

Additive Main Effects and Multiplicative Interaction and Genotype Main Effect and Genotype by Environment Interaction Effects-Biplot Analysis of Sorghum Grain Yield in Uganda

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Abstract

Genotype-by-environment interaction analysis is vital for cultivar release, and to identify suitable crop production sites. The current study aimed to determine sorghum grain yield stability and adaptability and to identify the most informative and representative environments for sorghum grain yield performance in Uganda. Sorghum grain yield data of eight (08) genotypes; ICSR 160, IS8193, IESV92043DL, IESV92172DL, GE17/1/2013A, GE35/1/2013A, SESO1, and SESO3 tested across eight (08) major sorghum production area in Uganda for two consecutive seasons of 2017 using randomised complete block design with 2 replications were analysed via Additive Main effects and Multiplicative Interaction (AMMI) and Genotype Main Effect and Genotype by Environment interaction effects (GGE) using PB tools. Genotype IESV92043DL was the ideal genotype in the entire test environments with mean grain yield of 2783 kg ha⁻¹ however genotype ICSR 160 had the highest grain yield of 2823 kg ha⁻¹ across all the test environment. On the other hand, GE17/1/2013A was the most stable and adapted genotype across all the test environment. Of the eight (08) environments tested, biplot analysis precisely grouped the test environments into two presumed mega-environments with the best genotype being IS8193 and ICSR 160. Out of eight (08) trial sites, two (02) environments; Abi and Mayuge were the most representative and informative environment for sorghum grain yield performance in Uganda.

Keywords: sorghum (*Sorghum bicolor*), multiplicative models, genotype, and yield stability

1. Introduction

Environment is important in determining the performance of crop genotypes especially for quantitative variables. Likewise the multiplicative effect of the genotype by environment [genotype by environment interaction (GEI)] further complicates the expressivity of the variables resulting in selection. This directs plant breeders to select genotypes that are suitable for certain environment. It is important to study genotypes response to different environments and henceforth select cultivars suitable for specific or diverse environments. However, cultivars that are adapted to diverse environments are the most desirable in breeding therefore understanding genotype by environment (GxE) interaction is very key in a plant breeding program before the variety is released to the uptake pathway. The yield potential of a variety is controlled by both the genetic and various environmental factors that vary over the years and locations. The study of quantitative traits like grain yield is further convoluted by GxE interaction; especially across many trial locations (Kaya et al., 2002). Therefore, evaluation of newly developed varieties across several environments is fundamental to estimate the magnitude of GEI, and for cultivar recommendation. Several statistical approaches have been used to analyse GEI for recommending specific or general selection in plant breeding. As noted by Lubadde et al. (2017), more than one method should be used for better comparison. In this study the Additive Main effects and Multiplicative Interaction (AMMI) and the Genotype Main Effect and Genotype by Environment interaction effects (GGE) models was adopted. Nyaligwa et al. (2018) acknowledged that AMMI and GGE models have been used by many breeders to analyse GEI. AMMI employs both analysis of variance (ANOVA) and principle component analysis (PCA) (Zobel et al., 1988) to analyse the main effects (additive effect) and the non-additive residual effect (Akter et al., 2014)

respectively to ascertain GEI for trait of interest such as sorghum grain yield in this current study. While GGE biplots on the other hand display both genotype and genotype by environment disparity for traits (Crossa et al., 2002). In this current study, both AMMI and GGE biplot was used for estimating yield stability and adaptability of improved sorghum genotype over the major sorghum production areas in Uganda as excellent tools for visual display and interpretation of multi environments data (Rakshit et al., 2017). Therefore, the objectives of this study were to (i) determine sorghum grain yield stability and adaptability, (ii) identify the most discriminating (informative) and representative environments for sorghum grain yield performance in Uganda and (iii) determine the presence of sorghum production mega environments in Uganda.

2. Materials and Methods

2.1 Trial Sites

The trial was conducted at eight (08) different sites namely Arua, Iganga, Mayuge, Namutumba, Pallisa, Serere, Oyam and Kitgum (Table 1 and Figure 1) that represent the major sorghum production areas in Uganda for two consecutive seasons (first and second seasons) of 2017. Each site and two consecutive seasons formed the eight (08) environment in which sorghum grain yield data were collected for AMMI and GGE biplot analysis.

2.2 Experimental Materials and Design

Eight (08) genotypes including two checks (SESO1 and SESO3) (Table 2) were used in this study. The trials were arranged in randomised complete block design with two replications per location. Each genotype was planted in a plot with 4 rows at spacing of 60 cm apart and 20 cm between plants within the row and each plot was measuring 4 m long.

Table 1. Characteristics of the locations used in the study

Code	Location	Geographical position		Elevation m	Mean Temp °C	Annual Rainfall mm	Agro-ecologies
		Latitude	Longitude				
E1	Arua	3°1'9"N	30°55'51"E	1215	23.9	1404	West Nile farmlands
E2	Iganga	0°36'33"N	33°28'7"E	1120	23.3	1313	Lake Victoria Crescent
E3	Kitgum	3°16'42"N	32°53'12"E	760	24.1	1125	North Eastern Central Grass Bush farmlands
E4	Mayuge	0°27'35"N	33°28'49"E	1,190	22.3	979	Lake Victoria Crescent
E5	Namutumba	0°50'10"N	33°41'10"E	1,080	22.0	1322	Lake Kyoga Basin
E6	Oyam	2°26'24"N	32°23'22"E	900	21.6	1500	Northern moist farmlands
E7	Pallisa	1°8'42"N	33°42'34"E	1,070	23.4	1353	Lake Kyoga Basin
E8	Serere	1°29'39"N	33°27'19"E	1140	23.8	1362	Lake Kyoga Basin

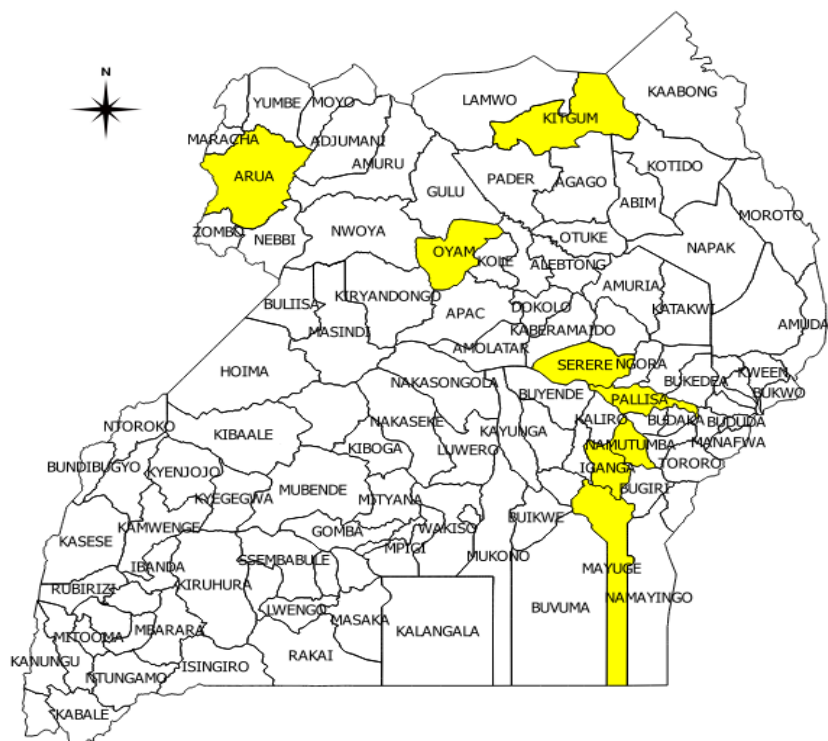


Figure 1. Map of Uganda showing the locations (marked in yellow) used in the study

The trials were weeded manually thrice for good crop establishment and no fertilizer was applied during the crop growing cycle however they were sprayed with cypermethrin to control pests at four weeks after crop emergence, then at intervals of two weeks for 6 weeks.

Table 2. List of sorghum genotype used in this study

Code	Genotypes Source	Pedigree or Origin	Variety status	Special attributes
G1	GE17/1/2013A (GE17)	USA, Perdue University	Pure line	Resistant to Smut and Striga, and early maturity
G2	GE35/1/2013A (GE35)	Texas	Pure line	Sweet stalk and seed, and resistant to striga
G3	ICSR 160	[(IS 12622Cx555) × (IS 3612Cx2219B)-5-1 × E 35-1], ICRISAT	Pure line	Suitable for lager beer production and drought tolerant/stay green trait.
G4	IESV 92043DL	KARI Mtama 1 × Seredo, ICRISAT	Pure line	Resistant to midge, drought tolerant, juicy sweet stalk suitable for forage.
G5	IESV92172DL	ICRISAT	Pure line	Short height and medium maturity with high threshability
G6	IS8193	Land Race from East Africa, ICRISAT	Pure line	Resistant to bird damage, drought and Striga tolerant.
G7	SES01 (M91057)-Check 1	[GPR 148 x E35-1] × CS 3541)	Released variety in Uganda	White seeded, early maturity and good for brewing.
G8	SES03 (SRN 39)-Check2	Sudan	Released variety in Uganda	Early maturing, high yielding, good for food and tolerant to striga, drought and bird damage.

2.3 Data Collection and Analysis

Grain yield data were collected on sorghum genotypes per the (IBPGR, 1993) descriptors. Harvesting was done manually at physiological maturity at all the trial sites. The grain yield data were analysed using combined analysis of AMMI and GGE biplot using PB tools (Version 1.4, <http://bbi.irri.org/products>) and the models were:

$$Y_{ij} = \mu + \delta_i + \beta_j + \sum_{k=1}^K \delta_{ik} \beta_{jk} + \epsilon_{ij} \text{ (for AMMI)} \tag{1}$$

$$Y_{ij} = \mu + \beta_j + \sum_{k=1}^K \delta_{ik} \beta_{jk} + \epsilon_{ij} \text{ (for GGE Biplot)} \tag{2}$$

Where, Y_{ij} is the mean yield of i^{th} genotype in j^{th} environment, μ is the overall mean, δ_i is the genotypic effect, β_j is the environment effect, λ_k is the singular value for PC axis k , δ_{ik} is the genotype eigen vector value for PC axis n , β_{jk} is the environment eigen vector value for PC axis k and ϵ_{ij} is the residual error assumed to be normally and independently distributed ($0, \sigma^2/r$), where σ^2 is the pooled error variance, and r is the number of replicates (Crossa et al., 2002; Gauch et al., 2008). The mean sorghum grain yield was separated by the least significant difference (LSD) test.

3. Results and Discussions

The sorghum grain yield results of the eight (08) sorghum genotypes across the eight (08) environments showed that genotype ICSR 160 had the highest mean grain yield of 2823 Kg per ha⁻¹, superseded by IESV92043DL, and IS8193 with grain yield of 2783 Kg ha⁻¹ and 2740 Kg ha⁻¹ respectively (Table 3). These genotypes consistently and significantly performed better than the checks across the environments. The combined analysis of variance across the environment for grain yield of eight (08) sorghum genotypes showed that the treatment, genotypes and environment components were significantly different ($P < 0.001$) unlike G×E interactions at 0.05 level. Our data therefore showed that genotypes and environments used during the study were different. Therefore, there was great diversity between the genotypes. The absence of GEI in this current study clearly indicates breeding for specific adaptability for the targeted trait. According to Andiku et al. (2019), presence of low or no G×E interactions in any study shows that screening programs for such important trait could be conducted centrally at one or two locations to minimise breeding costs.

Table 3. Grain yield of eight sorghum genotypes across the environments

Environment	Abi	Iganga	Kitgum	Mayuge	Namutumba	Oyam	Pallisa	Serere	Genotype means
Genotype	----- Grain sorghum yield (Kg ha ⁻¹) -----								
GE17/1/2013A	1808	2441	2031	3702	2862	3376	2024	2104	2544
GE35/1/2013A	1532	2694	2014	3278	2512	3334	1948	2124	2430
ICSR 160	1710	2985	2122	4091	3264	3610	2167	2637	2823
IESV92043DL	1856	2977	2127	3859	3224	3566	2082	2576	2783
IESV92172DL	1739	2488	1987	3208	2882	2837	1967	1647	2344
IS8193	2126	3077	2239	3563	2864	3382	2199	2471	2740
SES01 (Check1)	1576	2507	2067	3596	2634	3426	2023	2016	2481
SES03 (Check2)	1524	2599	2001	3752	3100	3156	1999	2097	2529
Mean	1734	2721	2074	3631	2918	3336	2051	2209	2584
LSD (0.05)	538.7ns								
C.V %	18.4								

Note. ns: not significant at level 0.05.

According to Akter et al. (2014), a genotype or an environment is assumed to have small interaction (stable) when the first Interaction Principal Component Axis (IPCA1) score is almost to zero or equivalent to zero. More still, the horizontal line (y-ordinate) is the IPCA1 value of zero while the vertical line represents the grand mean for grain yield (Figure 2) where a genotype or environment on the right side of the vertical line are high yielding unlike their counter parts on the left hand side of the vertical line. However, genotypes and environments that appear on perpendicular and horizontal lines have similar mean and interaction patterns respectively (Akter et al., 2019). Consequently, our study provided a visual expression of the relationships between the IPCA1 and means of genotypes and environments as shown in Figure 2. The AMMI biplot showed four groupings of genotypes; IESV92172DL (G5) generally low yielding and unstable, GE17/1/2013A (G1), GE35/1/2013A (G2), SES01 (G7), and SES03 (G8), low yielding and moderately stable, IESV92043DL (G4) high yielding and the moderately stable while ICSR 160 (G3) and IS8193 (G6) are high yielding but unstable.

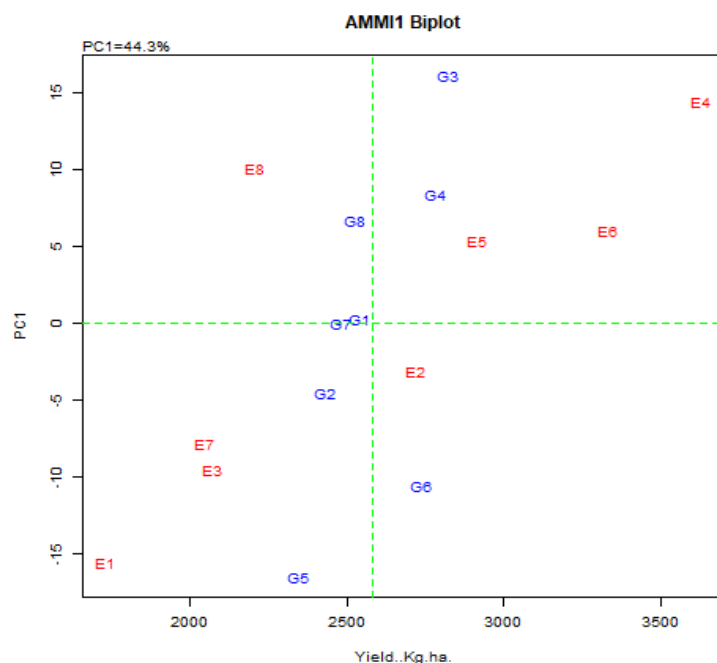


Figure 2. AMMI biplot (genotypes and environments plotted against their IPCA1 scores) for sorghum grain yield in Kg per hectare

Out of the eight (08) environments, half of the environments; Iganga (E2), Mayuge (E4), Namutumba (E5) and Oyam (E6) were high yielding since they were positioned on the right side of the vertical line with Iganga (E2) being the most stable environment since its Interaction Principal Component Axis (IPCA) scores was close to zero than other environments while the low yielding environments were positioned at the left side of the vertical line [Arua (E1), Kitgum (E3), Pallisa (E7) and Serere (E8)]. The genotype or environment IPCA scores (either positive or negative) displays their stability in the AMMI biplot. The more the IPCA score is close to zero (low interaction), the more stable the genotype or environment as opposed to environments (or genotypes) with large first IPCA scores (high interactions).

The pattern of GEI was cross-validated from distribution of eight sorghum genotypes over eight environments on the AMMI display of the first and second IPCA of genotypes and the environment (AMMI 2 model) as proposed by Vargas et al. (2001). This second model of AMMI helps to further examine adaptation of the genotypes across the environment (Figure 3). More still, (Purchase, 1997) explained the stability pattern of genotype display in AMMI 2 model where he emphasised that the stable genotypes are closer to the centric ring of the biplot. Based on this argument, Figure 3 results further showed that, GE17/1/2013A (G1) and SESO1 (G7) being more stable based on their closeness to the centric ring of the biplot. Conversely, ICSR 160 (G3) and IESV92172DL (G5) had diffused position therefore they were considered unstable across the study environment. The AMMI 2 model biplot further showed that genotypes ICSR 160 (G3) and IESV92172DL (G5) and environments Abi (E1), Mayuge (E4) and Namutumba (E5) contributed more to the GE interaction effect.

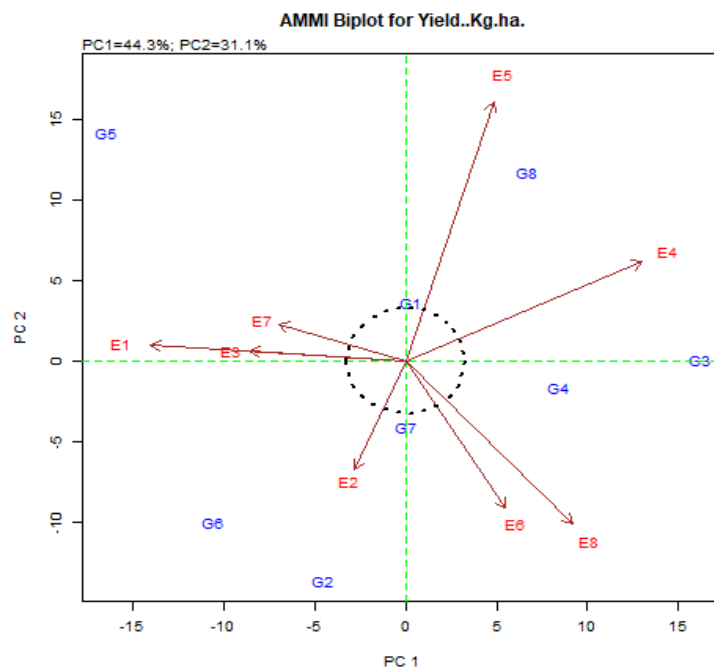


Figure 3. AMMI 2 biplot (IPCA2 scores plotted against IPCA1 scores) for sorghum grain yield in Kg per hectare

SESO3 (G8) and ICSR 160 (G3) were specifically adapted to Namutumba (E5) and Mayuge (E4) respectively. On contrary, GE35/1/2013A (G2) and IS8193 (G6) were specifically adapted to Iganga (E2). The observed results can be attributed to fundamental GEI (Wallace et al., 1995). More still, the GGE biplot informative and representativeness is of great significant measure of testing environments. The visual length of the environment vectors which is proportional to the standard deviation within the respective environments determines the environmental discriminatory ability. Superior environmental discriminating ability is displayed by the extensiveness of the environment vector. Consequently, in this study, the environmental vector biplot identified Abi (E1), Mayuge (E4) and Namutumba (E5) as favourably informative (discriminating) for the trial genotypes, as revealed by the extensive environment vectors (Figure 3) therefore exert strong interaction with genotype. Informative test environments precisely fix differences among the genotype accordingly inform breeders on selection decision. Iganga (E2) was non informative (least discriminating) of the eight (08) environments followed by Pallisa (E7), as revealed by the minuscule environment vector. The non-informative trial environments like Iganga (E2) and Pallisa (E7) tends to furnish little information on the genotypes therefore should not be used as trial environments. More still, a trial environment with smaller Average-Environment Axis (AEA) angle is more representative than their counter parts. The AEA (the line that passes through the average environment and the biplot origin) measures the representativeness of the average environment. Trial environments that are both informative and representative are superior environments for selecting overall genotype with good adaptability. Therefore, testing sorghum genotype for grain yield solely in Abi (E1) and Mayuge (E4) is adequate based on their representative and informative ability for sorghum grain yield in the study. Namutumba (E5) is informative but not representative due to its dispersed position; hence such environment can be used for rapid elimination of unstable genotypes during the selection process (Tukamuhabwa et al., 2012) under a single mega-environment or for selecting genotypes under mega-environments for specific adaptability. Use of those particular environments with non-informative and representative ability for assessing sorghum grain yield may give ambiguous results due to their low informative and representative ability. Yan and Rajcan (2002) defined the superior environment as the environment with substantial PC1 scores (informative) and small PC2 scores (representative) as observed for Abi (E1).

GGE biplot for the environment vector view for the stability study of genotypes for sorghum grain yield over the eight (08) environments identified the genotype IESV92043DL (G4) as the stable genotypes with fairly high sorghum grain yield mean performance (Figure 4). The biplot origin represents a stable genotype with grand mean value and thus zero contribution of the additive effect of genotype and multiplicative interactions shows the stability of the genotype. However, based on the same principle, SESO1 (G7) was identified as stable genotype but with low sorghum grain yield mean performance. This result was not surprising since SESO1 (G7)

was a released registered commercial cultivar which has already adapted in these environments. The distance between two genotypes estimates the Euclidean distance between them consequently measuring the dissimilarity between the genotypes. In this study, all the used genotypes are quite different in their genetic make-up with respect to sorghum grain yield due to their diffuse position (Figure 4). Out of the eight (08) environments, Mayuge (E4) was found to be the most superior environment in terms of sorghum grain yield performance and genotype, ICSR 160 (G3) was best adapted to Mayuge (E4) and Namutumba (E5) while IESV92043DL (G4) was specifically best adapted to Oyam (E6). Therefore, ICSR 160 (G3) and IESV92043DL (G4) with a particular adaptation to environments; Mayuge (E4)/Namutumba (E5) and Oyam (E6) respectively could be selected and recommended for specific adaptability as observed in this study.

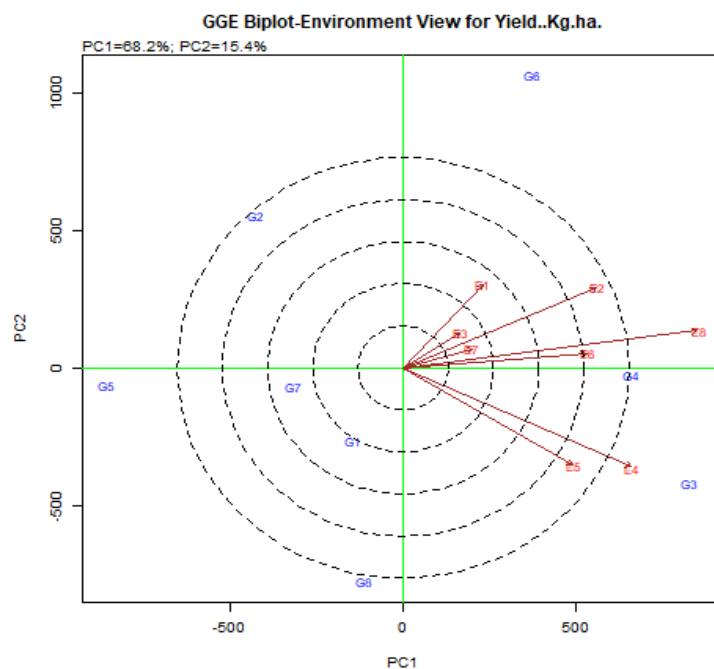


Figure 4. GGE biplot for the environment vector view to show similarities among the environments

On contrary, genotype focused biplot (Figure 5) conveyed that IESV92043DL (G4) is the most stable genotype for sorghum grain yield in the entire study environment while ICSR 160 (G3) is the superior genotype, succeeded by IESV92043DL (G4) and IS8193 (G6) respectively. However, IESV92043DL (G4) was depicted as superior genotype in the entire study environments due to its outstanding relative stability and adaptability couple with moderate sorghum grain yield from AMMI and GGE biplots display. This is a desirable plant breeding trait consequently such genotype can be recommended for possible release as a variety to up take pathway. The genotypic stability displayed in the study indicated that it performs well regardless of the GxE interaction thus wide adaptability of the genotype.

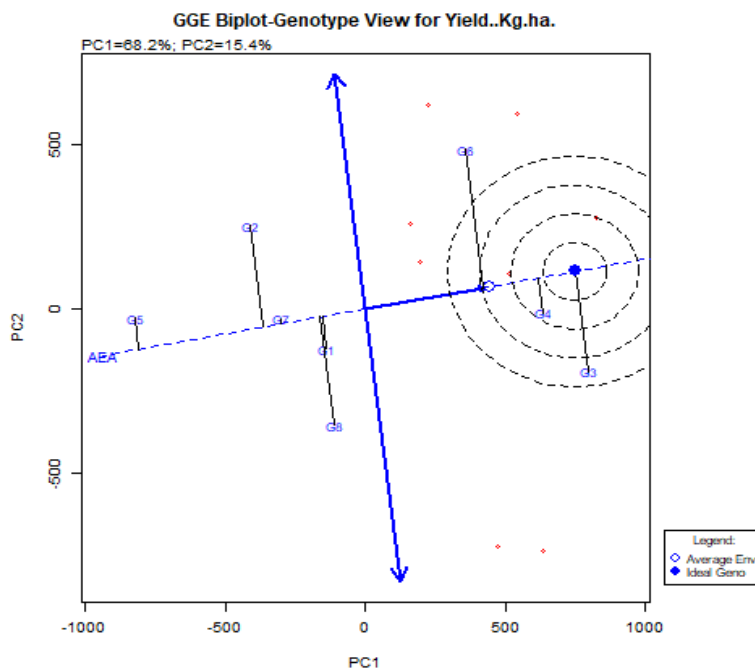


Figure 5. GGE biplot for the genotype view to show genotype ranking relative to an ideal genotype

The dynamic stability displayed by the genotypes calls for specific selection of genotypes suitable for particular environments (Andiku et al., 2019). However, genotypes; GE17/1/2013A (G1), GE35/1/2013A (G2), IESV92172D (G5), SESO1 (G7), and SESO3 (G8) recorded low yield unlike their counter parts [ICSR 160 (G3), IESV92043DL (G4) and IS8193 (G6)] that had high yields as evidenced by their positioning on the right side of the AEC abscissa (single-headed line (Figure 5). These high yielding genotypes could be selected for possible release as a variety. On the other hand, genotypes with below-average mean (left side of the AEC abscissa); SESO1 (G7) and GE17/1/2013A (G1) which are stable could be selected. The extensiveness of the non-headed line to the AEC regardless of the direction, indicates that genotype is unstable (high level of GEI) in the entire test environments. Conversely, genotypes IESV92043DL (G4)/SESO1 (G7) and GE17/1/2013A (G1) were fairly stable as well as high and low yielding respectively in terms of grain yield performance.

Physical envision of the which-won-where pattern of Multi Environment Yield Trials (METs) data is very crucial for understanding possible existence of different mega-environments (ME) in the production area as cited by Singh et al. (2019). The display of GGE-biplot clearly shows which-won-where pattern, as such it concisely summarises the GEI pattern of a trial as displayed for sorghum grain yield data in Figure 6. In the current study, there are four sectors with two mega environments namely Mega Environment I consisting of Abi (E1), Iganga (E2), Kitgum (E3), and Pallisa (E7) with the best genotype being IS8193 (G6). Mega environment II had the environments; Mayuge (E4), Namutumba (E5), Oyam (E6) and Serere (E8) with the best genotype being ICSR 160 (G3). These results suggested that genotypes with high grain yield for these two mega environments were ICSR 160 (G3) and IS8193 (G6) as observed under AMMI biplot (Figure 2). However Mega Environment II also had IESV92043DL (G4) with specific adaptability to Oyam (E6). These Mega Environment suggests feasible existence of different mega environments for sorghum production across the country. According to Oral et al. (2018), environments that are positioned within the same sector have strong correlations, and GEI suggesting effect of the environment on the genotypes and the presence of mega environment which is observed in this current study.

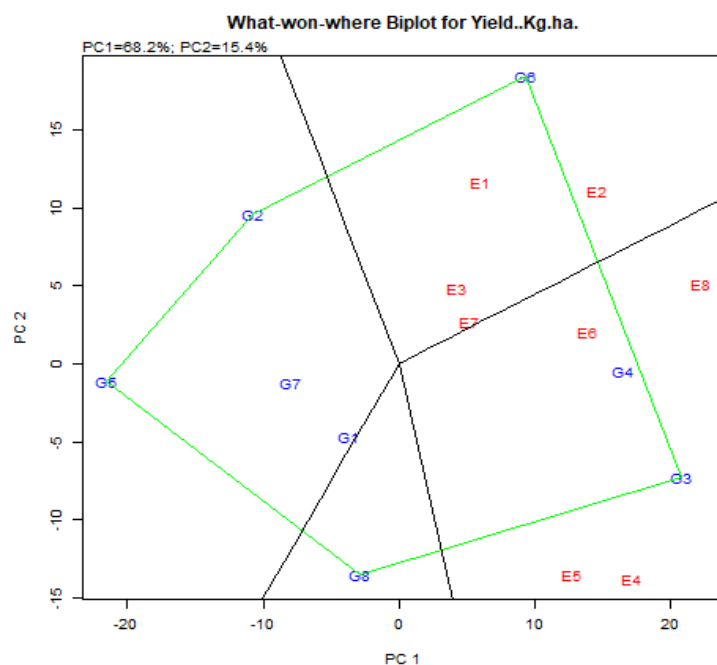


Figure 6. IPCA2 scores plotted against IPCA1 scores based on sorghum grain yield across eight environments to show the which-won-where pattern

The fascinating point from this GGE biplot view is that the genotypes [ICSR 160 (G3), IESV92043DL (G4), and IS8193 (G6)] that fall within the two mega environments were genotypes that out-performed the registered commercial released cultivar [(SES01(G7) and SES03 (G8)]. No environments fell into sectors with genotypes; GE17/1/2013A (G1), GE35/1/2013A (G2), IESV92172DL (G5), SES01(G7) and SES03 (G8) as vertices, suggesting that these genotypes did not perform well in any of the eight (08) environments. However, this Mega Environment pattern needs further verifying through setting repeated seasonal trials across the study location since this Mega Environment pattern was solely deduced from two seasons data of 2017 without considering subsequent years.

4. Conclusion

In this study, both the AMMI and GGE models identified IESV92043DL (G4) as the ideal genotype as it was stable and high yielding across the entire study environments. Using the same data, the three (03) promising sorghum genotypes [ICSR 160 (G3), IESV92043DL (G4) and IS8193 (G6)] with grain yield gain of 11.6%, 10.0% and 8.3% over the check (SES03) respectively were identified and released as varieties in Uganda; NAROSORG1, NAROSORG3, and NAROSORG2 respectively. On the other hand, stable genotype GE17/1/2013A (G1) with below-average yield mean of 2544 Kg ha⁻¹ was released as NAROSORG4 because of being resistant to covered kernel smut.

Abi (low yielding) and Mayuge (high yielding) were the most representative and informative environment in the country for sorghum grain yield performance and only testing sorghum genotypes for grain yield performance in these two environments can be enough. Namutumba can be used for rapid elimination of unstable genotypes during the selection process since it was informative but not representative.

The test environments for sorghum grain yield performance were delineated into two presumed mega-environments but this Mega Environment pattern needs further verifying through setting repeated seasonal trials across the study location since this Mega Environment pattern was solely deduced from two seasons data of 2017 without considering subsequent years.

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