

GENOTYPE-BY-ENVIRONMENT INTERACTION AND GRAIN YIELD STABILITY OF LOWLAND RICE GENOTYPES IN THE NORTHERN SAVANNA ZONES OF GHANA

¹*S.O. Abebrese, ¹A. Yeboah, ¹H.A. Yemyoliya and ¹M. Mawunya

¹ CSIR-Savanna Agricultural Research Institute, P.O. Box TL 52, Tamale, Ghana

*Corresponding author: sam555oppa@yahoo.com

Abstract

Grain yield stability is important for farmers in diverse and unpredictable environments and seasons. This study assessed the grain yield, genotype by environment interaction ($G \times E$) and grain yield stability of some lowland rice genotypes within the Northern Savanna zones of Ghana. The trials were laid out in a randomized complete block design (RCBD) with four replicates across two locations for three years. Grain yield of genotypes ranged from 0.8 to 4.1 t/ha with an average of 2.3 t/ha. Significant differences ($p < 0.05$) were observed for genotype effects, location effects, year effects, genotype by location interaction effects as well as location by year interaction effects. Stability analysis with the genotype main effect plus genotype by environment interaction (GGE) biplot identified WAS 122-13-WAS-10-WAR as a high yielding and stable genotype that can be cultivated across the test environments. EXBAIKA and L2-4 were also identified as high yielding but unstable genotypes that could be recommended for specific locations within the test environments.

Keywords

Multi-environment trials, genotype stability, rice, genotype \times environment interaction, GGE biplot

Introduction

Rice has become part of the diet of many Ghanaian homes due to its relative ease of cooking and changes in consumer preference especially those in the urban centres (Ragasa and Chapoto, 2017). It is now the second most consumed cereal after maize (Asante et al., 2020; Ragasa et al., 2013). Rice is also considered as a cash crop for many farmers because most rice farmers on average sell about 70% of their total rice harvest (MoFA, 2016). The per capita rice consumption which was estimated around 40 kg/person in 2016, keeps rising due to population growth and continual annual increase in consumption (Ragasa and Chapoto, 2017).

To meet the increasing demand, rice breeders develop improved and resilient varieties to help increase productivity and production. In doing so, breeders test promising genotypes over a wide range of targeted environments to ensure that results apply on farmers' field (Kang, 2002; Shrestha et al., 2020). During the analysis of such evaluations, a relative change in genotypes performances are sometimes observed across the diverse environments. This change in performances, referred to as genotype-by-environment interaction ($G \times E$), results from an interplay of genetic and nongenetic effects (Dia et al., 2016; Zobel et al., 1988). A significant $G \times E$ effects implies that genotypes do not show consistent performance across the test environments (Adjebeng-Danquah et al., 2016; Adu et al., 2019; Kang, 2002). Such significant $G \times E$, often makes breeders' selection complicated and selection efficiency misconstrued (Dia et al., 2016; Kang, 2002; Osei et al., 2018). A way breeders have devised to ensure progress in selection efficiency is to test genotypes in different environmental conditions to detect the presence or absence of significant $G \times E$ in order to assess the stability of genotypes

being tested (Akinwale et al., 2014; Kang, 2002).

Analysis of variance (ANOVA) is first carried out on the parameter under study to detect the presence or absence of significant $G \times E$. Significant $G \times E$ if absent, indicates a stable performance of the genotype's parameter across the tested environments whereas the presence of significant $G \times E$ indicates unstable performance of the parameter (Dia et al., 2016; Kang, 2002; Yan and Tinker, 2006). If $G \times E$ is significant, a further analysis is often performed to estimate the stability of the genotypes across the test environments (Kang, 2002; Zobel et al., 1988). The stability of a genotype gives an indication of its consistency in performance across a range of test environments (Akinwale et al., 2014; Kang, 2002). Stability analysis provides a general summary of the response patterns of genotypes to environmental changes (Zobel et al., 1988). This at the end, enables a breeder to make sound decision as to which of the varieties to recommend across a set of test environments and those for specific environments (Akinwale et al., 2014; Yan and Tinker, 2006). Several statistical methods, reflecting on different aspects of stability have been proposed (Yan and Tinker, 2006). These statistical methods vary from univariate models, such as regression slope, environmental variance, deviation from regression, Kang's yield-stability as well as multivariate models, such as additive main effects and multiplicative interaction (AMMI) and genotype main effect plus genotype environment interaction (GGE) biplot (Akinwale et al., 2014; Verma et al., 2015; Yan et al., 2000). Among these, the GGE biplot; which consists of a set of biplot interpretation methods whereby important questions regarding evaluating genotypes and test environments can be visually addressed is considered more versatile and innovative (Akinwale et al., 2014; Nath et al., 2013; Shrestha et al., 2020; Yan and Tinker, 2006).

Rice does very well in the Northern savanna zones of Ghana where bulk of the local rice is produced (Ragasa and Chapoto, 2017; Ragasa et al., 2013). In northern Ghana, rice is grown in different environments (transitional, guinea and sudan savannas) which differ in soil, climatic, disease and insect pressure using varying management practices (Katsura et al., 2016). Information on genotype-by-environment interaction ($G \times E$) interaction and grain yield stability is therefore important for breeders and farmers in such diverse and unpredictable environments and seasons. This study was conducted to assess the grain yield, genotype-by-environment interaction ($G \times E$) and yield stability of some promising lowland rice genotypes within the Northern savanna agro-ecological zones.

Materials and Methods

Plant materials and experiment locations

Thirteen lowland rice genotypes including a check from different sources (Table 1) were evaluated at Nyankpala (9° 25' 41" N, 0° 56' 42" W, 183 m) and Salaga (8° 33' 25" N, 0° 31' 04" W, 156 m) in 2008, 2009 and 2010. The Nyankpala site is in the Guinea savanna agro-ecological zone. The guinea savanna has a mean temperature of 29.5°C, mean rainfall of 1100 mm and annual relative humidity of 70% (Amekudzi et al., 2015). The Salaga site is in the transitional savanna agro-ecological zone. The transitional savanna zone has annual mean temperature of 28.2°C annual mean rainfall of 1200 mm and annual relative humidity of 67% (Amekudzi et al., 2015). The two sites were rainfed lowland ecologies. The soil at Nyankpala belongs to the acrisols whereas that of Libi is plinthosols (Effland et al., 2009).

Table 1. Genotypes used for the study

Genotype code	Genotype	Source	Status
V1	WAS 163-B-5-3	Afica Rice	Test entry
V2	WAS 122-13-WAS-10-WAR	Afica Rice	Test entry
V3	L2-4	Afica Rice	Test entry
V4	WAS 122 IDSA-11-WAS	Afica Rice	Test entry
V5	JASMINE 85	CSIR-SARI	Local check
V6	WAS 161-B-6-F/FR-1	Afica Rice	Test entry
V7	PERFUME IRRIGATED	Thailand	Test entry
V8	LONG GRAIN ORDINARY 1	Thailand	Test entry
V9	LONG GRAIN ORDINARY 2	Thailand	Test entry
V10	HEAVY JASMINE (105 days)	Thailand	Test entry
V11	LIGHT JASMINE (95 days)	Thailand	Test entry
V12	EXBAIKA	Legon, UG	Test entry
V13	DIGANG	CSIR-SARI	Test entry

Experimental design and trial management

The trials were laid out in a randomized complete block design (RCBD) with four replications across locations in a plot size of 15 m². Seeds were directly sown and thinned to one seedling per hill with a planting distance of 20 cm within and between rows. Recommended fertilizer rate of 90:60:60 kg NPK/ha was applied in two splits. Basal application of 60:60:60 was applied two weeks after germination. Top dressing with 30 kg

N in the form of urea was done at the booting stage. Weeds were controlled manually whenever necessary. Other standard agronomic practices were followed as recommended.

Data collection and analysis

Data were collected on grain yield, yield components and reaction to diseases based on International Rice Research Institute's Standard Evaluation System for Rice (IRRI, 2013). Excluding border rows, grains per plot were harvested, winnowed and dried. Grain weight per plot at 14% moisture content were extrapolated to tons per hectare t/ha (IRRI, 2013). Grain yield data from each location were subjected to Analysis of Variance (ANOVA) individually using GenStat statistical package (12th Edition) (Payne et al., 2009) to explore differences among genotypes and pooled across locations and years to determine genotype by environment interactions ($G \times E$). Comparison among genotype means were by the least significant difference (LSD) at 5% level of significance. GGE biplot analyses were performed with R statistical package (GGEbiplotGUI) as by Frutos et al. (2014) to determine grain yield stability of the genotypes evaluated across locations and years. The GGE Biplot analysis was based on environment-focused singular value partition (SVP = 2), without scaling (scaling = 0) and no transformation (transform = 0) (Yan and Tinker, 2006).

Results and Discussion

Analysis of variance

Significant differences were observed in all the component sources of variation and their interactions except the three-way interaction between variety, location and years (Table 2). Significant differences ($p < 0.001$) existed amongst the location effects, year effects, variety effects, variety by location interaction effects as well as location by year interaction effects. Significant differences ($p < 0.05$) existed amongst the interaction between variety and year effects (Table 2). The test locations contributed 52.73% of the total variation explained in the sum of squares for grain yield whereas genotypes and year explained 8.63% and 1.88% respectively (Table 2).

Mean yield performance of genotypes

The yield across locations and years ranged from 0.8 to 4.1 t/ha with an average 2.3 t/ha. The lowest yield was recorded at Salaga in 2008 cropping season whereas the highest was at Nyankpala in 2010 season (Table 3). Nyankpala in the 2010 cropping season recorded the highest location mean yield whereas Salaga in the 2010 cropping season recorded the lowest (Table 3). There were significant differences among genotypes at each environment except at Salaga in 2008 (Table 3).

Biplot Analyses

The biplot explained a total variation of 81.24% by both axes (Axis1 56.45% and Axis2 24.79%). The Nyankpala 2010 cropping season had the longest environmental vector and

Table 2. ANOVA table and percentage of variation explained by sources of variations

Source of variation	df	Sum of Sq.	Mean Sq.	Total Variation Explained (%)	Percent G×E Explained
Rep	3	5.62	1.87***	1.69	
Location	1	175.44	175.44***	52.73	
Year	2	6.26	3.13***	1.88	
Variety	12	28.73	2.39***	8.63	
Variety×Location	12	22.02	1.84***	6.62	42.70
Location×Year	2	9.5	4.75***	2.86	18.42
Variety×Year	24	11.83	0.49*	3.56	22.94
Variety×Location×Year	24	8.22	0.34ns	2.47	15.94
Residuals	231	65.11	0.28	19.57	

*** = significant at ($p < 0.001$), * = significant at ($p < 0.05$), ns = not significant, df = degree of freedom, Sq = square, G = genotype, E = environment, Rep = replication.

Table 3. Mean Yield of Genotypes across locations and years

Codes	Genotypes	Ny_08	Sa_08	Ny_09	Sa_09	Ny_10	Sa_10	Mean
V1	WAS 163-B-5-3	3.6	1.5	3.5	2.0	4.1	1.5	2.7
V2	WAS 122-13-WAS-10-WAR	3.2	1.6	3.4	2.1	4.0	1.5	2.6
V3	L2-4	3.9	1.2	3.9	1.4	4.1	1.2	2.6
V4	WAS 122 IDSA-11-WAS	2.6	1.5	3.6	2.0	2.7	1.1	2.2
V5	JASMINE 85	2.5	1.4	3.2	1.9	3.5	1.3	2.3
V6	WAS 161-B-6-F/FR-1	3.7	1.6	3.0	1.5	3.3	1.2	2.4
V7	PERFUME IRRIGATED	2.2	1.3	2.8	1.6	3.0	1.4	2.1
V8	LONG GRAIN ORDINARY 1	2.5	0.8	2.1	1.2	2.7	0.9	1.7
V9	LONG GRAIN ORDINARY 2	3.2	1.7	3.7	2.3	3.3	1.0	2.5
V10	HEAVY JASMINE	2.7	1.5	2.5	2.0	1.6	1.1	1.9
V11	LIGHT JASMINE	2.0	2.0	2.8	2.3	2.9	1.3	2.2
V12	EXBAIKA	2.6	2.2	3.4	2.4	4.0	1.5	2.7
V13	DIGANG	2.7	2.0	2.9	2.6	3.3	1.4	2.5
Mean		2.9	1.6	3.1	1.9	3.3	1.3	2.3
CV		18.1	21.0	18.5	23.4	35.1	24.2	
LSD _(0.05)		0.7	ns	0.4	0.3	1.3	0.4	

Ny_08 = Nyankpala 2008 season, Sa_08 = Salaga 2008 season, Ny_09 = Nyankpala 2009 season, Sa_09 = Salaga 2009 season, Ny_10 = Nyankpala 2010 season, Sa_10 = Salaga 2010 season.

small angle with the average environment axis and was therefore the most discriminatory and representative among the six test environments (Figure 1). Nyankpala in the 2008 cropping season was the most discriminatory but non-representative environment because it had the longest environmental vector but large angle with the average environmental axis (Figure 1).

Figure 2 presents the relationships that exist among the six test environments. Nyankpala in 2009 and Nyankpala in 2010 cropping seasons were positively correlated which suggests that the two environments could give a similar evaluation result. Salaga in 2008 and Salaga in 2009 were also positively correlated. Salaga in 2010 and Nyankpala in 2008 cropping seasons however had no association with any of the test environments (Figure 2).

For the mean versus stability overview of the GGE Biplot (Figure 3), EXBAIKA (V12) had the highest mean whereas

LONG GRAIN ORDINARY 1 (V8) had the least mean yield. L2-4 (V3) was the most unstable whereas LONG GRAIN ORDINARY 2 (V9) and WAS 122-13-WAS-10-WAR (V2) were the most stable genotypes (Figure 3). WAS 122-13-WAS-10-WAR (V2) was a high yielding stable genotype than LONG GRAIN ORDINARY 2 (V9). L2-4 (V3) and EXBAIKA (V12) were high yielding but unstable whereas LONG GRAIN ORDINARY 1 (V8) was low yielding and unstable genotype (Figure 3).

Figure 4 identified WAS 122-13-WAS-10-WAR (V2) as the most "ideal" genotype. This genotype points on the average environment axis in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of average environment axis highest mean performance.

EXBAIKA (V12) was the winning genotype for Salaga in 2008, 2009 and 2010 whereas L2-4 (V3) won at Nyankpala in

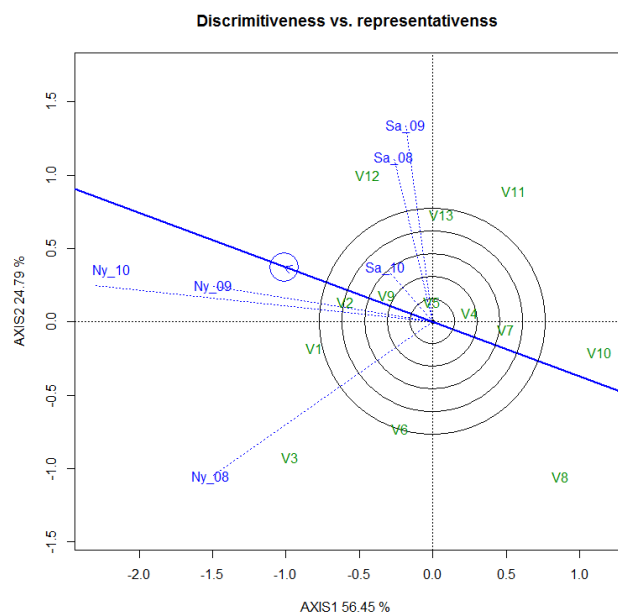


Figure 1. Discriminatory power versus representative overview of the test environments

Ny_10 = Nyankapala 2010, Ny_09 = Nyankapala 2009, Ny_08 = Nyankapala 2008, Sa_10 = Salaga 2010, Sa_09 = Salaga 2009, Sa_08 = Salaga 2008

2008, 2009 and 2010 (Figure 5). The remaining vertices genotypes [LIGHT JASMINE (V11), HEAVY JASMINE (V10) and LONG GRAIN ORDINARY 1 (V8)] which had no environment attached to the sectors in which they fell did not win in any environments (Figure 5).

Rice is cultivated in diverse environments globally (Van Tran, 1998). In Ghana, rice is cultivated in three ecologies (irrigated lowland, rainfed lowland and upland) across the various agro-ecological zones (Ragasa et al., 2013). Whereas the irrigated lowlands constitute about 10% of the available production area with an average yield of 4.5 t/ha, the rainfed lowland constitute about 84% of the production area with an average yield of 2.5 t/ha. The remaining 6%, goes for the upland ecology with average yield of about 1.5 t/ha (Ragasa and Chapoto, 2017). The rainfed lowlands contributes the most to Ghana's local production and is characterized by low yields resulting from seasonal weather variability particularly rainfall (Katsura et al., 2016). The average yield of 2.3 t/ha across locations and years, though lower than the average yield of 2.5 t/ha for the rainfed lowland ecology, is typical of rice yields within the Northern savanna zones of Ghana (Ragasa et al., 2013). Genotypes effects were significant in most of the test environments despite the variable cultivating factors. The emergence of environmental effects as the largest contributor to the total variation is typical of most rice varietal trials within the West African sub region (Katsura et al., 2016). This could be partly attributed to the variable climatic and soil characteristics of the two agro-ecological zones (Amekudzi et al., 2015; Effland et al., 2009). Grain

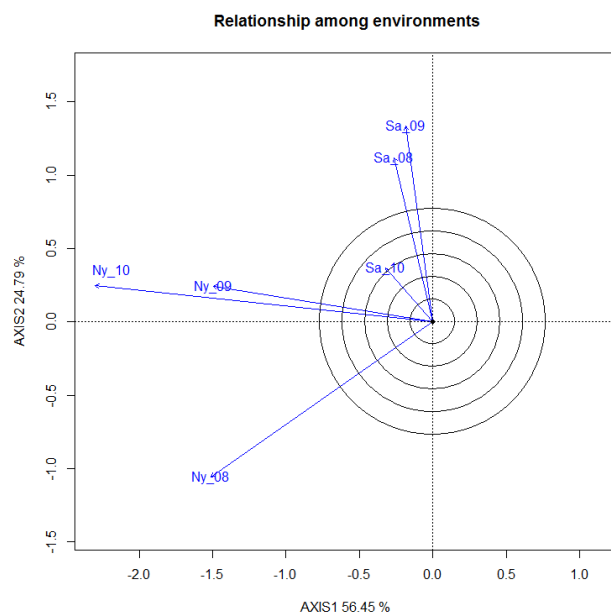


Figure 2. Relationships among test environments; Ny_10=Nyankapala 2010.

Ny_09 = Nyankapala 2009, Ny_08 = Nyankapala 2008, Sa_10 = Salaga 2010, Sa_09 = Salaga 2009, Sa_08 = Salaga 2008

yield of rice is reported to vary with management, climatic and soils factors (Nassir and Ariyo, 2011; Sharifi et al., 2017). Since the trials across the locations and years were managed with a standard protocol, seasonal weather variability could be the major contributing factor of the environmental effect. Breeders normally select cultivars with wide adaptation to be able to manage such wide environmental variation

The genotype main effect plus genotype by environment interaction (GGE) biplot is considered the most versatile and innovative methodology in biplot graphic analysis applied in plant breeding (Verma et al., 2015; Yan et al., 2000; Yan and Tinker, 2006). It produces a graphical display of results which facilitates a better understanding of complex genotype x environment interaction in multi-environment trials (Akinwale et al., 2014; Nassir and Ariyo, 2011). After the ANOVA had shown significant mean squares for GxE, GGE biplot graphically analyse the nature of the interactions considering only the G and GxE effects simultaneously, removing the environment (E) effect (Yan and Tinker, 2006). For the discriminatory and representative overview of the test environments (Figure 1), the Nyankapala 2010 cropping season had the longest environmental vector and small angle with the average environment axis as suggested by Yan and Tinker (2006). It was therefore the most discriminatory and representative among the six test environments. An environment which has longer environmental vector but large angle with the average environment axis is considered the most discriminatory but non-representative of the environments. Such environments are suitable for selecting specifically adapted genotypes (Yan and Tinker, 2006). Nyankapala in the 2008 cropping season

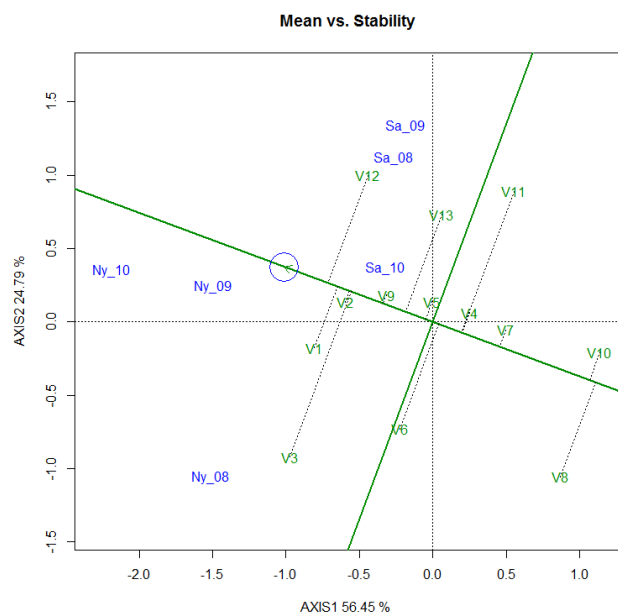


Figure 3. Mean versus stability view of the genotypes; Ny_10=Nyankpala 2010.

Ny_09 = Nyankpala 2009, Ny_08 = Nyankpala 2008, Sa_2010 = Salaga 2010, Sa_09 = Salaga 2009, Sa_08 = Salaga 2008

was the most discriminatory but non-representative among the environments.

The similarity between two environments is determined by both the length of their vectors and the cosine of the angle between them. The existence of acute angle between two environments indicates a positive correlation, an obtuse angle indicates a negative relationship while right angle indicates no correlation (Yan and Tinker, 2006). Positive association among two sets of environments indicates the same information about genotypes performance could be obtained from either and hence can be dropped to reduce cost. Presence of negative association suggests that the environments do not give same information and hence one cannot represent the other (Yan and Tinker, 2006). Nyankpala in 2009 and Nyankpala in 2010 cropping seasons were positively correlated which suggests that a similar information could be drawn from these two environments. Salaga in 2008 and 2009 were also positively correlated. Nonetheless, Salaga in 2010 and Nyankpala in 2008 cropping seasons had no association with any of the test environments (Figure 2) which means different information could be drawn from these environments.

For the mean versus stability overview of the GGE Biplot (Figure 3), individual genotype mean yield performance is compared to the grand mean yield performance to reveal those that are above and below the grand mean. The average environment axis (AEA) [small circle with an arrow] points to the direction of highest mean yield across environments. The closer a genotype is to the average environment axis, the higher the genotype's performance above the grand mean and vice versa. Therefore, EXBAIKA (V12) had the highest

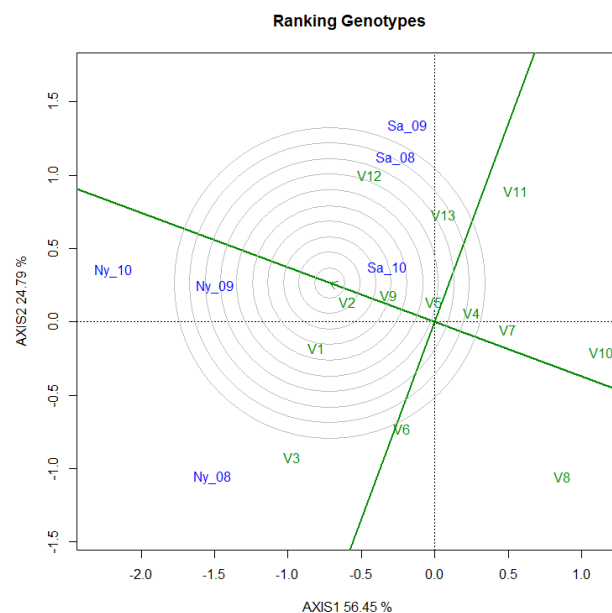


Figure 4. Ideal genotype overview of the test genotypes.

Ny_09 = Nyankpala 2009, Ny_08 = Nyankpala 2008, Sa_2010 = Salaga 2010, Sa_09 = Salaga 2009, Sa_08 = Salaga 2008

mean whereas LONG GRAIN ORDINARY 1 (V8) had the least mean yield. The stability of genotype's performance across environments was assessed using the AEC which is the line that passes through the biplot origin opposite to the average environment axis (AEA). The ACE points to greater variability in either direction. The longer the length of the genotype's projections unto the AEA, the more unstable the genotype and vice versa (Yan and Tinker, 2006). Therefore, L2-4 (V3) was the most unstable whereas LONG GRAIN ORDINARY 2 (V9) and WAS 122-13-WAS-10-WAR (V2) were the most stable genotypes (Figure 3). The concept of stability is meaningful when the stability is accompanied by high mean yield performance (Akinwale et al., 2014). Genotypes that combine high mean yield performance with stability across a wide range of environments is of much importance in regions with variable cultivating factors such as in the savanna agro-ecologies (Katsura et al., 2016; Shrestha et al., 2020). Therefore, WAS 122-13-WAS-10-WAR (V2) was a high yielding stable genotype than LONG GRAIN ORDINARY 2 (V9). L2-4 (V3) and EXBAIKA (V12) were considered high yielding but unstable. Such genotypes could be recommended for specific environments. However, LONG GRAIN ORDINARY 1 (V8) was low yielding and unstable genotype which cannot be recommended neither across nor for specific environment. As elaborated by Yan and Tinker (2006), Figure 4 defines an "ideal" genotype (the centre of the concentric circles) to be a point on the average environment axis ("absolutely stable") in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of average environment axis highest mean performance. Therefore, genotypes located closer to the ideal genotype are more

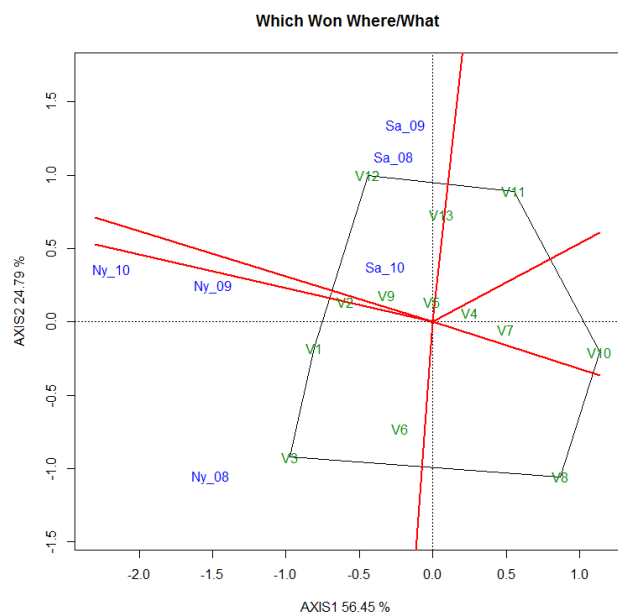


Figure 5. Which-won-where view of the test genotypes.
Ny_09 = Nyankpala 2009, Ny_08 = Nyankpala 2008, Sa_2010 = Salaga 2010, Sa_09 = Salaga 2009, Sa_08 = Salaga 2008.

favourable than the others. Thus, WAS 122-13-WAS-10-WAR (V2) is more favourable than LONG GRAIN ORDINARY 2 (V9) and LONG GRAIN ORDINARY 2 (V9) is also more desirable than WAS 163-B-5-3 (V1).

Conclusion

Given the significant genotype by environment interaction effect, promising rice genotypes are recommended to be evaluated across a number of locations and seasons within the Northern savanna agro-ecological zones. This should be accompanied with a thorough stability analyses to help select varieties that are adapted to specific environments and those with broad adaptation across a set of environments. WAS 122-13-WAS-10-WAR was identified as a high yielding and stable genotype that can be cultivated across the test environments. EXBAIKA and L2-4 which were high yielding but unstable could be recommended for specific environments. Since breeders normally select varieties that can adapt to a wide range of environments, WAS 122-13-WAS-10-WAR is the best genotype for cultivation within the northern savanna zones. Aside identifying stable and unstable genotypes, the discriminatory and representative view and the relationship among test environments view of the GGE biplot were also useful in delineating the test environments into the most representative among the test environments to inform future testing projects and also for rationale use of resources.

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