

## USE OF GGE BIPLLOT FOR TARGETING EARLY MATURING MAIZE CULTIVARS TO MEGA-ENVIRONMENTS IN WEST AFRICA

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### ABSTRACT

Maize (*Zea mays* L.) is an important staple food consumed by people with varying food preferences and socio-economic backgrounds in West Africa (WA). Genotype by environment interactions (G×E) exist in WA implying the need for extensive testing of cultivars in multiple environments over years before cultivar realistic recommendations can be made. This study examined the effect of G×E on the performance and stability of early cultivars and to identify core test locations in the mega-environments of WA. Across locations, 2004 TZE-W Pop STR C<sub>4</sub> produced the highest grain yield and was the most stable cultivar. DMR-ESRW QPM produced the lowest yield. The test environments contributed about 83.4% of the total variation in grain yield, while genotypes accounted for 1.5% and G × E, 11%. Test environments were classified into four mega-environments, namely, Katibougou, Sotouboua, Ejura, and Bagou as the first group; the second group consisted of Manga, Nyankpala, Bagauda, Yendi, Angaredebou, Mokwa, Katibougou, and Zaria; while the third group comprise of Ativeme, and Ikenne; and the fourth, Ina. Test locations Ejura, Sotouboua and Bagou and Katibougou were highly correlated in their ranking of the genotypes in group 1, suggesting that a promising early maturing cultivar selected in one of these locations in one country will also be suitable for production in the other locations within the same mega-environments in different countries. Kita was identified as the ideal location, while Zaria was close to the ideal location.

*Key Words:* Genotypes, multiple environment, *Zea mays*

### RÉSUMÉ

Le maïs (*Zea mays* L.) est une nourriture principale consommé par des personnes à préférence alimentaires et un passé socio-économique variés en Afrique de l'Ouest. Une interaction Génotype et Environnement (G×E) était trouvée, impliquant ainsi le besoin en test extensive des cultivars sur plusieurs années avant toute recommandation. Le but de cette étude était d'examiner l'effet G×E sur la performance et la stabilité des cultivars précoces, ainsi que d'identifier le test principal de milieu dans les méga-environnements de l'Afrique de l'Ouest. A travers les milieux, 2004 TZE-W Pop STR C<sub>4</sub> avait produit le rendement en grain le plus élevé et était le cultivar le plus stable. DMR-ESRW QPM avait induit le rendement le moins élevé. La contribution du test d'environnements était d'environ 83.4% de la variation totale du rendement en grain, pendant que les génotypes et G × E présentaient 1.5% et 11%, respectivement. Les tests d'environnements étaient classifiés en quatre méga-environnements à savoir, Katibougou, Sotouboua, Ejura, and Bagou comme premier groupe; Manga, Nyankpala, Bagauda, Yendi, Angaredebou, Mokwa,

Katibougou, and Zaria comme deuxième groupe, alors que le troisième groupe comprenait Ativeme, et Ikenne et le quatrième, Ina. Le test de milieux Ejura, Sotouboua, Bagou et Katibougou étaient hautement corrélé sur le plan ranking des génotypes au sein du groupe 1, suggérant qu'un cultivar précoce promettant sélectionné dans un de ces milieux dans un pays sera approprié pour la production dans d'autres milieux au sein des mêmes méga-environnements dans différents pays. Kita était identifié comme un milieu idéal, alors que Zaria était proche du milieu idéal.

*Mots Clés:* Génotypes, environnement multiple, *Zea mays*

## INTRODUCTION

Maize is an important staple food in West and Central Africa (WCA), accounting for about 15% of the total calorific intake of the rural communities (Badu-Apraku *et al.*, 2011). It is grown in highly heterogeneous environments (Menkir, 2003) and is consumed by people with varying food preferences and socio-economic backgrounds (Badu-Apraku *et al.*, 2006). To meet these demands, maize breeders at the International Institute of Tropical Agriculture (IITA) work in partnership with national programmes in West Africa (WA) to develop maize varieties adapted to the different agro-ecological zones and farming systems of WCA. The diverse maize growing areas are plagued by high incidence of diseases, insect pests and parasitic plants, especially *Striga hermonthica*, recurrent drought and low soil fertility.

The multi-environment trials (METs) have demonstrated the existence of  $G \times E$  (Fakorede and Adeyemo, 1986; Badu-Apraku *et al.*, 1995; 2003; 2007; 2008) and have justified extensive testing of cultivars in multiple environments over several years to aid decisions on cultivar recommendations.

Often, however, national maize research programmes of WCA are compelled to conduct cultivar evaluation in a few locations owing to resource limitation which sometimes limit the application of their results. From the results of Yan *et al.* (2007), it is important to properly examine environments for uniqueness and for information that would enable the separation and ranking of genotypes. This allows stratification and identification of core locations where testing of cultivars can be done without losing valuable information about genotypes. Furthermore, stratification of maize evaluation environments can help increase heritability of

measured traits, accelerate the rate of gain from selection, strengthen the potential competitiveness for seed production and maximise grain yields for farmers (Gauch and Zobel, 1997).

It is, therefore, important to improve our understanding of the agro-ecosystems of WCA and determine if it could be subdivided into different mega-environments to facilitate a more meaningful cultivar evaluation and recommendation. The result of such a study would simplify the selection of locations for METs that would permit inclusion of sample of environments that adequately cover the range of environmental conditions of the target geographical region.

Gauch and Zobel (1996, 1997) defined a mega-environment as a portion of a crop species' growing region with a homogenous environment in which some genotypes perform similarly. They used the maize MET dataset for identification of maize mega-environments. Menkir (2003) used Geographic Information System (GIS) to analyse long-term data collected on seven climatic variables relevant to maize production to refine the stratification of the sub-region into well-defined agro ecological zones. GIS separated the locations into four distinct zones, namely, mid-altitude, rainforest, moist savannah, and dry savannah.

Setimela *et al.* (2007) used the maize MET data set of CIMMYT and agro-climatic data to identify maize mega-environments for sub-Saharan Africa including WCA. The WCA sub-region was stratified into four distinct groups viz. dry savannah, wet savannah, dry mid-altitude and wet mid-altitude.

The GGE biplot graphically displays genotype main effect plus  $G \times E$  of a MET in a way that facilitates visual evaluation of cultivars and mega-environment identification (Yan *et al.*

2000). Badu-Apraku *et al.* (2008) and Badu-Apraku and Lum (2010) used the GGE biplot analysis to decompose the G×E in WCA and to obtain information on the early maturing maize cultivars that were suitable for *Striga*-infested and *Striga*-free environments and to investigate stability of cultivars in the various environments. However, GGE biplot has not been used to define core test locations for early maturing maize germplasm in maize variety evaluations in WA. Furthermore, the signing of the protocol on seed by the Heads of States of the Economic Community of West Africa (ECOWAS) member countries in 2009, and the availability of the West African Catalogue of Plant Species and Varieties (COAFEV), offer a unique opportunity for movement of good quality seed of improved maize varieties and hybrids across borders of the ECOWAS countries for production and marketing.

Presently, a variety released in any ECOWAS member country does not need to be released again in other member countries within the sub-region. This new development in the seed sectors of the ECOWAS member countries calls for the identification of core testing locations in each of the current mega-environments in WA to facilitate the selection of high yielding and stable cultivars for seed production and marketing across the member countries of ECOWAS. The seed catalogue which contains the list of varieties whose seeds can be produced and commercialised within the territories of the 17 member countries is an aggregate of the varieties registered in the national catalogues of the Member States.

The objective of this research was to use the dataset of the RUVT-Early and the GGE biplot technique to summarise the effects of G and G×E in early maturing maize cultivars, and identify core test locations in each mega-environment in WA.

## MATERIALS AND METHODS

**Regional uniform variety trials - early.** The regional early variety trials have since 1987 been organised by the West and Central Africa Collaborative Maize Research Network (WECAMAN) and IITA in collaboration with the

National Agricultural Research Systems (NARS) of WCA. The trials serve as the vehicle for systematically and extensively testing and disseminating elite early maize cultivars across WCA. Both the National Agricultural Research Systems (NARS) and IITA nominate their best cultivars for evaluation in the trials.

Eighteen elite early maturing maize cultivars, comprising six normal endosperm and twelve Quality Protein Maize (QPM) cultivars (Table 1) were evaluated between 2006 and 2008 in the Regional Uniform Variety Trials - Early (RUVT-Early) at 15 sites representing the dry savanna, moist savanna and forest/savanna transition zones of WA (Table 2, Fig. 1). A QPM cultivar, DMR-ESRW QPM was included as the reference check in the trials at all sites. A standard protocol was adopted at each site. The evaluations were conducted under rain-fed conditions in all locations.

Trials were planted when rains at each test site had started. A randomised complete block design with four replications was used in the evaluations. Each plot consisted of 4 rows, each 5-m long, spaced 0.75 m apart with 0.40 m spacing between plants within the row. Three seeds were sown per hill and later thinned to two plants per stand to obtain a final population density of 66,666 plants per hectare. To optimise crop performance at each site, fertiliser application and pest control were carried out based on the recommendations for the respective sites in each country.

**Collection of agronomic data.** Observations were recorded on the two centre rows of each plot for days to 50% silking, number of ears per plant (EPP), plant and ear heights and root lodging (% plants leaning more than 30° from vertical). Others included stalk lodging (broken at or below highest ear node), ear aspect, number of plants harvested, number of ears harvested and per cent moisture in the grain. Days to anthesis (DA) and days to silking (DS) were computed as the number of days from planting to when 50% of the plants had shed pollen and had emerged silks, respectively. Anthesis-silking interval (ASI) was determined as the difference between 50% silking and anthesis. Plant and ear heights were measured as the distance from the base of the plant to the

TABLE 1. Characteristics of the 18 maize varieties evaluated in the RUVT-Early at 15 locations in West and Central Africa

Variety	Code	Parentage	Grain type*	Reaction to Striga hermonthica	Reaction to drought stress
EV DT-W 99 STR QPM C0	EWQ	(TZE-W Pop ' 1368 STR) TZE-W Pop S4F <sub>2</sub> set 1, source of QPM	White-D	Tolerant	Tolerant
POOL18SR/AK9331DMRSR/AK9331DMRSR (QPM)	P18B	9331 DMRESR and pool 18	Yellow-D/F	Tolerant	Tolerant
TZE-W Pop STR QPM C0	TWQ	TZE-W Pop STR QPM	White-D/F	Tolerant	Tolerant
POOL18SR/ACR94TZECOMP5-Y/ACR94TZECOMP5-Y (QPM)	P18C	Backcross of ACR94TZECOMP5-w with Pool 18SR to develop QPM variety	Yellow-F	Tolerant	Susceptible
Early STR Syn F2	ESS	Advanced Striga resistant early inbred lines from TZE Comp 3 and TZE comp 4	White-F/D	Tolerant	Susceptible
TZE-Y Pop STR QPM C0	TYQ	Various	Yellow-D/F	Tolerant	Tolerant
2004 TZE-W Pop STR C4	20TW	TZE-W Pop DT STR C <sub>4</sub>	White-D/F	Tolerant	Tolerant
2004 TZE-Y Pop STR C4	20TW	TZE-Y Pop DT STR C <sub>4</sub>	Yellow-D/F	Tolerant	Tolerant
POOL18SR/AK94DMRESR-Y/AK94DMRESR-Y (QPM)	P18A	DMRESR-Y/AK94DMRESR-Y and Pool 18	Yellow-D/F	Tolerant	Tolerant
DMR-ESRW QPM (RE)	DM	DMR-ESRW x QPM source	White-D/F	Susceptible	Susceptible
BG 97 TZE Comp. 3x4	BG97	TZE Comp 3 and TZE Comp 4	White-D/F	Susceptible	Susceptible
EV DT-Y 2000 STR QPM C0	EYQ	(Pool 16 DT ' 1368 STR) S6 F <sub>2</sub> QPM source	White-F/D	Tolerant	Tolerant
98 Syn WEC QPM C0	98S	(Pool 16 DT ' 1368 STR) S4 F <sub>2</sub> , QPM Source	White-F/D	Tolerant	Tolerant
TZE-Y Pop STR C0 S6 QPM C0	TYSC	TZE-Y Pop STR C0 S6, QPM source	Yellow-F/D	Tolerant	Tolerant
TZECOMP3X4-SYN	TCP4	TZE Comp 4 and TZE Comp3	Yellow-F/D	Susceptible	Susceptible
POOL15SR/ACR94TZECOMP5-W/ACR94TZECOMP5-W (QPM)	P15	Backcross of ACR94TZECOMP5-w with Pool 15SR to develop QPM variety	White-F	Tolerant	Susceptible
TZE-W Pop x 1368 STR QPM C0	TWXQ	TZE-W Pop ' 1368 STR	White-F/D	Tolerant	Tolerant
TZE Comp 3 DT C1	TCP3	TZE Composite	White-F/D	Susceptible	Tolerant

\* D = dent; F = flint.

TABLE 2. Description of the test locations for the Regional Uniform Variety Trials (RUVT) of early maturing varieties conducted in West Africa, 2006-2008

Country	Location	Code	Agro ecological zone <sup>†</sup>	Latitude	Longitude	Altitude (m ASL)	Rainfall during growing season (mm)
Nigeria	Mokwa	MOK	SGS	9°18'N	5°4'E	457	1100
Nigeria	Ikenne	IKN	FT	6°53'N	3°42'E	60	1200
Nigeria	Bagauda	BG	NGS	12°01'N	8°19'E	520	840
Nigeria	Zaria	ZA	NGS	12°00'N	8°22'E	640	1120
Togo	Ativeme	ATV	FT	6°25'N	1°06'E	100	1360
Togo	Sotouboua	SO	SGS	0°59'N	8°34'E	374	1200
Ghana	Ejura	EJ	FT	7°38'N	1°37'E	90	1460
Ghana	Nyankpala	NYP	NGS	9°25'N	0°58'E	340	800
Ghana	Yendi	YD	SGS	9°26'N	0°10'W	157	1300
Ghana	Manga	MAN	SS	11°01'N	0°16'W	270	718
Benin	Ina	INA	SGS	9°58'N	2°44'W	358	899.5
Benin	Angaredébou	ANG	SS	11°32'N	3°05'W	297	1000
Benin	Bagou	BF	SGS	11°28'N,	2°23'W	303	1125
Mali	Kita	KX	SS	13°05'N,	09°25'W	393	1000
Mali	Katibougou	KT	SS	12°50'N	8°09'W	285	700

<sup>†</sup> SGS = southern Guinea savanna; NGS = northern Guinea savanna; FT = Forest-savanna Transitional zone; SS = Sudan savanna

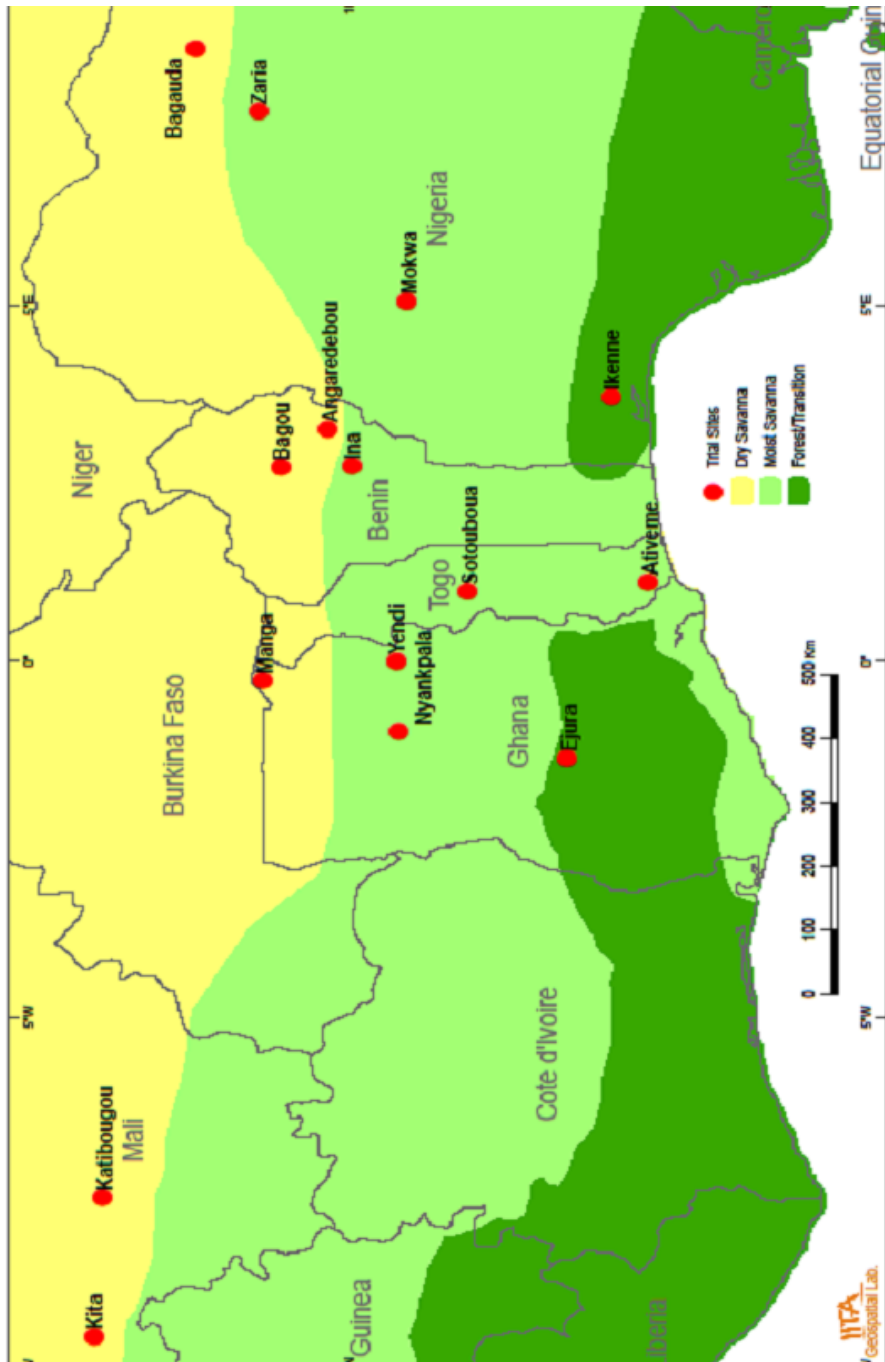


Figure 1. Locations in the major agroecological zones in West Africa used for testing early maize varieties in the RUVT.

height of the first tassel branch and the node bearing the upper ear, respectively.

Root lodging (percentage of plants leaning more than 30° from the vertical), stalk lodging (percentage of plants broken at or below the highest ear node), and disease reaction, were also recorded. Husk cover was rated on a scale of 1 to 5, where 1 = husk tightly arranged and extended beyond the ear tip and 5 = ear tips exposed. Plant aspect was scored on a scale of 1 to 5, where 1 = excellent plant type and 5 = poor plant type. Ear aspect was based on a scale of 1 to 5, where 1 = clean, uniform, large, and well-filled ears and 5 = ears with undesirable features. Data on maydis leaf blight, (*Bipolaris maydis*) was recorded between 2-4 week period after 50% silking. About 10 plants were scored in the central part of the plot using a 1-5 rating scale where:

1 = slight infection	Very few lesions on leaves, usually only on the lower leaves of the plant.
2 = light infection	Few to moderate lesions on leaves below top ear, no lesions on leaves above the top ear.
3 = moderate infection	Moderate to large number of lesions on leaves below top ear, few lesions on leaves above the top ear.
4 = heavy infection	Large number of lesions on leaves below top ear, moderate to large number of lesions on leaves above the top ear.
5 = very heavy infection	All leaves with large number of lesions leading to premature death of the plant and light ears.

Also, data were recorded on rust, *Puccinia polysora*, or *Puccinia sorghi* within 2-4 week period after 50% silking using a scale of 1-5 or 1-9 where 1=no rust and 5 or 9= severe rust. Number of ears per plant (EPP) was obtained by dividing the total number of ears per plot by the number of plants harvested. Grain yield was calculated based on 80% (800 g grain kg<sup>-1</sup> ear weight) shelling percentage and adjusted to 150 g kg<sup>-1</sup> moisture content. Even though data were collected on several traits, only those on the most important traits in the studies are presented in the results.

**Statistical analysis.** Analyses of variance (ANOVA), combined across environments were performed on plot means for grain yield, DS, ASI, EPP, plant height, plant and ear aspects, percentage stalk lodging, husk cover with PROC GLM in SAS using a RANDOM statement with the TEST option (SAS Institute, 2002). In the combined ANOVA, the year, location, G x E interaction and replicates were considered as random factors, while entries were considered as fixed effects. Means were separated using the LSD at P<0.05. ANOVA was done for each site and across sites and years.

Data relating to scores and counts were natural logarithm-transformed before the analyses of variance. Subsequently, the data on grain yield were subjected to GGE biplot analysis to decompose the G x E interactions. The GGE biplots were constructed using the first two principal components (PC1 and PC2) that were derived from subjecting environment-centred grain yield means for each location (averaged over years) to singular value decomposition. The data were not transformed ('Transform=0'), not standardised ('Scale=0'), and were environment-centred (Centering=2'). This provided information on the cultivars that were suitable for the different environments, investigation of stability of cultivars in the various environments and identification of the mega-environments. The analyses were done using GGE biplot, a Windows that fully automates biplot analysis (Yan, 2001). The programme is available at [www.ggebiplot.com](http://www.ggebiplot.com)



(verified 1 December 2009). The GGE biplot Model 3 equation used is as follows:

$$Y_{ij} - Y_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

Where:

$Y_j$  is the average yield across all genotypes in environment  $j$ ;

$\lambda_1$  and  $\lambda_2$  are the singular values for PC1 and PC2, respectively;

$\xi_{i1}$  and  $\xi_{i2}$  are the PC1 and PC2 scores, respectively, for genotype  $i$ ;

$\eta_{j1}$  and  $\eta_{j2}$  are the PC1 and PC2 scores, respectively, for environment  $j$ ; and

$\varepsilon_{ij}$  is the residual of the model associated with the genotype  $i$  in environment  $j$ .

The decision as to whether each group of locations could be considered as representative of a mega-environment was based on the similarity of grouping of winning genotypes across years (Yan *et al.*, 2000; 2007).

## RESULTS AND DISCUSSION

**Field performance of early maturing maize cultivars.** Combined analysis across sites and locations for the nineteen genotypes in the RUVT - early revealed that genotypes, environments and Genotype x year interaction ( $G \times E$ ) were significantly ( $P < 0.05$ ) different for all traits measured except EPP, plant height, ear height, plant aspect, ear aspect and husk cover for which the  $G \times E$  was not significant (Table 2). The test environments contributed about 83.4% of the total variation in grain yield; while the genotypes accounted for about 1.5%, and  $G \times E$  sources of variation, about 11% (Table 3). The contribution of locations to the environmental variation was nearly eight times that of years and about double the contribution of the interaction of years with locations to the environmental variation.  $G \times$  year interaction

accounted for more than half of the  $G \times E$  sum of squares.

Grain yield across the environments ranged from 2835 kg ha<sup>-1</sup> for the reference QPM cultivar, DMRE-SR-W QPM, to 3563 kg ha<sup>-1</sup> for the drought tolerant and *Striga* resistant cultivar, 2004 TZE-W Pop STR C<sub>4</sub>. However, there were no significant ( $P > 0.05$ ) differences in grain yield among the five top ranking cultivars. It is striking to note that the QPM cultivar, TZE-W Pop STR QPM C<sub>0</sub>, was comparable in grain yield to 2004 TZE-W Pop STR C<sub>4</sub>, both of which were derived from the same source population, TZE-W Pop DT STR C<sub>4</sub>. This indicates that QPM cultivars with comparable performance to the normal endosperm type are available in our programme. Similar findings were reported by Badu-Apraku and Lum (2010).

The highly significant cultivar  $\times$  environment interaction for grain yield and most measured traits justified the use of the GGE biplot to decompose the cultivar  $\times$  environment interactions to determine the yield potential and stability of the early cultivars and to investigate the best core test locations in the various mega-environments in WA using the GGE biplot tool (Yan *et al.*, 2000; 2005; 2010; Yan, 2001; Setimela *et al.*, 2007) and adopting the cultivar and environment codes listed in all Figures and Tables.

**GGE biplot analysis of grain yield response and stability of early cultivars.** The principal component (PC) axis 1 explained 34.9% of total variation; while PC2 explained 16.2% and, thus these two axes accounted for 51.1% of the total variation for grain yield (Fig. 1). These results suggest that the biplot of PC1 and PC2 adequately approximated the environment-centred data.

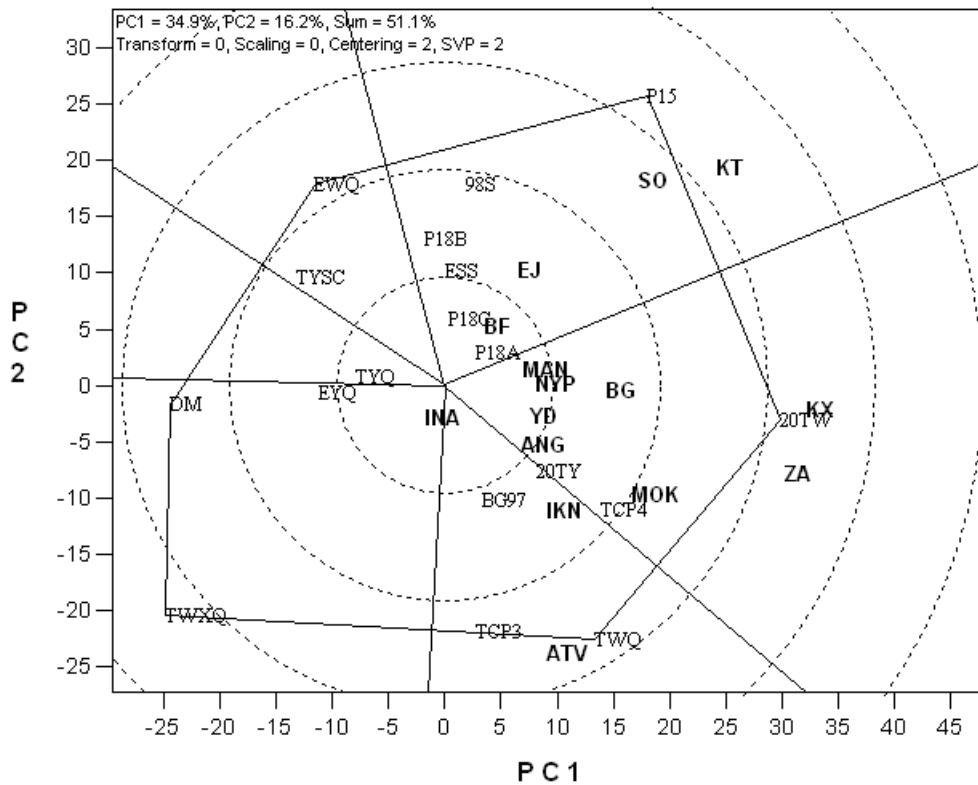
The GGE biplot for grain yield of the 18 early-maturing maize cultivars evaluated at fifteen locations across WA from 2006 to 2008 is shown in Figures 1 and 2. According to Yan (2001) and Yan *et al.* (2000; 2005; 2010), in the polygon view (Fig. 2), the vertex cultivar in each sector represents the highest yielding cultivar in the location that falls within that particular sector. Based on this information, P15 was the highest



TABLE 3. Grain yield and other agronomic traits of 18 early maturing maize varieties evaluate in West and Central Africa between 2006 and 2008

Variety	Code	Grain yield (kg ha <sup>-1</sup> )	Ears per plant	Days to 50 % silk	Anthesis-silking interval	Days to 50 % anthesis	Plant height (cm)	Ear height (cm)	Plant aspect	Ear aspect	Husk cover
2004 TZE-W Pop STR C4	20TW	3563	0.9	56	3	54	168	76	2.2	2.2	2.3
TZCOMP3X4-SYN	TCP4	3438	0.9	56	3	54	163	73	2.4	2.2	2.1
TZE-W Pop STR QPM C0	TWQ	3363	0.9	56	3	53	166	75	2.3	2.2	2.3
2004 TZE-Y Pop STR C4	20TY	3361	1.0	56	2	54	177	79	2.3	2.0	2.3
BG 97 TZE Comp. 3x4	BG97	3296	0.9	55	3	53	163	69	2.3	2.2	2.3
POOL15SR/ACR94TZCOMP5-W/ACR94TZCOMP5-W (QPM)	P15	3242	0.9	57	3	55	166	73	2.4	2.5	2.4
TZE Comp 3 DT C1	TCP3	3237	1.0	56	2	54	166	77	2.2	2.2	2.0
Early STR Syn F2	ESS	3217	0.9	57	3	55	164	72	2.4	2.2	2.1
POOL18SR/AK94DMRESR-Y/AK94DMRESR-Y (QPM)	P18A	3204	0.9	56	3	54	168	75	2.4	2.3	2.2
POOL18SR/ACR94TZCOMP5-Y/ACR94TZCOMP5-Y (QPM)	P18C	3196	0.9	55	3	53	162	71	2.5	2.5	2.3
TZE-Y Pop STR QPM C0	TYQ	3190	0.9	56	3	54	171	77	2.5	2.3	2.4
POOL18SR/AK9331DMRSR/ AK9331DMRSR (QPM)	P18B	3162	1.0	56	3	54	160	69	2.5	2.5	2.2
EV DT-W 99 STR QPM C0	EWQ	3126	1.0	56	3	54	163	70	2.4	2.5	2.3
EV DT-Y 2000 STR QPM C0	EYQ	3099	0.9	57	3	54	172	78	2.3	2.4	2.4
98 Syn WEC QPM C0	98S	3094	0.9	56	3	54	167	76	2.3	2.3	2.3
TZE-Y Pop STR C0 S6 QPM C0	TYSC	2992	0.9	57	3	54	168	74	2.5	2.6	2.4
TZE-W Pop x 1368 STR QPM C0	TWXQ	2839	0.9	57	3	54	161	71	2.5	2.4	2.2
DMR-ESRW QPM (RE)	DM	2835	1.0	58	3	55	164	72	2.5	2.4	2.2
S.E		262.1	0.1	0.9	0.3	0.9	4.5	3.3	0.2	0.2	0.1
Probability of F for Genotype (G)		**	**	**	**	**	**	**	**	**	**
Probability of F for Environment (E)		**	**	**	**	**	**	**	**	**	**
Probability of F for G x E		**	ns	**	*	**	ns	ns	ns	ns	ns

\*, \*\* Significant at P &lt; 0.05 and 0.01, respectively; ns = not significant.



Location	Country	Code
Mokwa	Nigeria	MOK
Ikenne	Nigeria	IKN
Bagauda	Nigeria	BG
Zaria	Nigeria	ZA
Ativeme	Togo	ATV
Ejura	Ghana	EJ
Nyanpala	Ghana	NYP
Ina	Benin	INA
Kita	Mali	KX
Katibougou	Mali	KT
Manga	Ghana	MAN
Angaredebou	Benin	ANG
Sotouboua	Togo	SO
Bagou	Benin	BF
Yendi	Ghana	YD

Variety	Code
EV DT- Y 2000 STR QPM C0	EYQ
TZE Comp 3 DT C1	TCP3
TZCOMP3X4-SYN	TCP4
POOL18SR/AK94DMRESR-Y/AK94DMRESR-Y (QPM)	P18A
POOL18SR/AK9331DMRSR/AK9331DMRSR (QPM)	P18B
POOL18SR/ACR94TZCOMP5-Y/ACR94TZCOMP5-Y (QPM)	P18C
POOL15SR/ACR94TZCOMP5-W/ACR94TZCOMP5-W (QPM)	P15
Early STR Syn F2	ESS
TZE-Y Pop STR QPM C0	TYQ
DMR-ESRW QPM (RE)	DM
TZE-Y Pop STR C0 S6 QPM C0	TYSC
EV DT-W 99 STR QPM C0	EWQ
98 Syn WEC QPM C0	98S
BG 97 TZE Comp. 3x4	BG97
TZE-W Pop STR QPM C0	TWQ
TZE-W Pop x 1368 STR QPM C0	TWXQ
2004 TZE-W Pop STR C4	20TW
2004 TZE-Y Pop STR C4	20TY

Figure 2. A Which-won where or which-is-best-at-what based on a genotype x environment yield data of 18 early maturing maize cultivars evaluated in 15 environments across West Africa between 2006 and 2008. The biplot was based on genotype-focused singular value partitioning (SVP = 2) and is therefore appropriate for visualizing the relationships among environments. Principal component (PC)1 and PC 2 explained 51.1 % of yield variation.

yielding cultivar at EJ, BF, SO and KT; 20TW was top-ranking at KX, ZA, MOK, BG, MAN, NYP, YD, ANG; TWQ was the vertex cultivar at ATV and IKN; TWXQ and DM were the winning cultivars at INA. The vertex cultivar, EWQ was the lowest-yielding cultivar at all or some locations. Furthermore, no environments fell into the sector with EWQ, indicating that this cultivar was not the best in any of the environments. This also implies that it was the poorest cultivar in some or all of the environments.

Cultivars within the polygon, particularly those located near TYQ were less responsive than the vertex cultivars. In the entry/tester view of the GGE biplot of grain yield for the 18 early maturing cultivars (Fig. 3), the genotypes were ranked along the average-tester axis (ATC abscissa), with an arrow pointing to a greater value based on their mean performance across all environments. The double-arrowed line separates entries with below-average means from those with above-average means. The average yield of the cultivars is approximated by the projections of their markers on the average-tester axis. The stability of the cultivars is measured by their projection onto the double-arrow line (average-tester coordinate [ATC] y axis). The greater the absolute length of the projection of a cultivar, the less stable it is (Yan *et al.*, 2000; 2005; 2010; Yan, 2001). Thus, 20TW was the highest yielding and most stable cultivar, while DM was the lowest yielding but very stable cultivar. The cultivars P15, TCP3 and TWQ were high yielding, but were the most unstable; while TWXQ was not only low yielding but also one of the least-stable cultivars.

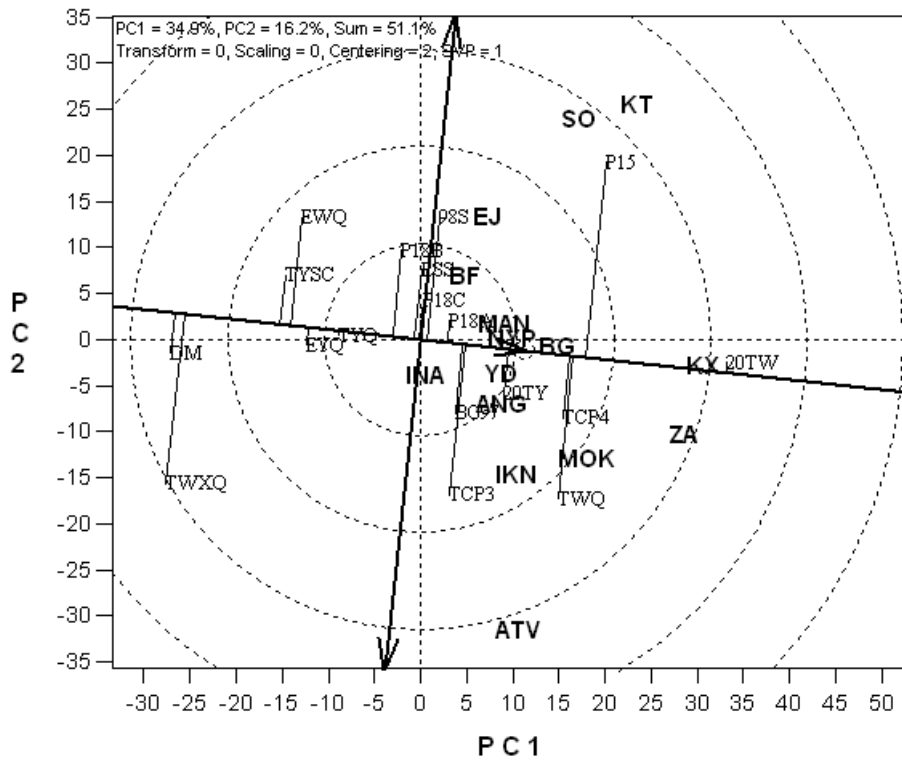
Figure 4 shows location groupings with similar rankings of the early maturing maize varieties as follows: KT, SO, EJ, and BF constitute the first group; the second group consists of MAN, NYP, BG, and KX; the third group contains YD, ANG, MOK, and ZA; the fourth group comprise ATV, IKN, with INA isolated from all the other locations.

**Discriminating power and representativeness of the test environments.** In the present study, test environments were classified into four mega-environments based on the

method of Yan *et al.* (2007), who proposed that test locations should be classified into three types. They indicated that the first group are locations with low genotype discrimination that should not be selected as test locations. The second group are locations with high genotype discrimination and representative of the mega-environments that are close to ideal and should be chosen for superior genotype selection. The third group are locations with high genotype discrimination that do not represent the mega-environment, which could be used for unstable genotype evaluation.

The discriminating power of an environment refers to the ability of an environment to identify an ideal test environment, while the representativeness refers to the ability of a test location to represent the mega-environment. The discriminating power *versus* representativeness view of GGE biplot analysis of the results of the test locations are presented in Figure 5. The small circle is the average-environment axis (AEA), and the arrow pointing to it is used to indicate the direction of the AEA (Yan and Tinker, 2005).

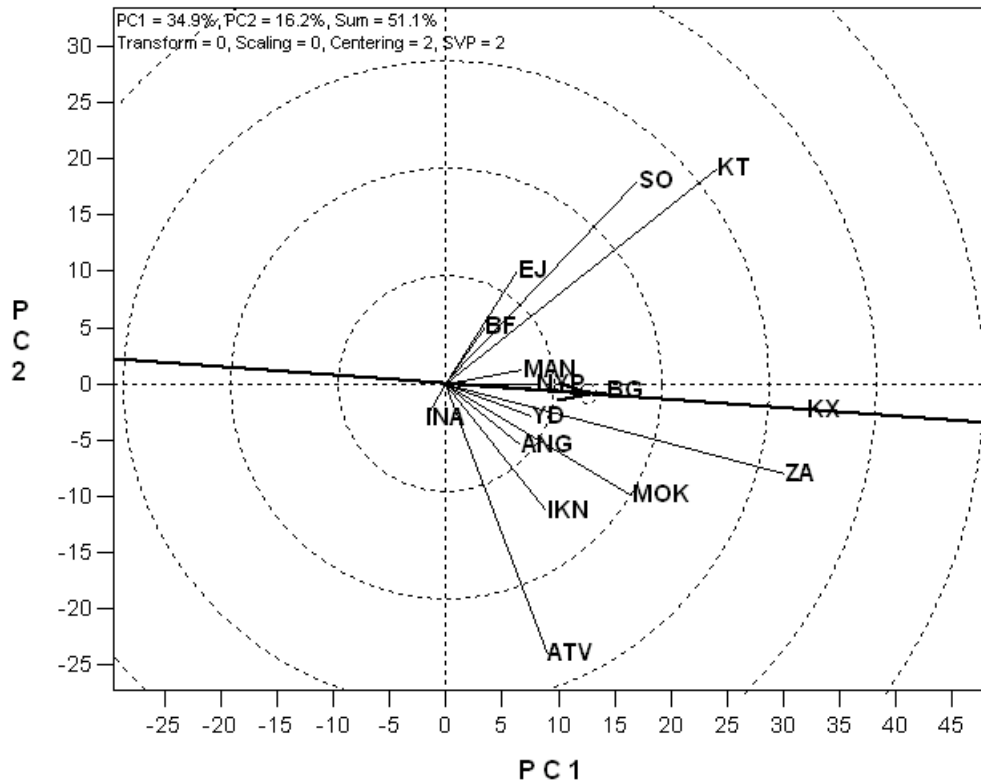
Test environments that have small angles with AEA are more representative of the mega-environment than those that have large angles with it. This implies that the cosine of the angle between any environment vector and the AEA approximates the correlation coefficient between the genotype values in that environment and the genotype means across the environments (Yan *et al.*, 2007). The environments that have shorter vectors are less informative compared to those with longer vectors and provide little or no information about the genotypes and could therefore be excluded when choosing test environments. Furthermore, shorter environmental vectors indicate that the specific environments were not strongly correlated with environments with longer vectors and that they were probably not strongly correlated with one another either. Thus, the short-vector environments BF, MAN, NYP, YD, ANG, and INA may be regarded as independent research environments and may be treated as unique and, therefore, essential research environments. On the other hand, the long-vector research



Location	Country	Code
Mokwa	Nigeria	MOK
Ikenne	Nigeria	IKN
Bagauda	Nigeria	BG
Zaria	Nigeria	ZA
Ativeme	Togo	ATV
Ejura	Ghana	EJ
Nyanpala	Ghana	NYP
Ina	Benin	INA
Kita	Mali	KX
Katibougou	Mali	KT
Manga	Ghana	MAN
Angaredebou	Benin	ANG
Sotouboua	Togo	SO
Bagou	Benin	BF
Yendi	Ghana	YD

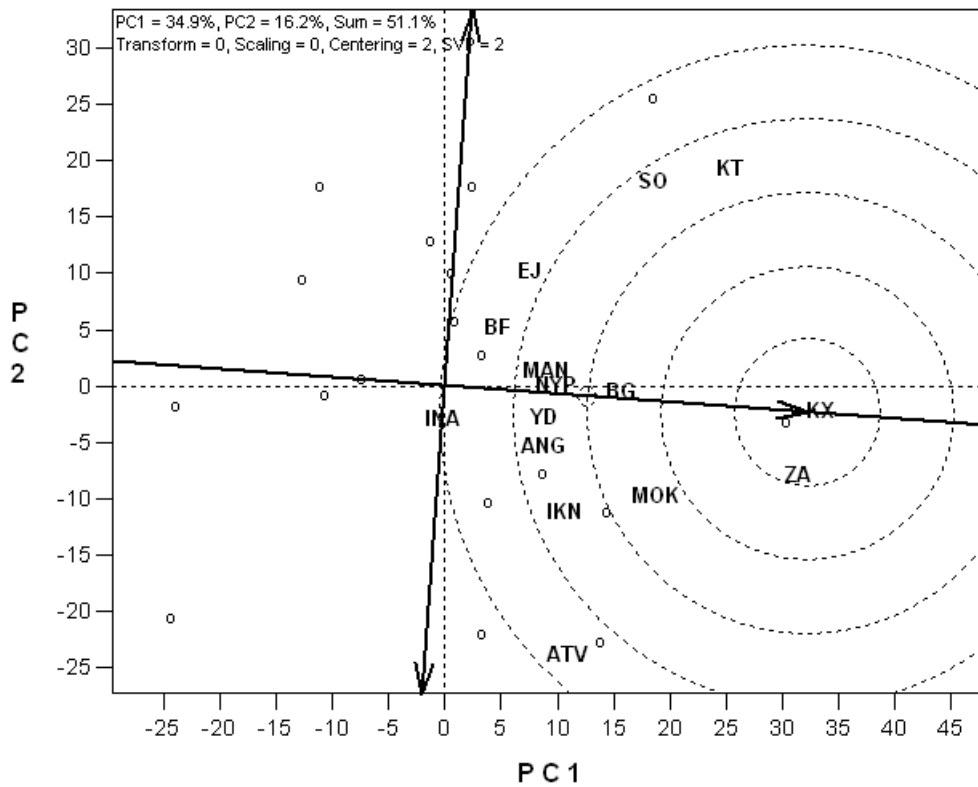
Variety	Code
EV DT- Y 2000 STR QPM C0	EYQ
TZE Comp 3 DT C1	TCP3
TZECOMP3X4-SYN	TCP4
POOL18SR/AK94DMRESR-Y/AK94DMRESR-Y (QPM)	P18A
POOL18SR/AK9331DMRSR/AK9331DMRSR (QPM)	P18B
POOL18SR/ACR94TZECOMP5-Y/ACR94TZECOMP5-Y (QPM)	P18C
POOL15SR/ACR94TZECOMP5-W/ACR94TZECOMP5-W (QPM)	P15
Early STR Syn F2	ESS
TZE-Y Pop STR QPM C0	TYQ
DMR-ESRW QPM (RE)	DM
TZE-Y Pop STR C0 S6 QPM C0	TYSC
EV DT-W 99 STR QPM C0	EWQ
98 Syn WEC QPM C0	98S
BG 97 TZE Comp. 3x4	BG97
TZE-W Pop STR QPM C0	TWQ
TZE-W Pop x 1368 STR QPM C0	TWXQ
2004 TZE-W Pop STR C4	20TW
2004 TZE-Y Pop STR C4	20TY

Figure 3. The 'mean vs. stability' view of the GGE biplot based on a genotype x environment yield data of 18 early maturing maize cultivars evaluated in 15 locations across West Africa between 2006-2008. The biplot was based on environment-focused singular value partitioning ('SVP = 1) and is therefore appropriate for visualizing the relationships among genotypes. Principal component (PC)1 and PC 2 explained 51.1 % of yield variation.



Location	Country	Code
Mokwa	Nigeria	MOK
Ikenne	Nigeria	IKN
Bagauda	Nigeria	BG
Zaria	Nigeria	ZA
Ativeme	Togo	ATV
Ejura	Ghana	EJ
Nyanpala	Ghana	NYP
Ina	Benin	INA
Kita	Mali	KX
Katibougou	Mali	KT
Manga	Ghana	MAN
Angaredebou	Benin	ANG
Sotouboua	Togo	SO
Bagou	Benin	BF
Yendi	Ghana	YD

Figure 4. The 'discriminating power and representativeness' view of GGE biplot based on a genotype x environment yield data of 18 early maturing maize cultivars evaluated in 15 locations across West Africa between 2006-2008. The biplot was based on genotype-focused singular value partitioning (SVP = 2) and is therefore appropriate for visualizing the relationships among environments. Principal component (PC)1 and PC 2 explained 51.1 % of yield variation.



Location	Country	Code
Mokwa	Nigeria	MOK
Ikenne	Nigeria	IKN
Bagauda	Nigeria	BG
Zaria	Nigeria	ZA
Ativeme	Togo	ATV
Ejura	Ghana	EJ
Nyanpala	Ghana	NYP
Ina	Benin	INA
Kita	Mali	KX
Katibougou	Mali	KT
Manga	Ghana	MAN
Angaredebou	Benin	ANG
Sotouboua	Togo	SO
Bagou	Benin	BF
Yendi	Ghana	YD

Figure 5. The biplot view showing the ranking of the 15 locations in West Africa based on both the discriminating ability and representativeness of the locations. The biplot was based on genotype-focused singular value partitioning ( $SVP = 2$ ) and is therefore appropriate for visualizing the relationships among environments. Principal component (PC) 1 and PC 2 explained 51.1% of yield variation.

TABLE 4. Combined analysis of variance with the proportions of the total variance attributable to the sources of variation for grain yield of 18 maize varieties evaluated at 15 locations in West and Central Africa between 2006 and 2008

Source of variation	df	ss	ms	% total variation	% G x E	% Environment
Treatment	587	3859680110	6575264**			
Genotype (G)	17	58639049	3449356**	1.5		
Environments (E)	44	3219248125	264680338**	83.4		
Year	2	42438703	21219351**			8.0
Location	14	2327446641	166246189**			62.8
Year x Location	28	849362781	77214798**			29.2
G x E	459	424296701	3612728**	11.0		
G x Year	34	64590068	1899708**		52.6	
G x Location	238	183735885	772000**		21.4	
G x Year x Location	187	175970748	941020**		26.0	
Pooled Error	1428	639454674	447797			

\*, \*\* Significant at probability level of 0.05 and 0.01, respectively; ns = not significant

environments EJ, SO, KT, KX, ZA, MOK, IKN, and ATV were more powerful in discriminating among the cultivars.

The environments which have long vectors and small angles with the AEC abscissa are ideal for selecting superior genotypes. Furthermore, test environments with long vectors and large angles with the AEC abscissa may not be used for selecting superior genotypes, but are useful in culling unstable genotypes (Yan *et al.*, 2007, 2010).

Based on the above information, environments BF, MAN, NYP, BG, YD, ANG, and NYP were highly correlated in their ranking of the genotypes, implying that these environments provided similar information about the genotypes. KT and ATV had long vectors and large angles with the AEC abscissa indicating that they may not be used in selecting superior genotypes, but may be used in culling unstable genotypes. KX and ZA had the longest vector lengths and small angles with the AEC abscissa and were, therefore, the most discriminating and representative test environments. KT and KX were located in the dry savanna, while ZA was in the moist savanna, which is characterised by moderately high rainfall (1100 mm of rainfall) and are moderately prone to risk of drought stress.

The second group of locations were SO, MOK and ATV, which are in the Southern Guinea

savanna. The third group comprised of IKN, BG, and EJ, which are in the forest savanna transition zone except Bagauda which is in the dry savanna; and the fourth group comprising INA, ANG, YD, NYP, MAN and BF in the dry savanna (Sudan savanna). The classification of Bagauda into the forest-savanna transition zone is not surprising since this location was characterised by excessive rainfall and waterlogging in 2008 and 2009 (Table 2). Similarly, NYP and YD, moist savanna sites, were grouped into the dry savanna agroecology due to low precipitation during the study period as shown in Table 2.

On the basis of representativeness, the locations EJ, SO and BF and KT were highly correlated in their ranking of the genotypes in Group 1, confirming that these locations produced similar information about the genotypes. The implication is that a promising early maturing cultivar selected in one of these locations in one country will also be suitable for production in the other locations within the environments in different countries. Similarly, MAN, NYP, BG, YD, ANG, MOK, KX, and ZA were highly correlated in their ranking of the genotypes in Group 2 and, therefore, a promising cultivar in one location will likely be adapted to the other locations. Selecting a cultivar out of these two locations, will likely result in varieties adapted to IKN and other locations within the same mega-environment. ATV and IKN were



highly correlated in their rankings of the genotypes and, thus, were grouped into the same mega-environment.

INA stood alone in its ranking of the genotypes. Its correlations with other locations were either weak or negative, indicating its uniqueness in the ranking of the genotypes. An ideal test location should effectively discriminate genotypes and represent their mega-environment (Yan and Rajan, 2002). The biplot display in Figure 4 identified KX as the ideal location in WA, while ZA was close to the ideal. The other locations were ranked on the basis of their discriminating power and representativeness in the following order: MOK, BG, IKN, ANG, YD, NYP, MAN, KT, SO, EJ, BF, ATV and INA. It is striking that KX, a dry savanna site in Mali was identified as the ideal location in this study. This could be attributed to the moderately high rainfall (1000 mm) at this location during the study period. The identification of Zaria as the closest to the ideal environment is not surprising and confirms our long time observation that it is an excellent location for testing for genotypes with high yield potential.

The four mega-environments stratified in this study do not correspond closely to the maize agroecological zones identified by maize breeders (Efron, 1985; Fajemisin *et al.*, 1985; Menkir *et al.*, 2003; Setimela *et al.*, 2007) (Fig. 1). For example, in the present study, the locations Katibougou, Sotouboua, Ejura, and Bagou were classified into one mega-environment. According to the classification of Figure 1, only Katibougou and Bagou represent the dry savanna, while Ejura and Sotouboua belong to the forest-savanna and the moist savanna, respectively. The second mega-environment was represented by Manga, Nyankpala, Bagauda, Yendi, Angaredebou, Mokwa, Kita and Zaria. According to the classification in Figure 1, Yendi, Zaria, Mokwa, and Nyankpala are in the moist savanna; while Manga, Bagauda, Angaredebou and Kita are classified into the dry savanna. The third mega-environment which comprised of Ativeme and Ikenne represent the forest-savanna transition zone; while Ina, which constituted the fourth mega-environment represent the moist savanna

( Fig. 1). The fewer locations sampled and the fact that there was no location in the mid-altitude agroecology included in our study might have accounted for the differences in the results of our study and those of earlier researchers.

## CONCLUSION

The results of this study show that G x E influences the ranking of the genotypes in different environments with some locations better for genotype evaluations than others. 2004 TZE-W, Pop STR C<sub>4</sub> is the highest yielding and most stable cultivar while DMR-ESRW QPM is the lowest yielding but very stable cultivar. The cultivars POOL15SR/ACR94TZECOMP5-W/ACR94TZECOMP5-W (QPM), TZE Comp 3 DT C<sub>1</sub>, and TZE-W Pop STR QPM C<sub>0</sub> are high yielding, but the most unstable. TZE-W Pop x 1368 STR QPM C<sub>0</sub> is not only low yielding but also one of the least-stable cultivars.

Test environments are divided into four mega-environments as follows: Katibougou, Sotouboua, Ejura, and Bagou constitute the first group, the second group consists of Manga, Nyankpala, Bagauda, Yendi, Angaredebou, Mokwa, Katibougou, and Zaria; while the third group comprises of Ativeme, Ikenne, and the fourth, Ina.

On the basis of representativeness, the locations Ejura, Sotouboua, Bagou, and Katibougou are highly correlated in their ranking of the genotypes in group 1, confirming that these locations produce similar information about the genotypes and that a promising early maturing cultivar selected in one of these locations in one country will also be suitable for production in the other locations within the same mega-environments in different countries. Similarly, Manga, Nyankpala, Bagauda, Yendi, Angaredebou, Mokwa, Katibougou and Zaria are highly correlated in their ranking of the genotypes in group 2 and therefore, a promising cultivar identified in one location will likely be adapted to the other locations. Selecting a cultivar out of these two locations will likely result in varieties adapted to Ikenne and other locations within the same mega-environment.

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