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Original paper

PERFORMANCE AND YIELD STABILITY OF QUALITY PROTEIN MAIZE (*ZEA MAYS* L.) HYBRIDS UNDER RAINFED CONDITION

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Quality protein maize (QPM) commercialization can combat the food and nutritional insecurity that is common in some developing nations of the world. Evaluation of QPM hybrids under varying rainfed environments provide valuable evidence for the selection of the most productive genotypes for the target environment. The present study was conducted at three locations to assess the agronomic performance and the grain yield stability of 11 QPM and 2 commercial hybrids (checks) over two years. There were significant ($p \geq 0.01$) differences among the environments in the expression of all measured traits while genotype as well as genotype × environment interaction also differed significantly for all the traits except for husk cover and Anthesis-silking interval. The tested QPM hybrids outperformed the local and reference checks by 17.28% and 29.47% respectively. The biplot explained 85.3% of the total variation in yield, with 65.4% attributed to principal component 1 and 19.9% to principal component 2. Three vertex hybrids, EWQH-25, EWQH-21 and Local Check, were identified as the most responsive in the environments within which they fall. Hybrid EWQH-21 produced the highest yield across all environments but was unstable. Therefore, hybrids EWQH-22, EWQH-9, and EWQH-13, with similar yield values and more stable performances were recognized as ideal across environments. Lapai 2017 (E2) proves to be both representative and discriminative, making it the ideal test environment for selecting hybrids with broad adaptability. The study concludes that EWQH-9, EWQH-13, and EWQH-22 be recommended for cultivation across the environments while EWQH-21 be recommended for the specific area of adaptation.

Key words: environment, genotype, genotype × environment interaction, grain yield, analysis of variance, stability analysis, biplot

Maize (*Zea mays* L.) is an annual crop with economic value that is expected to surpass wheat as the most important cereal crop in the world by 2025 (FAOSTAT 2017; Bhadmus *et al.* 2021). On a global level, it is one of the most grown crops because it can adapt to different climatic conditions, (Kamara *et al*. 2020) and also has various industrial and non-industrial uses. The normal endosperm maize consumed as food by humans and as feed by livestock is an excellent source of calories, but deficient in two essential amino acids lysine and tryptophan (Siwela 2020).

Protein and amino acid deficiency are more pronounced in Africa because, maize among the cereal protein is responsible for supplying between 17 to 60% of the daily protein intake in the continent

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(Krivanek 2007) therefore, predisposing individuals to the adverse effect of protein malnutrition. The most affected individuals by micronutrient deficiencies are infants, toddlers, pregnant women, and nursing mothers (Hwalla *et al*. 2017). The use of quality protein maize (QPM) is not only feasible but has also emerged as a sustainable option to tackle protein malnutrition in human and animal diets because of the increased levels of the essential amino acids lacking in the normal maize endosperm (Zaidi *et al*. 2008). The superiority of the nutritional composition of QPM maize genotypes over the non-QPM has also been reported.

In crop improvement, the standard for the selection of a potential variety for commercial release includes a high productivity index and consistent performance over a wide range of environmental conditions (Ayiga-Aluba *et al*. 2018). Testing of newly improved genotypes at various locations and years helps in the assessment of their stability which aids the breeding efficiency of potential cultivars for commercialization (Oyekunle *et al.* 2017). It is also important to test these same genotypes across the ecologies for general acceptability by crop producers who are often resource-limited farmers under their typical growing conditions. Differences in varietal performance could occur because of varying weather conditions (for example edaphic) that are specific to each environment. This will help ascertain if the performance of a particular variety is location-specific over a range of environments.

The attainment of this goal is usually hindered by the presence of genotype × environment interaction (GEI); a complication of the breeding procedure that makes selection of superior genotypes difficult across test locations. Genotype × environment interaction has been reported to be responsible for the observed differences between grain yield and stability of genotypes (Badu-Apraku *et al.* 2020). The ranking of genotypes in terms of performance often differs from one location to another such that a genotype that performs well in one environment may not perform well in another because of GEI (Makumbi *et al*. 2015). This often causes complications in the identification of superior genotypes in multi-environment trials and sometimes necessitates the release of different maize genotypes for different regions for cultivation to increase yield while decreasing production costs. Several researchers have used various statistical tools to evaluate GEI and its effects on varietal performance for grain yield and stability. These include additive main effects and multiplicative interaction (AMMI) in tropical maize (Kassa *et al*. 2013), genotype main effect with genotype × environment interaction (GGE) in tropical maize (Makumbi *et al.* 2015) and GGE biplots among intermediate drought tolerant maize varieties (Ruswandi *et al*. 2021). The GGE biplot which is a derivative of two components; the yield ratio and the yield *per se* as it relates to genotype × environment interaction (Yan & Holland 2010) seems to be the favoured above other methods because it allows the prediction of the mean yield of the genotypes coupled with the identification of the genotype that is most stable in each environment (Yan *et al*. 2014). This gives it an edge over other tools in terms of efficiency. Several researchers have also validated the efficiency of the GGE biplot (Tonk *et al*. 2010; Haruna *et al*. 2017; Olaoye *et al*. 2017; Oliveira *et al*. 2017; Sserumaga *et al*. 2018) in apportioning genotypes to specific environments that are considered favourable in achieving their maximum potential. The objectives of this study were to evaluate the grain yield performance of eleven stress-tolerant QPM and two hybrid checks in six environments, analyse their GEI for grain yield and identify hybrids that are high-yielding and stable across the test environments.

MATERIAL AND METHODS

Genetic materials

The materials used for the study consist of one local check variety, a reference check (RE) and eleven (11) early maturing quality protein maize hybrids collected from the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria, developed under the stress Tolerant Maize for Africa project (Table 1).

Locations of the experiment

The field experiment was conducted at the Teaching and Research Farm, University of Ilorin, Ilorin, Kwara State, Ibrahim Badamosi Babangida Uni-

versity, Lapai and College of Agriculture, Mokwa both in Niger State. The study was conducted over two successive years (2017 and 2018). The combination of years and locations was therefore treated as environments. Environments 1, 2, 3, 4, 5, and 6 represent Ilorin 2017, Lapai 2017 and Mokwa 2017, Ilorin 2018, Lapai 2018 and Mokwa 2018, respectively (Table 2).

Experimental procedure

The eleven QPM hybrids and two checks were evaluated at each location for two years (2017 & 2018) in a Randomized Complete Block Design with double rows of 5 m in length and 75 cm × 40 cm spacing between and within rows. Two maize seeds were sown per hill, and this gave a population density of 66,666 plants/ha. At all locations, weeds were controlled using Extra force (Atrazine and Metolachlor) at 3 L/ha and Paraforce (paraquat) at 5 L/ha. The trials received 60 kg/ha N, 60 kg/ha P_2O_5, 60 kg/ha K_2O at 2 weeks after sowing (WAS) and were top-dressed with urea at 60 kg/ha at 5 WAS. Each experimental set was replicated three times at all locations and all the trials were conducted under rainfed conditions.

Data collection and analysis

Data were recorded each year on a whole plot basis for days to anthesis/pollen shed (PS), days to silking (DS), ear height (EH), plant height (PH), ear aspect (EA), and plant aspect (PA). PS and DS are taken as the number of days from sowing to when 50% of the plants in a plot have shed pollen and extruded silk respectively. PH and EH are taken with the use of a meter rule as the mean height of plants in a plot in centimetres [cm] from the base of the plant to the beginning of the tassel branch and from the base to the node bearing the uppermost ear respectively. PA and EA were taken when the ear was fully developed between silk extrusion and harvest and rated on a scale of 1 to 5 where 1 = excellent overall phenotypic appeal and 5 = poor overall phenotypic appeal of the plant and ears respectively. Husk cover (HUSK) was scored when the ears were fully developed on a scale of 1 – 5 where 1 = husks tightly arranged and covered the ear fully without showing the ear tips tip and 5 = exposed ear tips. The details of how the measurements of the other characters were carried out were described by Badu-Apraku *et al*. (2012) and Bankole *et al*. (2017). The Anthesis-silking interval (ASI) was estimated as

T a b l e 1

List of the 11 QPM and 2 commercial hybrids (checks) used in the study

Code	Genotype	Source	Features (maturity and color)
1.	EWQH-9	IITA	Early, White
2.	EWQH-13	IITA	Early, White
3.	EWQH-14	IITA	Early, White
4.	EWQH-18	IITA	Early, White
5.	EWQH-20	IITA	Early, White
6.	EWQH-21	IITA	Early, White
7.	EWQH-22	IITA	Early, White
8.	EWQH-24	IITA	Early, White
9.	EWQH-25	IITA	Early, White
10.	EWQH-26	IITA	Early, White
11.	EWQH-27	IITA	Early, White
12.	CHECK (RE)	IITA	Early, White
13.	Local check	Ilorin	Early, White

IITA – International Institute of Tropical Agriculture; RE – reference check; QPM – quality protein maize.

Table 2

Description of the experimental sites

Env.	Location/Year	State	Latitude	Longitude	Altitude [m]	Mean annual rainfall [mm]	Temperature range [°C]	Soil type
1	Ilorin (2017)	Kwara	8°3`N	4°32`E	289	1,200	23 – 34	Sandy loam
2	Lapai (2017)	Niger	9°40`N	6°43`E	263	1,100	16 – 34	Sandy loam
3	Mokwa (2017)	Niger	9°18`N	5°40`E	457	1,100	17 – 37	Sandy loam
4	Ilorin (2018)	Kwara	8° 3`N	4° 32`E	289	1,200	23 – 34	Sandy loam
5	Lapai (2018)	Niger	9° 40`N	6° 43`E	263	1,100	16 – 34	Sandy loam
6	Mokwa (2018)	Niger	9°18`N	5°40`E	457	1,100	17 – 37	Sandy loam

Note: Env – Environment.

the difference between the days to silk extrusion and pollen shed per plot, ears per plant was estimated as the ratio of the ears harvested per plot to the plants harvested while grain yield was however computed from the field weight of the ears harvested per plot with an assumed shelling percentage of 80%.

The collected data were subjected to analysis of variance (ANOVA) using SAS software (SAS, 2009). The combined ANOVA across locations and years was performed to determine if there was a significant difference in the performance of the genotypes across locations. Means for which genotypes differed significantly were separated using the Least Significant Difference (*LSD*). Significant GEI was further subjected to genotype main effect plus genotype × environment interaction (GGE) biplot analysis to partition the GEI into principal component axes using GEA-R. The GGE biplots were generated using the first two principal components (PC1 and PC2). Information on yield performance and stability of the QPM hybrids were analysed by the biplot based on the position of their label relative to the abscissa (horizontal axis) and ATC coordination axis (vertical axis) respectively. Genotypes were classified along the average-tester axis (ATA abscissa) and had an arrow indicating a superior value which was based on their average performance across all environments. The line possessing a double arrow separates entries with values below the mean from those above the mean. The stability of the genotype is measured by their projection onto the double-arrow line average-tester coordinate (ATC) axis.

RESULTS

Combined analysis of variance for grain yield and other agronomic traits of the eleven QPM and two commercial hybrid (checks)

The results obtained from the combined analyses of variance for the eleven QPM and two commercial hybrids (checks) showed that the expression of grain yield and all other agronomic traits were influenced by the test environment and the effect was highly significant ($p \leq 0.01$) (Table 3). The influence of the environment was higher than average for all characters. The highest contribution of environment to all measured traits was observed for plant aspect (PA) and husk cover (HC) which accounted for 74% and 58%, respectively. The environment had the greatest effect on grain yield (GY), accounting for about 49% of the total variation. The main genotypic effect (G) was significant for grain yield and most of the measured traits except for ASI, PH and HC. The interactive effects of G × E were highly significant ($p \leq 0.01$) for grain yield and plant aspect, and significant ($p \leq 0.05$) for days to anthesis (DP), days to silk extrusion (DS), plant height (PH), and ear height (EH). However, no significant difference was observed for the anthesis-silk interval (ASI), husk cover, ear aspect (EA), and ear per plant (EPP).

Mean performance for grain yield and agronomic characters of eleven QPM and two commercial hybrids (checks)

The grain yield of the genotypes ranged from 2.25 t/ha (local check) to 3.19 t/ha (EWQH-9) with an average yield of 2.87 t/ha (Table 4). All tested QPM hybrids performed better than the local (2.25 t/ha) and reference check hybrids (2.66 t/ha) for grain yield. The highest-yielding hybrid, EWQH-9, exceeded the yield of the local and the reference commercial check (CHK (RE)) by 29.47% and 16.61% respectively. The average performance of the hybrids for GY in different environments showed that the three hybrids EWQH-9, EWQH-21, and EWQH-13 gave the highest yields of 3.19 t/ha, 3.13 t/ha, and 3.07 t/ha, respectively. Most hybrids had similar ASI values, while hybrid EWQH-25 had the longest interval of 4 days. The average height of the hybrids is 127 cm, with local check recording the greatest height at 136 cm, while hybrid EWQH-22 was the shortest at 122 cm. Hybrid EWQH-25 had the highest ear placement at 62 cm, while hybrid EWQH-20 had the lowest at 53 cm; the average ear height recorded was 57 cm.

GGE (genotype main effect and genotype × environment interaction) biplot analysis of grain yield and stability of the 11 QPM and 2 commercial hybrids (checks)

The polygon view of the GGE biplot for grain yield of the eleven QPM and two commercial hybrids (checks) across 6 environments is presented in Figure 1. The biplot explained 85.3% of the total variation for grain yield, with 65.4% attributed to principal component axis 1 (PC1) and 19.9% to principal component 2 (PC2). Three (3) QPM hybrids are located at the edges of the polygon, which is usually referred to as the vertex and the cultivar positioned at such points is called the vertex cultivar. Genotypes 9 (EWQH-25), 6 (EWQH-21) and 13 (Local check) are the vertex genotypes. Hybrids 9 (EWQH-25), 12 (EWQH-9) and 2 (EWQH-13) were the highest-yielding in E2 (Lapai 2017) and E3 (Mokwa 2017), while 6 (EWQH-21) and 7 (EWQH-22) yielded the highest in E1 (Ilorin 2017) and E4 (Ilorin 2018). Hybrid 13 (Local check), although the most responsive in E5 (Lapai 2018), gave the lowest yield in all other test environments. Hybrids 11 (EWQH-27), 3 (EWQH-14), 10 (EWQH 26), 5 (EWQH-20), 8 (EWQH-24), 4 (EWQH-18), and 1 (CHECK (RE)) fell within the polygon.

Performance and stability of the 11 QPM and two commercial hybrids (checks)

In Figure 2, the hybrids were ranked along the average tester axis (average-environment coordinate (AEC) abscissa) with the arrow pointing to a greater mean performance value across environments. Local check and CHECK (RE) were the least productive of the stable hybrids as they recorded the lowest performance in terms of yield. Hybrids 10 (EWQH-26), 5 (EWQH-20), and 8 (EWQH-24)

T a b l e 3

Mean squares from combined ANOVA of grain yield and agronomic characters of eleven QPM and two commercial hybrids (checks) evaluated across six environments

Source of variation	*df*	Contribution [%]	GY	DP	DS	ASI	PH	EH	HC	PA	EA
Environment	5	49.32	19.57^{++}	446.43^{++}	422.60^{++}	1.56^{++}	$9{,}802.72^{++}$	$3{,}374.09^{++}$	15.18^{++}	27.01^{++}	23.31^{++}
Rep (ENV)	12	2.48	0.41	18.15^{++}	20.88^{++}	0.33	$1{,}426.13^{++}$	177.93^{++}	0.10	0.42^{++}	0.58
GEN	12	6.71	1.11^{++}	18.45^{++}	19.45^{++}	0.42	259.38	124.50^{++}	0.12	0.30^{+}	0.74
ENV × GEN	60	17.54	0.58^{++}	7.22^{+}	7.35^{+}	0.34	210.74^{+}	80.20^{+}	0.31	0.28^{++}	0.44
Error	144	23.95	0.33	5.06	5.08	0.38	146.32	54.03	0.23	0.16	0.47

$^{+}$, $^{++}$ significantly different at 0.05 and 0.01 levels of probability respectively.
Note: Env – environment; Rep – replicate; *df* – degree of freedom; GY – grain yield; DP – days to pollen shed; DS – days to silking; ASI – anthesis-silking interval; PH – plant height; EH – ear height; HC – husk cover; PA – plant aspect; EA – ear aspect; GEN – genotype; ANOVA – analysis of variance; QPM – quality protein maize.

were the most stable with slightly above-average performance as they were located closest to the AEC abscissa. Hybrids 12 (EWQH-9), 2 (EWQH-13), and 7 (EWQH-22) were the most stable hybrids with the highest yield performance. On the other hand, hybrids 6 (EWQH-21) and 9 (EWQH-25) recorded the highest yield, but also the most unstable across environments.

Discriminating power and representativeness of the test environments

The discriminating power versus representativeness of the GGE biplot analysis is presented in Figure 3. In this study, long vector environments such as E2 (Lapai 2017) are the most discriminating, followed by E4 (Ilorin 2018), and thus were very informative, while E5 (Lapai 2018) and E6 (Mokwa 2018) with the shortest vector length are considered the least discriminating and provide little information about the QPM hybrids. E6, which is closest to the AEA, is the only environment in its mega-environment and therefore has no other environment other than itself to represent. E3 (Mokwa 2017), E4 (Ilorin 2018), and E1 (Ilorin 2017), while not representative, can be used to select hybrids that are specifically adapted to these environments.

DISCUSSION

Evaluation of improved maize genotypes in locations that are like those of the farmers in sub-Sahara

T a b l e 4

Mean performance for grain yiled and agronomic characters of 11 QPM and 2 commercial hybrids (checks) selected maize hybrids evaluated across six environments

Genotypes	Grain yield [t/ha]	Days to pollen shed	Days to silking	Anthesis silking intervals [days]	Plant height [cm]	Ear height [cm]	Husk cover [1 – 5]	Plant aspect [1 – 5]	Ear aspect [1 – 5]	Ear per plant (no)
EWQH-13	3.07	52	54	2	124	56	2	2	2	1
EWQH-14	2.72	52	55	3	130	58	2	2	2	1
EWQH-18	2.95	52	54	2	126	56	2	2	2	1
EWQH-20	2.90	52	53	3	125	53	2	2	3	1
EWQH-21	3.13	52	54	3	127	60	2	2	3	1
EWQH-22	3.00	51	53	2	122	57	2	2	2	1
EWQH-24	2.91	53	55	2	124	57	2	2	2	1
EWQH-25	3.03	52	54	4	130	62	2	2	2	1
EWQH-26	2.80	53	55	3	127	57	2	2	3	1
EWQH-27	2.72	53	55	2	124	54	2	2	2	1
EWQH-9	3.19	53	55	2	125	57	2	2	2	1
Check (RE)	2.66	52	54	2	133	58	2	2	2	1
Local check	2.25	55	57	2	136	61	2	2	3	1
MEAN	2.87	52	54	2	127	57	2	2	2	1
LSD values	0.38	1.48	1.49	0.41	7.97	4.84	0.32	0.26	0.45	0.01
SD	0.97	4.02	3.97	0.63	21.02	11.92	0.75	0.89	0.98	0.01
SE	0.06	0.27	0.26	0.04	1.37	0.78	0.05	0.06	0.06	0.00
CV [%]	20.09	4.29	4.14	31.07	9.51	12.79	24.58	20.47	29.07	1.36

Note: *LSD* – least significant difference; *CV* – coefficient of variation; SD – standard deviation; SE – standard error; RE – reference check; QPM – quality protein maize.

Africa is important in the selection of high-yielding adapted ones. The significant environmental effect on the expression of the grain yield and most of the other agronomic traits implies that the overall mean performances of the QPM hybrids differed from one environment to the other which is also a reflection of their response to differences in climatic and edaphic variations in the locations/years of assessment. This underscores the need to conduct multi-locational trials to identify adapted genotypes with good performance for traits of interest. The observed difference is in line with the findings of previous authors such as Bharti *et al*. (2017) and Matongera *et al*. (2023).

The high environmental effect on grain yield (GY), compared to the genotypic and G × E interactive effect of the total variation in grain yield, is consistent with the findings of Badu-Apraku *et al.* (2003), Rwasimitana *et al.* (2021) and Dosho *et al.* (2022) who reported that the largest proportion of total variation in multi-environment trials was attributed to environment/location. The significant effect of grain yield and most of the measured traits depicts differences in the genetic composition for those traits and this is in line with the finding of Oyekunle *et al.* (2017), who reported significant genotypic effects for grain yield and other traits except for husk cover and plant aspect.

The selection of stable genotypes with desired traits across environments can be complicated even though heritable variation among genotypes is requisite for a successful breeding project. The highly significant interactive effects of the G × E effect for GY indicated that the hybrids performed differentially in each of the test environments. It follows that selecting superior hybrids based on the data from a single environment is not reliable, which underscores the need for multi-environment testing of

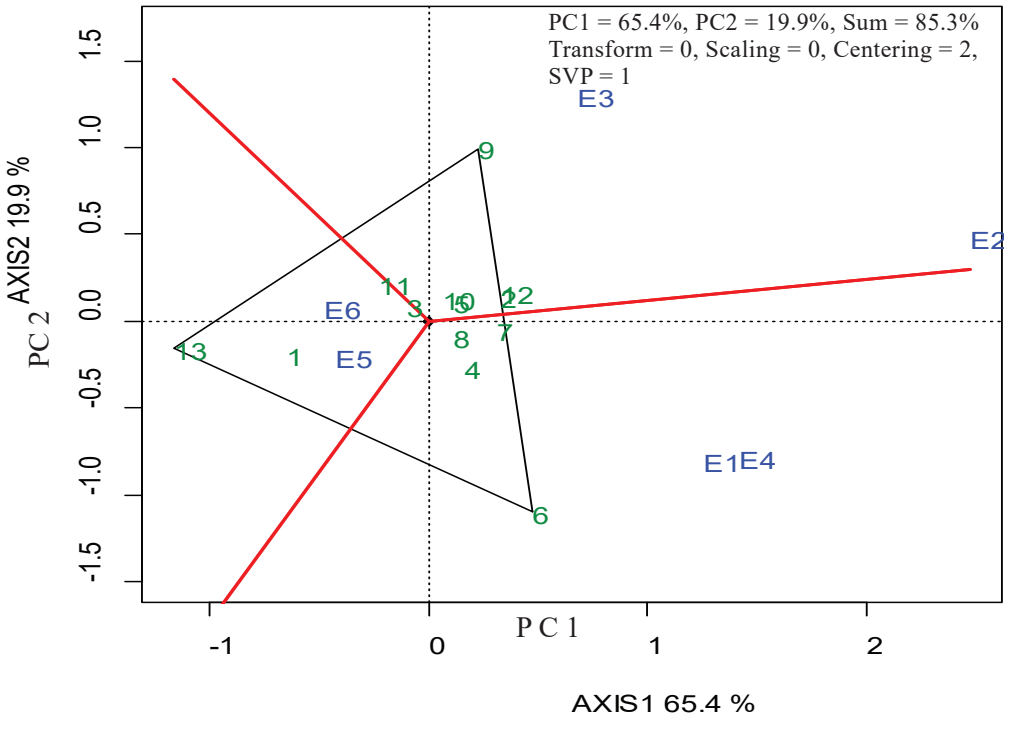


Figure 1. Polygon view of GGE biplot based on grain yield of eleven QPM and two checks evaluated across six environments. Note: Environments: E1 – Ilorin 2017; E2 – Lapai 2017; E3 – Mokwa 2017; E4 – Ilorin 2018; E5 – Lapai 2018; E6 – Mokwa 2018. Hybrids' code: 1 – CHECK (RE – reference check); 2 – EWQH-13; 3 – EWQH-14; 4 – EWQH-18; 5 – EWQH-20; 6 – EWQH-21; 7 – EWQH-22; 8 – EWQH-24; 9 – EWQH-25; 10 – EWQH-26; 11 – EWQH-27; 12 – EWQH-9; 13 – Local Check. PC1 – principal component 1; PC2 – principal component 2; SUM – sum of PC1 and PC2; SVP – single value portioning; GGE – genotype main effect + genotype × enviromment; QPM – quality protein maize.

the hybrids in different years before recommending genotypes in the sub-region or for specific agroecology.

Mean performance for grain yield and agronomic characters eleven QPM and two commercial hybrids (checks)

The superior performance of all tested QPM hybrids over the local and reference check hybrids was notable however the mean grain yield was slightly lower than those reported by Ayiga-Aluba *et al.* (2018) who reported a mean yield of 3.8 t/ha. Most hybrids had similar ASI values, but differences existed for other measured traits. The local check recorded the greatest height but had a low yield which depicts that the non-performance of the variety was not because of morphological traits. The result confirmed that the tested hybrids had sufficient variation for improvement of the measured traits.

GGE (genotype main effect and genotype × environment interaction) biplot analysis of grain yield and stability of the 11 QPM and two commercial hybrids (checks)

The significant G × E interaction for GY necessitated the use of the GGE biplot to separate the G × E interaction, determine the yield potential and stability of the QPM hybrids, and identify the ideal test site among the six test environments. The GGE biplot is effective in determining the best-performing cultivar in each environment and the most suitable environment for each cultivar (Yan & Kang 2003; Yan & Tinker 2006; Yan *et al.* 2007). The hybrids are located at the edges of the polygon, which is usually referred to as the vertex and the genotypes positioned at such points are called the vertex genotypes. The vertex hybrids positioned in each sector of a polygon view represent the highest yielding in the environments that fall within the particular sec-

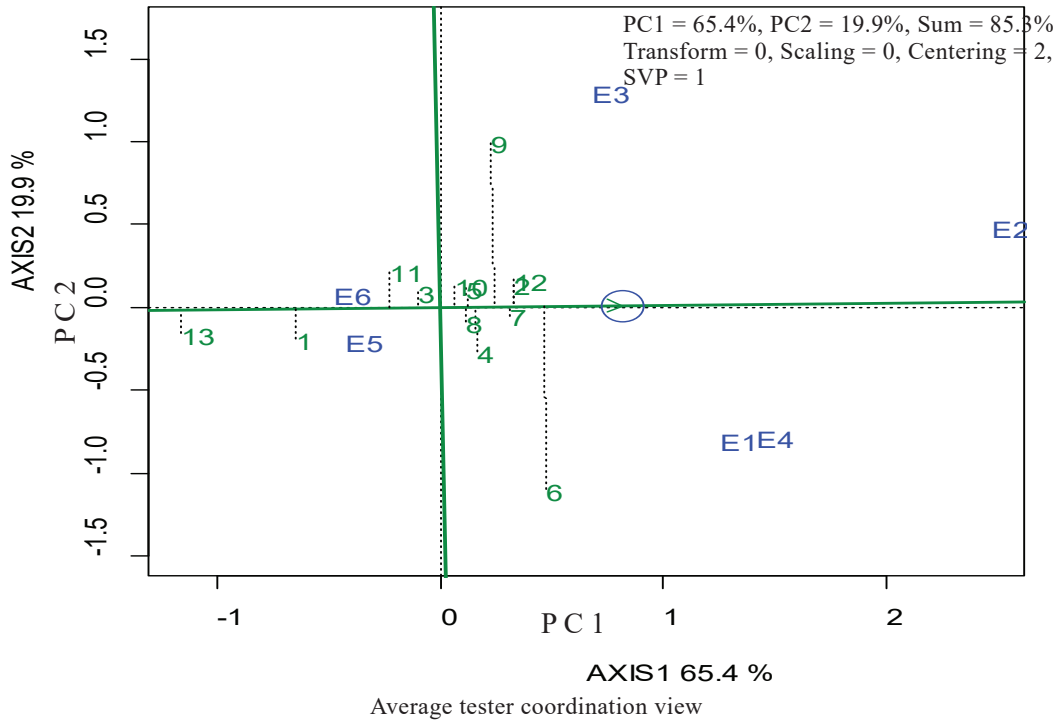


Figure 2. Mean versus stability view of GGE biplot showing the mean performance and stability of the eleven QPM and two commercial hybrids (checks).
Note: Environments: E1 – Ilorin 2017; E2 – Lapai 2017; E3 – Mokwa 2017; E4 – Ilorin 2018; E5 – Lapai 2018; E6 – Mokwa 2018. Hybrids' code: 1 – CHECK (RE – reference check) ; 2 – EWQH-13; 3 – EWQH-14; 4 – EWQH – 18; 5 – EWQH-20; 6 – EWQH-21; 7 – EWQH-22; 8 – EWQH-24; 9 – EWQH-25; 10 – EWQH-26; 11 – EWQH-27; 12 – EWQH-9; 13 – local check. PC1 – principal component 1; PC2 – principal component 2; SUM – sum of PC1 and PC2; SVP – single value portioning; GGE – genotye + genotype × enviromment; QPM – quality protein maize.

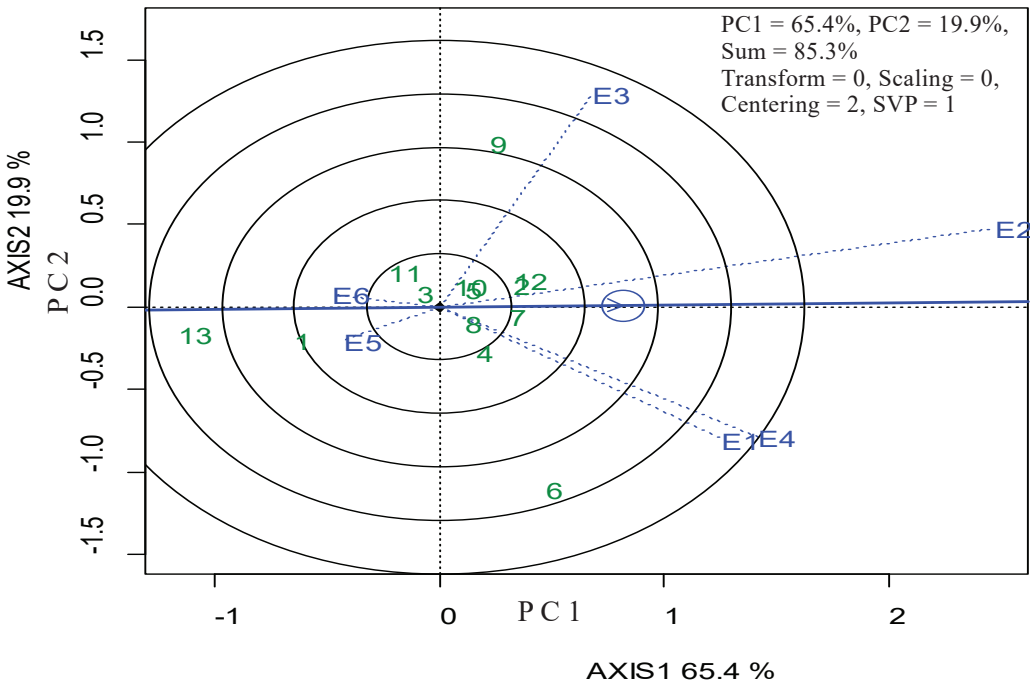
tor (Yan & Tinker 2005). Consequent to the distance from the biplot origin, the hybrids positioned at the vertex ought to be the most responsive (Yan & Rajcan 2002). The vertex genotypes are considered the most responsive hybrids while those that fall within the polygon are less responsive compared to the vertex hybrids.

Performance and stability of the 11 QPM and two commercial hybrids (checks)

The line with an arrow passing through the biplot origin is called the Average-Environment Coordinate (AEC). The arrow specifies the positive end of the axis and ranks the genotypes in terms of their average performance in all environments. The double-arrowed line separates the hybrids with below-average grain yield from those with above-average grain yield. The average yield of the hybrids is approximated by the projections of their markers on the average-tester axis. The stability of the hybrids was measured by their projection of the double arrow line (y-axis of the average-tester coordinate). The greater the absolute length of the projection of a genotype, the less stable the hybrid (Yan *et al.* 2007). On this basis, Local reference check hybrids were the least productive of the stable hybrids as they recorded the lowest performance in terms of yield. The closeness of some of the hybrids to the AEC abscissa implied that their rankings were very consistent across sites. The hybrids that fall into that category are referred to as ideal across the environments (Badu-Apraku *et al.* 2012).

Discriminating power and representativeness of the test environments

The discriminating power, which refers to the ability of a test environment to differentiate genotypes (Yan *et al.* 2007) can be measured through the vector length of the environments in the biplot. The longer the length of the vector, the more discriminating the environment is. The long vector length of environments of E2 (Lapai 2017) makes it the most



Discrimitiveness vs. representativeness view

Figure 3. Vector view of GGE biplot showing ideal environments based on their discriminating power and representativeness.
Note: Environments: E1 – Ilorin 2017; E2 – Lapai 2017; E3 – Mokwa 2017; E4 – Ilorin 2018; E5 – Lapai 2018; E6 – Mokwa 2018.
Hybrids' code: 1 – CHECK (RE – reference check); 2 – EWQH-13; 3 – EWQH-14; 4 – EWQH – 18; 5 – EWQH-20; 6 – EWQH-21; 7 – EWQH-22; 8 – EWQH-24; 9 – EWQH-25; 10 – EWQH-26; 11 – EWQH-27; 12 – EWQH-9; 13 – local check.
PC1 – principal component 1; PC2 – principal component 2; SUM – sum of PC1 and PC2 ; SVP – single value portioning; GGE – genotye + genotype × enviromment.

discriminating, followed by E4 (Ilorin 2018), and thus were very informative, while E5 (Lapai 2018) and E6 (Mokwa 2018) with the shortest vector length are considered the least discriminating and provide little information about the QPM hybrids. Therefore, they should not be used as test environments (Yan & Tinker 2006).

On the other hand, the representativeness of test environments shows the ability of a test environment to represent the mega-environment and can be determined by the degree of the angle measured between the test environments and the Average Environment Axis (AEA). Test environments with a smaller angle to the AEA are considered more representative of the other environment than those with large angles (Yan *et al.* 2007). In this study, E6, which is closest to the AEA, is the only environment in its mega-environment and therefore has no other environment other than itself to represent.

Test environments that are both the most discriminating and representative are regarded as the ideal test environments for selecting generally adapted genotypes (Yan & Tinker 2006) while discriminating, but non-representative test environments are useful for selecting specifically adapted genotypes when the target environments can be divided into mega-environments. However, in a single environment, they can also be useful to screen out unstable genotypes and should not be used for selection. Therefore, E3 (Mokwa 2017), E4 (Ilorin 2018), and E1 (Ilorin 2017), while not representative, can be used to select hybrids that are specifically adapted to these environments. However, E2 (Lapai 2017) is both representative and discriminating making it the ideal test environment for selecting the most suitable hybrids with broad adaptability.

CONCLUSIONS

This study concludes that E3 (Mokwa 2017), E1 (Ilorin 2017) and E4 (Ilorin 2018), although not representative, can be used to select hybrids specifically adapted to these environments. However, E2 (Lapai 2017), both representative and discriminating, is the ideal test environment for selecting the most suitable hybrids with broad adaptability. The study also identified hybrids 12 (EWQH-9), 2 (EWQH-13) and 7 (EWQH-22) as the most stable hybrids with the highest yield performance in all environments and are therefore have been nominated for testing in farmers' fields.

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