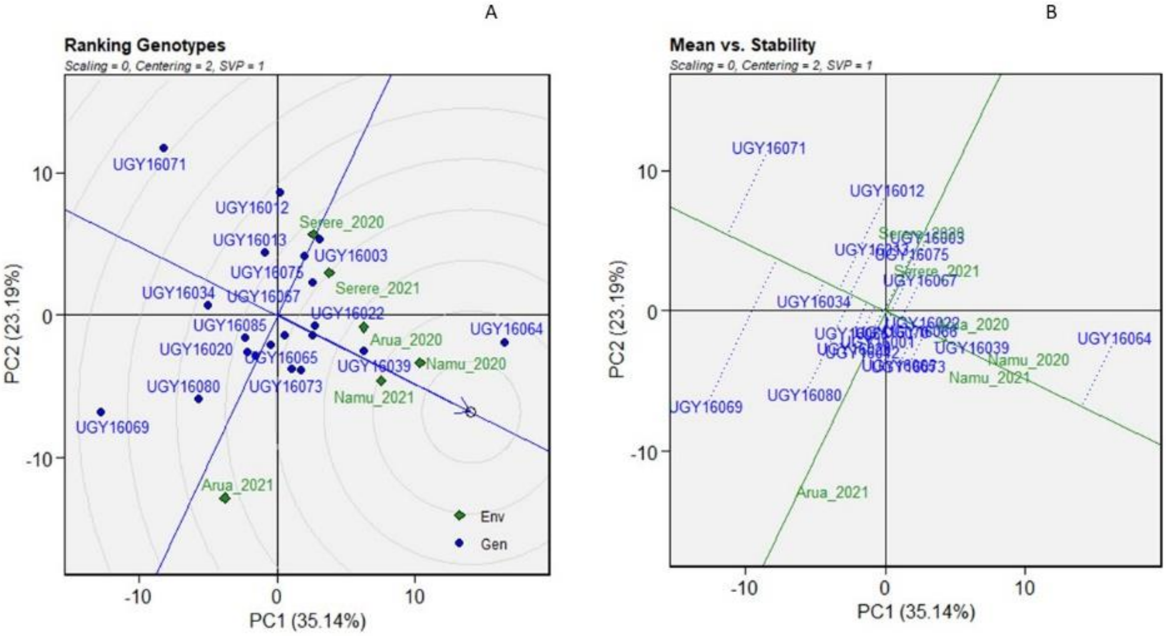

Figure 6. A GGE ranking biplot (A) showing the mean performance and stability (B) for dry matter content of 20 yam genotypes evaluated in six environments

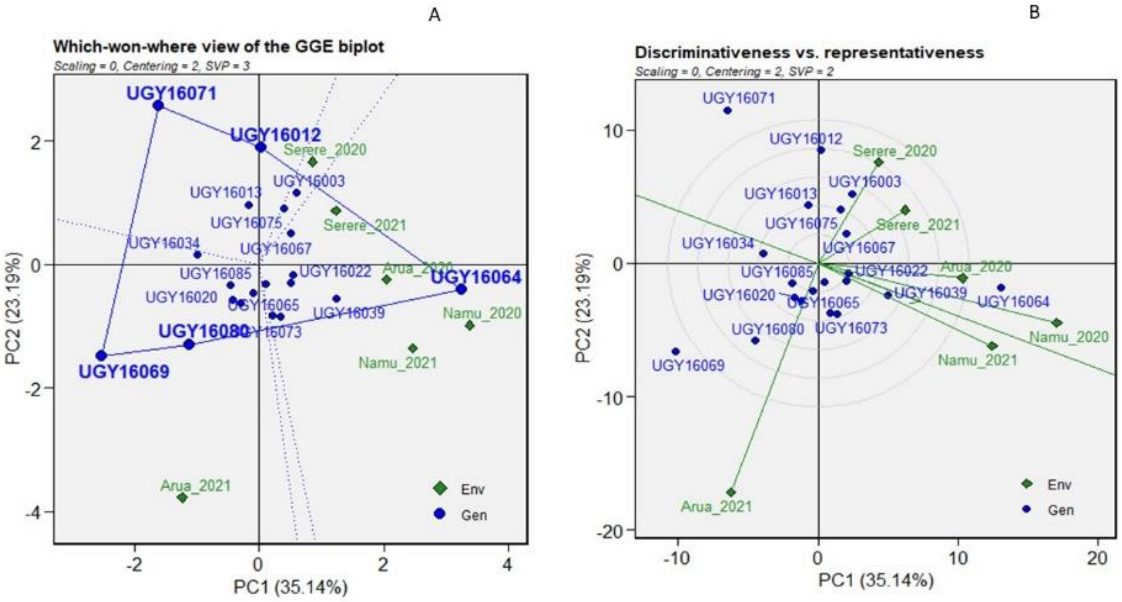

Figure 7. A GGE scatterplot based on symmetrical scaling for the "*which-won-where*" pattern (A) and the discriminating power and representativeness of test environments (B) for dry matter content involving 20 yam genotypes evaluated in six environments

3.4 Pearson correlations among traits studied

A highly significant negative correlation (r = -0.85, d.f. = 19) was observed between yam mosaic virus and total yield of yams whilst a non-significant positive correlation (r = 0.35, d.f = 19) was observed between dry matter content and yam mosaic virus.

4. Discussion

The overall goal of this study was to evaluate the performance of Uganda yam genotypes across six test environments for yield, viral disease resistance, and dry matter content. The significant variation in these genotypes for mosaic virus resistance, total weight of yam, and dry matter content presents an important opportunity for yam breeding in Uganda. This variability could serve as the foundation for making progress in the genetic improvement of yams for these traits via selection. In this study, genotype x environment effects were highly significant for all traits studied, indicating significant variation in genotype means performance across environments which had a significant impact on the studied genotypes. The high genotype by environment interaction effect on the traits leads to the obvious conclusion that selection for the traits can be effectively achieved by evaluating target genotypes in different environments due to different environmental conditions. Tuber yield and dry matter content in yam, like other quantitative traits, are strongly impacted by genotype-environment interaction [9,15]. This characteristic makes the selection of such genotypes for universal adaption difficult. According to Nduwumuremyi et al. [25], the existence of a strong genotype-environment interaction impact for quantitative variables like tuber yield, dry matter content and yam mosaic virus might hinder efforts to choose superior genotypes for diverse environments. This is because such performance cannot be duplicated in environments with varying environmental conditions [26].

Different yam genotypes have intrinsic varietal traits and preferences for various environmental situations (Otoo et al., 2006), particularly for introduced genotypes into new environments. As a result, genotypes must be assessed across several locations to discover specific places that best fit them and where such genotypes may achieve their maximum yield potential [9]. This means that a standard yam variety selection approach for traits such as high dry matter content, high tuber yield, and yam mosaic virus requires additional environments for screening resistance [2]. Breeders can use stability analysis to measure the level of genotype-environment interaction and classify genotypes as widely or narrowly adapted based on stability indices [28]. As a result, breeding programs in Uganda aimed at developing yams for the above qualities should subject genotypes to multilocational assessment, with an emphasis on traits that are heavily impacted by environmental impacts. Although this technique is more expensive, it provides greater precision in determining the top-performing genotypes in terms of dry matter content, tuber yield, and yam mosaic virus resistance.

The genotype main effect and genotype x environment (GGE) biplot depicts the genotype main effect as well as genotype x environment interaction [29]. The "*which-won-where*" pattern of the GGE biplot's polygon view-based interaction is effective for identifying elite genotypes in single or multiple settings [30]. The use of GGE biplots in this work showed genotypes that coupled high mean performance with high stability, as well as preferences and adaption to particular specific situations. In terms of dry matter content, genotype UGY16069 was best suited to the Arua 2021 environment, whereas genotype UGY16003 performed best in Serere 2020. Genotype UGY16054, on the other hand, was adapted to four environments: Namulonge 2020, Namulonge 2021, Arua 2020, and Serere 2021. Nonetheless, the ranking GGE biplot revealed that genotype UGY16071 performed overall best, despite being rather unstable throughout the test conditions. However, genotype performance for total weight of yam indicated that UGY16034 was the greatest performer but unstable, whereas genotype UGY16020 was suited to two primary environments, Serere 2021 and Serere 2020. Other genotypes, such as UGY16085, were adapted to a single environment, Namulonge 2021, whereas genotype UGY16034 captured three major environments (Arua 2020, Namulonge 2020, and Arua 2021). A similar outcome was observed for the yam mosaic virus, where the most common vertex genotypes were UGY16073, UGY16039, and UGY16003 identified as adapters for different environments. Earlier research on genotype x environment analyses has also found this phenomenon of distinct adaptability or environmental preferences by various yam genotypes. In Ghana, Otoo et al. [2] used the GGE biplot to identify uniquely suited cultivars in 16 settings in research comprising 12 *Dioscorea rotundata* genotypes, validating the environmental uniqueness of distinct yam genotypes per this current study.

According to Dhillon et al. [31], a genotype is deemed stable if its yielding ability varies little when planted in different conditions. Furthermore, Yan and Tinker [23] and Gurmu et al. [32] proposed that stable genotypes are those whose variances remain largely consistent from one environment to the next. A persistently underperforming genotype, on the other hand, can be stable. As a result, in addition to greater performance for that attribute of interest, stability should always be addressed. According to a report by Purchase et al. [33], a yield stability index that combines ranking based on high yield and stability (based on the AMMI stability value) into a single index, and the AMMI analysis reveals certain genotypes that are stable across environments [34]. According to the findings of this study, genotype UGY16022 was stable but not the best performer in terms of yam mosaic virus severity score across contexts. Furthermore, for total yield yam, genotype UGY16070 was the least performer, though it was relatively stable compared to other genotypes; for dry matter content, genotype UGY16071 was the best performer but very unstable across the six test environments; and for total yield of yam, genotype UGY16070 was the least performer, though it was relatively stable compared to other genotypes. This means that the genotype (UGY16070) responded positively to favorable environmental conditions and performed well under less favorable settings, implying particular adaptation.

Those types of genotypes would be ideal for high-input agriculture under favorable environmental circumstances. Literature defines such genotypes as being resistive to environmental situations, and they continue to be the best insurance for farmers under difficult situations. Furthermore, certain genotypes tend to respond favourably to favorable environments while maintaining moderate yields, dry matter content, and disease resistance under hard conditions. Such genotypes are often chosen for specific settings where they may fully realize their production potential. The yield of locally cultivated genotypes such as UGY16085 and UGY16012 remained highest in the current investigation, despite being unstable across the six environments. The dry matter content of genotypes UGY16022 and UGY16064, on the other hand, remained considerably high across settings, while disease-resistant genotypes were UGY16020, UGY16034, UGY16042, and UGY16080 throughout the six test environments. In addition, this was obvious and reflected in the performance of the genotypes across environments. Further, similar observations were made from the correction between dry matter content and total weight of yam where a non-significant but weak and negative relationship was observed.

5. Conclusions

The study revealed significant GEI effects for yam mosaic virus, the total yield of yam, and dry matter content in the yam genotypes evaluated and significant genotypic variation for the studied traits which could provide resources for making selections for further genetic improvement through hybridization. Genotypes UGY16022 and UGY16066 were the most stable genotypes with relatively high dry matter content across the test environments. All the six test environments used for the study were relevant for the research and development of yams. In general, genotypes UGY16020, UGY16034, UGY16042, and UGY16080 had a high tolerance to yam mosaic virus disease, and were relatively high yielding, hence good candidates for improving other genotypes in the future. For a combination of all three traits (virus resistance, dry matter content, tuber yield), genotypes UGY16022 and UGY16066 showed the best stability i.e., closest to the ideal genotype. Since these genotypes present promising high yields with substantial dry matter content and yam mosaic virus resistance, there is a need to further evaluate them with farmers targeting official release in Uganda

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W.E.; funding acquisition, R.E, T.A, and R.A. All authors have read and agreed to the published version of the manuscript.

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